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(54) **TWO COMBINED MUTATIONS THAT INTRODUCE THE SECOND ENTRY PATHWAY TO SYNTHESIZED LIGNIN FROM TYROSINE IN PLANTS**

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(57) **ABSTRACT**

The present invention provides engineered phenylalanine ammonia-lyase (PAL) enzymes comprising one or more mutations that increase the enzymes' tyrosine ammonia-lyase (TAL) activity. Also provided are plants comprising the engineered PAL enzymes and methods of using these plants to sequester CO_2 or produce phenylpropanoid-derived products.

Specification includes a Sequence Listing.

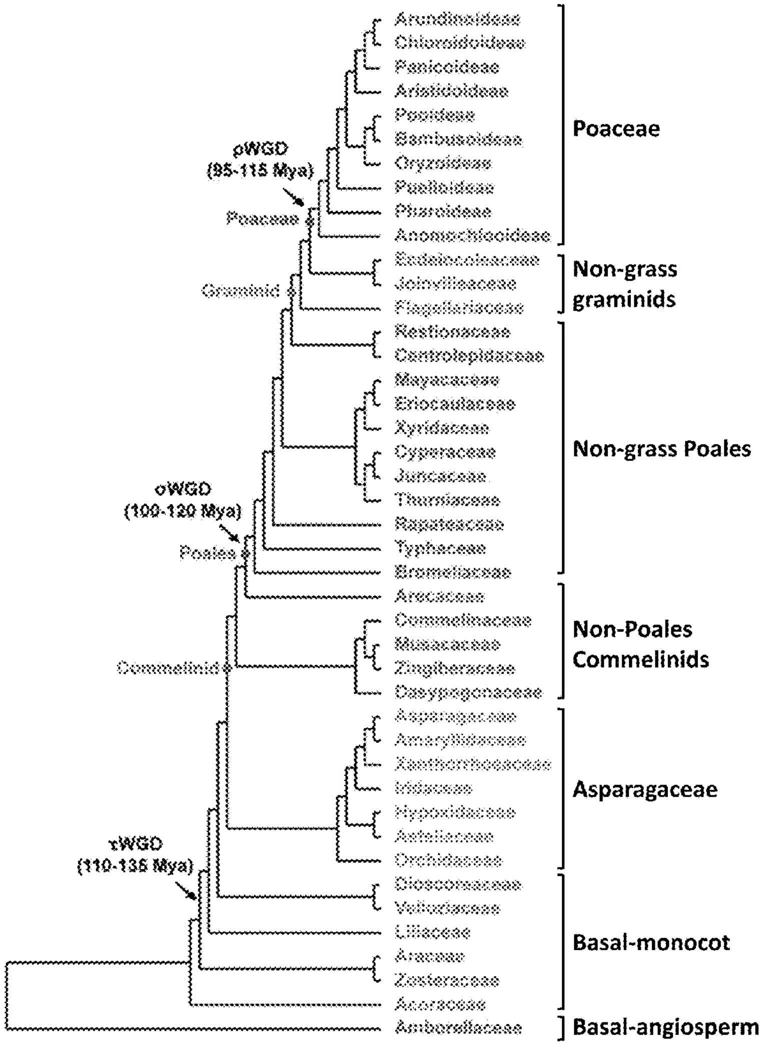


Figure 1A

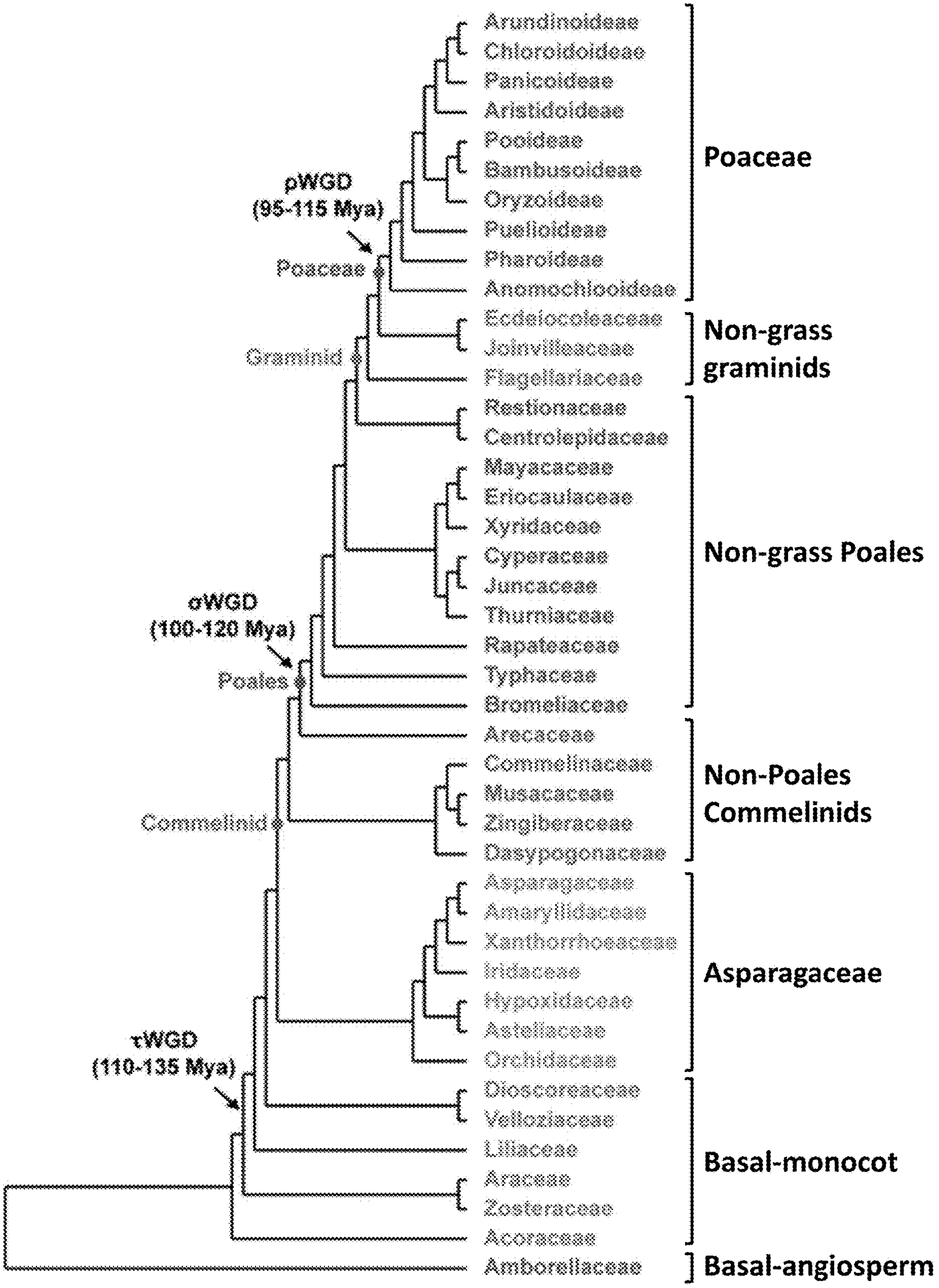

Arundinoideae
Chloroidoideae
Panicoideae
Aristidoideae
Pooideae
Bambusoideae
Oryzoideae
Puelioideae
Pharoideae
Anomochlooideae
Poaceae
pWGD
(95-115 Mya)
Poaceae
Ecdeiocoleaceae
Joinvilleaceae
Flagellariaceae
Non-grass graminids
Graminid
Restionaceae
Centrolepidaceae
Mayacaceae
Eriocaulaceae
Xyridaceae
Cyperaceae
Juncaceae
Thurniaceae
Rapateaceae
Typhaceae
Bromeliaceae
Non-grass Poales
σWGD
(100-120 Mya)
Poales
Arecaceae
Commelinaceae
Musacaceae
Zingiberaceae
Dasypogonaceae
Non-Poales Commelinids
Commelinid
Asparagaceae
Amaryllidaceae
Xanthorrhoeaceae
Iridaceae
Hypoxidaceae
Asteliaceae
Orchidaceae
Asparagaceae
τWGD
(110-135 Mya)
Dioscoreaceae
Velloziaceae
Liliaceae
Araceae
Zosteraceae
Acoraceae
Basal-monocot
Amborellaceae
Basal-angiosperm

Figure 1B

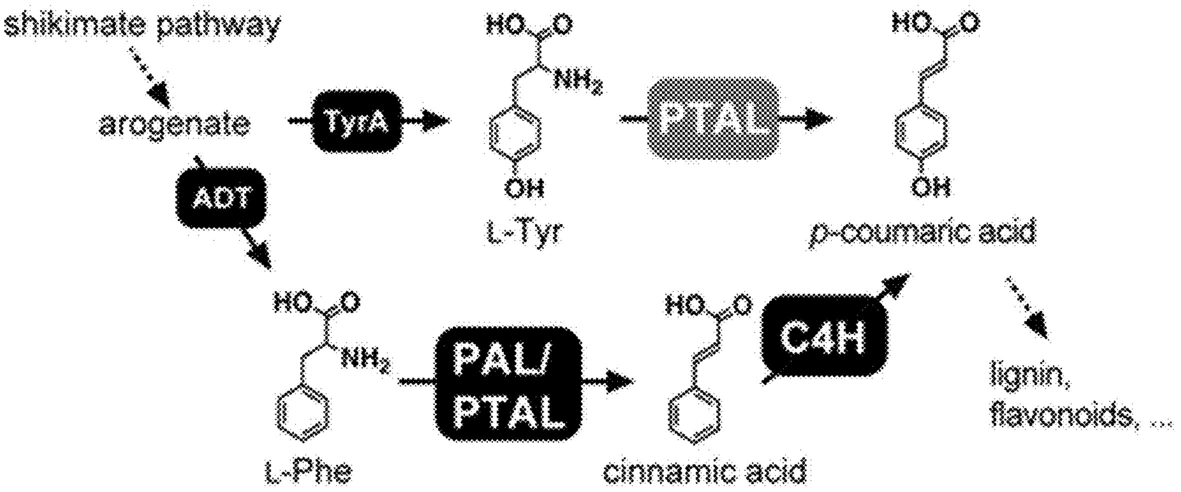

shikimate pathway
arogenate
TyrA
ADT
L-Tyr
PTAL
p-coumaric acid
L-Phe
PAL/
PTAL
cinnamic acid
C4H
lignin,
flavonoids, ...

Figure 2A

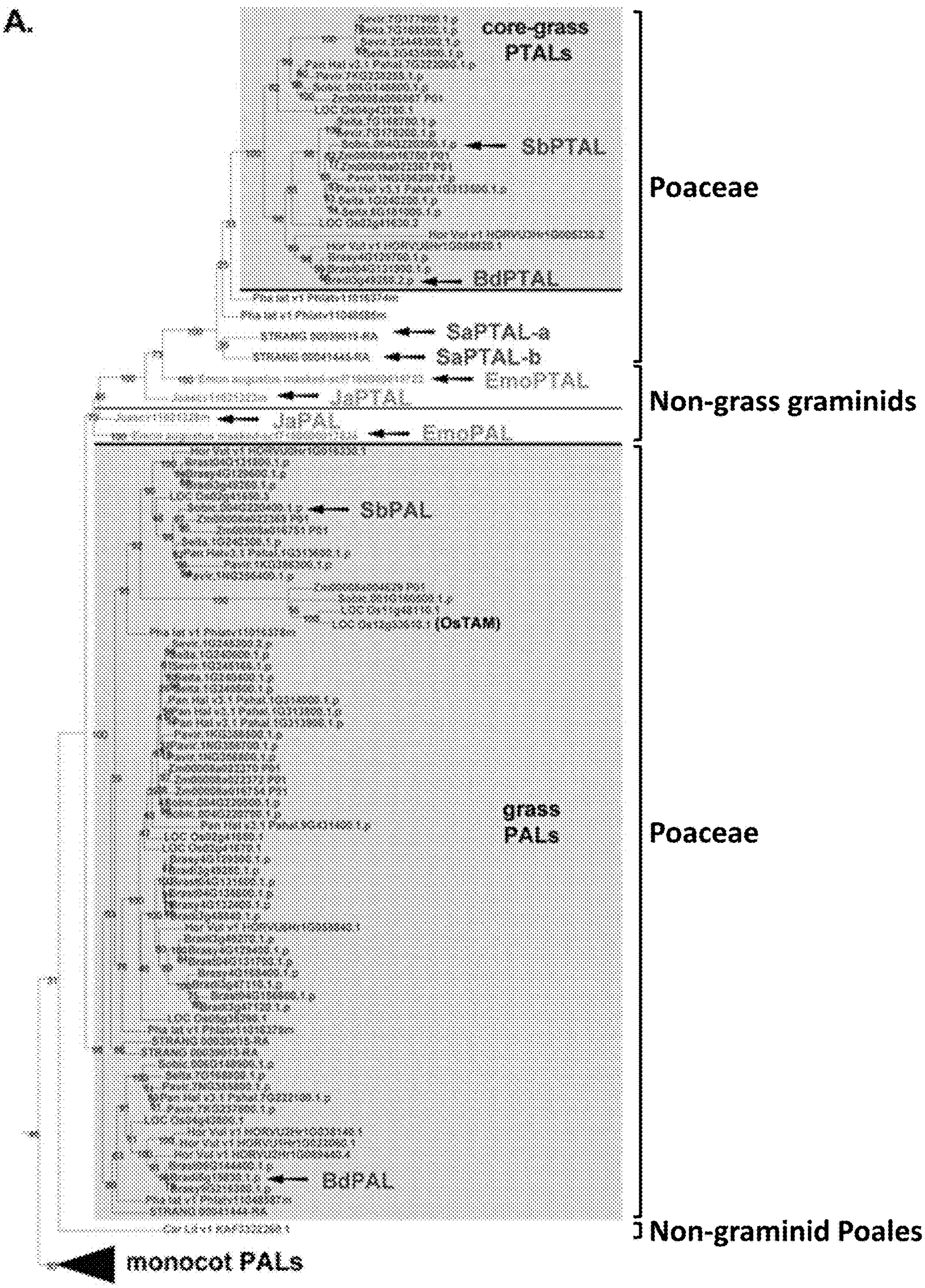

A.
core-grass PTALs
SbPTAL
BdPTAL
Poaceae
SaPTAL-a
SaPTAL-b
EmoPTAL
JaPTAL
Non-grass graminids
JaPAL
EmoPAL
SbPAL
(OsTAM)
grass PALs
Poaceae
BdPAL
Non-graminid Poales
monocot PALs

Figure 2B

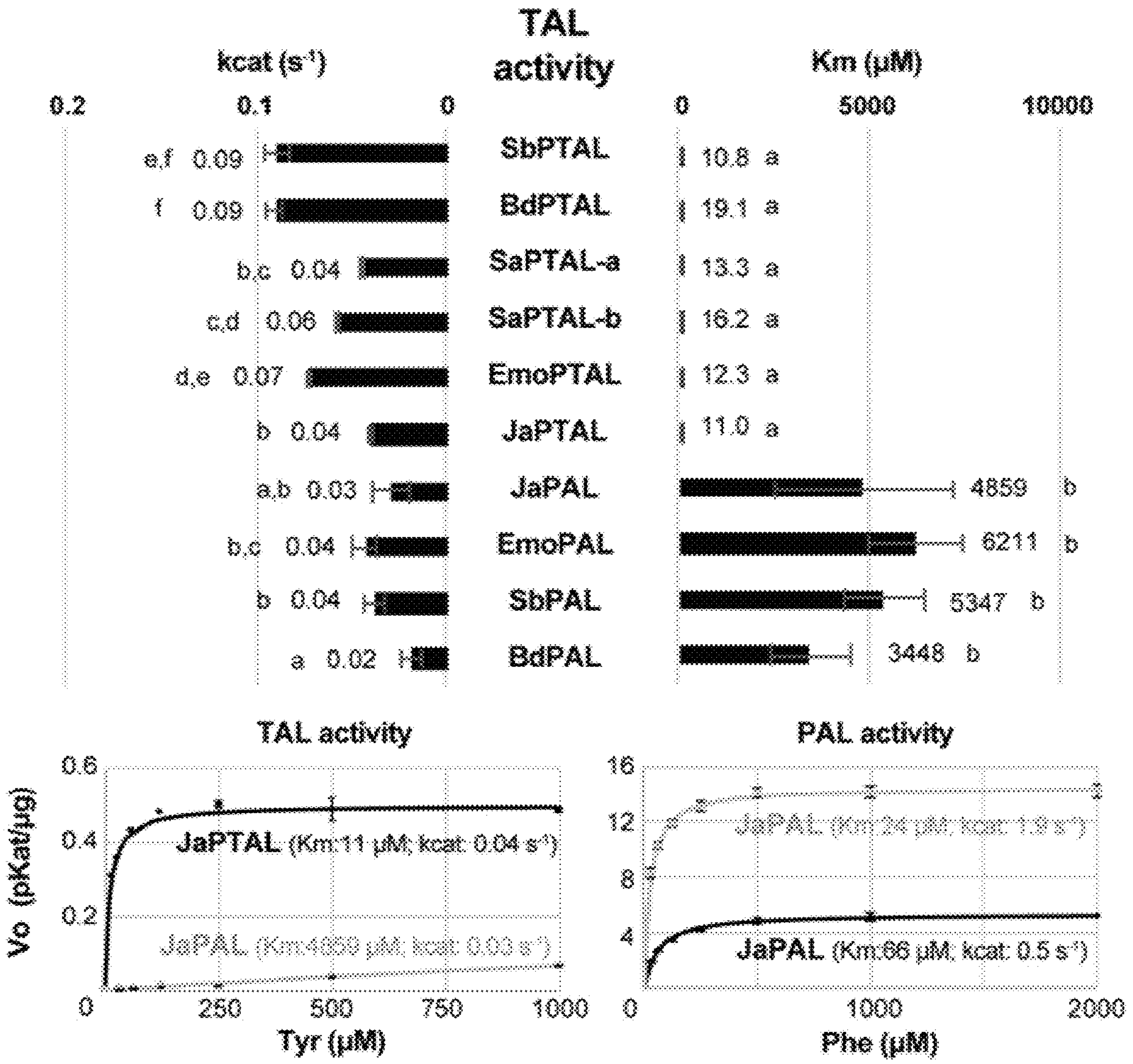

TAL activity
kcat (s-1)
0.2
0.1
0
Km (µM)
0
5000
10000
e,f 0.09
SbPTAL
10.8 a
f 0.09
BdPTAL
19.1 a
b,c 0.04
SaPTAL-a
13.3 a
c,d 0.06
SaPTAL-b
16.2 a
d,e 0.07
EmoPTAL
12.3 a
b 0.04
JaPTAL
11.0 a
a,b 0.03
JaPAL
4859 b
b,c 0.04
EmoPAL
6211 b
b 0.04
SbPAL
5347 b
a 0.02
BdPAL
3448 b
TAL activity
Vo (pKat/µg)
0.6
0.4
0.2
0
JaPTAL (Km:11 µM; kcat: 0.04 s-1)
JaPAL (Km:4859 µM; kcat: 0.03 s-1)
250
500
750
1000
Tyr (µM)
PAL activity
16
12
8
4
0
JaPAL (Km:24 µM; kcat: 1.9 s-1)
JaPAL (Km:66 µM; kcat: 0.5 s-1)
1000
2000
Phe (µM)

Figure 2C

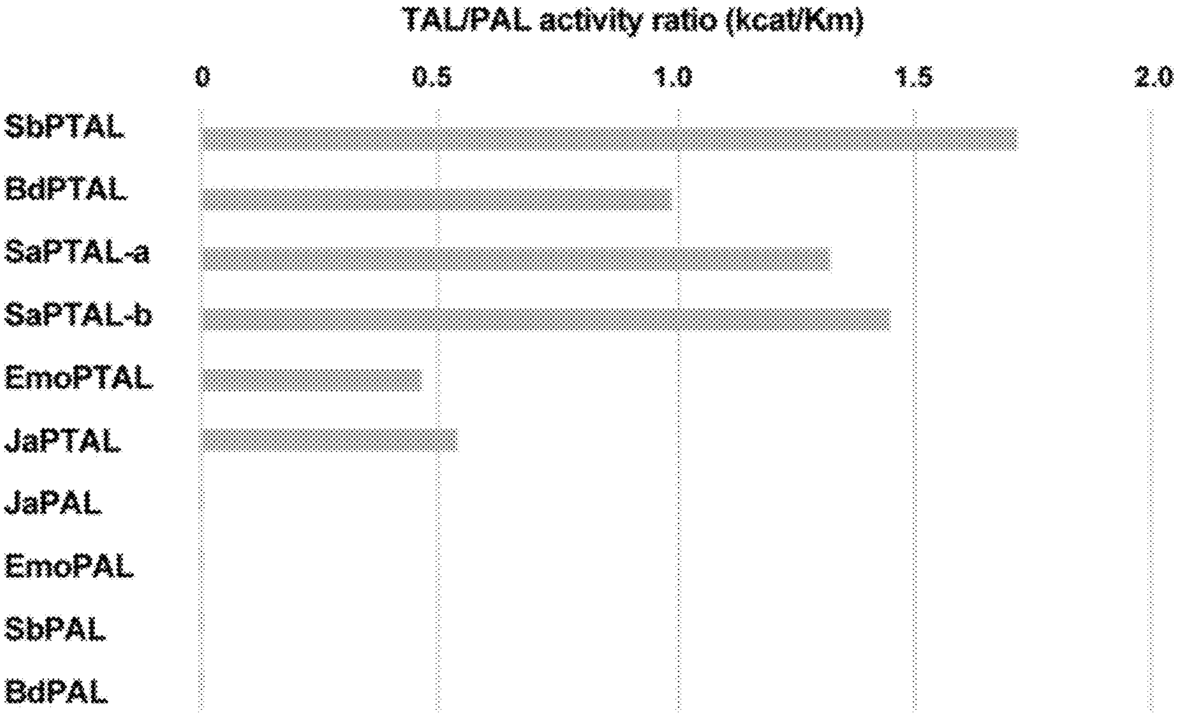

TAL/PAL activity ratio (kcat/Km)
0
0.5
1.0
1.5
2.0
SbPTAL
BdPTAL
SaPTAL-a
SaPTAL-b
EmoPTAL
JaPTAL
JaPAL
EmoPAL
SbPAL
BdPAL

Figure 3A

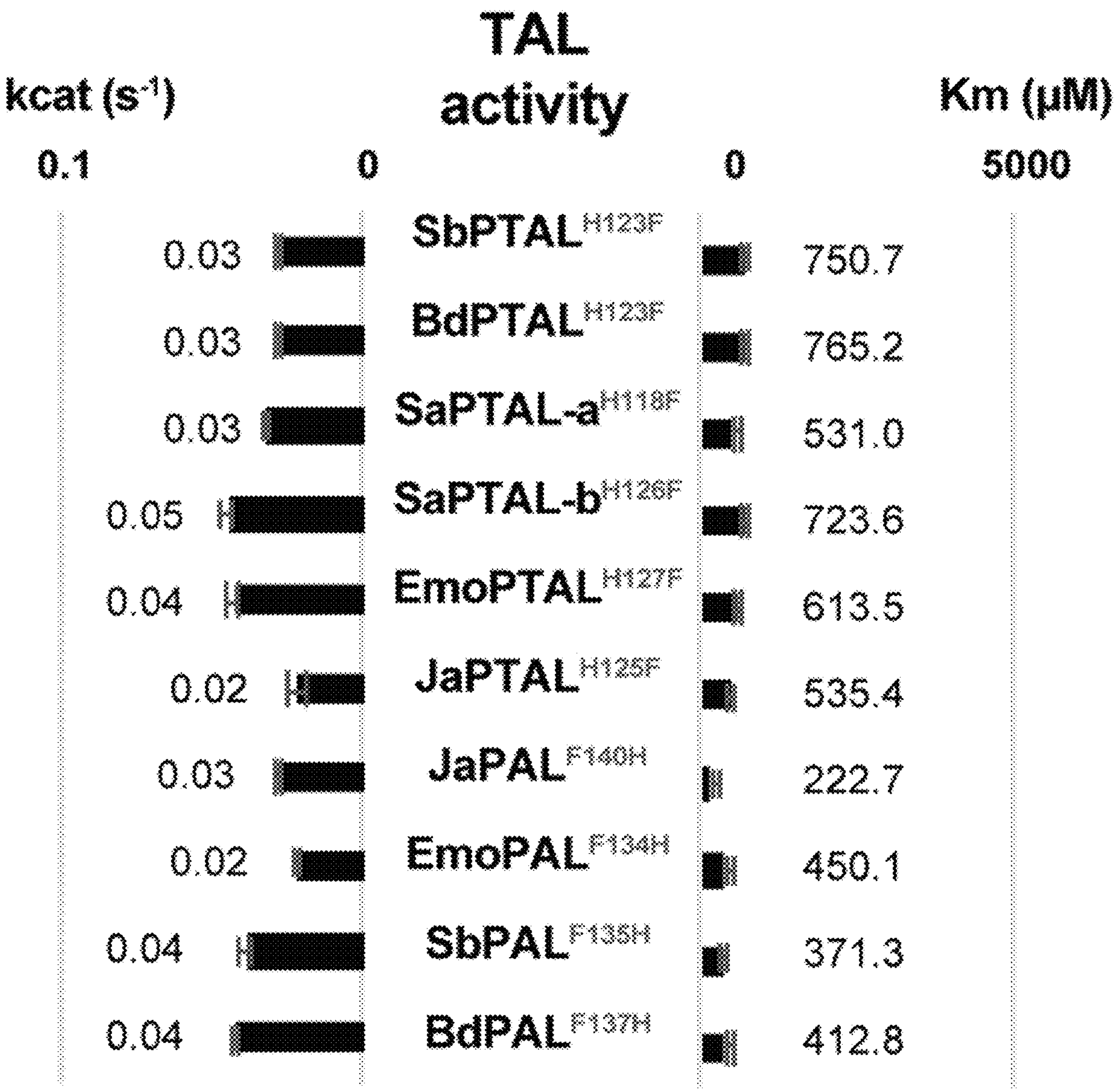

TAL activity
kcat (s-1)
Km (µM)
0.1
0
0
5000
SbPTAL H123F 0.03 750.7
BdPTAL H123F 0.03 765.2
SaPTAL-a H118F 0.03 531.0
SaPTAL-b H126F 0.05 723.6
EmoPTAL H127F 0.04 613.5
JaPTAL H125F 0.02 535.4
JaPAL F140H 0.03 222.7
EmoPAL F134H 0.02 450.1
SbPAL F135H 0.04 371.3
BdPAL F137H 0.04 412.8

Figure 3B

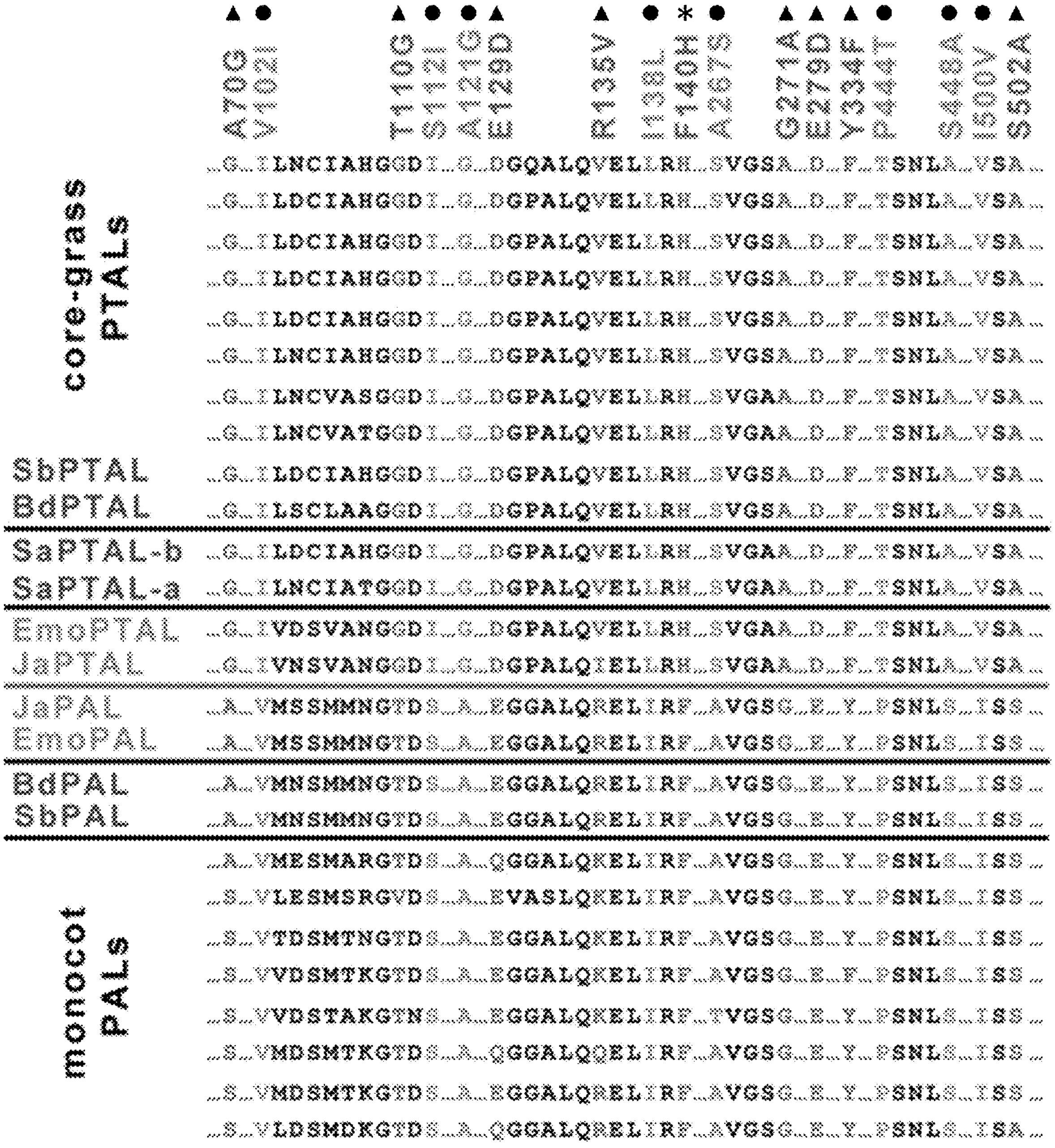
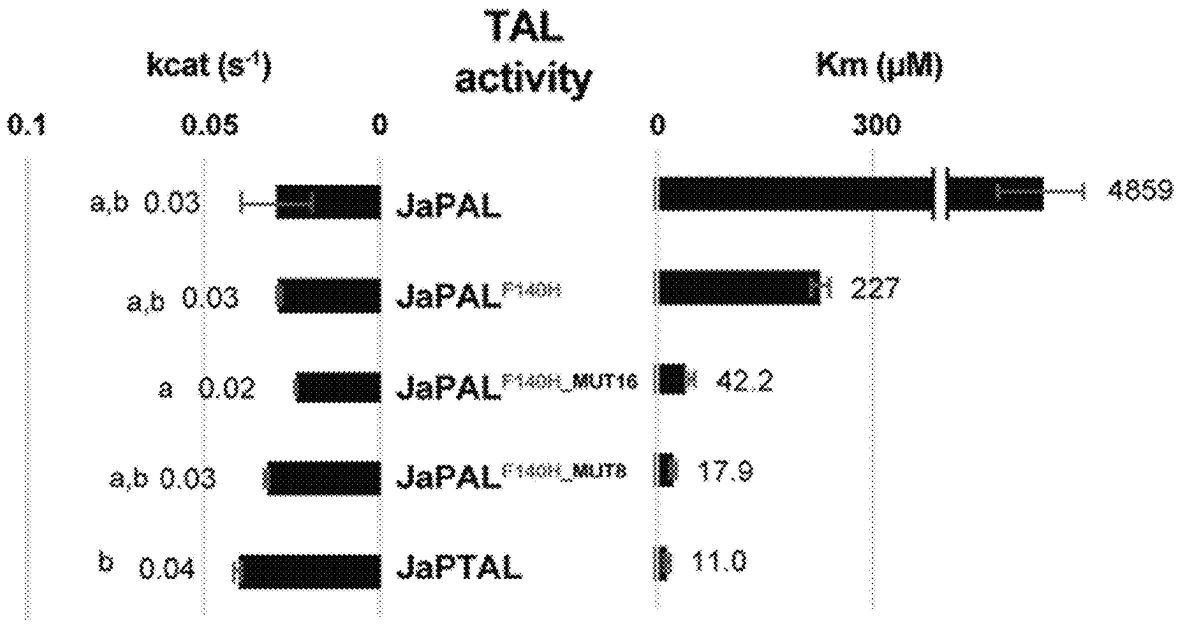

▲ A70G
● V102I
▲ T110G
● S112I
● A121G
▲ E129D
▲ R135V
● H138L
* F140H
● A267S
▲ G271A
▲ E279D
▲ Y334F
● P444T
● S448A
● I500V
▲ S502A
core-grass PTALs
...G...ILNCIAHGGDI...G...DGQALQVELLRH...SVGSA...D...F...TSNLA...VSA...
...G...ILDCIAHGGDI...G...DGPALQVELLRH...SVGSA...D...F...TSNLA...VSA...
...G...ILDCIAHGGDI...G...DGPALQVELLRH...SVGSA...D...F...TSNLA...VSA...
...G...ILDCIAHGGDI...G...DGPALQVELLRH...SVGSA...D...F...TSNLA...VSA...
...G...ILDCIAHGGDI...G...DGPALQVELLRH...SVGSA...D...F...TSNLA...VSA...
...G...ILNCIAHGGDI...G...DGPALQVELLRH...SVGSA...D...F...TSNLA...VSA...
...G...ILNCVASGGDI...G...DGPALQVELLRH...SVGAA...D...F...TSNLA...VSA...
...G...ILNCVATGGDI...G...DGPALQVELLRH...SVGAA...D...F...TSNLA...VSA...
SbPTAL ...G...ILDCIAHGGDI...G...DGPALQVELLRH...SVGSA...D...F...TSNLA...VSA...
BdPTAL ...G...ILSCLAAGGDI...G...DGPALQVELLRH...SVGSA...D...F...TSNLA...VSA...
SaPTAL-b ...G...ILDCIAHGGDI...G...DGPALQVELLRH...SVGAA...D...F...TSNLA...VSA...
SaPTAL-a ...G...ILNCIATGGDI...G...DGPALQVELLRH...SVGAA...D...F...TSNLA...VSA...
EmoPTAL ...G...IVDSVANGGDI...G...DGPALQVELLRH...SVGAA...D...F...TSNLA...VSA...
JaPTAL ...G...IVNSVANGGDI...G...DGPALQIELLRH...SVGAA...D...F...TSNLA...VSA...
JaPAL ...A...VMSSMMNGTDS...A...EGGALQRELIRF...AVGSG...E...Y...PSNLS...ISS...
EmoPAL ...A...VMSSMMNGTDS...A...EGGALQRELIRF...AVGSG...E...Y...PSNLS...ISS...
BdPAL ...A...VMNSMMNGTDS...A...EGGALQRELIRF...AVGSG...E...Y...PSNLS...ISS...
SbPAL ...A...VMNSMMNGTDS...A...EGGALQRELIRF...AVGSG...E...Y...PSNLS...ISS...
monocot PALs
...A...VMESMARGTDS...A...QGGALQKELIRF...AVGSG...E...Y...PSNLS...ISS...
...S...VLESMSRGVDS...A...EVASLQKELIRF...AVGSG...E...Y...PSNLS...ISS...
...S...VTDSMTNGTDS...A...EGGALQKELIRF...AVGSG...E...Y...PSNLS...ISS...
...S...VVDSMTKGTDS...A...EGGALQKELIRF...AVGSG...E...F...PSNLS...ISS...
...S...VVDSTAKGTNS...A...EGGALQKELIRF...TVGSG...E...Y...PSNLS...ISS...
...S...VMDSMTKGTDS...A...QGGALQQELIRF...AVGSG...E...Y...PSNLS...ISS...
...S...VMDSMTKGTDS...A...EGGALQRELIRF...AVGSG...E...Y...PSNLS...ISS...
...S...VLDSMDKGTDS...A...QGGALQRELIRF...AVGSG...E...Y...PSNLS...ISA...

Figure 3C


TAL activity
kcat (s-1)
Km (μM)
0.1
0.05
0
0
300
a,b 0.03
JaPAL
4859
a,b 0.03
JaPALF140H
227
a 0.02
JaPALF140H_MUT16
42.2
a,b 0.03
JaPALF140H_MUT8
17.9
b 0.04
JaPTAL
11.0

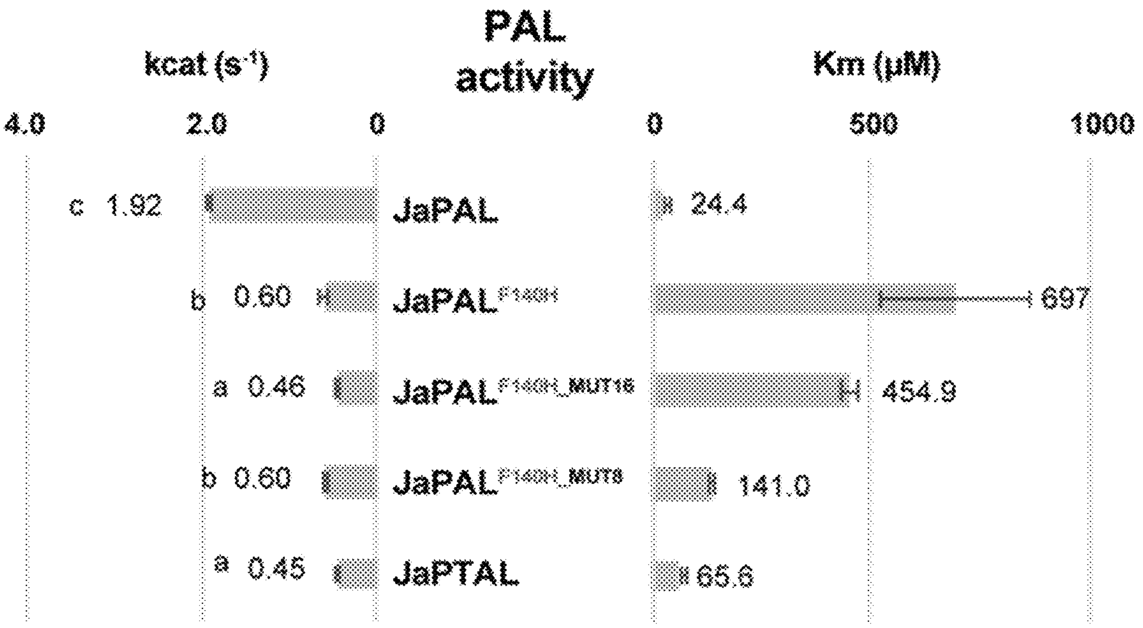

PAL activity
kcat (s-1)
Km (μM)
4.0
2.0
0
0
500
1000
c 1.92
JaPAL
24.4
b 0.60
JaPALF140H
697
a 0.46
JaPALF140H_MUT16
454.9
b 0.60
JaPALF140H_MUT8
141.0
a 0.45
JaPTAL
65.6

Figure 4A

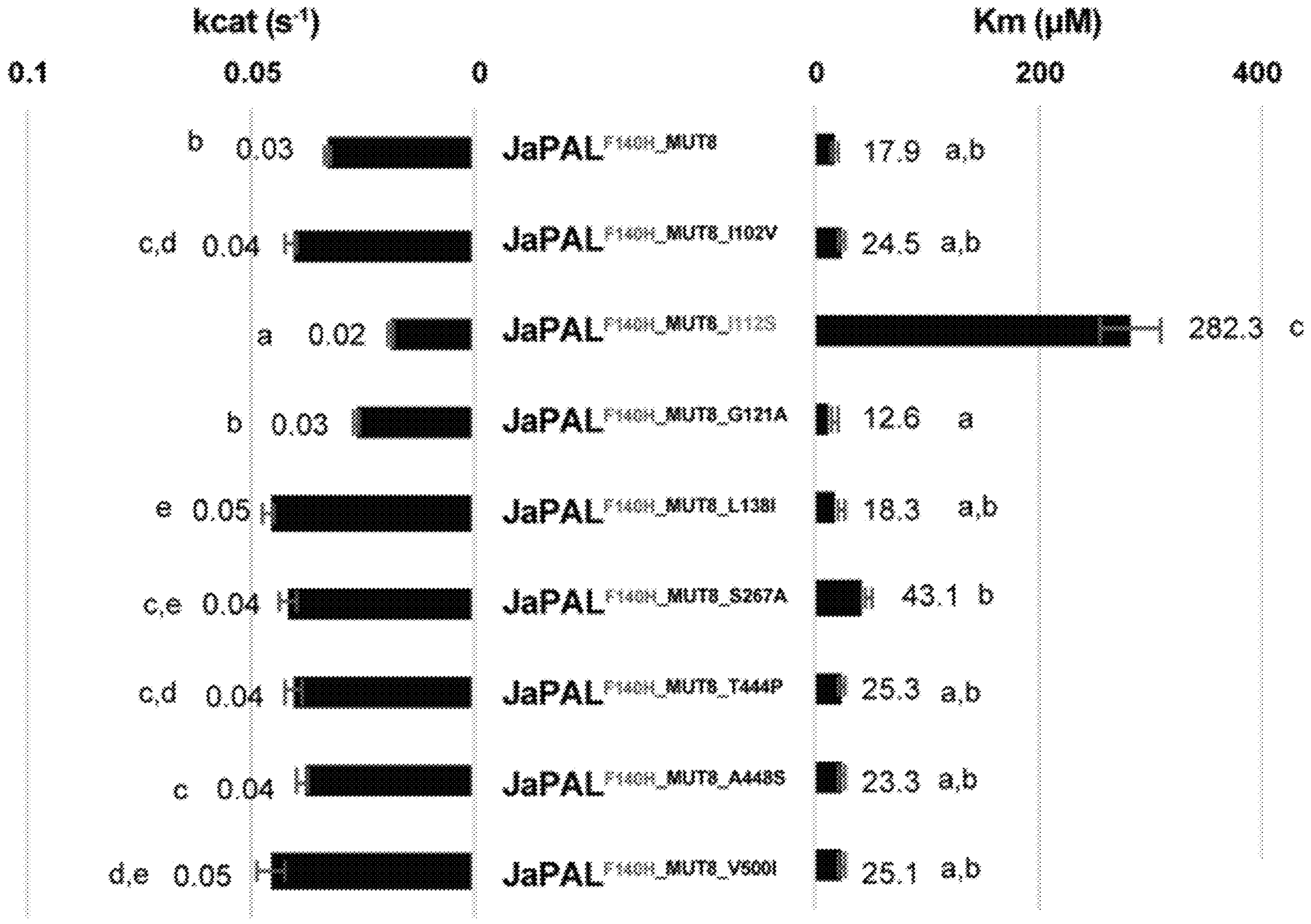

kcat (s^{-1})
0.1
0.05
0
Km (μM)
0
200
400
b 0.03 $\mathrm{JaPAL}^{F140H\_MUT8}$ 17.9 a,b
c,d 0.04 $\mathrm{JaPAL}^{F140H\_MUT8\_I102V}$ 24.5 a,b
a 0.02 $\mathrm{JaPAL}^{F140H\_MUT8\_I112S}$ 282.3 c
b 0.03 $\mathrm{JaPAL}^{F140H\_MUT8\_G121A}$ 12.6 a
e 0.05 $\mathrm{JaPAL}^{F140H\_MUT8\_L138I}$ 18.3 a,b
c,e 0.04 $\mathrm{JaPAL}^{F140H\_MUT8\_S267A}$ 43.1 b
c,d 0.04 $\mathrm{JaPAL}^{F140H\_MUT8\_T444P}$ 25.3 a,b
c 0.04 $\mathrm{JaPAL}^{F140H\_MUT8\_A448S}$ 23.3 a,b
d,e 0.05 $\mathrm{JaPAL}^{F140H\_MUT8\_V500I}$ 25.1 a,b

Figure 4B

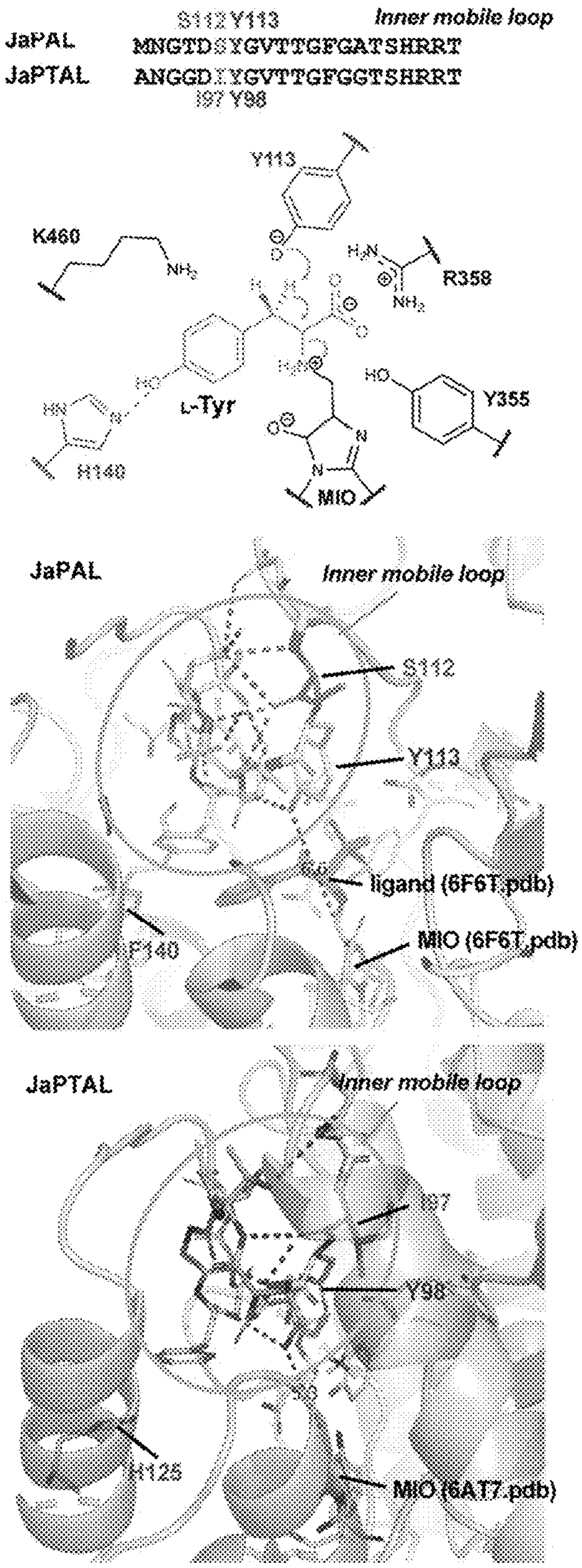

S112 Y113
Inner mobile loop
JaPAL MNGTDSYGVTTGFGATSHRRT
JaPTAL ANGGDIYGVTTGFGGTSHRRT
I97 Y98
Y113
K460
NH2
H2N
R358
NH2
H2N
L-Tyr
HO
HN
N
H140
HO
Y355
N
N
MIO
JaPAL
Inner mobile loop
S112
Y113
ligand (6F6T.pdb)
F140
MIO (6F6T.pdb)
JaPTAL
Inner mobile loop
I97
Y98
H125
MIO (6AT7.pdb)

Figure 4C

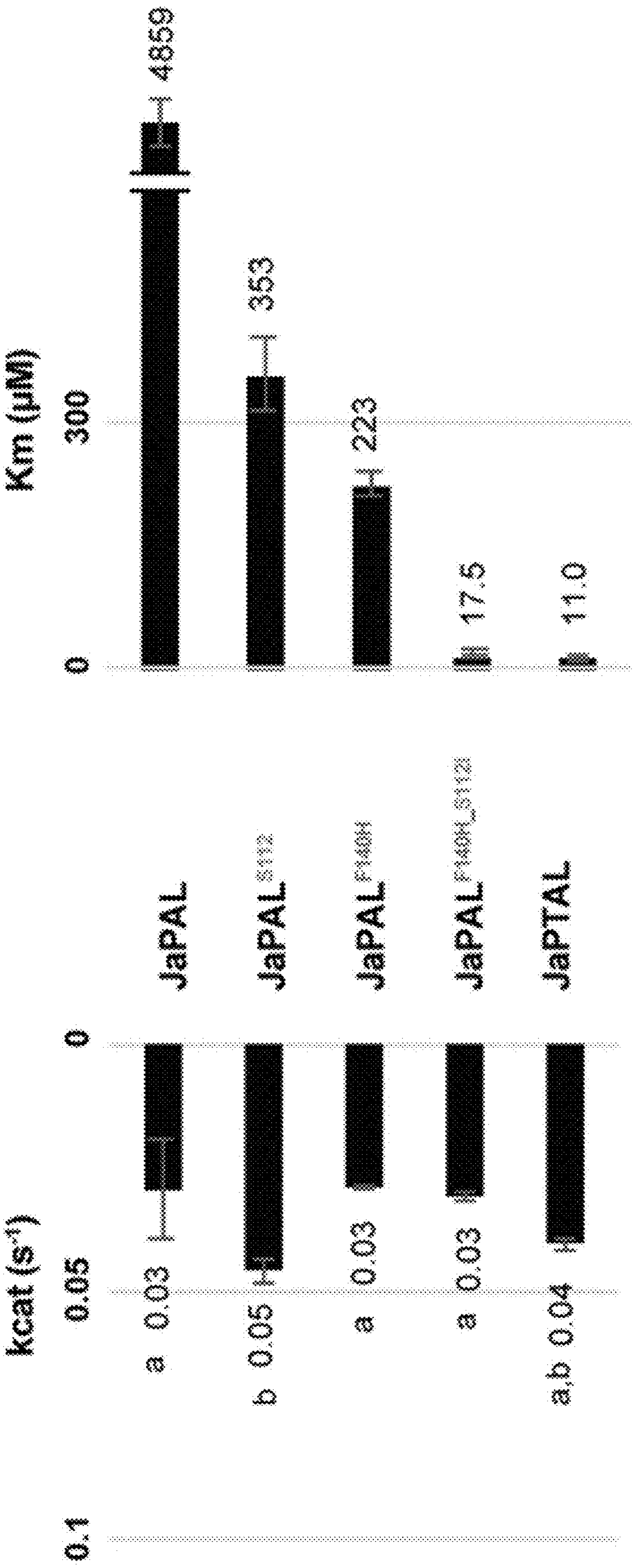

Kcat (s-1)
0
0.05
0.1
a 0.03
b 0.05
a 0.03
a 0.03
a,b 0.04
JaPAL
JaPAL S112
JaPAL F140H
JaPAL F140H_S112
JaPTAL
Km (µM)
0
300
4859
353
223
17.5
11.0

Figure 4D

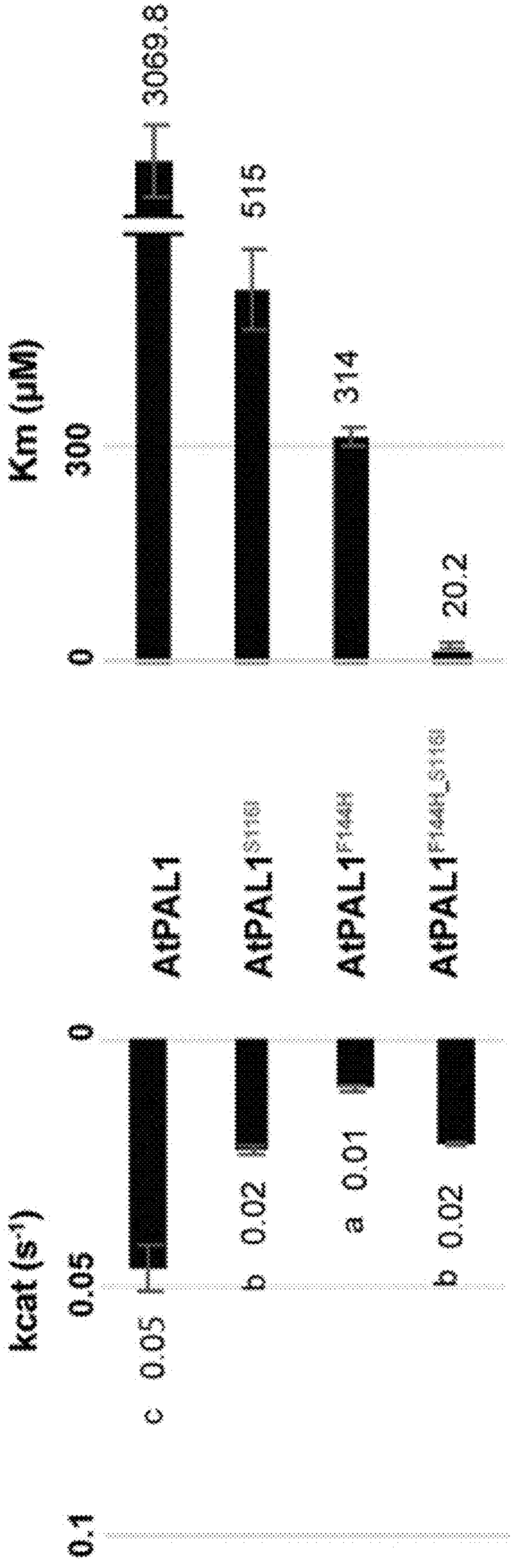

kcat (s-1)
0.1
0.05
0
c 0.05
b 0.02
a 0.01
b 0.02
AtPAL1
AtPAL1S116
AtPAL1F144H
AtPAL1F144H_S116
Km (μM)
0
300
3069.8
515
314
20.2

Figure 5

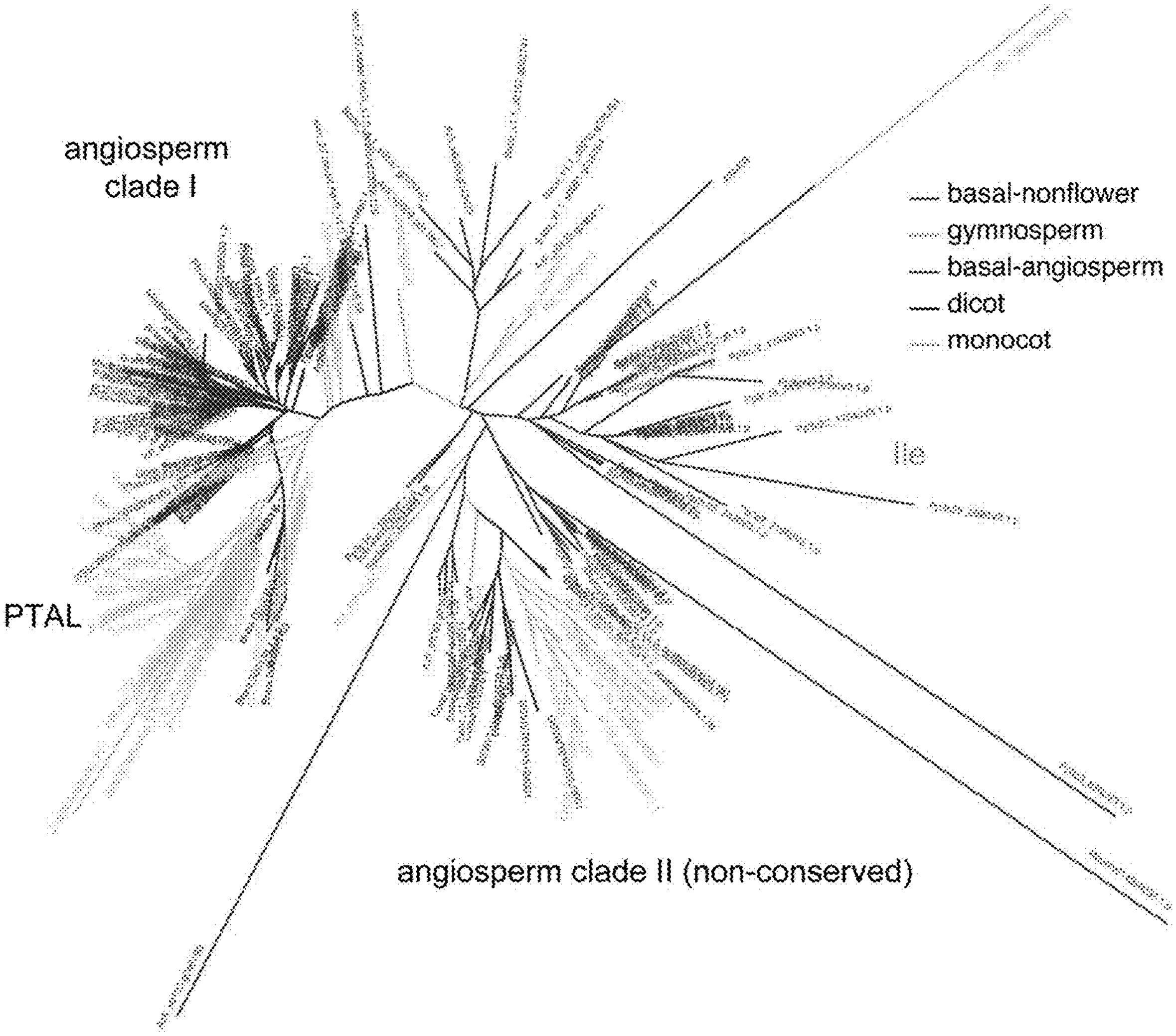

angiosperm clade I
PTAL
angiosperm clade II (non-conserved)
IIe
basal-nonflower
gymnosperm
basal-angiosperm
dicot
monocot

Figure 6

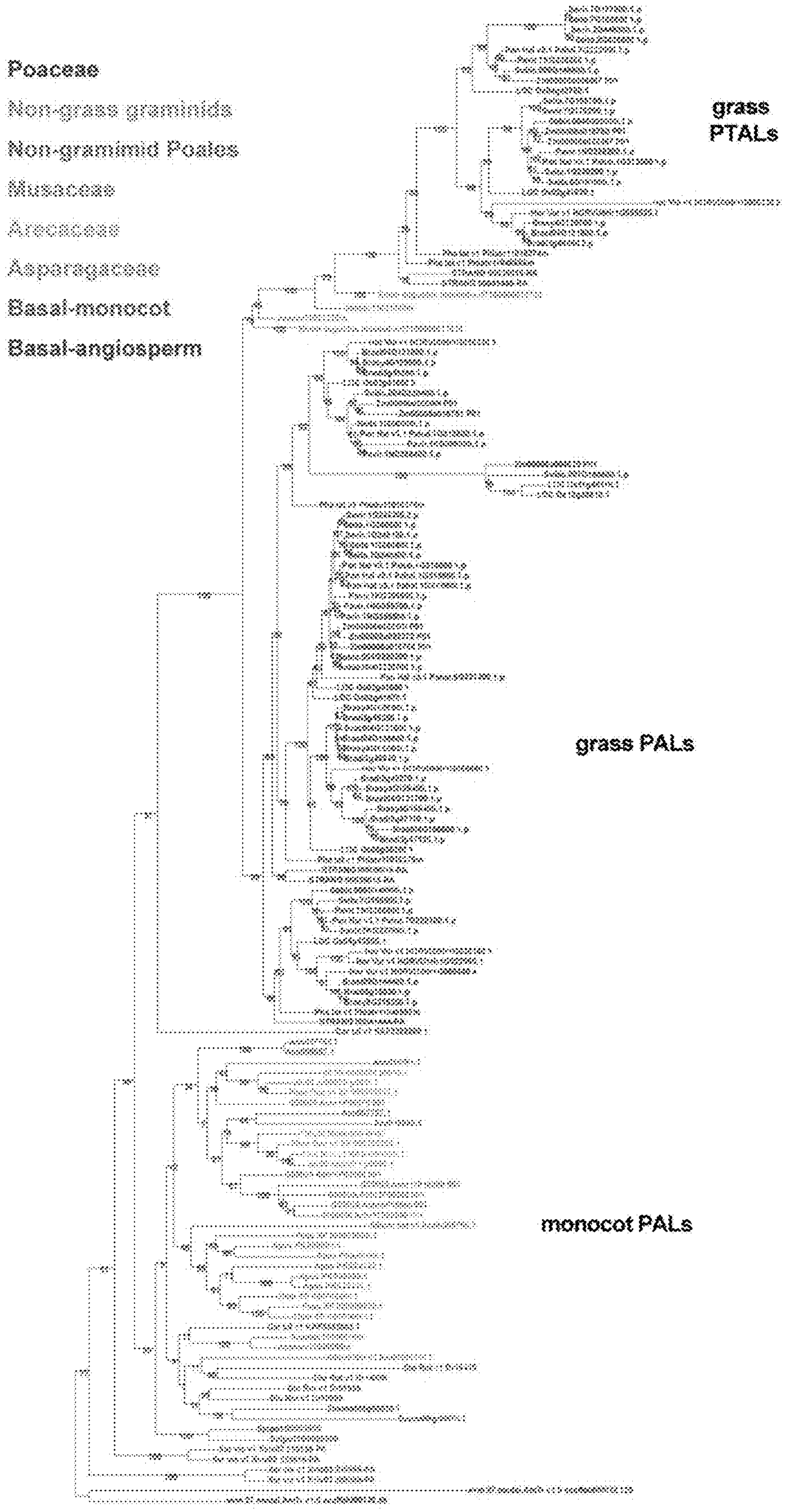

Poaceae
Non-grass graminids
Non-gramimid Poales
Musaceae
Arecaceae
Asparagaceae
Basal-monocot
Basal-angiosperm
grass PTALs
grass PALs
monocot PALs

Figure 7

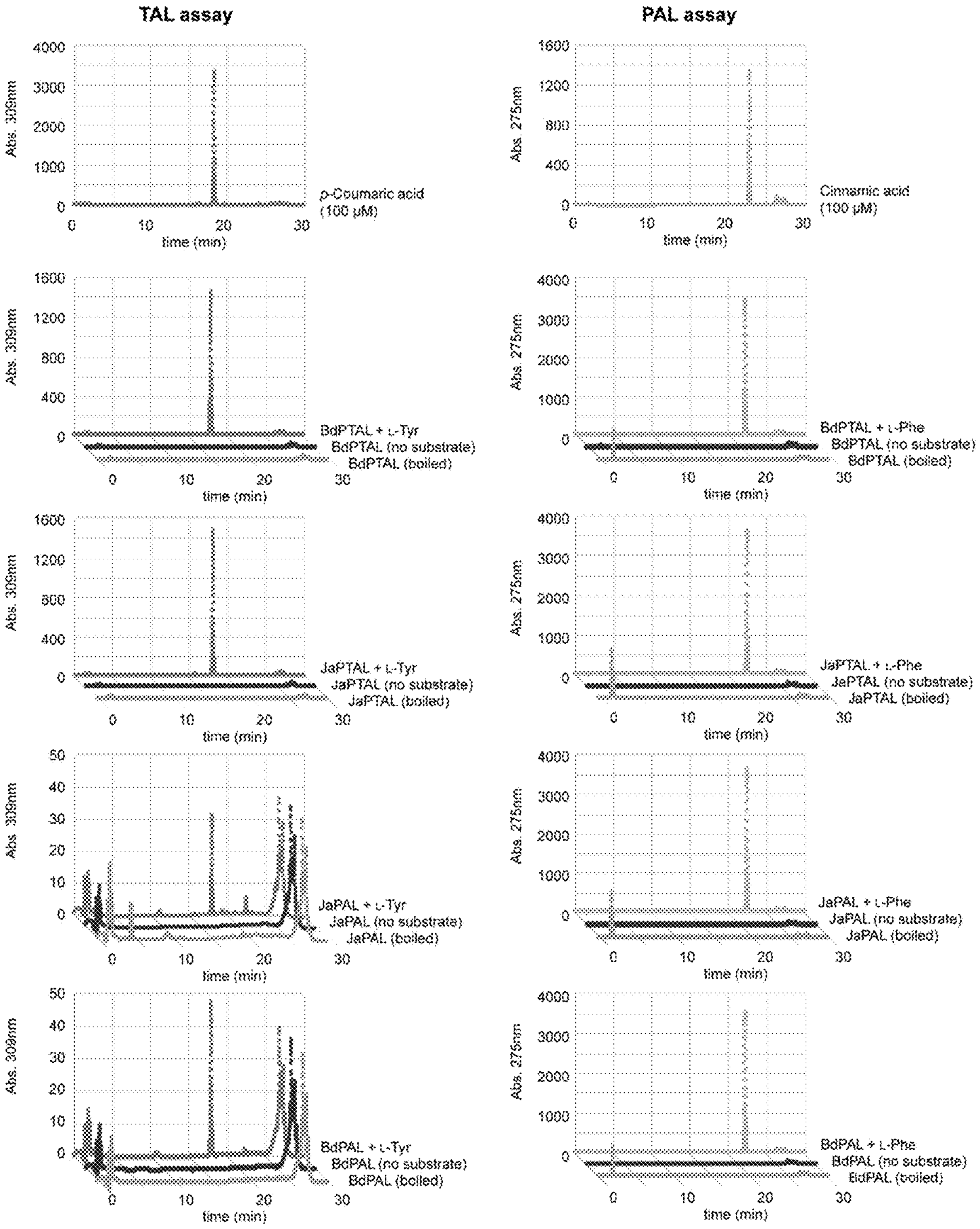

TAL assay
PAL assay
Abs. 309nm
4000
3000
2000
1000
0
0
10
20
30
time (min)
p-Coumaric acid
(100 μM)
Abs. 275nm
1600
1200
800
400
0
Cinnamic acid
(100 μM)
BdPTAL + L-Tyr
BdPTAL (no substrate)
BdPTAL (boiled)
BdPTAL + L-Phe
BdPTAL (no substrate)
BdPTAL (boiled)
JaPTAL + L-Tyr
JaPTAL (no substrate)
JaPTAL (boiled)
JaPTAL + L-Phe
JaPTAL (no substrate)
JaPTAL (boiled)
50
40
30
20
10
JaPAL + L-Tyr
JaPAL (no substrate)
JaPAL (boiled)
JaPAL + L-Phe
JaPAL (no substrate)
JaPAL (boiled)
BdPAL + L-Tyr
BdPAL (no substrate)
BdPAL (boiled)
BdPAL + L-Phe
BdPAL (no substrate)
BdPAL (boiled)

Figure 8

```
Sevir.6G187100.1.p                                     .......... .......... .......... ....MAG... ..........
Seita.6G181000.1.p                                     .......... .......... .......... ....MAG... ..........
Sevir.1G245000.1.p                                     .......... .......... .......... ....MAG... ..........
Seita.1G240200.1.p                                     .......... .......... .......... ....MAG... ..........
PhHAL.1G306700.1.p                                     .......... .......... .......... ....MAG... ..........
Pavir.1NG356200.1.p                                    .......... .......... .......... ....MAG... ..........
Zm00008a016750_P01                                     .......... .......... .......... ....MAG... ..........
Zm00008a022367_P01                                     .......... .......... .......... ....MAG... ..........
Sobic.004G220300.1.p                                   .......... .......... .......... ....MAG... ..........
Sevir.7G178200.1.p                                     .......... .......... .......... ....MAS... ..........
Seita.7G168700.1.p                                     .......... .......... .......... ....MAS... ..........
Osa_LOC_Os02g41630.1                                   .......... .......... .......... ....MAG... ..........
Bradi3g49250.2.p                                       .......... .......... .......... ....MAG... ..........
Pavic.7KG228255.1.p                                    .......... .......... .......... ....MAS... ..........
Pavic.7NG355500.1.p                                    .......... .......... .......... ....MAS... ..........
PhHAL.7G213600.1.p                                     .......... .......... .......... ....MAS... ..........
Zm00008a006867_P01                                     .......... .......... .......... ....MAS... ..........
Sobic.006G148800.1.p                                   .......... .......... .......... ....MAS... ..........
Seita.2G435800.1.p                                     .......... .......... .......... ....MAC... ..........
Sevir.2G448300.1.p                                     .......... .......... .......... ....MAC... ..........
Sevir.7G177900.1.p                                     .......... .......... .......... ....MAC... ..........
Seita.7G168500.1.p                                     .......... .......... .......... ....MAC... ..........
Osa_LOC_Os04g43760.1                                   .......... .......... .......... ....MAS... ..........
STRANG_00041445-RA                                     .......... .......... .......... ....MVA... ..........
STRANG_00039013-RA                                     .......... .......... .......... ....MAS... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1   .......... .......... .......... ....MACL.. ..........
Joascv11021323m                                        .......... .......... .......... ....MAF... .......... ; PTAL
Joascv11021328m                                        .......... .......... .......... ....MEC... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1  .......... .......... .......... ....MEC... ..........
Flagellaria_indica_Trinity_comp23995_c0_seq1           .......... .......... .......... ....MECQQN .......... ; basal grass PAL
Seita.1G240400.1.p                                     .......... .......... .......... ....MAC... ..........
Sevir.1G245166.1.p                                     .......... .......... .......... ....MAC... ..........
Seita.1G240500.1.p                                     .......... .......... .......... ....MAC... ..........
Sevir.1G245232.1.p                                     .......... .......... .......... ....MAC... ..........
Seita.1G240600.1.p                                     .......... .......... .......... ....MEC... ..........
Sevir.1G245300.2.p                                     .......... .......... .......... ....MEC... ..........
PhHAL.1G307000.1.p                                     .......... .......... .......... ....MAC... ..........
PhHAL.1G307100.1.p                                     .......... .......... .......... ....MAC... ..........
PhHAL.1G307200.1.p                                     .......... .......... .......... ....MEC... ..........
Pavir.1NG356700.1.p                                    .......... .......... .......... ....MAC... ..........
Pavir.1NG356800.1.p                                    .......... .......... .......... ....MEC... ..........
Pavic.1KG386500.1.p                                    .......... .......... .......... ....MEC... ..........
Sobic.004G220600.2.p                                   .......... .......... .......... ....MAC... ..........
Sobic.004G220500.1.p                                   .......... .......... .......... ....MAC... ..........
Sobic.004G220700.1.p                                   .......... .......... .......... ....MAC... ..........
Zm00008a016754_P01                                     .......... .......... .......... ....MEC... ..........
Zm00008a022372_P01                                     .......... .......... .......... ....MEC... ..........
Zm00008a022370_P01                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                   .......... .......... .......... ....MAC... ..........
Osa_LOC_Os02g41680.1                                   .......... .......... .......... ....MEC... ..........
Bradi3g47110.1.p                                       .......... .......... .......... ....MAC... ..........
Bradi3g47120.1.p                                       M......... .......... .......... ...TMAS... ..........
Bradi3g49270.1.p                                       .......... .......... .......... ....MAR... ..........
Bradi3g48840.1.p                                       .......... .......... .......... ....MEC... ..........
Bradi3g49280.1.p                                       .......... .......... .......... ....MEC... ..........
Osa_LOC_Os05g35290.1                                   .......... .......... .......... ....MEC... ..........
Pavir.1KG386300.1.p                                    .......... .......... .......... ....MEC... ..........
Pavic.1NG356400.1.p                                    .......... .......... .......... ....MEC... ..........
PhHAL.1G306800.1.p                                     .......... .......... .......... ....MEC... ..........
Seita.1G240300.1.p                                     .......... .......... .......... ....MEC... ..........
Sevir.1G245100.1.p                                     .......... .......... .......... ....MEC... ..........
Zm00008a016751_P01                                     .......... .......... .......... ....MEC... ..........
Zm00008a022369_P01                                     .......... .......... .......... ....MEC... ..........
Sobic.004G220400.1.p                                   .......... .......... .......... ....MEC... ..........
Osa_LOC_Os02g41650.1                                   .......... .......... .......... ....MEC... ..........
Osa_LOC_Os11g48110.1                                   .......... .......... .......... ....MEC... ..........
Osa_LOC_Os12g33610.1                                   .......... .......... .......... ....MEC... ..........
Sobic.001G160500.1.p                                   .......... .......... .......... ....MEC... ..........
Zm00008a004629_P01                                     .......... .......... .......... ....MEC... ..........
Bradi3g49260.1.p                                       .......... .......... .......... ....MEC... ..........
STRANG_00039013-RA                                     .......... .......... .......... ....MEC... ..........
STRANG_00039015-RA                                     .......... .......... .......... ....MEC... ..........
Pavir.7KG237600.1.p                                    .......... .......... .......... ....MEC... ..........
PhHAL.7G214000.1.p                                     .......... .......... .......... ....MEC... ..........
Pavir.1NG361819.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                    .......... .......... .......... ....MEC... ..........
Sevir.7G178300.1.p                                     .......... .......... .......... ....MEC... ..........
Seita.7G168800.1.p                                     .......... .......... .......... ....MEC... ..........
Zm00008a006866_P01                                     .......... .......... .......... ....MEC... ..........
Sobic.006G148900.1.p                                   .......... .......... .......... ....MEC... ..........
Pavir.4KG229700.2.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                   .......... .......... .......... ....MEC... ..........
Osa_LOC_Os08g21670.1                                   .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                       .......... .......... .......... ....MEY... ..........
STRANG_00041444-RA                                     M......... .......... EP........ ....LSC... ..........
STRANG_00041441-RA                                     .......... .......... .......... .......... ..........
STRANG_00041440-RA                                     .......... .......... .......... .......... ..........
STRANG_00059682-RA                                     .......... .......... .......... ....MFCPDQ PRRTAPQDRL ; grass PAL
Aco013943.1                                            .......... .......... .......... .......... ..........
Aco007727.1                                            .......... .......... .......... ....MEC... ..........
Apos_PKA46439.1                                        .......... .......... .......... ....MEHAAD ..........
Apos_PKA58411.1                                        .......... .......... .......... ....MEHAAD ..........
Apos_PKA64143.1                                        MLQEDPGRSL SDKRRNFSSL NFFFELLLIS YPPSMEQSKK ..........
Dcat_XP_020704813.1                                    .......... .......... .......... ....ME.... ..........
Pequ_XP_020589728.1                                    .......... .......... .......... ....ME.... ..........
Dcat_XP_020702280.1                                    .......... .......... .......... ....MERVKG ..........
Apos_PKA59591.1                                        .......... .......... .......... ....MDHSKV ..........
Apos_PKA60166.1                                        .......... .......... .......... ....MDHVKE ..........
Pequ_XP_020579535.1                                    .......... .......... .......... ....MDACK. ..........
Spipo11G0025500                                        .......... .......... .......... ....MEAATQ V.........
Spipo1G0002500                                         .......... .......... .......... ....MEAAGQ I.........
GSMUA_Achr8P18960_001                                  .......... .......... .......... ....ME.... ..........
GSMUA_Achr11P22840_001                                 .......... .......... .......... ....ME.... ..........
GSMUA_Achr5P18560_001                                  .......... .......... .......... ....ME.... ..........
GSMUA_Achr2P00240_001                                  .......... .......... .......... ....ME.... ..........
GSMUA_Achr11P16280_001                                 .......... .......... .......... ....ME.... ..........
GSMUA_Achr5P03950_001                                  .......... .......... .......... ....MEF... ..........
p5.00_sc00071_p0098.1                                  .......... .......... .......... ....MESAHE ..........
CALSI_Maker00040467                                    .......... .......... .......... ....MEEGHQ ..........
Aco008987.1                                            .......... .......... .......... ....MEEVE. ..........
Aco027752.1                                            .......... .......... .......... ....MEEVE. ..........
GSMUA_Achr1P09070_001                                  .......... .......... .......... ....MEFAPK AQ........
p5.00_sc00334_p0013.1                                  .......... .......... .......... ....ME.... ..........
p5.00_sc00076_p0011.1                                  .......... .......... .......... ....ME.... ..........
Aco010091.1                                            .......... .......... .......... ....MERAPS S.........
Aoff_XP_020259774.1                                    .......... .......... .......... ....ME.... ..........
Aoff_XP_020259795.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                    .......... .......... .......... ....ME.... ..........
Aoff_XP_020248601.1                                    .......... .......... .......... ....M..... ..........
Aoff_XP_020272851.1                                    .......... .......... .......... ....MSHV.. ..........
Aoff_XP_020272852.1                                    .......... .......... .......... ....MSHV.. ..........
Acamev1I004816m                                        .......... .......... .......... ....ME.... ..........
Acamev1I046066m                                        .......... .......... .......... ....MEHSL. ..........
Zosma445g00020.1                                       .......... .......... .......... ....MDAMDL CQ........
Zosma69g00670.1                                        .......... .......... .......... ....M..... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59            .......... .......... .......... ....MEFSAH Q.........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129           .......... .......... .......... ....MKSVS. ..........
CALSI_Maker00043687                                    .......... .......... .......... ....MASED. .APS......
CALSI_Maker00043684                                    .......... .......... .......... ....MASPD. .GPV......
p5.00_sc01789_p0001.1                                  .......... .......... .......... ....MASPN. .TVP......
p5.00_sc00066_p0001.1                                  .......... .......... .......... ....MAEPGK ..........
CALSI_Maker00043685                                    .......... .......... .......... ....MAEPRK ..........
Aco020618.1                                            .......... .......... .......... ....MASENP KGST......
GSMUA_Achr9P15990_001                                  .......... .......... .......... ....MDSPG. .SYI......
Zosma49g00480.1                                        .......... .......... .......... ....MALAKK F.........
Zosma115g00180.1                                       .......... .......... .......... ....MANSTK SAM.......
Spipo15G0044700                                        .......... .......... .......... ....MAAQIN .GLV......
Acamev1I008810m                                        .......... .......... .......... ....MASTE. .APT......
Acamev1I024102m                                        .......... .......... .......... ....MASTE. .AIT......
Acamev1I050170m                                        .......... .......... .......... ....MASSTE .GLS......
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177           .......... .......... .......... ....MAENGP ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178           .......... .......... .......... ....MAETA. ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181           .......... .......... .......... ....MADSVF .......... ; monocot PAL
```

Figure 8(continued)

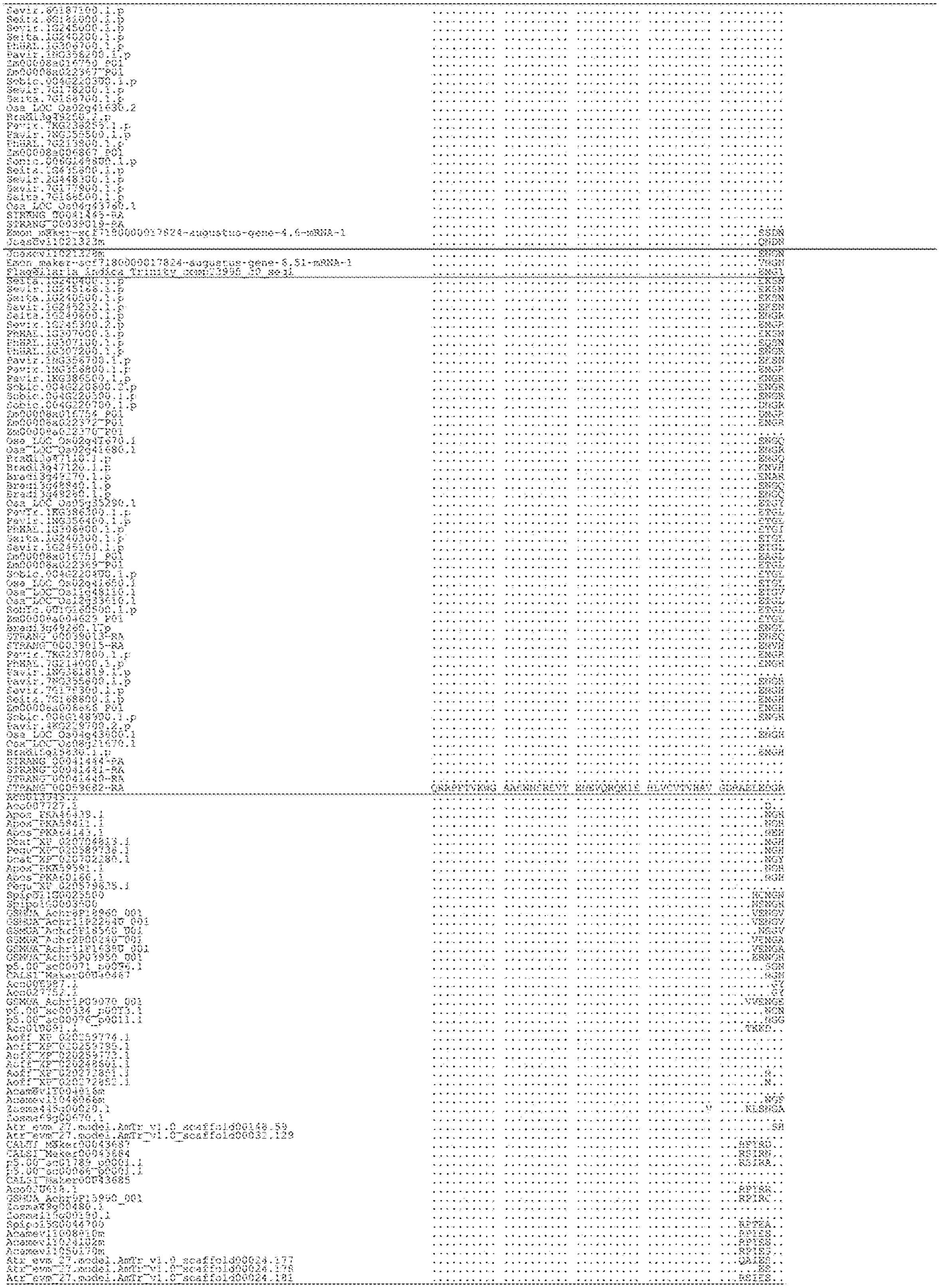


Figure 8(continued)

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Sevir.6G187100.1.p                                     .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                    .......... .......... .......... .......... ..........
Zm00008a016750_P01                                     .......... .......... .......... .......... ..........
Zm00008a022367_P01                                     .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                   .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                   .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                       .......... .......... .......... .......... ..........
Pavir.7KG238255.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                    .......... .......... .......... .......... ..........
PhHAL.7G213900.1.p                                     .......... .......... .......... .......... ..........
Zm00008a006867_P01                                     .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                   .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                     .......... .......... .......... .......... ..........
Sevir.2G448300.1.p                                     .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                   .......... .......... .......... .......... ..........
STRANG_00041445-RA                                     .......... .......... .......... .......... ..........
STRANG_00039019-RA                                     .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1   .V........ .......... .......... .......... ..........
Joascv11021323m                                        .V........ .......... .......... .......... ..........
-----------------------------------------------------------------------------------------------------------
Joascv11021328m                                        .V.AAVAAV. .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1  .G.AAA.... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1           .A.AAAVA.. .......... .......... .......... ..........
-----------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                     .V.AA..... .......... .......... .......... ..........
Sevir.1G245166.1.p                                     .V.AA..... .......... .......... .......... ..........
Seita.1G240500.1.p                                     .V.AA..... .......... .......... .......... ..........
Sevir.1G245232.1.p                                     .V.AA..... .......... .......... .......... ..........
Seita.1G240600.1.p                                     .V.AAA.... .......... .......... .......... ..........
Sevir.1G245300.2.p                                     .V.AAA.... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                     .V.AA..... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                     .V.AA..... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                     .V.A...... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                    .V.AT..... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                    .G.A...... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                    .V.A...... .......... .......... .......... ..........
Sobic.004G220600.2.p                                   .V.AAT.... .......... .......... .......... ..........
Sobic.004G220500.1.p                                   .V.AAT.... .......... .......... .......... ..........
Sobic.004G220700.1.p                                   .V.AAT.... .......... .......... .......... ..........
Zm00008a016754_P01                                     .V.AAT.... .......... .......... .......... ..........
Zm00008a022372_P01                                     .V.AAT.... .......... .......... .......... ..........
Zm00008a022370_P01                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                   .V.AAD.... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                   .V.SAN.... .......... .......... .......... ..........
Bradi3g47110.1.p                                       .V..AA.... .......... .......... .......... ..........
Bradi3g47120.1.p                                       .V..SA.... .......... .......... .......... ..........
Bradi3g49270.1.p                                       .V.AAA.... .......... .......... .......... ..........
Bradi3g48840.1.p                                       .F..AA.... .......... .......... .......... ..........
Bradi3g49280.1.p                                       .F..AA.... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                   .V.AAA.... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                    .V.RSL.... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                    .V.RSL.... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                     .V.RSL.... .......... .......... .......... ..........
Seita.1G240300.1.p                                     .V.RSL.... .......... .......... .......... ..........
Sevir.1G245100.1.p                                     .V.RSL.... .......... .......... .......... ..........
Zm00008a016751_P01                                     .LVRSSL... .......... .......... .......... ..........
Zm00008a022369_P01                                     .V.RSL.... .......... .......... .......... ..........
Sobic.004G220400.1.p                                   .V.RSL.... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                   .V.RSL.... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os12g33610.1                                   .VDRPLN... .......... .......... .......... ..........
Sobic.001G160500.1.p                                   .VDRPPR... .......... .......... .......... ..........
Zm00008a004629_P01                                     .VDRPL.... .......... .......... .......... ..........
Bradi3g49260.1.p                                       .V.GSL.... .......... .......... .......... ..........
STRANG_00039013-RA                                     .V..AA.... .......... .......... .......... ..........
STRANG_00039015-RA                                     .V..AA.... .......... .......... .......... ..........
Pavir.7KG237800.1.p                                    .V.AAA.... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                     .V..AA.... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                    .V..AA.... .......... .......... .......... ..........
Sevir.7G178300.1.p                                     .V.VAA.... .......... .......... .......... ..........
Seita.7G168800.1.p                                     .V.VAA.... .......... .......... .......... ..........
Zm00008a006866_P01                                     .V..AA.... .......... .......... .......... ..........
Sobic.006G148900.1.p                                   .A.AGA.... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                   .VAAAA.... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                   .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                       .A..AT.... .......... .......... .......... ..........
STRANG_00041444-RA                                     .V..AA.... .......... .......... .......... ..........
STRANG_00041441-RA                                     .......... .......... .......... .......... ..........
STRANG_00041440-RA                                     .......... .......... .......... .......... ..........
STRANG_00059682-RA                                     .CDGVMGTLA KAGRGRGGGG VVGRGGAGGR GRGGAGVVGR GGAAGRGRGG
-----------------------------------------------------------------------------------------------------------
Aco013943.1                                            .......... .......... .......... .......... ..........
Aco007727.1                                            .A........ .......... .......... .......... ..........
Apos_PKA46439.1                                        .L........ .......... .......... .......... ..........
Apos_PKA58411.1                                        .L........ .......... .......... .......... ..........
Apos_PKA54143.1                                        .L........ .......... .......... .......... ..........
Dcat_XP_020704813.1                                    .A........ .......... .......... .......... ..........
Pequ_XP_020589738.1                                    .A........ .......... .......... .......... ..........
Dcat_XP_020702380.1                                    .A........ .......... .......... .......... ..........
Apos_PKA59591.1                                        .A........ .......... .......... .......... ..........
Apos_PKA60166.1                                        .G........ .......... .......... .......... ..........
Pequ_XP_020579635.1                                    .V........ .......... .......... .......... ..........
Spipo31G0025500                                        .G........ .......... .......... .......... ..........
Spipo1G0003500                                         .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                  .G........ .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                 HG........ .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                  HA........ .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                  YT........ .......... .......... .......... ..........
GSMUA_Achr11P16380_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                  HA........ .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                  .A........ .......... .......... .......... ..........
CALSI_Maker00040467                                    .G........ .......... .......... .......... ..........
Aco006987.1                                            .......... .......... .......... .......... ..........
Aco027752.1                                            .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                  .A........ .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                  .A........ .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                  .A........ .......... .......... .......... ..........
Aco010091.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                    .G........ .......... .......... .......... ..........
Aoff_XP_020272852.1                                    .G........ .......... .......... .......... ..........
Acamev1I004816m                                        .......... .......... .......... .......... ..........
Acamev1I046066m                                        .T........ .......... .......... .......... ..........
Zosma445g00020.1                                       .T........ .......... .......... .......... ..........
Zosma69g00670.1                                        .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59            .S........ .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129           .......... .......... .......... .......... ..........
CALSI_Maker00043687                                    .LRPPTLPIP I......... .......... .......... ..........
CALSI_Maker00043684                                    .LRPPTLPIP A......... .......... .......... ..........
p5.00_sc01789_p0001.1                                  .LRPPTLPVP A......... .......... .......... ..........
p5.00_sc00066_p0001.1                                  ....PSEPNV C......... .......... .......... ..........
CALSI_Maker00043685                                    .......... .......... .......... .......... ..........
Aco020610.1                                            .PRPPTLPVP T......... .......... .......... ..........
GSMUA_Achr9P15990_001                                  .PRPPTLPVP T......... .......... .......... ..........
Zosma79g00480.1                                        .......... .......... .......... .......... ..........
Zosma115g00180.1                                       .......... .......... .......... .......... ..........
Spipo15G0044700                                        .PRPPTLPLP K......... .......... .......... ..........
Acamev1I008610m                                        .LRPPTLPLP T......... .......... .......... ..........
Acamev1I024102m                                        .LRPPTLPLP T......... .......... .......... ..........
Acamev1I050170m                                        .LRPPTLPLP T......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177           .CRPATLPLP I......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178           .CRPPSLLLP N......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181           .CRPPTLPLP N......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                      .......... .......... ......NGL. .......... ..........
Seita.6G181000.1.p                                      .......... .......... ......NGL. .......... ..........
Sevir.1G245000.1.p                                      .......... .......... ......NGL. .......... ..........
Seita.1G240200.1.p                                      .......... .......... ......NGL. .......... ..........
PhHAL.1G306700.1.p                                      .......... .......... ......NGL. .......... ..........
Pavir.1NG356200.1.p                                     .......... .......... ......NGL. .......... ..........
Zm00008a016750_P01                                      .......... .......... ......NGA. .......... ..........
Zm00008a022367_P01                                      .......... .......... ......NGA. .......... ..........
Sobic.004G220300.1.p                                    .......... .......... ......NGA. .......... ..........
Sevir.7G178200.1.p                                      .......... .......... ......NTA. .......... ..........
Seita.7G168700.1.p                                      .......... .......... ......NTA. .......... ..........
Osa_LOC_Os02g41630.2                                    .......... .......... ......NGP. .......... ..........
Bradi3g49250.1.p                                        .......... .......... ......NGA. .......... ..........
Pavir.7KG238255.1.p                                     .......... .......... ......NTA. .......... ..........
Pavir.7NG355500.1.p                                     .......... .......... ......NTA. .......... ..........
PhHAL.7G213800.1.p                                      .......... .......... ......NTA. .......... ..........
Zm00008a006867_P01                                      .......... .......... ......NTA. .......... ..........
Sobic.006G148500.1.p                                    .......... .......... ......NTA. .......... ..........
Seita.2G435800.1.p                                      .......... .......... ......NTA. .......... ..........
Sevir.2G448300.1.p                                      .......... .......... ......NTA. .......... ..........
Sevir.7G177900.1.p                                      .......... .......... ......NTA. .......... ..........
Seita.7G168500.1.p                                      .......... .......... ......STA. .......... ..........
Osa_LOC_Os04g43760.1                                    .......... .......... ......QTAD .......... ..........
STRANG_00041445-RA                                      .......... .......... ......QSDS .......... ..........
STRANG_00039019-RA                                      .......... .......... ......Q... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1    .......... .......... .......... .......... ..........
Joascv11021323m                                         .......... .......... .......... .......... ..........
--------------------------------------------------------------------------------------------------------------
Joascv11021328m                                         .......... .......... .....NGSN. .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1   .......... .......... ......NGS. .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1            .......... .......... ......NGAA AREE...... ..........
--------------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                      .......... .......... ......NGD. .......... ..........
Sevir.1G245166.1.p                                      .......... .......... ......NGD. .......... ..........
Seita.1G240500.1.p                                      .......... .......... ......NGD. .......... ..........
Sevir.1G245232.1.p                                      .......... .......... ......NGD. .......... ..........
Seita.1G240600.1.p                                      .......... .......... ......NGD. .......... ..........
Sevir.1G245300.2.p                                      .......... .......... ......NGD. .......... ..........
PhHAL.1G307000.1.p                                      .......... .......... ......NGD. .......... ..........
PhHAL.1G307100.1.p                                      .......... .......... ......NGD. .......... ..........
PhHAL.1G307200.1.p                                      .......... .......... ......NGD. .......... ..........
Pavir.1NG356700.1.p                                     .......... .......... ......NGD. .......... ..........
Pavir.1NG356800.1.p                                     .......... .......... ......NGD. .......... ..........
Pavir.1KG386500.1.p                                     .......... .......... ......NGD. .......... ..........
Sobic.004G220600.2.p                                    .......... .......... ......NGD. .......... ..........
Sobic.004G220500.1.p                                    .......... .......... ......NGD. .......... ..........
Sobic.004G220700.1.p                                    .......... .......... ......NGD. .......... ..........
Zm00008a016754_P01                                      .......... .......... ......NGD. .......... ..........
Zm00008a022372_P01                                      .......... .......... ......NSD. .......... ..........
Zm00008a022370_P01                                      .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                    .......... .......... ......GIN. .......... ..........
Osa_LOC_Os02g41680.1                                    .......... .......... ......GMS. .......... ..........
Bradi3g47110.1.p                                        .......... .......... ......NG.. .......... ..........
Bradi3g47120.1.p                                        .......... .......... ......DGYL .......... ..........
Bradi3g49270.1.p                                        .......... .......... ......NG.. .......... ..........
Bradi3g48840.1.p                                        .......... .......... ......NGT. .......... ..........
Bradi3g49280.1.p                                        .......... .......... ......NGT. .......... ..........
Osa_LOC_Os05g35290.1                                    .......... .......... ......ADG. .......... ..........
Pavir.1KG386300.1.p                                     .......... .......... ......HGD. .......... ..........
Pavir.1NG356400.1.p                                     .......... .......... ......HGD. .......... ..........
PhHAL.1G306800.1.p                                      .......... .......... ......HGD. .......... ..........
Seita.1G240300.1.p                                      .......... .......... ......HGD. .......... ..........
Sevir.1G245100.1.p                                      .......... .......... ......HGD. .......... ..........
Zm00008a016751_P01                                      .......... .......... ......NGE. .......... ..........
Zm00008a022369_P01                                      .......... .......... ......NGE. .......... ..........
Sobic.004G220400.1.p                                    .......... .......... ......NGD. .......... ..........
Osa_LOC_Os02g41650.1                                    .......... .......... ......NGD. .......... ..........
Osa_LOC_Os11g48110.1                                    .......... .......... ......NGS. .......... ..........
Osa_LOC_Os12g33610.1                                    .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                    .......... .......... ......NGAA .......... ..........
Zm00008a004629_P01                                      .......... .......... .......NSS .......... ..........
Bradi3g49260.1.p                                        .......... .......... ......NGE. .......... ..........
STRANG_00039013-RA                                      .......... .......... ......NGN. .......... ..........
STRANG_00039015-RA                                      .......... .......... ......NGN. .......... ..........
Pavir.7KG227800.1.p                                     .......... .......... ......TGN. .......... ..........
PhHAL.7G214000.1.p                                      .......... .......... ......SGN. .......... ..........
Pavir.1NG361819.1.p                                     .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                     .......... .......... ......NGN. .......... ..........
Sevir.7G178300.1.p                                      .......... .......... ......NGN. .......... ..........
Seita.7G168800.1.p                                      .......... .......... ......NGN. .......... ..........
Zm00008a006866_P01                                      .......... .......... ......SGNG .......... ..........
Sobic.006G148900.1.p                                    .......... .......... ......SGN. .......... ..........
Pavir.4KG229700.2.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                    .......... .......... ......NGS. .......... ..........
Osa_LOC_Os08g21670.1                                    .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                        .......... .......... ......YGD. .......... ..........
STRANG_00041444-RA                                      .......... .......... ......NGN. .......... ..........
STRANG_00041441-RA                                      .......... .......... .......... .......... ..........
STRANG_00041440-RA                                      .......... .......... .......... .......... ..........
STRANG_00059682-RA                                      AGRIGRIGVV RGENMLGEGG AAGRLGGGEL VREKKNLQHG GDVAWGEEVL
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Aco013943.1                                             .......... .......... .......... .......... ..........
Aco007727.1                                             .......... .......... ......NGV. .......... ..........
Apos_PKA46439.1                                         .......... .......... ......NG.K VDD....... ..........
Apos_PKA58411.1                                         .......... .......... ......NG.K VDD....... ..........
Apos_PKA64143.1                                         .......... .......... ......KG.. .......... ..........
Dcat_XP_020704813.1                                     .......... .......... ......NGIA VME....... ..........
Pequ_XP_020589738.1                                     .......... .......... ......NGVA VME....... ..........
Dcat_XP_020702280.1                                     .......... .......... ......NGAK AME....... ..........
Apos_PKA59591.1                                         .......... .......... ......NG.. AME....... ..........
Apos_PKA60166.1                                         .......... .......... ......NG.. ELN....... ..........
Pequ_XP_020579635.1                                     .......... .......... ......NG.. .......... ..........
Spipo11G0025500                                         .......... .......... ......N..V KLE....... ..........
Spipo1G0003500                                          .......... .......... ......SG.. VLE....... ..........
GSMUA_Achr8P18960_001                                   .......... .......... ......NG.. .......... ..........
GSMUA_Achr11P22840_001                                  .......... .......... ......NG.. FAD....... ..........
GSMUA_Achr5P18560_001                                   .......... .......... ......NG.. .......... ..........
GSMUA_Achr2P00240_001                                   .......... .......... ......NS.. ETD....... ..........
GSMUA_Achr11P16360_001                                  .......... .......... ......AG.. .......... ..........
GSMUA_Achr5P03950_001                                   .......... .......... ......NG.. .......... ..........
p5.00_sc00071_p0096.1                                   .......... .......... ......NG.. AVK....... ..........
CALSI_Maker00040467                                     .......... .......... ......NG.. AVD....... ..........
Aco006987.1                                             .......... .......... .......... .......... ..........
Aco027752.1                                             .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                   .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                   .......... .......... ......NG.. .......... ..........
p5.00_sc00076_p0011.1                                   .......... .......... ......KS.. .......... ..........
Aco010091.1                                             .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                     .......... .......... ......N... .......... ..........
Aoff_XP_020259795.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                     .......... .......... ......N... .......... ..........
Aoff_XP_020248601.1                                     .......... .......... .......G.. .......... ..........
Aoff_XP_020272851.1                                     .......... .......... ......NG.. .......... ..........
Aoff_XP_020272852.1                                     .......... .......... ......NG.. .......... ..........
Acamev11004816m                                         .......... .......... .......... ..N....... ..........
Acamev11046066m                                         .......... .......... ......NGSV NQN....... ..........
Zosma445g00020.1                                        .......... .......... ......NG.. ETD....... ..........
Zosma69g00670.1                                         .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59             .......... .......... ......NGK. LD........ ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129            .......... .......... .......... .......... ..........
CALSI_Maker00043687                                     .......... .......... ......DGVN F......... ..........
CALSI_Maker00043684                                     .......... .......... ......DGIN P......... ..........
p5.00_sc01789_p0001.1                                   .......... .......... ......EGIN P......... ..........
p5.00_sc00066_p0001.1                                   .......... .......... ......IHSR P......... ..........
CALSI_Maker00043685                                     .......... .......... .......... PSE....... ..........
Aco020618.1                                             .......... .......... ......DGIN F......... ..........
GSMUA_Achr9P15990_001                                   .......... .......... ......DGIN P......... ..........
Zosma79g00480.1                                         .......... .......... .......... S......... ..........
Zosma115g00180.1                                        .......... .......... ........IR S......... ..........
Spipo15G0044700                                         .......... .......... ......DGIN P......... ..........
Acamev11008610m                                         .......... .......... ......AGKN P......... ..........
Acamev11024102m                                         .......... .......... ......AGDN F......... ..........
Acamev11050170m                                         .......... .......... ......GGKN P......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177            .......... .......... ......ESTS I......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178            .......... .......... ......STTS I......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181            .......... .......... ......STPE P......... ..........
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Figure 8(continued)

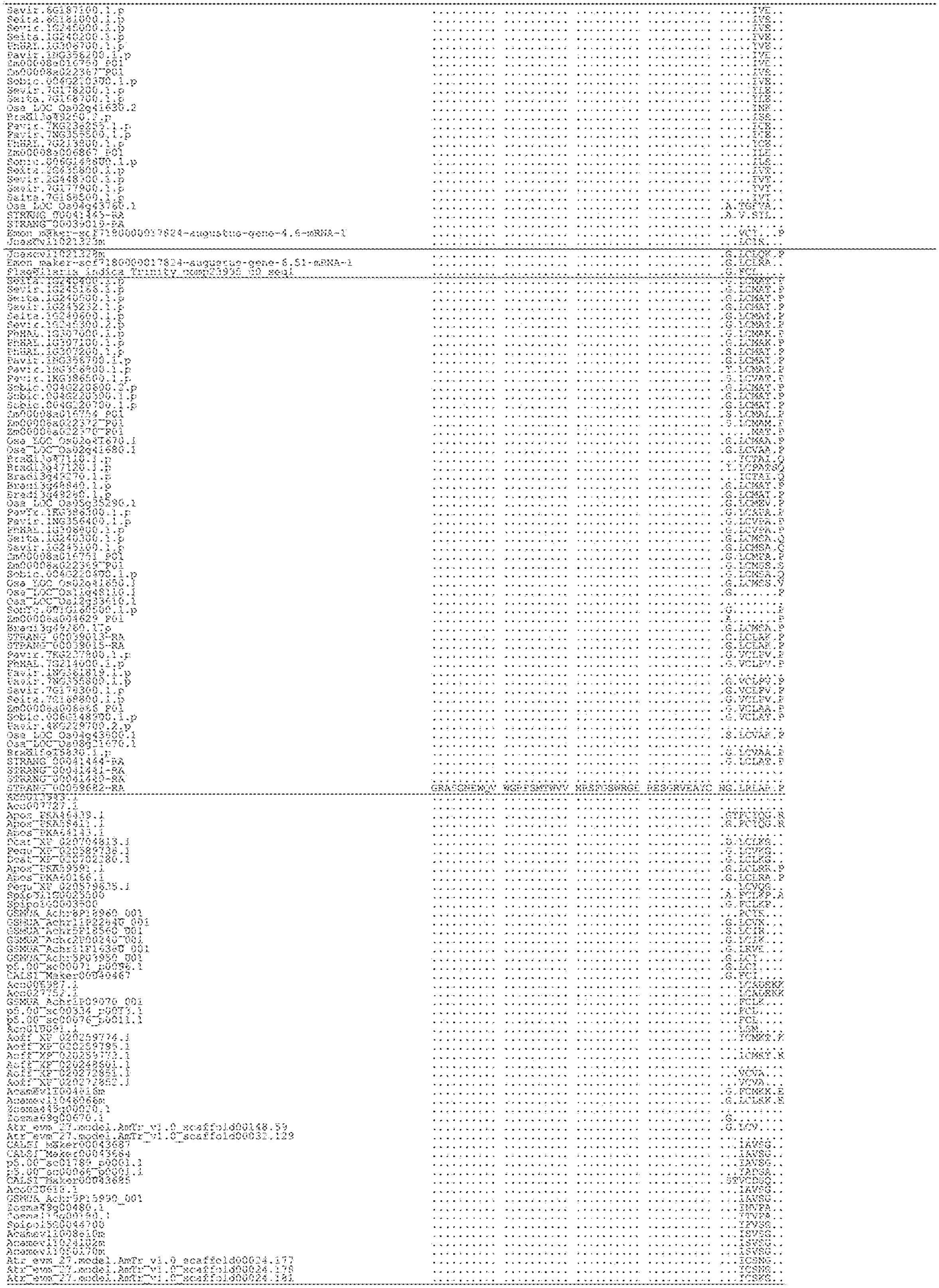

Figure 8(continued)

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Sevir.6G187100.1.p                                    .......... .........N DPLNWGAAAA EL..AGSHLD EVKRMVAQAR
Seita.6G181000.1.p                                    .......... .........N DPLNWGAAAA EL..AGSHLD EVKRMVAQAR
Sevir.1G245000.1.p                                    .......... .........N DPLNWGAAAA EL..AGSHLD EVKRMVAQAR
Seita.1G240200.1.p                                    .......... .........N DPLNWGAAAA EL..AGSHLD EVKRMVAQAR
PhHAL.1G306700.1.p                                    .......... .........N DPLNWGAAAA EL..AGSHLD EVKRMVAQAR
Pavir.1NG356200.1.p                                   .......... .........N DPLNWGAAAA EL..AGSHLD EVKRMVAQAR
Zm00008a016750_P01                                    .......... .........S DPLNWGAAAA EL..AGSHLD EVKRMVAQAR
Zm00008a022367_P01                                    .......... .........S DPLNWGAAAA EL..AGSHLD EVKRMVAQAR
Sobic.004G220300.1.p                                  .......... .........S DPLNWGAAAA EL..SGSHLD EVKRMVAQAR
Sevir.7G178200.1.p                                    .......... .........S DPLNWGKAAA EM..AGSHLD EVKRMVAQFR
Seita.7G168700.1.p                                    .......... .........S DPLNWGKAAA EM..AGSHLD EVKRMVAQFR
Osa_LOC_Os02g41630.2                                  .......... .........E DPLNWGAAAA EM..AGSHLD EVKRMVAQFR
Bradi3g49250.2.p                                      .......... .........K DPLNWGAAAA EL..TGSHLD EVKRMVAQFR
Pavir.7KG238255.1.p                                   .......... .........S DPLNWGKAAA EM..AGSHLD EVKRMVAQFR
Pavir.7NG355500.1.p                                   .......... .........S DPLNWGKAAA EM..AGSHLD EVKRMVAQFR
PhHAL.7G213800.1.p                                    .......... .........S DPLNWGKAAA EM..AGSHLD EVKRMVAQFR
Zm00008a006867_P01                                    .......... .........S DPLSWGKAAA EL..TGSHLD EVKRMVAQFR
Sobic.006G148800.1.p                                  .......... .........S DPLSWGKAAA EL..TGSHLD EVKRMVAQFR
Seita.2G435800.1.p                                    .......... .........S DPLNWGKAAA EL..TGSHLD EVKRMVAQSR
Sevir.2G448300.1.p                                    .......... .........S DPLNWGKAAA EL..TGSHLD EVKRMVAQSR
Sevir.7G177900.1.p                                    .......... .........S DPLNWGKAAA EL..TGSHLD EVKRMVAQSR
Seita.7G168500.1.p                                    .......... .........S DPLNWGKAAA EL..TGSHLD EVKRMVAQSR
Osa_LOC_Os04g43760.1                                  .......... .........S DPLSWGKAAL EM..TGSHLD EVKRMVAQSR
STRANG_00041445-RA                                    .......... .........R DPLNWGKAAE EL..TGSHFD EVKRMVAQFR
STRANG_00039019-RA                                    .......... .........R DPLNWAAAAA EL..TGSHLD EVKRMVAQFR
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1  .......... .........K DALNWAKAAE EL..AGSHLE EVKRMVAEFR
Joascv11021323m                                       .......... .........K DPLNWGKAAE EL..TGSHLD EVKRMVAESR
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Joascv11021328m                                       ......QH.. .........A DPLNWGKAAG EL..MGSHLE EVKRMVAEFR
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1 .......G.. .........G DPLNWGKAAE EM..AGSHLE EVKRMVAEFR
Flagellaria_indica_Trinity_comp23935_c0_seq1          .......... .........S DPLNWGKAAE EV..KGSHLE EVKRMVAEFR
-------------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVADYR
Sevir.1G245166.1.p                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVADYR
Seita.1G240500.1.p                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVADYR
Sevir.1G245232.1.p                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVADYR
Seita.1G240600.1.p                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVADYR
Sevir.1G245300.2.p                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVADYR
PhHAL.1G307000.1.p                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
PhHAL.1G307100.1.p                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
PhHAL.1G307200.1.p                                    ......R... .........G DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
Pavir.1NG356700.1.p                                   ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
Pavir.1NG356800.1.p                                   ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
Pavir.1KG386500.1.p                                   ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
Sobic.004G220600.2.p                                  ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
Sobic.004G220500.1.p                                  ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
Sobic.004G220700.1.p                                  ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
Zm00008a016754_P01                                    ......RA.. .........A DPLNWGKAAE EM..MGSHLD EVKRMVAEYR
Zm00008a022372_P01                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
Zm00008a022370_P01                                    ......R... .........A DPLNWGKAAE EL..MGSHLD EVKRMVAEYR
Osa_LOC_Os02g41670.1                                  ......R... .........A DPLNWGKAAE EM..SGSHLD EVKRMVAEYR
Osa_LOC_Os02g41680.1                                  ......R... .........A DPLNWGKATE EM..TGSHLD EVKRMVAEYR
Bradi3g47110.1.p                                      ......H... .........A DPLNWGKAAE AL..TGSHLE EVKRMVAEYR
Bradi3g47120.1.p                                      ......H... .........A DPLNWGKAAE AL..TGSHLE EVKRMVAEYR
Bradi3g49270.1.p                                      ......H... .........A DPLNWGKAAE EL..TGSHLD EVKRMVVEYR
Bradi3g48840.1.p                                      ......S... .........A DPLNWGKAAE EL..TGSHLD EVKRMVAEYR
Bradi3g49280.1.p                                      ......R... .........A DPLNWGKAAE EL..TGSHLD EVKRMVAEYR
Osa_LOC_Os05g35290.1                                  ......R... .........A DPLNWGKAAE EM..AGSHLD EVKRMVAEYR
PavTr.1KG386300.1.p                                   ...APRA... .........A DPLNWGKAAE DL..SGSHLG EVQRMVAEFR
Pavir.1NG356400.1.p                                   ...AAAR... .........A DPLNWGKAAE DL..SGSHLG EVQRMVAEFR
PhHAL.1G306800.1.p                                    ..AAAAR... .........A DPLNWGKAAE DL..SGSHLG EVQRMVAEFR
Seita.1G240300.1.p                                    ..AAAPR... .........A DPLNWGKAAE DL..SGSHLD EVKRMVAEFR
Sevir.1G245100.1.p                                    ..AAAPR... .........A DPLNWGKAAE DL..SGSHLD EVKRMVAEFR
Zm00008a016751_P01                                    ......R... .........A DPLNWGKAAE GL..SGSHLD EVKRMVAEFR
Zm00008a022369_P01                                    SAAAAPR... .........A DALNWGKAAE DL..SGSHLD EVKRMVVEFR
Sobic.004G220400.1.p                                  ..AAPRG... .........A DPLNWGKAAE DL..SGSHLE EVKRMVAEFR
Osa_LOC_Os02g41650.1                                  ..SAPPR... .........A DPLNWGKAAD EL..AGSHLD EVKRMVEDFR
Osa_LOC_Os11g48110.1                                  ......R... ........GS DPLYWGKAAE GV..AGSHLE EVKRMVVEYR
Osa_LOC_Os12g33610.1                                  .......... .........G DPLYWGKAAE GL..AGSHLD EVKRMVVEYR
SobTc.001G160500.1.p                                  ......HVVD .........D DPLNWGKAAE DL..TGSHLD DVRRMVEEYR
Zm00008a004629_P01                                    ......R..T .........G DPLKWGKAAE GL..TGSHLD EVKRMVEEYR
Bradi3g49260.1.p                                      .....PRA.. ........AA DPLNWAKTAE EL..AGSHLE EVKRMVAQFR
STRANG_00039013-RA                                    ......Q... .........A DPLNWGKAAE EL..TGSHLD EVKRMVAEYR
STRANG_00039015-RA                                    ......H... .........A DPLNWGAAAS EL..TGSHLD EVKRMVAHFR
Pavir.7KG227800.1.p                                   .....PR... .........A DPLNWGKAAE NL..AGSHLE AVKRMVEEYR
PhHAL.7G214000.1.p                                    .....PR... .........A DPLNWGKAAE DL..AGSHLE AVKRMVEEYR
Pavir.1NG361819.1.p                                   .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                   .....PR... .........A DPLNWGKAAE DL..AGSHLS AVKRMVSEYR
Sevir.7G178300.1.p                                    .....PR... .........A DPLNWGKAAE EL..SGSHLE AVKRMVEEYR
Seita.7G168800.1.p                                    .....PR... .........A DPLNWGKAAE DL..SGSHLE AVKRMVEEYR
Zm00008a006866_P01                                    ......R... .........A DPLNWVKAAE DL..AGSHLD AVKRMVEEYR
Sobic.006G148900.1.p                                  .....RA... .........A DPLNWGKAAE DL..TGSHLE AVKRMVEEYR
Pavir.4KG229700.2.p                                   .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                  ......R... .........A DPLNWGKAAE EL..SGSHLD AVKRMVEEYR
Osa_LOC_Os08g21670.1                                  .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                      ...LAPR... .........A DPLNWGKAAE EL..SGSHLD AVKRMVEEYR
STRANG_00041444-RA                                    ......Q... .........A DPLNWGKAAA EL..TGSHLD EVKRMVAEYR
STRANG_00041441-RA                                    .......... .......... .......... .......... ..........
STRANG_00041440-RA                                    .......... .......... ..LNWGKAAE EL..TGSHLD EVKHLVAQYR
STRANG_00059682-RA                                    ......Y... .........A DPLNWGTAAV EL..TGSHLE EVKRMVAESR
-------------------------------------------------------------------------------------------------------------
Aco017943.1                                           .......... .......... ..NGGGSKPR AA..KGRQAD GTA.......
Aco007727.1                                           .......... ....V....T DPLGWAAAAA AAAESGSHLE EVKRMVEEFR
Apos_PKA46439.1                                       .......... .........R DPLGWRAAAE AV..SKSHLD EVKRMVEEFL
Apos_PKA58411.1                                       .......... .........R DPLGWRAAAE AV..SKSHLD EVKRMVEEFL
Apos_PKA54143.1                                       .......... .W.......P DALGWVAAAA AM..ERSHLS EVKRMVDEFR
Dcat_XP_020704813.1                                   .......... .........S DPLGWVAAAK AA..EGSHLD EVKRMVEDFR
Pequ_XP_020589738.1                                   .......... .........R DPLGWAAAAK AA..EGSHLD EVKRMVEEFR
Dcat_XP_020702280.1                                   .......... .........R DQLGWAAAAK AL..EGSHLD EVKRMVKEFR
Apos_PKA59591.1                                       .......... .......... DPLNWGAAAE AL..SGSHLD EVKRMVEEFR
Apos_PKA60166.1                                       .......... .........A DPLNWGSAAA AM..EGSHLD EVKRMVEEFR
Pequ_XP_020579635.1                                   .......... .........H DPLNWGAAAA EL..QGSHLD EVKRMVEEFR
Spipo31G0025500                                       ......A.AA AAPAVAPVSG DPLNWGAAAD SL..SGSHLD EVKRMVEDFR
Spipo1G0003500                                        ......TIAA .........G DPLNWGAAAE SL..SGSHLE EVKRMVEEFR
GSMUA_Achr8P18960_001                                 .......... .........A DPLNWGAAAE AM..TGSHLD DVKRMVEEFR
GSMUA_Achr11P22840_001                                .......... .........A DPLNWGAAAE AL..TGSHLD EVKRMVEEFR
GSMUA_Achr5P18560_001                                 .......... .........T DPLNWGAAAE AV..TGSHLE EVKRMVGEFR
GSMUA_Achr2P00240_001                                 .......... .........A DAINWATAAE AL..SGNHLD EVRRMVEESR
GSMUA_Achr11P16380_001                                .......... .........T DPLNWAAAAE AL..AGSHLD EVRRMTWEFR
GSMUA_Achr5P03950_001                                 .......... .........K DPLNWAAAAE AL..TGSHLD EVKKMVAESR
p5.00_sc00071_p0096.1                                 .......... .........K DPLNWVAAAE AL..TGSHFD EVKRMVEEFR
CALSI_Maker00040467                                   .......... .........K DPLNWIAAAE SL..TGSHLD EVKRMVELFR
Aco006987.1                                           ......Q... .........R DPLNWGRAAE AM..SGSHLE EVKRMVEEFR
Aco027752.1                                           ......Q... .........R DPLNWGRAAE AM..SGSHLE EVKRMVEEFR
GSMUA_Achr1P09070_001                                 .......... .........A DPLNWIKAAE SL..TGSHLD EVKRMVEEFR
p5.00_sc00334_p0073.1                                 .......... .........P DPLKWAKAAE EL..SGSHLD EVKLMVEEYR
p5.00_sc00076_p0011.1                                 .......... .........P DPLHWAKAAE AL..TGSHLD EVKHMVEEYR
Aco010091.1                                           .......... .........E DPLNWAGAAE PT..KVSHFD EVKRMVEEFR
Aoff_XP_020259774.1                                   ......Q... .........A DPLNWGAAAE AL..TGSHLD EVKRMVEDFR
Aoff_XP_020259795.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                   ......Q... .........A DPLNWGAAAE AL..TGSHLD EVKRMVEDFR
Aoff_XP_020248601.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                   .......... .........A DPLNWGAAAQ SL..SGSHLD EVKKMVKDYR
Aoff_XP_020272852.1                                   .......... .........A DPLNWGAAAQ SL..SGSHLD EVKKMVKDYR
Acamev1I004816m                                       ......E.EV .........V DPLNWAKSAE FL..MGSHLE EVKRMVEEFR
Acamev1I046066m                                       ......A.AS .........T DPLNWAKSTE FL..MGSHLE EVKRMVEEFR
Zosma445g00020.1                                      .......... .........A DPLNWGAAAE EL..TGSHLQ EVKRMVEDFN
Zosma69g00670.1                                       .......... .........A DPLKWEEAAE GM..KGSHVA EVKQMIEDFR
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59           .......... .........S DPLNWTAMAE TF..KGSHLE EVKKMVSEFQ
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129          .......... .........T DPLNWGSFA. ....EGSHLS LVKKLVDEFR
CALSI_Maker00043687                                   .........T S..YV....P HPPHWKKAAE AL..DCAHFN EVHRMISQFS
CALSI_Maker00043684                                   .........T S..YV....P HPPHWSKAAE AL..DCAHFD EVHRMISQFS
p5.00_sc01789_p0001.1                                 .........T S..YV....P NPPHWKKAAE AL..DCAHFD EVHRMISQFS
p5.00_sc00066_p0001.1                                 .........S A..YI....S DPYHWKKAAE TL..SSAYFD EVRRMITQFS
CALSI_Maker00043685                                   .........A T..FI....S DPDPWKKAAE TL..SSTYFD EASRMITQFS
Aco020618.1                                           .........T S..YV....P DPPHWAAAAD AL..PCTHFD DVHRMVAQFS
GSMUA_Achr9P15990_001                                 .........T S..YV....P DPPHWSKAAE AL..SCAHFD EVHRMITQFS
Zosma79g00480.1                                       .........T QTPEA....S KTSHWTKASE AI..QSNHFD EVPRMISQFS
Zosma115g00190.1                                      .........V S..PM....A PAQHWKQASE AI..QSNHFD EVRQMITQFS
Spipo15G0044700                                       .........D S..YI....P DPPHWKSAAE AL..QCTHSE EVRRMISQFQ
Acamev1I008610m                                       .........N S..YV....S NPPHNQKASE AL..LCTHFD EVRKMVDQYR
Acamev1I024102m                                       .........N S..YV....S NPPHWKKASE AL..LCTHFD EVRKMVDQYR
Acamev1I050170m                                       .........N S..YV....S NPPHWKKAAE AL..LCTHFD EVRKMVRQYR
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177          ........FH S..TV....T PPPHWKKASE AL..EISHFQ EVSKMISQFN
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178          ........LH S..NV....T PPPHWKSASE AL..KTSHSH EVSKMISQFN
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181          ........LH S..TV....T PPPHWKKASE AF..KTSHSE EVPKMISQFN
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Figure 8(continued)

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Sevir.6G187100.1.p                                      Q.PVVKIEG. STLRV▒QVAA VAAAKD.... .......AS. ..........
Seita.6G181000.1.p                                      Q.PVVKIEG. STLRV▒QVAA VAAAKD.... .......AS. ..........
Sevir.1G245000.1.p                                      Q.PVVKIEG. STLRV▒QVAA VASARD.... .......AS. ..........
Seita.1G240200.1.p                                      Q.PVVKIEG. STLRV▒QVAA VASARD.... .......AS. ..........
PhHAL.1G306700.1.p                                      Q.PVVKIEG. STLRV▒QVAA VAAARD.... .......AS. ..........
Pavir.1NG356200.1.p                                     Q.PVVKIEG. STLRV▒QVAA VAAARD.... .......AS. ..........
Zm00008a016750_P01                                      Q.PVVKIEG. STLRV▒QVAA VASARD.... .......AS. ..........
Zm00008a022367_P01                                      Q.PVVKIEG. STLRV▒QVAA VASAKD.... ........A. ..........
Sobic.004G220300.1.p                                    Q.PVVKIEG. STLRV▒QVAA VASAKD.... .......AS. ..........
Sevir.7G178200.1.p                                      E.PLVKIEG. SSLPV▒QVAA VAAAKD.... .......AS. ..........
Seita.7G168700.1.p                                      E.PLVKIEG. SSLPV▒QVAA VAAAKD.... .......AS. ..........
Osa_LOC_Os02g41630.2                                    E.PLVKIQG. ATLRV▒QVAA VAQAKD.... .......AA. ..........
Bradi3g49250.2.p                                        E.PVVKIEG. ASLRV▒QVAA VAQAKD.... .......AA. ..........
Pavir.7KG238255.1.p                                     E.PLVKIEG. SSLRV▒QVAA VAVAKD.... .......AS. ..........
Pavir.7NG355500.1.p                                     E.PLVKIEG. SSLRV▒QVAA VAAAKD.... .......AS. ..........
PhHAL.7G213900.1.p                                      E.PLVKIEG. SSLPV▒QVAA VAAAKD.... .......AS. ..........
Zm00008a006867_P01                                      D.PVVKIEG. SSLRV▒QVAA VAAAKD.... .......AS. ..........
Sobic.006G148800.1.p                                    D.PVVKIEG. STLRV▒QVAA VAAAKD.... .......AS. ..........
Seita.2G435800.1.p                                      E.PIVRVDG. SRLHV▒KVAA VAAAKD.... .......AS. ..........
Sevir.2G448300.1.p                                      E.PIVRVDG. SRLHV▒KVAA VAAAKD.... .......AS. ..........
Sevir.7G177900.1.p                                      E.PVVRVDG. SRLHV▒QVAA VAAAKD.... .......AS. ..........
Seita.7G168500.1.p                                      E.PVVRVDG. SRLHV▒QVAA VAAAKD.... .......AS. ..........
Osa_LOC_Os04g43760.1                                    E.AVVKIEG. SSLRV▒QVAA VSAAKD.... .......AS. ..........
STRANG_00041445-RA                                      E.PAVTIEG. ASLRV▒QVAS VAAARD.... .......GA. ..........
STRANG_00039019-RA                                      E.PQVKIEG. ASLKV▒QVAA VAAARD.... .......AA. ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1    S.PAVKIEG. ASLPV▒QVAA VAG.AE.... .......AA. ..........
Joascv11021323m                                         T.PVVKIQG. ASLRI▒QVAA VAV.PE.... ........T. ..........
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Joascv11021328m                                         A.PVVKIEG. ASLRI▒QVAA VAA.GE.... ........A. ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1   A.PAVKIEG. ASLRI▒QVAA VAA.EG.... ........A. ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1            A.PVVPLEG. ASLKI▒QVAA VAEGKK.... ......AAA. ..........
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Seita.1G240400.1.p                                      Q.PLVKIEG. ASLNI▒QVAA VAN.G..... ........A. ..........
Sevir.1G245166.1.p                                      Q.PLVKIEG. ASLNI▒QVAA VAN.G..... ........A. ..........
Seita.1G240500.1.p                                      Q.PLVKIEG. ASLNI▒QVAA VAN.G..... ........A. ..........
Sevir.1G245232.1.p                                      Q.PLVKIEG. ASLNI▒QVAA VAN.G..... ........A. ..........
Seita.1G240600.1.p                                      Q.PLVKIEG. ASLNI▒QVAA VAN.G..... ........A. ..........
Sevir.1G245300.2.p                                      Q.PLVKIEG. ASLNI▒QVAA VAN.G..... ........A. ..........
PhHAL.1G307000.1.p                                      Q.PLVKIEG. ASLRI▒QVAA VAN.G..... ........A. ..........
PhHAL.1G307100.1.p                                      Q.PLVKIEG. ASLPI▒QVAA VAN.G..... ........A. ..........
PhHAL.1G307200.1.p                                      Q.PLVKIEG. ASLRI▒QVAA VAN.G..... ........A. ..........
Pavir.1NG356700.1.p                                     Q.PLVKIEG. ASLRI▒QVAA VAN.G..... ........A. ..........
Pavir.1NG356800.1.p                                     Q.PLVKIEG. ASLRI▒QVAA VAN.G..... ........A. ..........
Pavir.1KG386500.1.p                                     Q.PLVKIEG. ASLRI▒QVAA VAN.G..... ........A. ..........
Sobic.004G220600.2.p                                    Q.PLVKIEG. ASLPI▒QVAA VAA.G..... ........A. ..........
Sobic.004G220500.1.p                                    Q.PLVKIEG. ASLRI▒QVAA VAA.G..... ........A. ..........
Sobic.004G220700.1.p                                    Q.PLVKIEG. ASLRI▒QVAA VAA.G..... ........A. ..........
Zm00008a016754_P01                                      Q.PLVKIEG. ASLRI▒QVAA VAA.G..... ........A. ..........
Zm00008a022372_P01                                      Q.PLVKIEG. ASLSI▒QVAA VAT.G..... ........A. ..........
Zm00008a022370_P01                                      Q.PLVKIEG. ASLSI▒QVAA VAA.G..... ........A. ..........
Osa_LOC_Os02g41670.1                                    Q.PLVKIEG. ASLPI▒QVAA VAA....... ........A. ..........
Osa_LOC_Os02g41680.1                                    Q.PLVKIEG. ASLRI▒QVAA VAA....... ........A. ..........
Bradi3g47110.1.p                                        Q.PVVTIEG. ASLSI▒KVAA VAA....... ........A. ..........
Bradi3g47120.1.p                                        Q.PVVTIEG. ASLSI▒KVAA VAA....... ........A. ..........
Bradi3g49270.1.p                                        E.PVVTIEG. ASLSI▒KVAA VAA....... ........A. ..........
Bradi3g48840.1.p                                        K.PVVTIEG. ATLSI▒KVAA VAA....... ........A. ..........
Bradi3g49280.1.p                                        K.PVVTIEG. ATLSI▒KVAA VAA....... ........A. ..........
Osa_LOC_Os05g35290.1                                    Q.PVVRIEG. ASLRI▒QVAA VAG....... ........A. ..........
PavTr.1KG386300.1.p                                     E.PLVRIQG. ASLSI▒QVAA VAA.G..... ........T. ..........
Pavir.1NG356400.1.p                                     E.PLVRIQG. ASLSI▒QVAA VAA.G..... ........A. ..........
PhHAL.1G306800.1.p                                      E.PLVKIQG. ASLSI▒QVAA VAA.G..... ........A. ..........
Seita.1G240300.1.p                                      E.PLVKIQG. ASLSI▒QVAA VAA.G..... ........A. ..........
Sevir.1G245100.1.p                                      E.PLVKIQG. ASLSI▒QVAA VAA.G..... ........A. ..........
Zm00008a016751_P01                                      E.PLVKIQG. ASLSV▒QVAA VAV.G..... ........AG G.........
Zm00008a022369_P01                                      E.PLVRIQG. ASLSI▒QVAA VAA.G..... ........AG ..........
Sobic.004G220400.1.p                                    D.PVVKIQG. ASLSI▒QVAA VAA.G..... ........A. ..........
Osa_LOC_Os02g41650.1                                    Q.PLVKIEG. ASLTI▒QVAA VAA.G..... ........A. ..........
Osa_LOC_Os11g48110.1                                    A.PLVKIDG. AMLSV▒KVAA VA..GE.... ........A. ..........
Osa_LOC_Os12g33610.1                                    A.PLVKIDG. AMLSV▒KVAA VA..GE.... ........A. ..........
SobTc.001G160500.1.p                                    M.PLVKIDG. AMLSV▒KVAA VA..GE.... ........AT ..........
Zm00008a004629_P01                                      V.PLVKIDG. AVLSV▒KVAA VA..G..... .......... ..........
Bradi3g49260.1.p                                        N.PLVKIEG. ATLGI▒QVAA VAA....... .......GA. ..........
STRANG_00039013-RA                                      E.PVVRIEG. AGLRI▒QVAA VAAAAD.... .......GG. ..........
STRANG_00039015-RA                                      E.PVVNIEG. AGLRI▒QVAA VAAAAD.... .......GV. ..........
Pavir.7KG237800.1.p                                     R.PLVRIEG. ASLTV▒QVAA VA........ .......AA. ..........
PhHAL.7G214000.1.p                                      R.PLVKIEG. ASLTV▒QVAA VA........ .......AA. ..........
Pavir.1NG361819.1.p                                     .......... .....▒.... .......... .......... ..........
Pavir.7NG355800.1.p                                     R.PLVKIEG. ASLTV▒QVAA VA........ .......AA. ..........
Sevir.7G178300.1.p                                      R.PLVRIEG. SSLTV▒QVAA VAN.G..... ........A. ..........
Seita.7G168800.1.p                                      R.PLVRIEG. SSLTV▒QVAA VAN.G..... ........A. ..........
Zm00008a006866_P01                                      R.PLVKIEG. ASLTV▒QVAA VA........ .......AA. ..........
Sobic.006G148900.1.p                                    R.PLVKIEG. ASLTV▒QVAA VA........ .......AA. ..........
Pavir.4KG229700.2.p                                     .......... .....▒.... .......... .......... ..........
Osa_LOC_Os04g43800.1                                    R.PVVTIEG. ASLTI▒QVAA VA........ .......SA. ..........
Osa_LOC_Os08g21670.1                                    .......... .....▒.... .......... .......... ..........
Bradi5g15830.1.p                                        R.PVVKMEG. ASLTI▒QVAA VA........ .......AG. ..........
STRANG_00041444-RA                                      K.PVVRIEG. ANLSI▒QVVA VALAGG.... .......AA. ..........
STRANG_00041441-RA                                      .......... .....▒.... .......... .......... ..........
STRANG_00041440-RA                                      K.PMVRIKG. TSLSI▒QVKA VAS....... ......AGGD A.........
STRANG_00059682-RA                                      L.PVVTIEG. AGLRI▒HVAA VATACG.... ......GGA. ..........
---------------------------------------------------------------------------------------------------------------
Aco013943.1                                             .......... .....▒.VAA VA..G..... ........A. ..........
Aco007727.1                                             A.PAVTLKG. VELKI▒QVAA VAMAKAVAPG VRVELAEAAR GGVEASSEWV
Apos_PKA46439.1                                         R.PSVKLEG. TALTI▒QVAA VAA.G..... ........A. ..........
Apos_PKA58411.1                                         R.PSVKLEG. TALTI▒QVAA VAA.G..... ........A. ..........
Apos_PKA54143.1                                         Q.PTVKLVG. AELKI▒QVAA VAS.G..... ........TM ..........
Dcat_XP_020704813.1                                     R.PVVMLEG. AELKI▒QVAA VAS.G..... ........A. ..........
Pequ_XP_020589738.1                                     Q.PLVLLEG. AELSI▒QVAA VAS.G..... ........A. ..........
Dcat_XP_020702280.1                                     S.PVVRLEG. AELKI▒QVAA VAA.G..... ........A. ..........
Apos_PKA59591.1                                         R.PEVKLEG. ADLKI▒QVAA VAA.G..... ........D. ..........
Apos_PKA60166.1                                         R.PAVRLEG. AALKI▒QVAA VAA.G..... ........S. ..........
Pequ_XP_020579635.1                                     R.PVVQLEG. E..XI▒QAAA VAI.G..... ........G. ..........
Spipo31G0025500                                         R.PLVRLEG. ADLKI▒QVAA VAS.G..... ........R. ..........
Spipo1G0003500                                          Q.PLVQLEG. ADLKI▒QVAA VAAAG..... ........G. ..........
GSMUA_Achr8P18960_001                                   Q.PLVKLEG. ATLKI▒QVAA VAM....... .......AAR ..........
GSMUA_Achr11P22840_001                                  R.PLVRLEG. ATLKI▒QVAA VAM....... .......APH ..........
GSMUA_Achr5P18560_001                                   Q.PLVRLEG. ATLKI▒QVAA VAT....... .......EPH ..........
GSMUA_Achr2P00240_001                                   R.PLVRLEG. ATLTI▒QVAA VAT....... .......A.. ..........
GSMUA_Achr11P16360_001                                  Q.PLVKLEG. STLKI▒QVAA IAA....... .......GAH ..........
GSMUA_Achr5P03950_001                                   Q.PLVSLEG. TTLKI▒RVAA VAG....... .......... ..........
p5.00_sc00071_p0096.1                                   Q.PMVRLEG. ASLKI▒QVAA VAM....... .......AE. ..........
CALSI_Maker00040467                                     Q.PSVKLEG. ATLKI▒QVAA VAV....... .......AE. ..........
Aco006987.1                                             R.PLVRLEG. ADLKI▒QVAA VAM....... .......GDF AQAQA.....
Aco027752.1                                             R.PLVRLEG. ADLKI▒QVAA VAM....... .......GDF AQAQA.....
GSMUA_Achr1P09070_001                                   K.PQVRLEG. ATLTI▒QVAA VAA....... .......AR. ..........
p5.00_sc00334_p0073.1                                   K.PLVRLEG. ATLPI▒QVAA VAT....... .......SK. ..........
p5.00_sc00076_p0011.1                                   K.PLVRLEG. ATLKI▒QVAA VAT....... .......SE. ..........
Aco010091.1                                             K.PLVRLAG. ANLTI▒QVAA VAA....... .......SE. ..........
Aoff_XP_020259774.1                                     N.PVVKLEG. ADLKI▒QVAA VAM....... .......GE. ..........
Aoff_XP_020259795.1                                     .......... .....▒.... .......... .......... ..........
Aoff_XP_020259773.1                                     N.PVVKLEG. ADLKI▒QVAA VAM....... .......GE. ..........
Aoff_XP_020248601.1                                     .......EG. .....▒.... .......... .......... ..........
Aoff_XP_020272851.1                                     E.GPVRIEG. ATLKV▒HVAA VAA....... .......GE. ..........
Aoff_XP_020272852.1                                     E.GPVRIEG. ATLKV▒HVAA VAA....... .......GE. ..........
AcamEv1I004816m                                         N.PLVCLEG. ADLKI▒QVAA VAA....... .......EG. ..........
Acamev1I046066m                                         N.PLVSLEG. ADLKI▒QVAA VAA....... .......GG. ..........
Zosma445g00020.1                                        N.PLVKIEG. ATLKI▒QVAA VAT....... .......... ..........
Zosma69g00670.1                                         N.PLVVLEG. KNLKI▒HVAA VAG....... ......DSS. ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59             K.PLVKLEG. HSLSI▒KVAA VAR....... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129            C.RTISLSG. TDLSI▒HVAA VSS....... .......GA. ..........
CALSI_Maker00043687                                     SVSSVKIEG. TTLTI▒DVAA VAR....... ......RAA. ..........
CALSI_Maker00043684                                     SVSSVKIEG. TALTV▒DVAA VAR....... ......CAA. ..........
p5.00_sc01789_p0001.1                                   SLSSVNIEG. TTLTV▒AVAA IAR....... ......RAA. ..........
p5.00_sc00066_p0001.1                                   ELTSICLQGT TSLTV▒QVAA ITR....... ......RSS. ..........
CALSI_Maker00043685                                     ELTSICLQG. TTLTV▒QVAA ITS....... ......RES. ..........
Aco020618.1                                             SVASVDLEG. TALTV▒QVAA VAR....... ......RPA. ..........
GSMUA_Achr9P15990_001                                   TLSSVDLEG. TTLTV▒QVAA VSR....... ......RLT. ..........
Zosma79g00480.1                                         NSESVNIEG. ASLTV▒QVSA IAR....... ......NSS. ..........
Zosma115g00180.1                                        QSQSVNIEG. TSLTV▒QVAA TTR....... ......RAD. ..........
Spipo15G0044700                                         STQTVDLQG. TTLTV▒QVAA VSR....... ......RQE. ..........
Acamev1I008610m                                         NSESVDLTG. TSLTV▒QVAA ITR....... ......RDE. ..........
Acamev1I024102m                                         NSPDVSLTG. TSLTV▒QVAA VTR....... ......RPT. ..........
Acamev1I050170m                                         NSSSVDLTG. TDLTV▒QVAA IAR....... ......RPK. ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177            QAQTVTLQG. TSFTV▒QVTA ITR....... ......RAH. ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178            QAHTVTLQG. TSLTV▒QVTA TTR....... ......RAN. ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181            QAQTVTLQG. TSLTV▒QVTA TTR....... ......QTG. ..........
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Figure 8(continued)

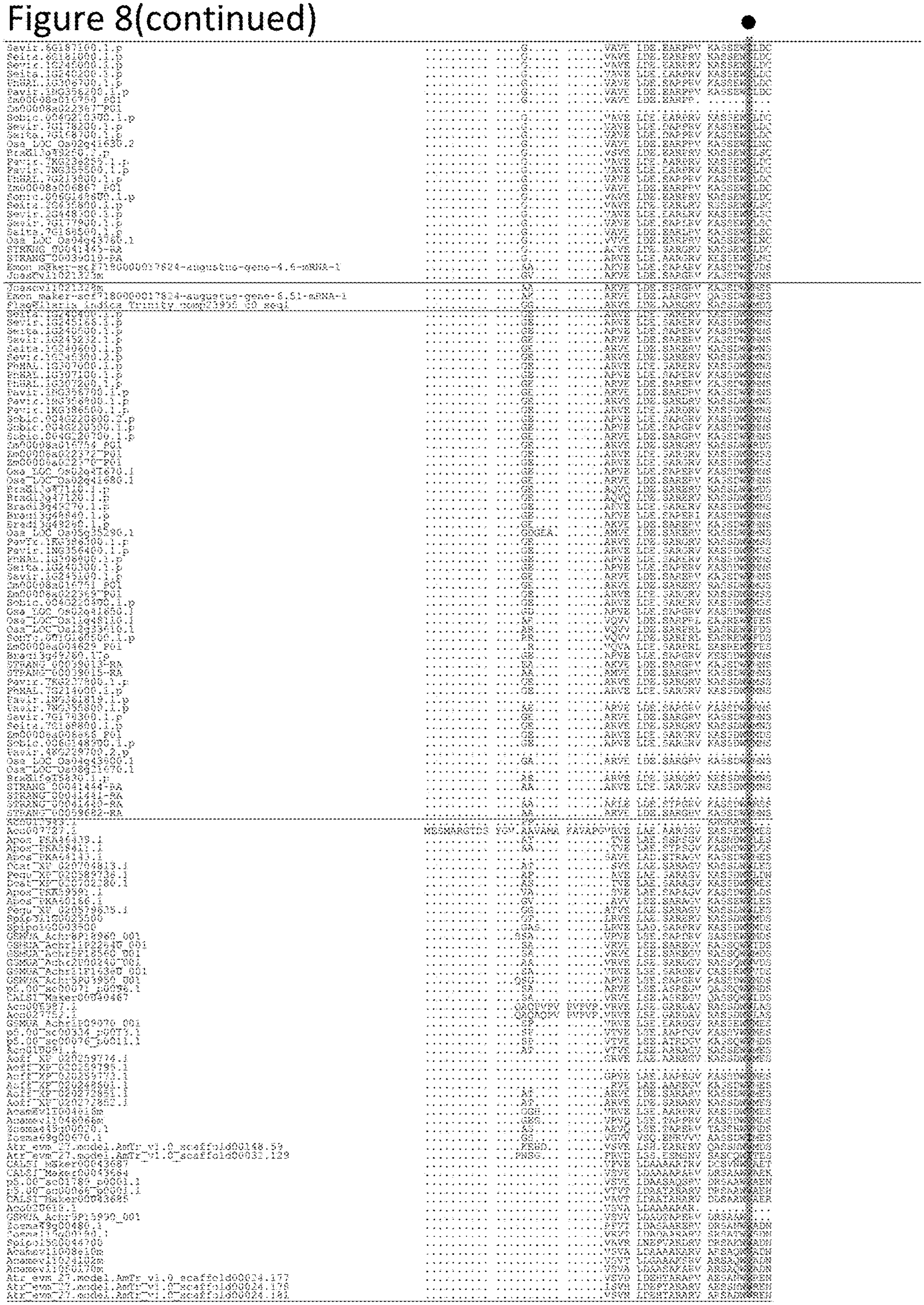

Figure 8(continued)

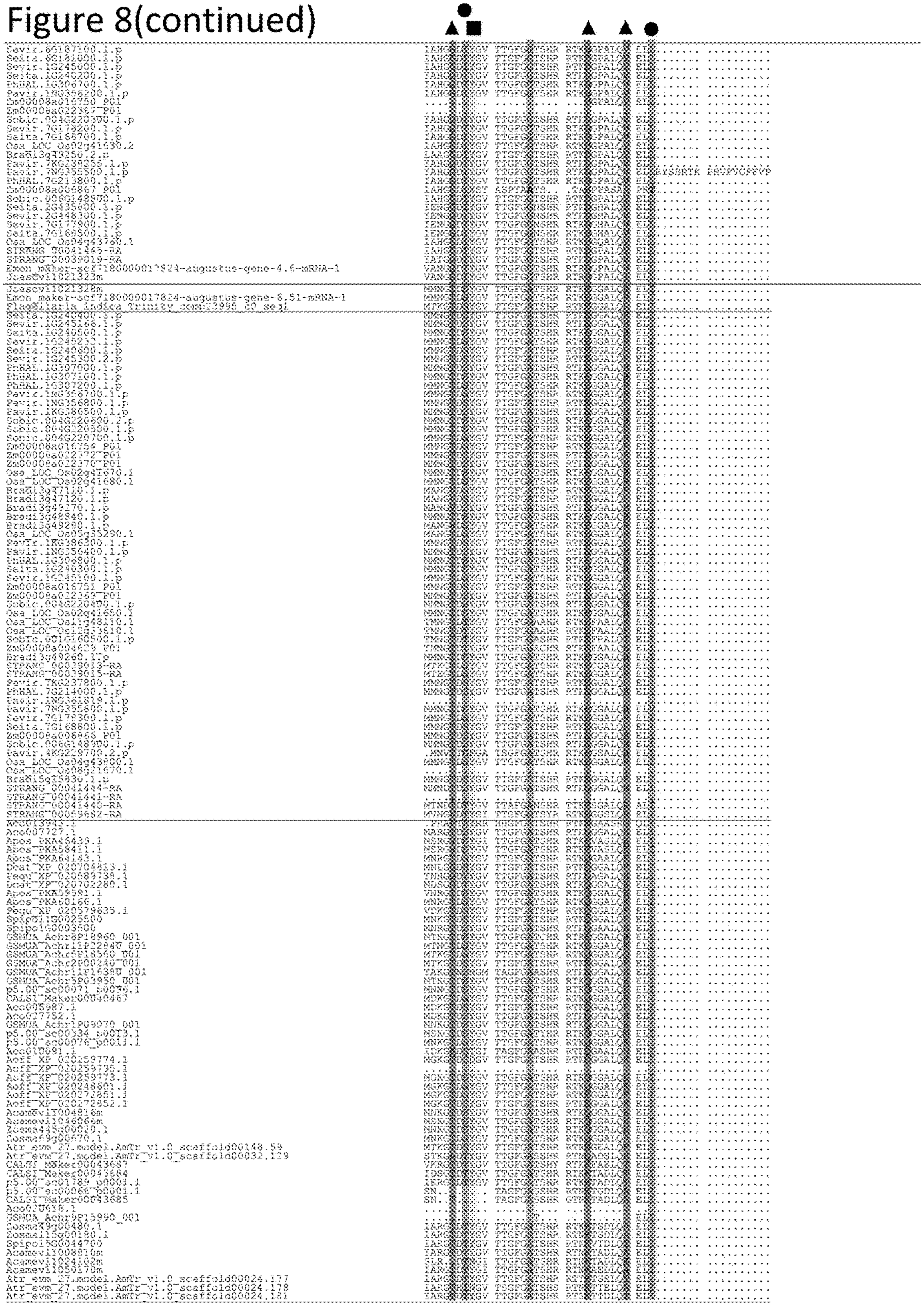

Figure 8(continued)

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Sevir.6G187100.1.p                                       .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                       .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                       .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                       .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                      .......... .......... .......... .......... ..........
Zm00008a016750_P01                                       .......... .......... .......... .......... ..........
Zm00008a022367_P01                                       .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                     .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                       .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                       .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                     .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                         .......... .......... .......... .......... ..........
Pavir.7KG232253.1.p                                      .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                      VQYAAPSDHV PAHWQRPVGG CKLQLVSTRL MSVSGSSLTT GARYVLFSRT
PhHAL.7G213800.1.p                                       .......... .......... .......... .......... ..........
Zm00008a006867_P01                                       ...AAPR... .......... .......... .........T GPRS......
Sobic.006G148800.1.p                                     .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                       .......... .......... .......... .......... ..........
Sevir.2G448700.1.p                                       .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                       .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                       .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                     .......... .......... .......... .......... ..........
STRANG_00041445-RA                                       .......... .......... .......... .......... ..........
STRANG_00039019-RA                                       .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1     .......... .......... .......... .......... ..........
Joascv1i021323m                                          .......... .......... .......... .......... ..........
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Joascv1i021328m                                          .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1    .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1             .......... .......... .......... .......... ..........
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Seita.1G240400.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                       .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                       .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                       .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                       .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                       .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                       .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG356900.1.p                                      .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                      .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                     .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                     .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                     .......... .......... .......... .......... ..........
Zm00008a016754_P01                                       .......... .......... .......... .......... ..........
Zm00008a022372_P01                                       .......... .......... .......... .......... ..........
Zm00008a022370_P01                                       .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                     .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                         .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                         .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                         .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                         .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                         .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                     .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                      .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                       .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                       .......... .......... .......... .......... ..........
Zm00008a016751_P01                                       .......... .......... .......... .......... ..........
Zm00008a022369_P01                                       .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                     .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                     .......... .......... .......... .......... ..........
Osa_LOC_Os12g33610.1                                     .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                     .......... .......... .......... .......... ..........
Zm00008a004629_P01                                       .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                         .......... .......... .......... .......... ..........
STRANG_00039013-RA                                       .......... .......... .......... .......... ..........
STRANG_00039015-RA                                       .......... .......... .......... .......... ..........
Pavir.7KG237800.1.p                                      .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                       .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                      .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                      .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                       .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                       .......... .......... .......... .......... ..........
Zm00008a006866_P01                                       .......... .......... .......... .......... ..........
Sobic.006G148900.1.p                                     .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                      .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                     .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                     .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                         .......... .......... .......... .......... ..........
STRANG_00041444-RA                                       .......... .......... .......... .......... ..........
STRANG_00041441-RA                                       .......... .......... .......... .......... ..........
STRANG_00041440-RA                                       .......... .......... .......... .......... ..........
STRANG_00059682-RA                                       .......... .......... .......... .......... ..........
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Aco013943.1                                              .......... .......... .......... .......... ..........
Aco007727.1                                              .......... .......... .......... .......... ..........
Apos_PKA46439.1                                          .......... .......... .......... .......... ..........
Apos_PKA58411.1                                          .......... .......... .......... .......... ..........
Apos_PKA54143.1                                          .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                      .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                      .......... .......... .......... .......... ..........
Dcat_XP_020702180.1                                      .......... .......... .......... .......... ..........
Apos_PKA59591.1                                          .......... .......... .......... .......... ..........
Apos_PKA60166.1                                          .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                      .......... .......... .......... .......... ..........
Spipo11G0025500                                          .......... .......... .......... .......... ..........
Spipo1G0003500                                           .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                    .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                    .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                    .......... .......... .......... .......... ..........
GSMUA_Achr11P16360_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                    .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                    .......... .......... .......... .......... ..........
CALSI_Maker00040467                                      .......... .......... .......... .......... ..........
Aco006987.1                                              .......... .......... .......... .......... ..........
Aco027752.1                                              .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                    .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                    .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                    .......... .......... .......... .......... ..........
Aco010091.1                                              .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                      .......... .......... .......... .......... ..........
Acamev1i004816m                                          .......... .......... .......... .......... ..........
Acamev1i046066m                                          .......... .......... .......... .......... ..........
Zosma445g00020.1                                         .......... .......... .......... .......... ..........
Zosma69g00670.1                                          .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59              .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129             .......... .......... .......... .......... ..........
CALSI_Maker00043687                                      .......... .......... .......... .......... ..........
CALSI_Maker00043684                                      .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                    .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                    .......... .......... .......... .......... ..........
CALSI_Maker00043685                                      .......... .......... .......... .......... ..........
Aco020618.1                                              .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                    .......... .......... .......... .......... ..........
Zosma79g00480.1                                          .......... .......... .......... .......... ..........
Zosma115g00180.1                                         .......... .......... .......... .......... ..........
Spipo15G0044700                                          .......... .......... .......... .......... ..........
Acamev1i008610m                                          .......... .......... .......... .......... ..........
Acamev1i024102m                                          .......... .......... .......... .......... ..........
Acamev1i050170m                                          .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177             .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178             .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181             .......... .......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                        .RELNAGIFG AGS.D.GH.T LPSEVTRAAM LVRINTLLQG YSGIRFEILE
Seita.6G181000.1.p                                        .KELNAGIFG AGS.D.GH.T LPSEVTRAAM LVRINTLLQG YSGIRFEILE
Sevir.1G245000.1.p                                        .KELNAGIFG TGS.D.GH.T LPSEVTRAAM LVRINTLLQG YSGIRFEILE
Seita.1G240200.1.p                                        .RELNAGIFG TGS.D.GH.T LPSEVTRAAM LVRINTLLQG YSGIRFEILE
PhHAL.1G306700.1.p                                        .PELNAGIFG TGR.D.GH.T LPSEVVRAAM LVRINTLLQG YSGIRFEILE
Pavir.1NG356200.1.p                                       .RELNAGIFS NDR.D.GH.T LPSETVRAAM LVRINTLLQG YSGIRFEILE
Zm00008a016750_P01                                        .KELNAGIFG TGS.D.GH.T LPSEVTRAAM LVRINTLLQG YSGIRFEILE
Zm00008a022367_P01                                        ..ELNAGIFG TGS.D.GH.T LPSEVTRAAM LVRINTLLQG YSGIRFEILE
Sobic.004G220300.1.p                                      .RELNAGIFG TGS.D.GH.T LPSEVVRAAM LVRINTLLQG YSGIRFEILE
Sevir.7G178200.1.p                                        .PELNAGIFG NGS.D.GH.T LPSEVSRAAM LVRINTLLQG YSGIRFEILE
Seita.7G168700.1.p                                        .PELNAGIFG NGS.D.GH.T LPSEVSRAAM LVRINTLLQG YSGIRFEILE
Osa_LOC_Os02g41630.2                                      .RELNAGIFS TGS.D.GH.T LPSETVRAAM LVRINTLLQG YSGIRFEILE
Bradi3g49250.2.p                                          .KELNAGIFG TGS.D.GH.S LPAEVTRAAM LVRINTLLQG YSGIRFEILE
Pavir.7KG238255.1.p                                       .KELNAGIFG NGS.D.GH.T LPSEVSRAAM LVRINTLLQG YSGIRFEILE
Pavir.7NG355500.1.p                                       CRELNAGIFG NGS.D.GH.T LPSEVSRAAM LVRINTLLQG YSGIRFEILE
PhHAL.7G213800.1.p                                        .PELNAGIFG NGS.D.GH.T LPSEVSRAAM LVRINTLLQG YSGIRFEILE
Zm00008a006867_P01                                        .RELNAGIFS NGS.D.GH.T LPSEVSRAAM LVRINTLLQG YSGIRFEILE
Sobic.006G148800.1.p                                      .KELNAGIFG NGS.D.GH.T LPSEVSRAAM LVRINTLLQG YSGIRFEILE
Seita.2G435800.1.p                                        .KELNAGIFG TGS.D.GH.T LPSQVSRAAM LVRINAIMQG YSGIRFEILE
Sevir.2G448300.1.p                                        .KELNAGIFG TGS.D.GH.T LPSQVSRAAM LVRINALMQG YSGIRFEILE
Sevir.7G177900.1.p                                        .PYLNAGIFG TGS.D.GH.T LPSQVSRAAM LVRINALMQG YSGIRFEILE
Seita.7G168500.1.p                                        .RYLNAGIFG TGS.D.GH.T LPSQVSRAAM LVRINALMQG YSGIRFEILE
Osa_LOC_Os04g43760.1                                      .KELNAGIFG NGS.D.GH.S LPSEVSRAAM LVRINTLLQG YSGIRFEILE
STRANG_00041445-RA                                        .KELNAGIFG TGS.H.GH.T LPTEVVRAAM LVPTNTLLQG YSGIRFEILE
STRANG_00039019-RA                                        .RELNAGIFG TGS.D.GH.T LPSEVARAAM LVRINTLLQG YSGIRFEILE
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1      .PELNAGIFG TGK.D.GH.V LPSEVTRAAM VVRINTLLQG YSGIRFEILE
JoascVi1021323m                                           .RELNAGIFG TGT.D.GH.V LPSAVTRAAM FVRINTLLQG YSGIRFEILE
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Joascv11021328m                                           .RELNAGVFG TGS.D.GH.V LPAAATRAAM LVRINTLLQG YSGIRFEILE
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1     .RELNAGVFG EDS.D.GH.V LPAPATRAAM LVRINTLLQG YSGIRFEILE
Flagellaria_indica_Trinity_comp23935_c0_seq1              .KELNAGIFG SGA.DSGH.V LPTPASRAAM LVRINTLLQG YSGIRFEILE
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Seita.1G240400.1.p                                        .KELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Sevir.1G245166.1.p                                        .RELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Seita.1G240500.1.p                                        .PELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Sevir.1G245232.1.p                                        .RELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Seita.1G240600.1.p                                        .KELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Sevir.1G245300.2.p                                        .KELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
PhHAL.1G307000.1.p                                        .RELNAGAFG TGT.D.GH.V LPGEATRAAM LVRINTLLQG YSGIRFEILE
PhHAL.1G307100.1.p                                        .RELNAGAFG TGT.D.GH.V LPGEATRAAM LVRINTLLQG YSGIRFEILE
PhHAL.1G307200.1.p                                        .RELNAGAFG TGT.D.GH.V LPGEATRAAM LVRINTLLQG YSGIRFEILE
Pavir.1NG356700.1.p                                       .RELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Pavir.1NG356800.1.p                                       .KELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Pavir.1KG386500.1.p                                       .KELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Sobic.004G220600.2.p                                      .RELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Sobic.004G220500.1.p                                      .RELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Sobic.004G220700.1.p                                      .RELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Zm00008a016754_P01                                        .KELNAGAFG IGT.DAGH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Zm00008a022372_P01                                        .KELNAGAFG TGA.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Zm00008a022370_P01                                        .KELNAGAFG TGA.D.GH.V LPADATRAAM LVRINTLLQG YSGIRFEILE
Osa_LOC_Os02g41670.1                                      .RELNAGAFG TGT.D.GH.V LSAEATRAAM LVRINTLLQG YSGIRFEILE
Osa_LOC_Os02g41680.1                                      .RELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Bradi3g47110.1.p                                          .KELNAGAFG TGS.D.GH.V LPAGATRAAM LVRINTLLQG YSGIRFEILE
Bradi3g47120.1.p                                          .KELNAGAFG TGS.D.GH.V LPAGATRAAM LVRINTLLQG YSGIRFEILE
Bradi3g49270.1.p                                          .KELNAGAFG TGS.D.GH.V LPAGATRAAM LVRINTLLQG YSGIRFEILE
Bradi3g48840.1.p                                          .RELNAGAFG TGS.D.GH.V LPAGATRAAM LVRINTLLQG YSGIRFEILE
Bradi3g49280.1.p                                          .RELNAGAFG TGS.D.GH.V LPAGATRAAM LVRINTLLQG YSGIRFEILE
Osa_LOC_Os05g35290.1                                      .RELNAGAFG TGA.D.GH.V LPAGATRAAM LVRINTLLQG YSGIRFEILE
PavTr.1KG386300.1.p                                       .KELNAGAFG TGA.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Pavir.1NG356400.1.p                                       .KELNAGAFG TGA.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
PhHAL.1G306800.1.p                                        .KELNAGAFG TGA.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Seita.1G240300.1.p                                        .RELNAGAFG TGA.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Sevir.1G245100.1.p                                        .RELNAGAFG TGA.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Zm00008a016751_P01                                        .KELNAGAFG TGA.D.GH.V LPAEATRAAM LVRVNTLLQG YSGIRFEILE
Zm00008a022369_P01                                        .KELNAGAFG TGA.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Sobic.004G220400.1.p                                      .KELNAGAFG TGA.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Osa_LOC_Os02g41650.1                                      .RELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
Osa_LOC_Os11g48110.1                                      .RYLNAGVFG ASRSD.GY.T LPTEVTRAAM LVRINTLTQG YSGIRFEILE
Osa_LOC_Os12g33610.1                                      .R........ ..RSD.GY.T LPTEVTRAAM LVRINTLTQG YSGIRFEILE
SobTc.001G160500.1.p                                      .KELNAGVFG ASSSD.GY.T LPAEVTRAAM LVRINTLTQG YSGIRFEILE
Zm00008a004629_P01                                        .KELNAGVFG ASSSD.GY.T LPPEVTRAAM LVRINTLTQG YSGIRFEILE
Bradi3g49260.1.p                                          .RELNAGAFG TGT.D.GH.V LPAEATRAAM LVRINTLLQG YSGIRFEILE
STRANG_00039013-RA                                        .RELNAGAFG TGT.D.GH.V LPAAATRAAM LVRINTLLQG YSGIRFEILE
STRANG_00039015-RA                                        .RELNAGAFG TGA.D.GY.V LPAPATRAAM LVRINTLLQG YSGIRFEILE
Pavir.7KG227800.1.p                                       .KELNAGAFG TGD.D.GH.V LPASATRAAM LVRINTLLQG YSGIRFEILE
PhHAL.7G214000.1.p                                        .KELNAGAFG TGD.D.GH.V LPASATRAAM LVRINTLLQG YSGIRFEILE
Pavir.1NG361819.1.p                                       .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                       .RELNAGAFG TGD.D.GH.V LPASATRAAM LVRINTLLQG YSGIRFEILE
Sevir.7G178300.1.p                                        .RELNAGAFG TGD.D.GH.V LPASATRAAM LVRINTLLQG YSGIRFEILE
Seita.7G168800.1.p                                        .RELNAGAFG TGD.D.GH.V LPASATRAAM LVRINTLLQG YSGIRFEILE
Zm00008a006866_P01                                        .KELNAGAFG TGD.D.GH.V LPASATRAAM LVRINTLLQG YSGIRFEILE
Sobic.006G148900.1.p                                      .KELNAGAFG TGD.D.GH.V LPAAATRAAM LVRINTLLQG YSGIRFEILE
Pavir.4KG229700.2.p                                       .RELNAGAFG TGD.D.GH.V LPAAATRAAM LVRINTLLQG YSGIRFQILE
Osa_LOC_Os04g43800.1                                      .RELNAGAFG NGD.D.GH.V LPAAATRAAM LVRINTLLQG YSGIRFEILE
Osa_LOC_Os08g21670.1                                      .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                          .KELNAGAFG TGE.D.GH.V LPAAATRAAM LVPVNTLLQG YSGIRFEILE
STRANG_00041444-RA                                        .KELNAGAFG TGE.D.GH.V LPTAATRAAM LVRINTLLQG YSGIRFEILE
STRANG_00041441-RA                                        .......... .......... .......... .......... ..........
STRANG_00041440-RA                                        .PYLNAGVFG TGTGDN...V LPAAATRGAM LVRINSLLQG YSGIRFEIVE
STRANG_00059682-RA                                        .RELNAGVFG TGA.D.GH.V LPAATTRAAM LVRINTLLQG YSGIRFEILE
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Aco013943.1                                               .KELNAGIFG SGR.ESGQ.T LPAAATRAAM LVRINTLLQG YSGIRFEILE
Aco007727.1                                               .KELNAGIFG SGP.KSEQ.T LPASATRAAM LVRINTLLQG YSGIRFEILE
Apos_PKA46439.1                                           .KELNAGIFG SGQ.DN...T LPPAATRAAM LVRINTLLQG YSGIRFEVLE
Apos_PKA58411.1                                           .PELNAGIFG SGQ.DN...T LPPAATRAAM LVRINTLLQG YSGIRFEILE
Apos_PKA54143.1                                           .RELNAGIFS SRT.EN...T LPPAAARAAM LVRINTLLQG YSGIRFEILE
Dcat_XP_020704813.1                                       .KELNAGIFG SNP.DN...T LSPSATRAAM LVRINTLLQG YSGIRFEILE
Pequ_XP_020589738.1                                       .KELNAGIFG SNP.NN...T LSPATTRAAM LVRINTLLQG YSGIRFEILE
Dcat_XP_020702280.1                                       .KELNAGIFG SGK.DN...T LPPAATRAAM LVRINTLLQG YSGIRFEILE
Apos_PKA59591.1                                           .PELNAGIFG SGK.EN...T LPATATRAAM LVRINTLLQG YSGIRFEILE
Apos_PKA50166.1                                           .RELNAGIFS SGE.EN...Q LPAPATRAAM LVRINTLLQG YSGIRFEILE
Pequ_XP_020579635.1                                       .KELNAGIFG SGN.SN...T LPSTTTRAAM LVRINTLLQG YSGIRFEILE
Spipo31G0025500                                           .KELNAGIFG SGD.DSANTT LPQSATRAAM LVRINTLLQG YSGIRFEIME
Spipo1G0003500                                            .KELNAGIFG SGA.DSGNTT LPPAATRAAM LVRVNTLLQG YSGIRFEILE
GSMUA_Achr8P18960_001                                     .PELNAGIFG SGN.ESGH.T LPPSAARAAM LVRINTLLQG YSGIRFEILE
GSMUA_Achr11P22840_001                                    .RELNAGIFS SGT.ESAH.T LPTPAARAAM LVRVNTLLQG YSGIRFEILE
GSMUA_Achr5P18560_001                                     .KELNAGIFG SGA.ESGH.T LPTPAARAAM LVRINTLLQG YSGIRFEILE
GSMUA_Achr2P00240_001                                     .KELNAGIFG SGR.ESGH.T LPASAARAAM LVPVNTLLQG YSGIRFEILE
GSMUA_Achr11P16380_001                                    .KELNVGIFG SGA.ESGH.T LPPSATRAAM LVRINTLLQG YSGIRFEILE
GSMUA_Achr5P03950_001                                     .PELNAGIFG SGSDQSGH.T LPPPATRAAM LVRINTLLQG YSGIRFEILE
p5.00_sc00071_p0096.1                                     .RELNAGIFG SSP.QSVH.T LPPSATRAAM LVRINTLLQG YSGIRFEILE
CALSI_Maker00040467                                       .KELNAGIFG SGL.ESSGHT LPSSATRAAM LVRINTLLQG YSGIRFEILE
Aco006987.1                                               .KELNAGIFG SGR.ESGQ.T LPASATRAAM LVRINTLLQG YSGIRFEILE
Aco027752.1                                               .KELNAGIFG SGR.ESGQ.T LPASATRAAM LVRINTLLQG YSGIRFEILE
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Figure 8(continued)

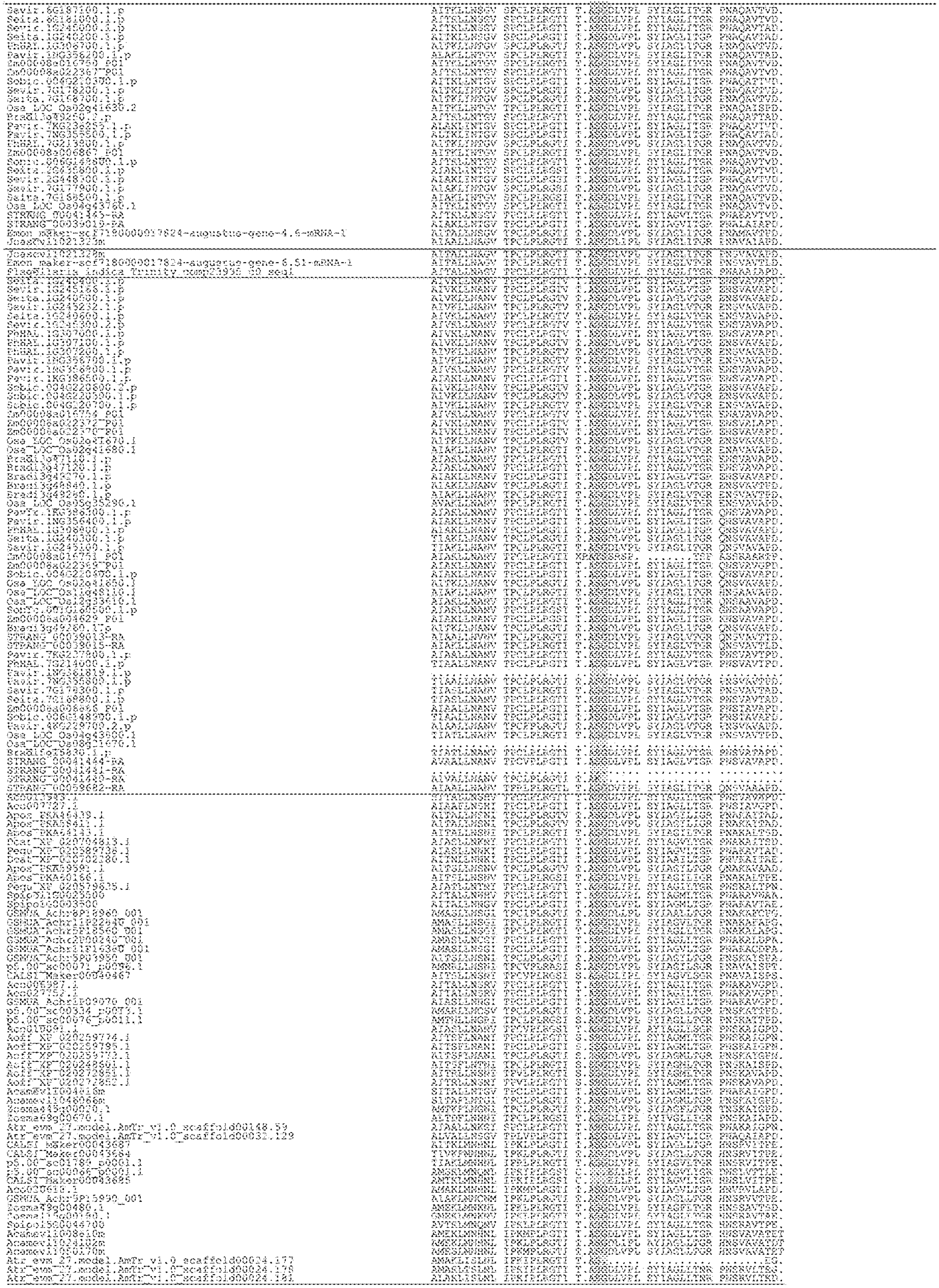

Figure 8(continued)

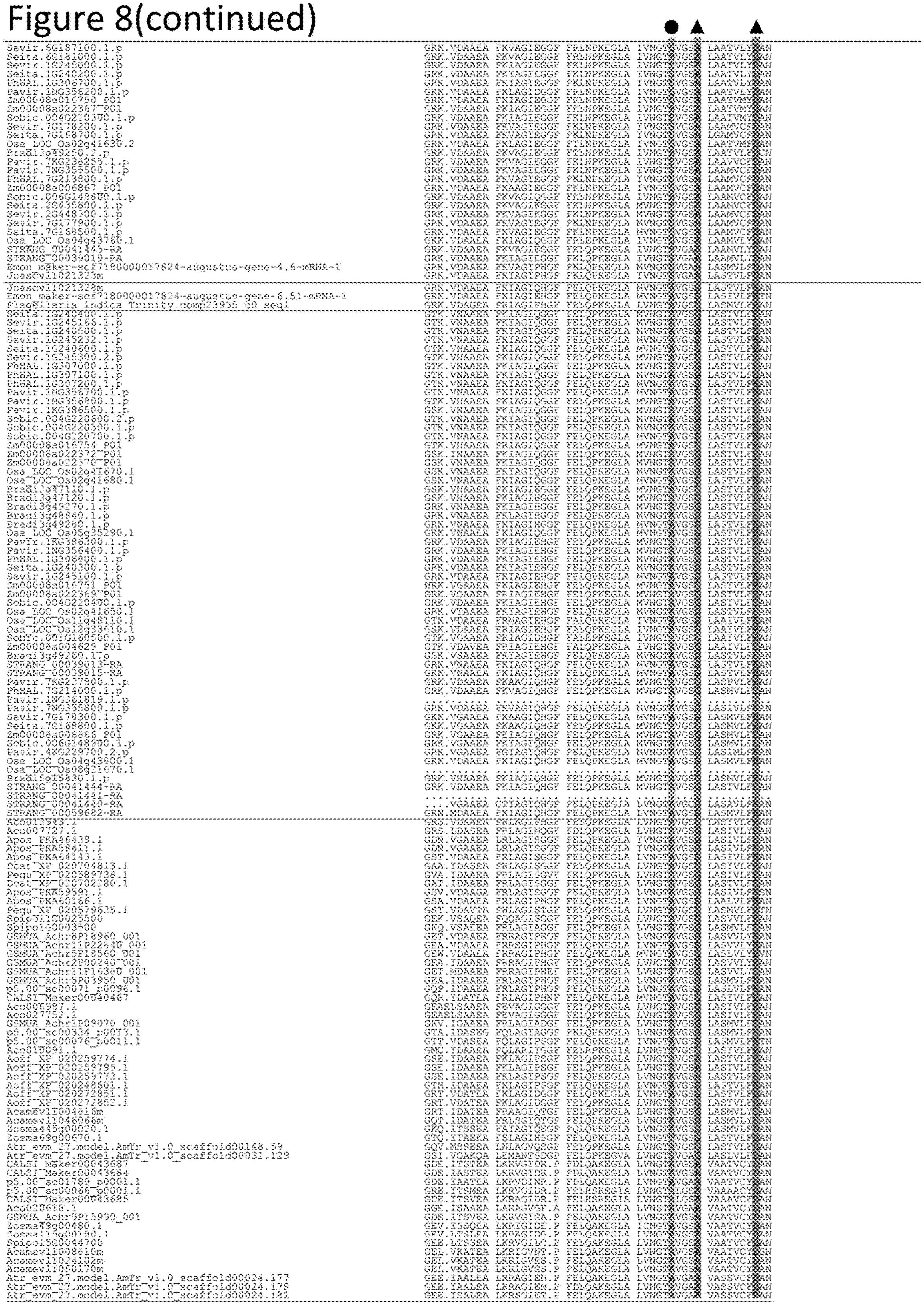

Figure 8(continued)

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Figure 8(continued)

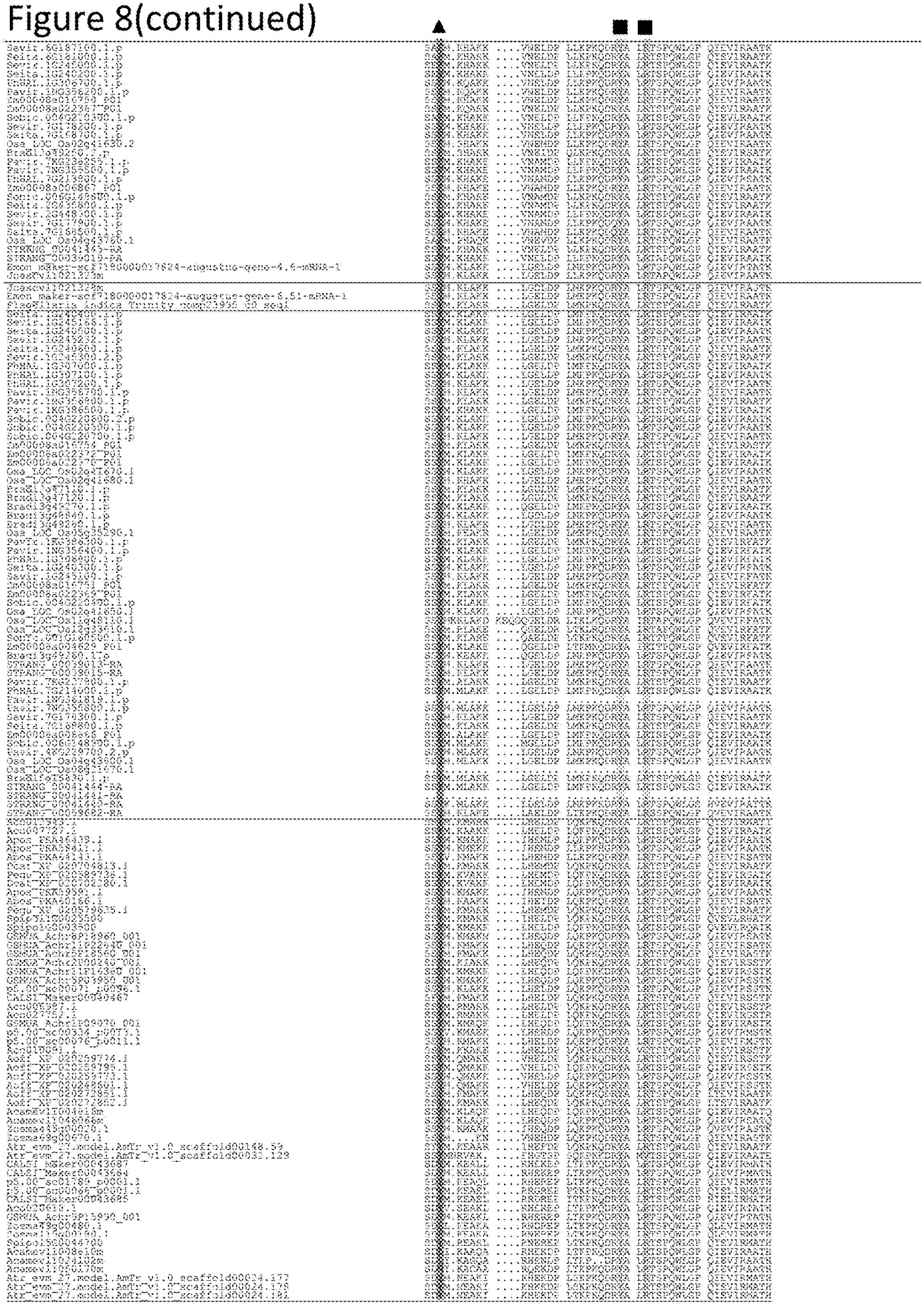

Figure 8(continued)

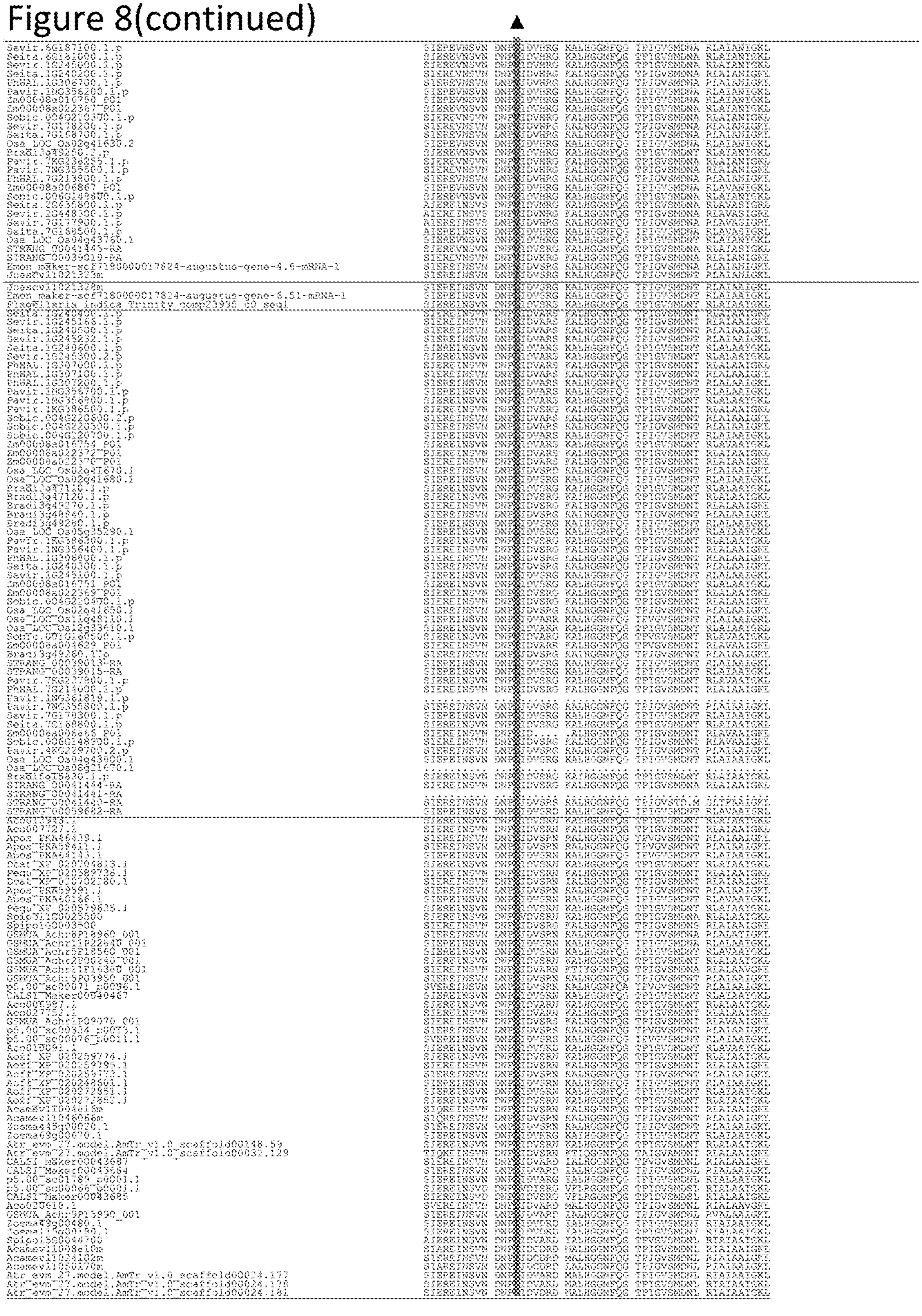

Figure 8(continued)

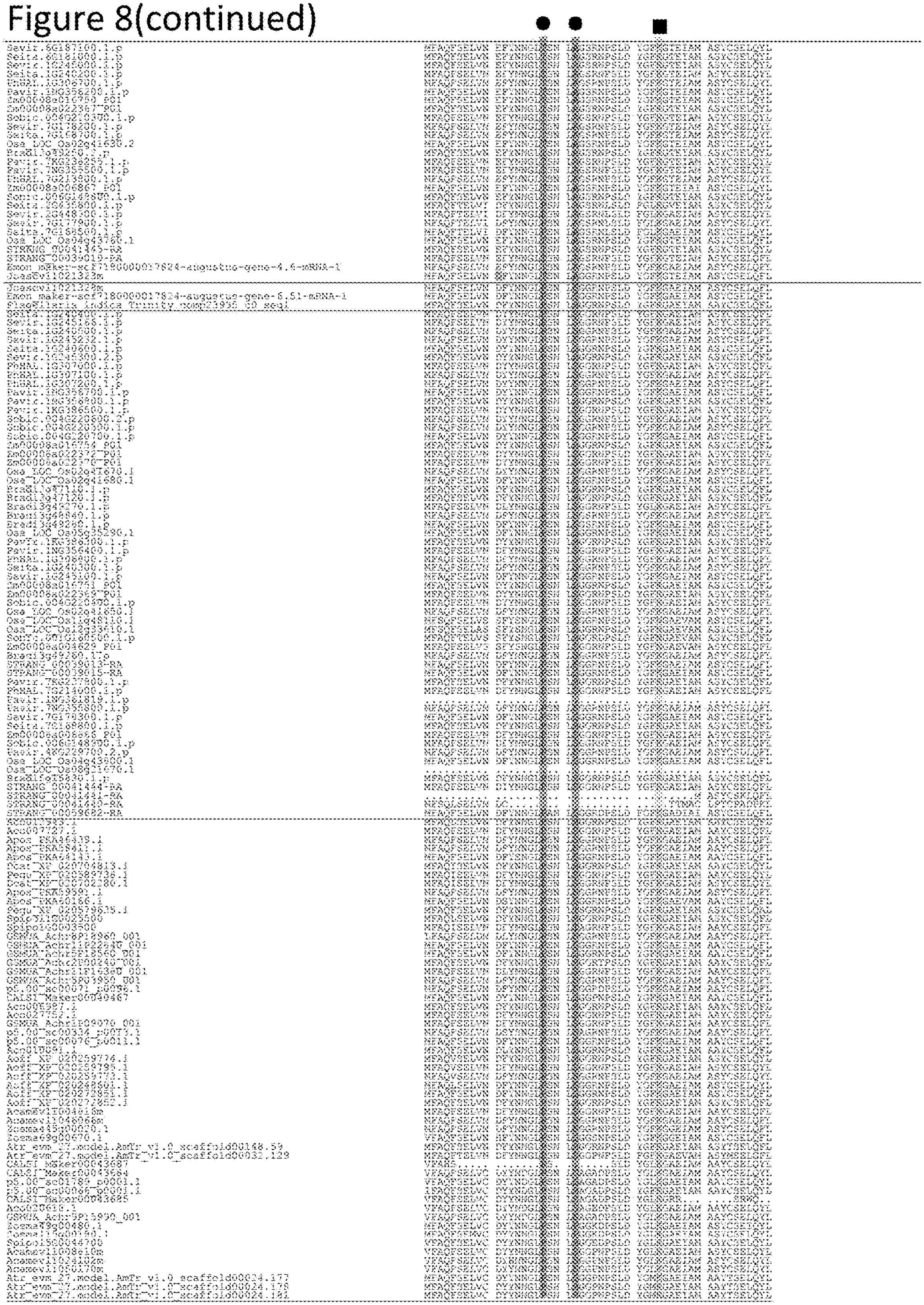

Figure 8(continued)

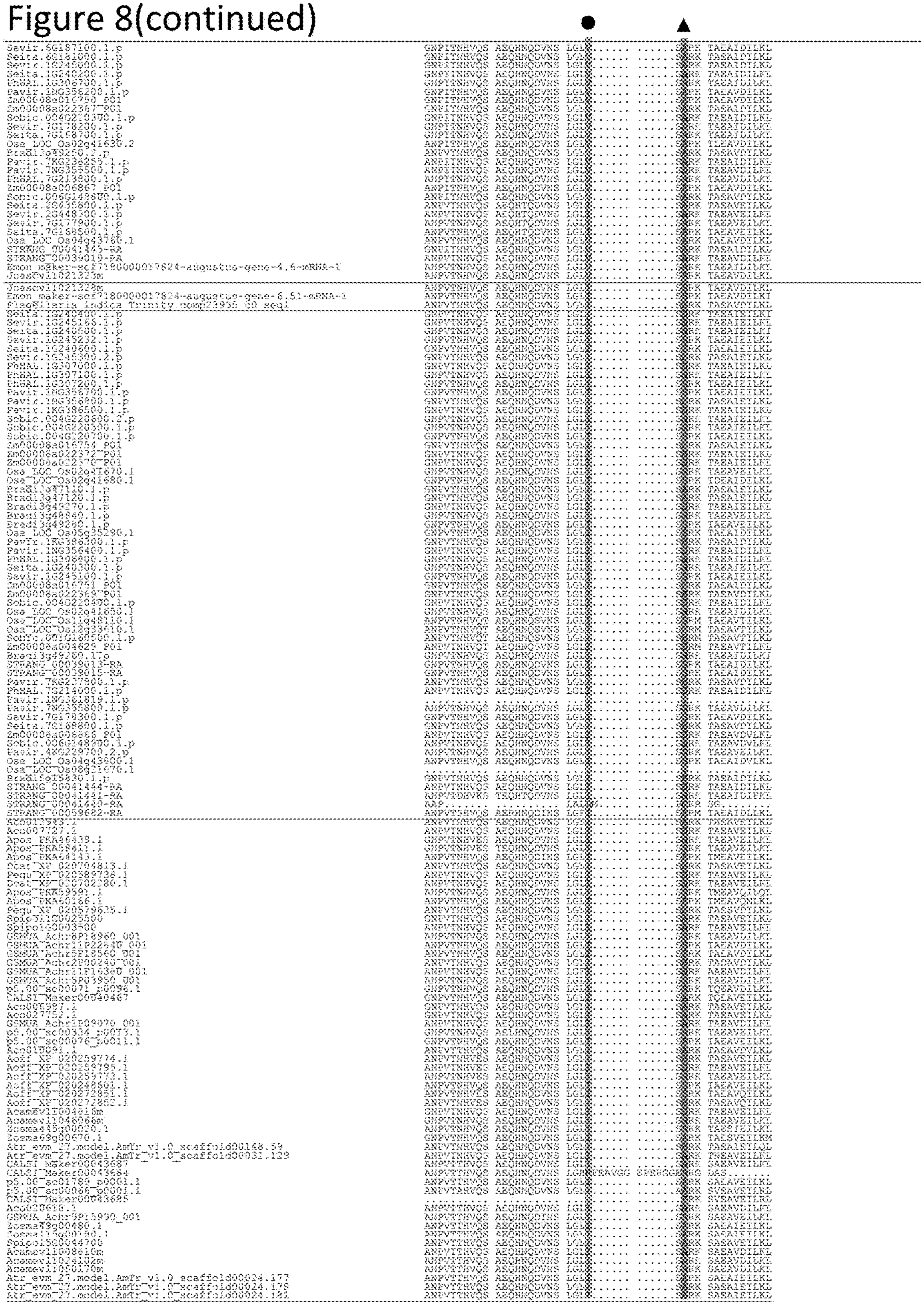

Figure 8(continued)

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Figure 8(continued)

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Seita.7G168500.1.p                                          CSARFSEKAL LAAIDRKAVY SYYDDPCSAS SSLMMTIRAV LVDHALA..N
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STRANG_00039019-RA                                          SNARFSEKAL ITSIDREAVF SYADDPCSAN YPLMQKIRAV LVDHAIT..N
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Joascv11021328m                                             HNARFSEKDL LTAIDREALF AYADDPCNPN YPLMQKLRAV LVEHALA..N
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1       HNARFSEKDL LTAIDREAVF AYADDPCSPN YPLMKKLRSV LVEHALA..N
Flagellaria_indica_Trinity_comp23935_c0_seq1                HNARFCEKDL LTAFDREAVF AYADDPCSAN YPLMQKLRAV LVEHALT..N
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Seita.1G240400.1.p                                          HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Sevir.1G245166.1.p                                          HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVEPALA..N
Seita.1G240500.1.p                                          HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVEPALA..N
Sevir.1G245232.1.p                                          HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Seita.1G240600.1.p                                          HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Sevir.1G245300.2.p                                          HVARFCSKDL LQSIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
PhHAL.1G307000.1.p                                          HAARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
PhHAL.1G307100.1.p                                          HAARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVEPALA..N
PhHAL.1G307200.1.p                                          HAARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Pavir.1NG356700.1.p                                         HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Pavir.1NG356800.1.p                                         HVARFCSKDL LQSIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Pavir.1KG386500.1.p                                         HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Sobic.004G220600.2.p                                        HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVEPALA..N
Sobic.004G220500.1.p                                        HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Sobic.004G220700.1.p                                        HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Zm00008a016754_P01                                          HVARFCSKDL LQSIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Zm00008a022372_P01                                          HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Zm00008a022370_P01                                          HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Osa_LOC_Os02g41670.1                                        HAARFCEKDL LQEIDREAVF AYADDPCSAN YPLMKKLRNV LVERALA..N
Osa_LOC_Os02g41680.1                                        HVARFCEKDL LKEIDREAVF AYADDPCSHN YPLMKKLRNV LVERALA..N
Bradi3g47110.1.p                                            HVARFSSKDL LQSIDREAVF AYADDPCNPN YPLMKKLRGV LVERALA..N
Bradi3g47120.1.p                                            HVARFSEKDL LQSIDREAVF AYADDPCNPN YPLMKKLRGV LVERALA..N
Bradi3g49270.1.p                                            HVSRFCEKDM LQEIDREAVF AYADDPCNHN YPLMKKLRGV LVESALA..N
Bradi3g48840.1.p                                            HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRSV LVERALS..N
Bradi3g49280.1.p                                            HVARFCEKDL LQEIEREAVF AYADDPCSAN YPLMKKLRGV LVERALS..N
Osa_LOC_Os05g35290.1                                        HVARFCEKDL LSEIDREAVF AYADDPCSAN YPLMKKLRSV LVERALA..N
Pavir.1KG386300.1.p                                         HIARFCEKDL QTAIDREAVF AYADDPCSPN YPLMQKLRAV LIEHALA..N
Pavir.1NG356400.1.p                                         HIARFCEKDL QTAIDREAVF AYADDPCSPN YPLMQKLRAV LIEHALA..N
PhHAL.1G306800.1.p                                          HIARFCEKDL QTAIDREAVF AYADDPCSAN YPLMQKLRAV LIEHALA..N
Seita.1G240300.1.p                                          HIARFCEKDL QTAIDREAVF AYADDPCSPN YPLMQKLRAV LIEHALA..N
Sevir.1G245100.1.p                                          HIARFCEKDL QTAIDREAVF AYADDPCSPN YPLMQKLRAV LIEHALA..N
Zm00008a016751_P01                                          HNARFCSKDL QTAIDREAVF AYADDPCSPN YALMQKLRAV LVEHALA..N
Zm00008a022369_P01                                          HNARFCEKDL QTAIDREAVF AYADDPCSPN YPLMQKLRAV LVEHALA..N
Sobic.004G220400.1.p                                        HNARFCEKDL QTAIDREAVF AYADDPCSPN YPLMQKLRAV LIEHALA..N
Osa_LOC_Os02g41650.1                                        HIARFCEKDL LTAIDREAVF AYADDPCSAN YPLMQKLRAV LIEHALA..N
Osa_LOC_Os11g48110.1                                        LAL......L GAAIDRVAVF TYAEDPCRSS LPLMQKLRAV LMEHALAN.N
Osa_LOC_Os12g33610.1                                        LAL......L GAAIDRVAVF TYAEDPCRSS LPLIQKLRAV LMDHALA..N
SobTc.001G160500.1.p                                        AAAQ.....L LGAVDRVAVF TYAEDPCRPS LPLMQKLRVV LMSHALGAAE
Zm00008a004629_P01                                          .........L LVAIDRVAVF TYAEDPCRPS YPLMQKLRAV LMSHALI..N
Bradi3g49260.1.p                                            HIARFCEKDL LTAIDREAVF AYADDPCSPN YPLMQKLRAV LIEHALA..N
STRANG_00039013-RA                                          HIARFCEKDL LTAIDREAVF AYADDPCSGT YPLMKNLRAV LVEHALA..N
STRANG_00039015-RA                                          HIARFCEKDL LTAIDREAVF AYADDPCNAS YPLMKNLRAV LVEHALA..N
Pavir.7KG227800.1.p                                         HSARFCEKDL LTAIDREAVF AYADDPCSAN YPLMQKMRSV LVEHALA..N
PhHAL.7G214000.1.p                                          HSARFCEKDL LTAIDREAVF AYADDPCSAN YPLMQKMRSV LVEHALA..N
Pavir.1NG361819.1.p                                         .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                         HSARFCEKDL LTAIDREAVF AYADDPCSTN YPLMQKMRSV LVEHALA..N
Sevir.7G178300.1.p                                          HNARFCEKDL LTAIDREAVF AYADDSCSAN YPLMQKMRSV LVEHALA..N
Seita.7G168800.1.p                                          HNARFCEKDL LTAIDREAVF AYADDSCSAN YPLMQKMRSV LVEHALA..N
Zm00008a006866_P01                                          HDARFCEKDL LTAIEREAVF AYADDPCSAT YPLMQKMRSV LVEHALA..N
Sobic.006G148900.1.p                                        HNARFCEKDL LTAIDREAVF AYADDPCSAN YPLMQKMRSV LVEHALA..N
Pavir.4KG229700.2.p                                         .......... .......... .......X.. .......... ..........
Osa_LOC_Os04g43800.1                                        HKARFCEKDL LQAIDREAVF AYADDPCSAN YPLMQKMRAV LIEHALA..N
Osa_LOC_Os08g21670.1                                        .......... .......... .......... ...MQKMRIV LIEHALA..N
Bradi5g15830.1.p                                            HNARFCEKDL LLTIDREAVF AYADDPCSAN YPLMQKMPAV LVEHALA..N
STRANG_00041444-RA                                          HIARFCEKDL LTAIDREAVF AYADDPCSNN YPLMQKLREV LVEHALA..N
STRANG_00041441-RA                                          HITRFC.KDL LEVIEREAVF TYAGDPCSEN YPLMQKLCAM HVEHILA..N
STRANG_00041440-RA                                          .......... .......... .....PSAPT .......... ..........
STRANG_00059682-RA                                          HTVPFSE.DL LTAIDREAVF AYADDPCSPK YPLMKNLRAV LLERALA..N
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Aco013943.1                                                 HPSRFCEKDL ITVIDREHVF SYADDPCSAT YPLMQKLRQV LVEHALG..N
Aco007727.1                                                 HPARFCVKDL IKVVDCEAAF SYADDPCSPS YLLMQKLRQV LVEHALK..N
Apos_PKA46439.1                                             HPSRFCEKDL IKMIDREYVF AYADDPCSST YPLMQKLRQV LVEHALT..N
Apos_PKA58411.1                                             HPSRFCEKDL IKMIDREYVF AYADDPCSST YPLMQKLRQM LVEHALT..N
Apos_PKA54143.1                                             HPSRFCEKDL IKVIDREYVF NYADDPCSSS YPLMQKLRQV LVDHALN..N
Dcat_XP_020704813.1                                         HPSRFCEKDL ITVIEREYVF AYADDPCCPT YPLMKNLRQV LVEHALN..N
Pequ_XP_020589738.1                                         HPSRFCEKDL IKVIDREYVF AYADDPCSST YPLMKNLRQV LVEHALN..N
Dcat_XP_020702280.1                                         HPSRFCEKDL IKVIDREYVF AYADDPCSST YPLMQNLRQV LVEHALN..N
Apos_PKA59591.1                                             HPSRFCEKDL IKVIDREYVF AYADDPCSFS YPLMQKLRQV LVDHAIG..N
Apos_PKA60166.1                                             HPARFCEKDL IKAIDREHVF AYADDPCSAS YPLMQKLRQV LVEHAIA..N
Pequ_XP_020579635.1                                         HPSRFCEKDL IKVIDREYVF SYADDPCSST YPLMPKLRAV LVEHALN..N
Spipo31G0025500                                             HPSRFCEKDL LKVVDREYVF AYADDPCLST YPLMQKLRQV LVEHALA..N
Spipo1G0003500                                              HPSRFCEKDL IRAVDREHVF TYADDPCSAT YPLMQKLRQV LVEHALT..N
GSMUA_Achr8P18960_001                                       .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                      HPSRFCEKDL ITVIDREHVF SYIDDPCSST YALMPKLRM. ..........
GSMUA_Achr5P18560_001                                       HPSRFCEKDL IMVVDREHVF SYIDDPCSST YALMPKLRMV L.........
GSMUA_Achr2P00240_001                                       QPSRFCEKDL ITIVDREHVF SYIDDPCSST YALMPKLRM. ..........
GSMUA_Achr11P16360_001                                      ....FCEKNL ITVADREHIF GYIDDPCSST YALMPKLRMA L.........
GSMUA_Achr5P03950_001                                       HPSRFCEKDL ITIIDREHVF SYVDDPCSST YPLMQKLRQ. ..........
p5.00_sc00071_p0096.1                                       HPSRFCEKDL IKVIDREYVF SYADDPCSST YTLMEKLRQV LVEHALR..N
CALSI_Maker00040467                                         HPSRFCEKDL IKVIDREYVF SYADDPCSST YTLMPKLRQV LVEHALN..N
Aco006987.1                                                 HPARFCEKDL IKVVDRDHVF AYADDPCSST YPLMQKLRQV LVEQALG..N
Aco027752.1                                                 HPARFCEKDL IKVVDRDHVF AYADDPCSST YPLMQKLRQV LVEQALG..N
GSMUA_Achr1P09070_001                                       HPARFCEKEL IKVVDREHVF TYVDDPCSAT YPLMQKLRQ. ..........
p5.00_sc00334_p0073.1                                       HPSRFCEKDL IRVIDGEYVF SYVDDPCSST YPLIQKLRQV LVEHALN..N
p5.00_sc00076_p0011.1                                       HPSRFCEKDL IKVIDREYVF AYIDDPCSPT YPLMQKLRQV LVEHALN..N
Aco010091.1                                                 QPSMFCVEGL IKVIDREHVF SYIDDPCSSA YPLVQKLRQA LVEHALS..K
Aoff_XP_020259774.1                                         HPSRFCEKEL IKVIDREYVF AYIDDPCSYT YPLMQKVRQV LVEHALN..N
Aoff_XP_020259795.1                                         HPSRFCEKEL IKVIDREYVF AYIDDPCSYT YPLMQKVRQV LVEHALN..N
Aoff_XP_020259773.1                                         HPSRFCEKEL IKVIDREYVF AYIDDPCSYT YPLMQKVRQV LVEHALN..N
Aoff_XP_020248601.1                                         HPSRFCELEL IKMIDREYVF AYIDEPCSYN YPLMQKLRQV LVEHALN..N
Aoff_XP_020272851.1                                         HPSRFCELDL IKVVEREPVF AYIDDPCSAT YPLMQKLRQV LVEHALT..N
Aoff_XP_020272852.1                                         HPSRFCELDL IKVVEREPVF AYIDDPCSAT YPLMQKLRQV LVEHALT..N
Acamev11004816m                                             HPSRFCEKDL IKVVDRESVY AYVDEPCSAT YPLMQKLRQV LVEHAIN..N
Acamev11046066m                                             HPSRFCEKDL IKVIDREYVF AYVDDPCSAT YPLMQKLRQV LVEHALN..N
Zosma445g00020.1                                            HPSRFCEKDL LKVVDREYVF SYIDDPCSAT YPLMQKLRSV LVDHALN..N
Zosma69g00670.1                                             HPSRFCEKDL IKVIDREQVF DYIDDPCNAT YPLMEKLRGV LVDHALG..N
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59                 LPSRFCEKDL LNVVEREYVF AYADDPCSSN YPLMQKLRGV LVEHALA..S
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129                SGSNLCE.EL LEVVEAEYAF SYIDDPCNPN YPLIQKLRGV LEGRVMA...
CALSI_Maker00043687                                         LETRFCEKDL IQVVEKQFVF SYIDDPAMPA YALMIQLREV LVEKALE...
CALSI_Maker00043684                                         LETRFCEKDL IQVVEKQFVF SYIDDPAMPA YALMLQLREV LVEKALE...
p5.00_sc01789_p0001.1                                       LETRFCEKDL IQVVEKQFVF SYIDDPGNPA YALMLQLREV LVEKALE...
p5.00_sc00066_p0001.1                                       SEARFWEKDL IQVVERLPVY SYIDDPSNAK NALMQQLRSA LVEKALE...
CALSI_Maker00043685                                         SEARFWEKDL IQVVERLPVY SYIDDPANAK YALMQQLREV LVEKALQ...
Aco020618.1                                                 SEARFCEKEL LQVVERQFVF SYIDDPAMPN YALMIQLREV LVEKALG...
GSMUA_Achr3P15990_001                                       TEARFCEKEL IQVAERQFVF SYIDDPANPS YALMLQLREV LVEKALE...
Zosma79g00480.1                                             SSTRFCEKEL LQVVEEQPVF SYIDDPANTS YALLLQLREV LVEKSLTS.E
Zosma115g00190.1                                            ARTRFCEKEL LQVVEEQPVF SYIDDPSNSS YALLLQLREV LVEKSLKS.S
Spipo15G0044700                                             LESRFCEKDL LQVVEEQPIF SYIDDPANPS YALLLQLREV LVEKSLN...
Acamev11008610m                                             LESRFCEKEL LEVVERQFVF SYIDDPANPS YALLLQLREV LVEKALKD.L
Acamev11024102m                                             .....CEKEL LNVVEHQPVF SYIEDPVNPS YALLLQLREV LVEKALKD.L
Acamev11050170m                                             LDTRFCEKEL LQVVEHQPVF SYIDDPTNPS YALLLQLREV LVERALKN.I
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177                LDTPFYEKEL LQVVDHQPVF SYLDDPANPS YALLLQLREV LVEKSLES.E
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178                LDTRFDEKEL LQVVDRQPVF SYLDDPANPS YALLLQLREV LVEKSLKS.E
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181                LDTRFYEKEL LQVVDRQPVF SYLDDPSNPS YALMLQLREV LVEKSLKS.N
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Figure 8(continued)

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Sevir.6G187100.1.p                                     GD......E PSVFSKITKF EEELRAVLPQ EVEAARVAV. AEGTAAVENR
Seita.6G181000.1.p                                     GD......E PSVFSKITKF EEELRAVLPQ EVEAARVAV. AEGTAAVENR
Sevir.1G245000.1.p                                     GD......E PSMFSKITKF EEELRAVLPQ EVEAARVAV. AEGTAAVENR
Seita.1G240200.1.p                                     GD......E PSMFSKITKF EEELRAVLPQ EVEAARVAV. AEGTAAVENR
PhHAL.1G306700.1.p                                     GDAER...E PSVFSKITKF EEELRAVLPR EVEAARVAV. AEGTASVPNR
Pavir.1NG356200.1.p                                    GDAER...E PSVFSKITKF EEELRAVLPR EVEAARVAV. AEGAAAVPNR
Zm00008a016750_P01                                     GDAER...E PSVFSRITKF EEELRAVLPH EVEAARVAV. AEGTAPVANR
Zm00008a022367_P01                                     GDAEK...E PSVFSKITKF EEELRAVLPQ EVEAARVAV. AEGTAPVANR
Sobic.004G220300.1.p                                   GDAER...E PSVFSKITKF EEELRAVLPR EVEAARVAV. AEGTAPVANR
Sevir.7G178200.1.p                                     GDAER...E PSVFSKITKF EEELRAVLPR EVEAARVAV. AEGTAPVANR
Seita.7G168700.1.p                                     GDAER...E PSVFSKITKF EEELRAVLPR EVEAARVAV. AEGTAPVANR
Osa_LOC_Os02g41630.2                                   GDAEP...E ASVFSKITKF EEELRSALPR EIEAARVAV. ANGTAPVANR
Bradi3g49250.2.p                                       SGVDNAGESE ATVFSKINKF EEELRAALPR EIEAARVAF. EKGTAPIPNL
Pavir.7KG238255.1.p                                    GEAEK..DAS ASVLSKINKL EEELREALPR EMEAARVAF. ETGAAPIANR
Pavir.7NG355500.1.p                                    GEAEK..DAS ASVFSKINKL EEELREALPR EMEAARVAF. ETGTAPIANR
PhHAL.7G213800.1.p                                     GEAEK..DAS ASVFSKINKF EEELREALPR EMEAARVAF. ETGTAPIANR
Zm00008a006867_P01                                     GEAEK..DAS ASVFSKINRF EEELREALPR EMEAARVAF. ETGAAPIANR
Sobic.006G148800.1.p                                   GEAEK..DAS ASVFSKINKF EEALREALPR EMEAARVAF. ETGTAPIGNR
Seita.2G435800.1.p                                     GEAEN..EAR APIFSKITKF EEELREALPR EMEKTRVAF. ETGTAPIGNR
Sevir.2G448300.1.p                                     GEAEN..EAR APIFSKITKF EEELREALPR EMEKTRVAF. ETGTAPIGNR
Sevir.7G177900.1.p                                     GEAEN..EAG APIFSKITKF EEELREALPR EMEKTRVAF. ETGTAPIGNR
Seita.7G168500.1.p                                     GEAEN..EAR APIFSKITKF EEELRSALPR EMEKTRVAF. ETGTAPIGNR
Osa_LOC_Os04g43760.1                                   GPAEK..DDG SSVFSKITAF EEELREALPR EMEAARVAF. ETGTAPTINR
STRANG_00041445-RA                                     GEDSK..EPA TSVFAKITKF EDELRTALPR EMEAARVAV. ENGTAPTANR
STRANG_00039019-RA                                     GDGEN..EPA AAVFAKITKF EDELRSALPR EMEAARVAF. ENGASQTPNR
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1   GEAER..VTD TSVFAKITKF EDELRAALPK EVEAVRAAV. ENGNAPIPNR
Joasev11021323m                                        GEAER..VAN TSVFAKITKF EEELRATLPK EVEAARVAV. ENRTAPTQNR
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Joasev11021328m                                        GEAEH..VAT TSVFAKITKF EEELRATLPK EVEAARVAV. ENGTAPTPNR
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1  GEAEL..AAE TSVFAKIAKF EEELRAALPS EVEAAWAAV. ENGTAATPNR
Flagellaria_indica_Trinity_comp23935_c0_seq1           GEAEL..SQD TSVFMKIAKF EEELRAALPK EVEAARAAV. ESGNAAIPNR
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Seita.1G240400.1.p                                     GTAEF..NAE TSVLAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPIR
Sevir.1G245166.1.p                                     GTAEF..NAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPIR
Seita.1G240500.1.p                                     GTAEF..NAE TSVLAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPIR
Sevir.1G245232.1.p                                     GTAEF..NAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPIR
Seita.1G240600.1.p                                     GTAEF..NAE TSVLAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPNR
Sevir.1G245300.2.p                                     GTAEF..NAD TSVLAKVAQF EEELRAALPN AVEAARAAV. ENGTAAIPNR
PhHAL.1G307000.1.p                                     GTAEF..NAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPNR
PhHAL.1G307100.1.p                                     GTAEF..NAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPNR
PhHAL.1G307200.1.p                                     GTAEF..NAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPNR
Pavir.1NG356700.1.p                                    GAAEF..SAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPNR
Pavir.1NG356800.1.p                                    GAAEF..SAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPNR
Pavir.1KG386500.1.p                                    GAAEF..NAE TSVFAKVAQF EEELRAALPK AVEAARASV. ENGTAAIPNR
Sobic.004G220600.2.p                                   GAAEF..DAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPNR
Sobic.004G220500.1.p                                   GAAEF..DAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPNR
Sobic.004G220700.1.p                                   GAAEF..DAE TSVFAKVAQF EEELRAALPK AVEAARAAV. ENGTAAIPNR
Zm00008a016754_P01                                     GTAEF..DAE TSVFAKVAQF EEELRTALPS AVEAARAAV. ENGTAAIPNR
Zm00008a022372_P01                                     GAAEF..NAE TSVFAKVAQF EDDLRAALPK AVEAARAAV. ENGTAGIPNR
Zm00008a022370_P01                                     GAAEF..NAE TSVFAKVAQF EEDLRAALPK AVEAARAAV. ENGTAAIPNR
Osa_LOC_Os02g41670.1                                   GAAEF..NAE TSVFAKVAQF EEELRAALPA AVLAARAAV. ENGTAATPNR
Osa_LOC_Os02g41680.1                                   GAAEF..NAD TSVFAKVAQF EEELRATLPG AIEAARAAV. ENGTAAIPSR
Bradi3g47110.1.p                                       GVAEF..DAE TSVFAKVARF EEELRAALPV AVEAARAAV. ESGTAEAPNR
Bradi3g47120.1.p                                       GVAEF..DAE TSVFAKVARF EEELRAALPV AVEAARAAV. ESGTAEAPNR
Bradi3g49270.1.p                                       GVAEY..NVE TSVFAKVAQF EEELRAALPK AVEAARAAV. ESGTAAIPNR
Bradi3g49840.1.p                                       GMAEF..NAE TSVFAKVAQF EEELRTVLPK AVEAARAAV. ESGTAATPNR
Bradi3g49280.1.p                                       GKAEF..NAE TSVFAKVAQF EEELRTALPK AVEAARSAV. ESGTAATPNR
Osa_LOC_Os05g35290.1                                   GAAEF..DAE TSVLAKVARF EEELRAALPR AVEAARAAV. ESGTAAAPNR
Pavir.1KG386300.1.p                                    GDAER..VAE TSIFAKITKF EEELRAVLPR EVEAARVAV. AEGAAPLPNR
Pavir.1NG356400.1.p                                    GDAER..VVE TSIFAKVAEF EQQVRAALPK GVEAARAAV. ESGNPMVPNR
PhHAL.1G306800.1.p                                     GDAER..VVE TSIFAKVAEF EQQVRAALPK EVEAARAAV. ESGRPMVPNR
Seita.1G240300.1.p                                     GDAER..VVE TSIFAKVAEF EQQVRAALPK EVEAARAAV. ESGRPMVPNR
Sevir.1G245100.1.p                                     GDAER..VVE TSIFAKVAEF EQQVRAALPK EVEAARAAV. ESGRPMVPNR
Zm00008a016751_P01                                     GDAER..DVD TSIFAKVAEF EQQVSAALPK EVEAARAAV. ENGSPLVPNR
Zm00008a022369_P01                                     GDAER..AAE TSIFAKVAEF EQQVRAALPK EVEAARAAV. ESGNPLVPNR
Sobic.004G220400.1.p                                   GDAER..VVE TSIFAKVAEF EQQVRAALPK EVEAARAAV. ESGNPLVPNR
Osa_LOC_Os02g41650.1                                   GDAER..VLE TSIFAKVAEF EQRVRAALPK EVEAARAAV. ENGTPLVPNR
Osa_LOC_Os11g48110.1                                   GD........ .ILLAKVAEF EQQLRAVLPD EVEAARAAV. ESGTA..PNR
Osa_LOC_Os12g33610.1                                   GD........ .NQLAKVAEF EQQLSAVLHD EVEAARAAV. ESGTA..PNR
SobTc.001G160500.1.p                                   GAVET..... TSILAKVAEF EQQLRAVLPD EVEAARAAV. ESGTA..PKP
Zm00008a004629_P01                                     GDSNIERPME TSILAKVAEF EKQLSAVLPD EVEAARAAV. ESGTT..PNR
Bradi3g49260.1.p                                       GLGER..ALE TSIFAKVAEF EQNLRAALPK EVEAARASV. ENGTPLAPNR
STRANG_00039013-RA                                     GEAER..NAE TSVFAKVAKF EEELRAALPK AVEAARASV. ENGTGPTPNR
STRANG_00039015-RA                                     GEAER..NVD TSVFTKVAEF EQQLSAALPK EVEAARAAV. ENGAATVPNR
Pavir.7KG227800.1.p                                    GEAEH..DPD TSVFAKLATF EEELRAALPR EVDAARAAV. ENGTAAIPNR
PhHAL.7G214000.1.p                                     GEAER..DPD TSVFAKVTAF EEELRAALPR EVDAARAAV. ESGTAAIPNR
Pavir.1NG361819.1.p                                    .......... .TVFAKVATF EEELRAALSR EVDAARGAV. ......IPNR
Pavir.7NG355800.1.p                                    GEAER..DPD TSVFGKVATF EEELRAALPT EVEASRAGV. EKGAAAIPNR
Sevir.7G178300.1.p                                     GEAER..DPE TSVFAKVATF EEEIRAALPR EVEAARAAV. ENGTAAIPNR
Seita.7G168800.1.p                                     GEAER..DPE TSVFAKVATF EEEIRAALPR EVEAARAAV. ENGTAAIPNR
Zm00008a006866_P01                                     GEAER..DPD TSVFAKVATF EEELRAALPR EVDAARAAV. ESGTAAIRNR
Sobic.006G148900.1.p                                   GEAER..DPE TSVFAKVATF EEELRAALPR EVDAARAAV. ENGTAAVPNR
Pavir.4KG229700.2.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                   GEAER..NVD TSVFAKVATF EEELRVALPR EVEAARAAV. ENGTAAKANR
Osa_LOC_Os08g21670.1                                   SEAER..NVN TSVFAKVAMF EEKLSAALPR EVEATPAAV. ENGTAAKANR
Bradi5g15830.1.p                                       GEAER..DVE TSVFAKLAAF EQELRAVLPK EVEAARAAV. ENGTATKQNP
STRANG_00041444-RA                                     GEAER..NVE TSVFAKIAMF EEELRAVLPR EVEAARAAV. ENGAAAKPNR
STRANG_00041441-RA                                     GEAKR..NGE TKFLAKITMF EE....VLPG EVKAIREAM. ENRATVNPNR
STRANG_00041440-RA                                     .......... .......... .......... .......... ..........
STRANG_00059682-RA                                     GEAER..DVE TSVLAKLASF EEELHAELPK AVEAARVAV. ENGGAPTPNR
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Aco013943.1                                            GEKEK..AYE TSIFQKITAF EEELKAQLPK EVEAVRAAV. ESGSSATANR
Aco007727.1                                            GEKEK..NSN SSIFQKITAF EEELKANLPK EVDAARVAF. ETGSSAIPNR
Apos_PKA46439.1                                        GENER..DPN SSIFQKITAF EEEIKSSLPK ELEAARANV. ENGSPAIANR
Apos_PKA58411.1                                        GEKEK..DVN FSIFQKITAF EEEIKSSLPK ELEAARANV. ENGSPAIANR
Apos_PKA54143.1                                        GDKEK..DPT SSIFQKIAAF EEEVKNAVTK DVETARAAV. ENGSPAISNR
Dcat_XP_020704813.1                                    GEKEK..DAN SSIFQKITAF EEEIKAVIPK EVEATRVAF. EKGSSTIGNR
Pequ_XP_020589738.1                                    GEKEK..DST SSIFQKIAAF EEEIKATVPK EVEAARAAF. EKGSSAIGNR
Dcat_XP_020702380.1                                    GEKEK..EAD SSIFQKITAF EEELKAVLPK EVEATRLAF. ENGTSTIGNR
Apos_PKA59591.1                                        GEKER..DVN TSIFQKILAF EEELKAVLPK EAEAARAAF. DNGSPAIANR
Apos_PKA60166.1                                        GEKEK..DSS ASIFQKIVDF EEEVKAIVPR EVEAARAAV. ESGSPAIENR
Pequ_XP_020579635.1                                    GDKEK..NSS TSIFQKISSF EAELKAAMPK EVEAARAAF. ENGSPAIENR
Spipo31G0025500                                        GEKEK..DSA TSIFQKVTAF EEELKMALPK EVEAAREAV. EKGAPAIPNR
Spipo1G0003500                                         GEKEK..DSN TSIFQKVAAF EEELKMTLPK EVEAVRAAF. DNGTAVIPNR
GSMUA_Achr8P18960_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P16380_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                  .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                  GEKEK..DAT TSIFQKITAF EQELKAVLPK EVEATRVAF. ENGNLPIENR
CALSI_Maker00040467                                    GEKER..DAS TSIFQKITAF EEELKAILPK EVEAARVAF. ENGSLPILNR
Aco006987.1                                            GEKEK..DPN NSIFQKIAAF EEELKAQLPK EVEAARVAF. ENGTSAIPNR
Aco027752.1                                            GEKEK..DPN NSIFQKIAAF EEELKAQLPK EVEAARVAF. ENGTSAIANR
GSMUA_Achr1P09070_001                                  .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                  GEKER..DPS SSIFQKIAAF EEELKTVLPR EVESARVAL. ENGRSAIANR
p5.00_sc00076_p0011.1                                  GEKEK..DPS SSIFQKISVF EEELKTLLPK EVEGARVAF. ENGNSAIANR
Aco010091.1                                            GEKEKDNDSS TFFLHRITAF EEELSARLPK DVEAAWVAF. GSGKSAIQNR
Aoff_XP_020259774.1                                    GEKER..DLN TSIFQKIAVF EEELKAVLPK EVEAARVAV. ENGSAAIANR
Aoff_XP_020259795.1                                    GEKER..DLN TSIFQKIAVF EEELKAVLPK EVEAARVAV. ENGSAAIANR
Aoff_XP_020259773.1                                    GEKER..DLN TSIFQKIAVF EEELKAVLPK EVEAARVAV. ENGSAAIANR
Aoff_XP_020248601.1                                    GEKEK..DVK TSIFQKIAAF EEELKAVLPK EVEAARVAV. EAGNAQIGNR
Aoff_XP_020272851.1                                    GDKEK..PVN TSIFHRIEEF EDELKALLPK EVEGVRMAF. ENGRLSIPNR
Aoff_XP_020272852.1                                    GDKEK..PVN TSIFHRISEF EDELKALLPK EVEGVRMAS. ENGRLSIPNR
Acamev11004816m                                        GEKER..EVG TSIFQKIGVF EEEIKAVLPK EVEAARVAY. EAGNASVGNR
Acamev11046066m                                        GEKER..EWS TSIFQKISLF EEELKAVLPK EVEAARAAY. EAGNSSVSNR
Zosma445g00020.1                                       GDKEK..DEA MSIFQKIAVF EEELIAALPK EVEAARLAV. EAGKPAIANR
Zosma69g00670.1                                        WEKET..DVS TSIFQKIPTF EAELKLTLPK EVDAARLAH. ENGNSVVGNR
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59            GEKEK..EMG SSIFERIGLF EQELKAILPK EVETARASV. EKGDSAIPKR
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129           ..AKK..EVG ILVLQKIEDF ELELKNHLPK EVELTREAI. EKGNSMIPNR
CALSI_Maker00043687                                    GSEEG..... MVMFKRITKF QEELKERLKE EVGRARERF. EKGDFIVGNR
CALSI_Maker00043684                                    GSEEG..... MVMFKRVFKF QEELKERLRE EVGRARERF. EKGDFIVGNR
p5.00_sc01789_p0001.1                                  GSEAG..... MAMFKRIPEF QEELRQRLRE EVGKARERF. GKGDFMVGNR
p5.00_sc00066_p0001.1                                  GNEEG..... RVVFKRISEF QEEARQRSPE EVERARERS. RKGDFVIGSP
CALSI_Maker00043685                                    GGEEE..... RVVFKSIPKF QEEVRERLKE EVGRARERF. GKGDFVIGNR
Aco020618.1                                            GSEEG..... MAAFKRIFQF QEELKRVLKE EVGKTREEFT SKKDEILKSR
GSMUA_Achr3P15990_001                                  GTEEG..... MAAFKRIPKF QEELGSALNE ELAKARERF. GRGDFIVGSR
Zosma79g00480.1                                        EDKDG..... YFVFKKITEF TNDLKVRVAK DVEVAREKI. EKGEYLVGKR
Zosma115g00190.1                                       KKEVG..... YSAFKKITVF KEDLKERVVK DVAVAPEEI. EKGVYMVGNR
Spipo15G0044700                                        KSEDG..... YAVFTRIPVF QEELKARLSE EVPQARQRS. EKGDFLVPNR
Acamev11008610m                                        KDDTS..... SVVFKRIPLF QEELKKRLTE EVLKARERF. DEGDFPVPNR
Acamev11024102m                                        NLPSS..... .VVFKKIPLF EEELKKRLSE EVAKARERF. DEGDFLVPNR
Acamev11050170m                                        NEENG....A GKVLKMIPVF QEELKRRLSE EVPKARERF. DKGDFEVPNR
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177           KEGDG..... FSIFKRIGVF QEELKARLRE EIPKARERF. DAGDFPVPNR
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178           KEGDG..... FSIFKRIGVF QEELKARLTE EIPKARERS. DAGDFPVPNR
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181           TEADG..... FSIFKRIGVF QEELKVRLSE EIPKARERS. DAGDFPVPNR
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Figure 8(continued)

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Sevir.6G187100.1.p                                         IKDSRS.... .......... ...FPLYRFV REELGCVFLT GEK.......
Seita.6G181000.1.p                                         IKDSRS.... .......... ...FPLYRFV REELGCVFLT GEK.......
Sevir.1G245000.1.p                                         IKDSRS.... .......... ...FPLYRFV REELGCVFLT GEK.......
Seita.1G240200.1.p                                         IKDSRS.... .......... ...FPLYRFV REELGCVFLT GEK.......
PhHAL.1G306700.1.p                                         IKDSRS.... .......... ...FPLYRFV REELGCVFLT GEK.......
Pavir.1NG356200.1.p                                        IKDSRS.... .......... ...FPLYRFV REELGCVFLT GEK.......
Zm00008a016750_P01                                         IADSRS.... .......... ...FPLYRFV RQELGCVFLT GEK.......
Zm00008a022367_P01                                         IADSRS.... .......... ...FPLYRFV REELGCVFLT GER.......
Sobic.004G220300.1.p                                       IADSRS.... .......... ...FPLYRFV REELGCVFLT GEK.......
Sevir.7G178200.1.p                                         IKDSRS.... .......... ...FPVYRFV REELGCVFLT GEK.......
Seita.7G168700.1.p                                         IKDSRS.... .......... ...FPVYRFV REELGCVFLT GEK.......
Osa_LOC_Os02g41630.2                                       IVESRS.... .......... ...FPLYRFV REELGCVFLT GEK.......
Bradi3g49250.2.p                                           IKDSRS.... .......... ...FPLYRFV REELGCVYLT GEK.......
Pavir.7KG238255.1.p                                        IEESRS.... .......... ...YPLYRFI RQDLGAVYLT GEK.......
Pavir.7NG355500.1.p                                        IEESRS.... .......... ...YPLYRFI RQDLGAVYLT GEK.......
PhHAL.7G213900.1.p                                         IKESRS.... .......... ...YPLYRFI RQDLGAVYLT GEK.......
Zm00008a006867_P01                                         IKESRS.... .......... ...YPLYRFI RQDLGAVYLT GEK.......
Sobic.006G148800.1.p                                       IKDSRS.... .......... ...YPLYRFI RQDLGAVYLT GEK.......
Seita.2G435800.1.p                                         IKESRS.... .......... ...YPLYRFI REDLGAVYLT GEK.......
Sevir.2G448300.1.p                                         IKESRS.... .......... ...YPLYRFI REDLGAVYLT GEK.......
Sevir.7G177900.1.p                                         IKESRS.... .......... ...YPLYRFI REDLGAVYLT GEK.......
Seita.7G168500.1.p                                         IKESRS.... .......... ...YPLYRFI REDLGAVYLT GEK.......
Osa_LOC_Os04g43760.1                                       IKESRS.... .......... ...FPLYRFV REELGCVYLT GEK.......
STRANG_00041443-RA                                         IKESRS.... .......... ...YPLYRFI REDLGAVYLT GEK.......
STRANG_00039019-RA                                         MKDSRS.... .......... ...YPLYRFI REDLGAVYLT GEK.......
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1       VKECRS.... .......... ...YPLYRFL REDLGTVYLT GEK.......
Joasev11021323m                                            IKESRS.... .......... ...YPLYRFV REDLGTAYLT GEK.......
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Joasev11021328m                                            IKECRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1      IKECRS.... .......... ...YPLYRFV REELGSGYLT GEK.......
Flagellaria_indica_Trinity_comp23935_c0_seq1               IKECRS.... .......... ...CPLYQFV REEVGTEYLT GEK.......
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Seita.1G240400.1.p                                         ITECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Sevir.1G245166.1.p                                         ITECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Seita.1G240500.1.p                                         ITECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Sevir.1G245232.1.p                                         ITECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Seita.1G240600.1.p                                         ITECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Sevir.1G245300.2.p                                         ITECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
PhHAL.1G307000.1.p                                         IAECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
PhHAL.1G307100.1.p                                         IAECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
PhHAL.1G307200.1.p                                         IAECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Pavir.1NG356700.1.p                                        IAECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Pavir.1NG356800.1.p                                        IAECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Pavir.1KG386500.1.p                                        IAECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Sobic.004G220600.2.p                                       ITECRS.... .......... ...YPLYRFV RQEVGAVYLT GEK.......
Sobic.004G220500.1.p                                       ITECRS.... .......... ...YPLYRFV RQEVGAVYLT GEK.......
Sobic.004G220700.1.p                                       ITECRS.... .......... ...YPLYRFV RQEVGAVYLT GEK.......
Zm00008a016754_P01                                         ITECRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Zm00008a022372_P01                                         IADCRS.... .......... ...YPLYRFV REELGAVYLT GEK.......
Zm00008a022370_P01                                         ITDCRSYPLY RFVREELGAV YLYPLYRFV REELGAVYLT GEK.......
Osa_LOC_Os02g41670.1                                       ITECRS.... .......... ...YPLYRFV REELGTAYLT GEK.......
Osa_LOC_Os02g41680.1                                       ITECRS.... .......... ...YPLYRFV REELGTKYLT GEK.......
Bradi3g47110.1.p                                           IAECRS.... .......... ...YPLYRFV RQELGTVYLT GEK.......
Bradi3g47120.1.p                                           IAECRS.... .......... ...YPLYRFV RQELGTVYLT GEK.......
Bradi3g49270.1.p                                           ITECRS.... .......... ...YPLYRFV REELGTVFLT GEK.......
Bradi3g48840.1.p                                           IKECRS.... .......... ...YPLYRFV REELGTAYLT GEK.......
Bradi3g49280.1.p                                           IKECRS.... .......... ...YPLYRFV REELGTAYLT GEK.......
Osa_LOC_Os05g35290.1                                       IAECRS.... .......... ...YPLYRFV REELGTAYLT GEK.......
PavTc.1KG386300.1.p                                        IKDSRS.... .......... ...FPLYRFV REELGCVFLT GEK.......
Pavir.1NG356400.1.p                                        IKECRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
PhHAL.1G306800.1.p                                         IKECRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
Seita.1G240300.1.p                                         IKECRS.... .......... ...YPLYRFV REELGAEYLT GEK.......
Sevir.1G245100.1.p                                         IKECRS.... .......... ...YPLYRFV REELGAEYLT GEK.......
Zm00008a016751_P01                                         IKECRS.... .......... ...YPLYRFV REEVGTEYLT GEK.......
Zm00008a022369_P01                                         IRECRS.... .......... ...YPLYRFV REEVGTEYLT GER.......
Sobic.004G220400.1.p                                       IKECRS.... .......... ...YPLYRFV REEVGTQYLT GEK.......
Osa_LOC_Os02g41650.1                                       IKECRS.... .......... ...YPLYRFV REEVGTEYLT GEK.......
Osa_LOC_Os11g48110.1                                       ISDCRS.... .......... ...YPLYRFV RKELGAEYLT GEK.......
Osa_LOC_Os12g33610.1                                       ITQCRS.... .......... ...YPLYRFV RKELGAEYLT GEK.......
SobTc.001G160500.1.p                                       IAECRS.... .......... ...YPLYRFV REELGAEYLT GEK.......
Zm00008a004629_P01                                         ITECRS.... .......... ...YPLYRFV REELGAEYLT GEK.......
Bradi3g49260.1.p                                           IKDCRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
STRANG_00039013-RA                                         IKACRS.... .......... ...YPLYRFV REELGTEYLS GEK.......
STRANG_00039015-RA                                         IKECRS.... .......... ...YPLYRFA REELGTDYLT GEK.......
Pavir.7KG227800.1.p                                        IAECRS.... .......... ...YPLYRFV RQELGTEYLT GEK.......
PhHAL.7G214000.1.p                                         IAECRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
Pavir.1NG361819.1.p                                        IAECRS.... .......... ...Y...... ...LAT.... ..........
Pavir.7NG355800.1.p                                        IAECRS.... .......... ...YPLYRFV RQELGTEYLT GEK.......
Sevir.7G178300.1.p                                         IAECRS.... .......... ...YPLYRFV REELGTQYLT GEK.......
Seita.7G168800.1.p                                         IAECRS.... .......... ...YPLYRFV REELGTQYLT GEK.......
Zm00008a006866_P01                                         IAECRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
Sobic.006G148900.1.p                                       IAECRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
Pavir.4KG229700.2.p                                        .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                       ITECRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
Osa_LOC_Os08g21670.1                                       ITECKS.... .......... ...YSLYRFV CKELRTEYLT GKKIDAVAKS
Bradi5g15830.1.p                                           IAECRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
STRANG_00041444-RA                                         ITECRS.... .......... ...YPLYRFV REELGAKYLT GEK.......
STRANG_00041441-RA                                         TLECWL.... .......... ...YPLYQFM REKLGVEDLT GEM.......
STRANG_00041440-RA                                         ...CRA.... .....PRG.. ...Y...... .......... ..........
STRANG_00059682-RA                                         VKECRS.... .......... ...YPLYRFV RDEAGAEYLT GEK.......
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Aco013943.1                                                IKECRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
Aco007727.1                                                VKECRS.... .......... ...YPLYRFI REELGTEYLT GER.......
Apos_PKA46439.1                                            IMECRS.... .......... ...YPLYRFV REELGSEFLT GEK.......
Apos_PKA58411.1                                            IMLCRS.... .......... ...YPLYRFV REELGSEFLT GEK.......
Apos_PKA54143.1                                            IKDCRS.... .......... ...YPIYRFV REELGTGFLS GNS.......
Dcat_XP_020704813.1                                        IKECRS.... .......... ...YPLYRFV REELGASFLT GEK.......
Pequ_XP_020589738.1                                        IKECRS.... .......... ...YPLYRFV REELGAGFLT GEK.......
Dcat_XP_020702280.1                                        IKDCRS.... .......... ...YPIYRFV REELGTSFLT GEE.......
Apos_PKA59591.1                                            IRDCRS.... .......... ...YPLYRFV K.EVGAGFLT GEK.......
Apos_PKA60166.1                                            IRECRS.... .......... ...YPLYRFV K.ETGAGFLT GEK.......
Pequ_XP_020579635.1                                        IKDCRS.... .......... ...YPLYRFV K.QVGAGFLT GEK.......
Spipo31G0025500                                            IEDCRS.... .......... ...YPLYKFV REELGTAMLT GEK.......
Spipo1G0003500                                             IKECRS.... .......... ...YPLYKFV REELGTSLLT GEK.......
GSMUA_Achr8P18960_001                                      ...CRS.... .......... ...YPLYRFV REELGTAYLT GEK.......
GSMUA_Achr11P22840_001                                     ..ECRS.... .......... ...YPLYRFV RKELGAAYLT GEK.......
GSMUA_Achr5P18560_001                                      ...CRS.... .......... ...YPLYRLV REELGVAYLT GEK.......
GSMUA_Achr2P00240_001                                      ..ECRS.... .......... ...YPLYRFV REELGTACLT GEK.......
GSMUA_Achr11P16380_001                                     ...CRS.... .......... ...YPLYRFV REELGTEYLT GEK.......
GSMUA_Achr5P03950_001                                      ..ECRS.... .......... ...YPLYRFV RAELGTGYLT GEK.......
p5.00_sc00071_p0096.1                                      IKDCRS.... .......... ...YPLYRFV K.ELGTGFLT GEK.......
CALSI_Maker00040467                                        IKECRS.... .......... ...YPLYRFV REELGAGYLT GEK.......
Aco006987.1                                                IQECRS.... .......... ...YPLYRFV REELGAGYLT GEK.......
Aco027752.1                                                IQECRS.... .......... ...YPLYRFV REELGAGYLT GEK.......
GSMUA_Achr1P09070_001                                      ..ECRS.... .......... ...YPLYRLV REELKTGFLT GEK.......
p5.00_sc00334_p0073.1                                      IQECRS.... .......... ...YPLYRFV REELDTGLLT GEK.......
p5.00_sc00076_p0011.1                                      IKECRS.... .......... ...YPLYRFV RDELDAGFLT GEK.......
Aco010091.1                                                IKECRS.... .......... ...YPLYKFV REELGTECLT GEK.......
Aoff_XP_020259774.1                                        IKECRS.... .......... ...YPLYRFV REELGTELLT GEK.......
Aoff_XP_020259795.1                                        IKECRS.... .......... ...YPLYRFV REELGTELLT GEK.......
Aoff_XP_020259773.1                                        IKECRS.... .......... ...YPLYRFV REELGTELLT GEK.......
Aoff_XP_020248601.1                                        IKECRS.... .......... ...YPLYKFV REELGTGLLT GEK.......
Aoff_XP_020272851.1                                        IKECRS.... .......... ...YPLYRLV REELGAEYLT GER.......
Aoff_XP_020272852.1                                        IKECRS.... .......... ...YPLYRLV REELGAEYLT GER.......
Acamev11004816m                                            IAECRS.... .......... ...YPLYRFV REELKTGLLT GEK.......
Acamev11046066m                                            IEECRS.... .......... ...YPLYKFV REELKTGLLT GEK.......
Zosma445g00020.1                                           IEECRS.... .......... ...YPLYKFV REELRTGLLT GEK.......
Zosma69g00670.1                                            IKDCRS.... .......... ...YPLYRFV TEELGVGLLT GEK.......
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59                IKECRS.... .......... ...YPIYKFV RSVLGTELLS GER.......
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129               IKECRS.... .......... ...YPLYRFV RSELEVGELS GER.......
CALSI_Maker00043687                                        IRKCRT.... .......... ...YPVYQLV REELGTELLT GKK.......
CALSI_Maker00043684                                        IRKCRT.... .......... ...YPVYQLV REELGTELLT GEK.......
p5.00_sc01789_p0001.1                                      IKKCRT.... .......... ...CPVYRFV REELGTELLT GEK.......
p5.00_sc00066_p0001.1                                      INKCRT.... .......... ...YPMYKFV REEVGTELLT GEK.......
CALSI_Maker00043685                                        ISKCRT.... .......... ...YPVYKFV REEVGTELLT GEK.......
Aco020618.1                                                IEKCRT.... .......... ...YPVYRFV RAEVGTEMLT GEK.......
GSMUA_Achr9P15990_001                                      IKKCRT.... .......... ...YPVYNFV REEVGTELLT GEK.......
Zosma79g00480.1                                            IGKCRT.... .......... ...NGVYQLV RNVAQTEILT GEK.......
Zosma115g00180.1                                           IRKCRT.... .......... ...KSVYDLV RKVAQTEILT GEK.......
Spipo15G0044700                                            ARRCRT.... .......... ...YPIYKLV RSVAGAEFLT GEK.......
Acamev11008610m                                            AKKGRT.... .......... ...SAVYEFV RGEVGTELLT GEK.......
Acamev11024102m                                            AKKGRT.... .......... ...YPVYEFV RGEVGTELLT GEK.......
Acamev11050170m                                            ANKCRT.... .......... ...YELYQFV RGEVGTELLT GEK.......
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177               IKGCRT.... .......... ...YPVYKFV RSEMGTALLS GTT.......
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178               IKRCRT.... .......... ...YPVYKFV RSEMGTALLR GTK.......
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181               IKKCRT.... .......... ...YPIYKFV RNEMGTALLS GTK.......
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Figure 8(continued)

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Sevir.6G187100.1.p                                     ........LK SPGEECNKVF VGISQ.GKLV D....PMLEC LK........
Seita.6G181000.1.p                                     ........LK SPGEECNKVF VGISQ.GKLV D....PMLEC LK........
Sevir.1G245000.1.p                                     ........LK SPGEECNKVF IGISQ.GKLI D....PMLEC LK........
Seita.1G240200.1.p                                     ........LK SPGEECNKVF IGISQ.GKLI D....PMLEC LK........
PhHAL.1G306700.1.p                                     ........LK SPGEECNKVF VGISE.GKLI D....PMLEC LK........
Pavir.1NG356200.1.p                                    ........LK SPGEECNKVF IGISE.GKLV D....PMLEC LK........
Zm00008a016750_P01                                     ........LK SPGEECNKVF LGISQ.GKLV D....PMLEC LK........
Zm00008a022367_P01                                     ........LK SPGEECNKVF VGISQ.GKLV D....PMLEC LK........
Sobic.004G220300.1.p                                   ........LK SPGEECTKVF NGINQ.GKLV D....PMLEC LK........
Sevir.7G178200.1.p                                     ........LK SPGEECNKVF IGISQ.GKLI D....PMLEC LK........
Seita.7G168700.1.p                                     ........LK SPGEECNKVF IGISQ.GKLI D....PMLEC LK........
Osa_LOC_Os02g41630.2                                   ........LK SPGEECNKVF LGISQ.GKLI D....PMLDC LK........
Bradi3g49250.2.p                                       ........LL SPGEECNKVF IGISQ.GKLI D....PMLEC LK........
Pavir.7KG238255.1.p                                    ........LK SPGEECNKVF LALSE.GKLI D....PMLEC LK........
Pavir.7NG355500.1.p                                    ........LK SPGEECNKVF LALSE.GKLI D....PMLEC LK........
PhHAL.7G213800.1.p                                     ........LK SPGEECNKVF LALSE.GKLI D....PMLEC LK........
Zm00008a006867_P01                                     ........LK SPGEECNKVF LALSE.GKLI D....PMLDC LK........
Sobic.006G148800.1.p                                   ........LK SPGEECNKVF LALSE.GKLI D....PMLEC LK........
Seita.2G435800.1.p                                     ........LK SAGEECNKVF LALSE.GKLI D....PMLGC LK........
Sevir.2G448300.1.p                                     ........LK SAGEECNKVF LALSE.GKLI D....PMLGC LK........
Sevir.7G177900.1.p                                     ........LK SAGEECNKVF LALSE.GKLI D....PMLGC LK........
Seita.7G168500.1.p                                     ........LK SAGEECNKVF LALSE.GKLI D....PMLGC LK........
Osa_LOC_Os04g43760.1                                   ........LK SPGEECNKVF LAISE.RKLI D....PMLEC LK........
STRANG_00041445-RA                                     ........LR SPGEECNKVF VAINQ.GKLV D....PLLEC LK........
STRANG_00039019-RA                                     ........LR SPGEECNKVF VAISQ.GKLV D....PLLDC LK........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1   ........LR SPGEECNKVF VAINE.GKLI D....PLLEC LK........
Joascv11021323m                                        ........LR SPGEECNKVF VAINQ.GKLI D....PLLEC LK........

Joascv11021328m                                        ........LR SPGEECNKVF VAINQ.GKLI D....PLLEC LK........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1  ........VR SPGEECNKVF VAINK.GKLI D....PLLDC LN........
Flagellaria_indica_Trinity_comp23935_c0_seq1           ........TR SPGEECNKVF VAINE.GKVI D....PLLEC LK........

Seita.1G240400.1.p                                     ........TR SPGEELNKVL VAINE.GKHI D....PLLEC LK........
Sevir.1G245166.1.p                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Seita.1G240500.1.p                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Sevir.1G245232.1.p                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Seita.1G240600.1.p                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Sevir.1G245300.2.p                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
PhHAL.1G307000.1.p                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
PhHAL.1G307100.1.p                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
PhHAL.1G307200.1.p                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Pavir.1NG356700.1.p                                    ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Pavir.1NG356800.1.p                                    ........TR SPGEELNKVL VAINL.GKHI D....PLLEC LK........
Pavir.1KG386500.1.p                                    ........AR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Sobic.004G220600.2.p                                   ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Sobic.004G220500.1.p                                   ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Sobic.004G220700.1.p                                   ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Zm00008a016754_P01                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Zm00008a022372_P01                                     ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Zm00008a022370_P01                                     ........TR SPGEELNKVL IAINQ.GKHI D....PLLEC LK........
Osa_LOC_Os02g41670.1                                   ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Osa_LOC_Os02g41680.1                                   ........TR SPGEELNKVL VAINE.GKHI D....PLLEC LK........
Bradi3g47110.1.p                                       ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Bradi3g47120.1.p                                       ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Bradi3g49270.1.p                                       ........TR SPGEELNKVL MAINQ.GKHI D....PLLEC LK........
Bradi3g48840.1.p                                       ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Bradi3g49280.1.p                                       ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Osa_LOC_Os05g35290.1                                   ........TR SPGEELNKVL VAINQ.GKHI D....PLLEC LK........
Pavir.1KG386300.1.p                                    ........LK SPGEECNKVF VGISE.GKLV D....PMLEC LK........
Pavir.1NG356400.1.p                                    ........TR SPGEELNKVL VAINQ.RKHI D....PLLEC LK........
PhHAL.1G306800.1.p                                     ........TR SPGEELNKVL VAINQ.RKHI D....PLLEC LK........
Seita.1G240300.1.p                                     ........TR SPGEELNKVL VAINE.RKHI D....PLLEC LK........
Sevir.1G245100.1.p                                     ........TR SPGEELNKVL VAINE.RKHI D....PLLEC LK........
Zm00008a016751_P01                                     ........TR SPGEELNKVL VAINQ.RKHI D....PLLEC LKXAINQ..R
Zm00008a022369_P01                                     ........TR SPGEELNKVL VAINQ.RKHI D....PLLEC LK........
Sobic.004G220400.1.p                                   ........TR SPGEELNKVL VAINQ.RKHV D....PLLEC LK........
Osa_LOC_Os02g41650.1                                   ........TR SPGEELNKVL VAINE.RKHI D....PLLEC LK........
Osa_LOC_Os11g48110.1                                   ........TR SPGEEVDKVV IAMNQ.RKHI N....PLLEC LS........
Osa_LOC_Os12g33610.1                                   ........TR SPGEEVDKVV IAMNQ.RKHI N....PLLEC LS........
Sobic.001G160500.1.p                                   ........TR SPGEEVDKVV IAMNQ.RKHI D....PLLEC LS........
Zm00008a004629_P01                                     ........TR SPGEEVDKVV IAMNQ.RKHI D....PLLQC LS........
Bradi3g49260.1.p                                       ........TR SPGEELNKVL VAMNQ.NKHI D....PLLEC LK........
STRANG_00039013-RA                                     ........TR SPGEELDKVL VAINQ.GKHI D....PLLEC LK........
STRANG_00039015-RA                                     ........AR SPGEEVDKVL VAINQ.GKHI D....PLLEC LK........
Pavir.7KG227800.1.p                                    ........TR SPGEEVNKVF VAMNA.GKHI D....AVLEC LK........
PhHAL.7G214000.1.p                                     ........TR SPGEEVNKVF VAMNA.GKHI D....AVLEC LK........
Pavir.1NG361819.1.p                                    .........R SPDEEVNKVF VAVNA.GKHI D....AMLEC LK........
Pavir.7NG355800.1.p                                    ........TR SPGEEVNKVF VAMNA.GKHI D....AVLEC LK........
Sevir.7G178300.1.p                                     ........TR SPGEEVDKVF VAMNL.GKHI D....AVLEC LK........
Seita.7G168800.1.p                                     ........TR SPGEEVDKVF VAMNL.GKHI D....AVLEC LK........
Zm00008a006866_P01                                     ........AR SPGEEVDKVF VAMNL.GKHI D....AVLEC LK........
Sobic.006G148900.1.p                                   ........TR SPGEEVNKVF VAMNL.GKHI D....AVLEC LK........
Pavir.4KG229700.2.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                   ........TR SPGEEVNKVF VAMNQ.GKHI D....ALLEC LK........
Osa_LOC_Os08g21670.1                                   QCSRRSSARR CPGKW..PLP RAAVENGTAP HAN..PITEC RSYSLYRPVR
Bradi5g15830.1.p                                       ........TR SPGEEVDKVF VAMNQ.GKHI D....ALLEC LK........
STRANG_00041444-RA                                     ........TR SPGEEVDKVF VAINQ.GKHI D....PLLEC LK........
STRANG_00041441-RA                                     ........TW SPDGEVDKVF VAINQ.GKHI D....PLLEC LK........
STRANG_00041440-RA                                     .......... .......... .......... .......... ..........
STRANG_00059682-RA                                     ........AR SPGEEVDKVF VAMNL.GKHI D....PLLDC LK........

Aco013943.1                                            ........VR SPGEEFDKVF VAINE.GKLI D....PLLEC LK........
Aco007727.1                                            ........VR SPGEECDKVF AAING.GLLI D....PLLEC LK........
Apos_PKA46439.1                                        ........VR SPGEEFDKVF NAICQ.GKAI N....PLLEC LK........
Apos_PKA58411.1                                        ........VR SPGEEFDKVF NAICQ.GKAI N....PLLEC LK........
Apos_PKA54143.1                                        ........VK SPGEEFDKVF DAICE.GKAI D....PLLEC LK........
Dcat_XP_020704813.1                                    ........VT SPGEEFDKVF EAISK.GKAI D....PLFEC LK........
Pequ_XP_020589738.1                                    ........VR SPGEEFDKVF DAISE.GKAI D....PLLEC LK........
Dcat_XP_020702380.1                                    ........VR SPGEEFDKVF NAICE.GKAI D....PLLEC LQ........
Apos_PKA59591.1                                        ........TR SPGEAFDKVF VAISE.GKVI D....PLLEC LK........
Apos_PKA50166.1                                        ........AR SPGEEFDKVF GAFCE.GKVI D....PLLEC LK........
Pequ_XP_020579635.1                                    ........IV SPGEEFDKVY NAICE.GKAI D....PLLEC LK........
Spipo31G0025500                                        ........VR SPGEEFDKVF TAISQ.GKVI D....PLENC LS........
Spipo1G0003500                                         ........VR SPGEEFDKVY VAISQ.GKVV D....PLEEC LR........
GSMUA_Achr8P18960_001                                  ........VR SPGEEFDKVF AAINR.GQLI D....PLLEC LK........
GSMUA_Achr11P22840_001                                 ........VR SPGEEFDKVF AAINK.GLLI D....PLMEC LK........
GSMUA_Achr5P18560_001                                  ........AR SPGEEFDKVF MAVNE.GLLI D....PLLEC LK........
GSMUA_Achr2P00240_001                                  ........VR SPGEEFDKVF VAING.GSLI D....PLLEC LK........
GSMUA_Achr11P16380_001                                 ........VR SPGEEFDKVF VAIDR.GLVI D....PLLEC LK........
GSMUA_Achr5P03950_001                                  ........VR SPGEDFDKLF AAINK.GMVI D....PLLEC LK........
p5.00_sc00071_p0096.1                                  ........VR SPGEEFDKVF VAINR.GMVI D....PLLEC LK........
CALSI_Maker00040467                                    ........AR SPGEEFNKVF VAISR.GLVI D....PLFEC LK........
Aco006987.1                                            ........VR SPGEEFNKVF NAICK.GKAI D....PMLEC LK........
Aco027752.1                                            ........VR SPGEEFNKVF NAICK.GKAI D....PMLEC LK........
GSMUA_Achr1P09070_001                                  ........VI SPGEEFDKVF DAICQ.GKVI D....PLLEC LK........
p5.00_sc00334_p0073.1                                  ........VR SPGEEFDKVF DAICE.AKVI E....PLLEC LK........
p5.00_sc00076_p0011.1                                  ........VR SPGEEFNKVF NAICE.GKVI D....PLLEC LK........
Aco010091.1                                            ........VR SPGEEFDKVF DAICQ.AKMI D....PLLEC LK........
Aoff_XP_020259774.1                                    ........VR SPGEEFDKVF VAISQ.GKMI D....AVLAC LK........
Aoff_XP_020259795.1                                    ........VR SPGEEFDKVF VAISQ.GKMI D....AVLAC LK........
Aoff_XP_020259773.1                                    ........VR SPGEEFDKVF VAISQ.GKMI D....AVLAC LK........
Aoff_XP_020248601.1                                    ........VR SPGEEFDKVF VAISE.GKVI D....PMLEC LR........
Aoff_XP_020272851.1                                    ........VR SPGEEFDKVF NAICG.GKLI D....PLLEC LS........
Aoff_XP_020272852.1                                    ........VR SPGEEFDKVF NAICG.GKLI D....PLLEC LS........
Acamev11004816m                                        ........VR SPGEEFDKVF VAISE.GKVI D....PLLEC LS........
Acamev11046066m                                        ........VR SPGEEFDKVF VAISQ.GKVI D....PLLEC LS........
Zosma445g00020.1                                       ........VR SPGEEFDKVF VAINE.GELV G....PLMEC LK........
Zosma69g00670.1                                        ........IR SPGEEFDKVF AAINR.GELI D....PLFHC LA........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59            ........QR SPGEEFDKVF EAIRG.GKII E....PLLDC VK........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129           ........TV SPGEEFNKVS IAINK.GKLI D....PLLEC LH........
CALSI_Maker00043687                                    ........KV SPGEHIEKVY QAIVE.GKVG S....VVVKC VE........
CALSI_Maker00043684                                    ........KV SPGEYIEKVY QAIGE.GKVG S....VVVKC VE........
p5.00_sc01789_p0001.1                                  ........KV SPGEYIEKVY QAIGE.GKVG S....VVVEC VE........
p5.00_sc00066_p0001.1                                  ........KV SPGEYIEKVY EAMKE.RKEF YYHIVYIMSV IH........
CALSI_Maker00043685                                    ........KV SPGEYIEKVC EAMKE.KRVG E....VIVEC IE........
Aco020618.1                                            ........RA SPGEHIEKVY AAMGEKGRIG E....VVVEC VG........
GSMUA_Achr9P15990_001                                  ........K. .......... .......... .....VVVKC VG........
Zosma79g00480.1                                        ........KV SPGECIEKVY DCILQ.GKLE D....VLVKC LS........
Zosma115g00180.1                                       ........KI SPGECIESVY EVFEQ.GKVE D....AILQC LD........
Spipo15G0044700                                        ........KI SPGECIEKVV DAIDE.GKLG D....ALSAC LA........
Acamev11008610m                                        ........KT SPGEQIEKVY EAMME.GKVE G....VLMRC LS........
Acamev11024102m                                        ........KT SPGEQIEKVY EAVME.GKVE E....VLMRC LS........
Acamev11050170m                                        ........KT SPGEYIEKVY SAMKE.GKVE D....VLMKC LP........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177           ........KV SPGEEIEKVY EGISE.GKLG N....VLLQC LS........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178           ........KV SPGEEIEKVY EGISE.GKLG N....VLLQC LS........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181           ........QT SPGEEIEKVY EGISE.GKLG K....VLLQC LS........
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Figure 8(continued)

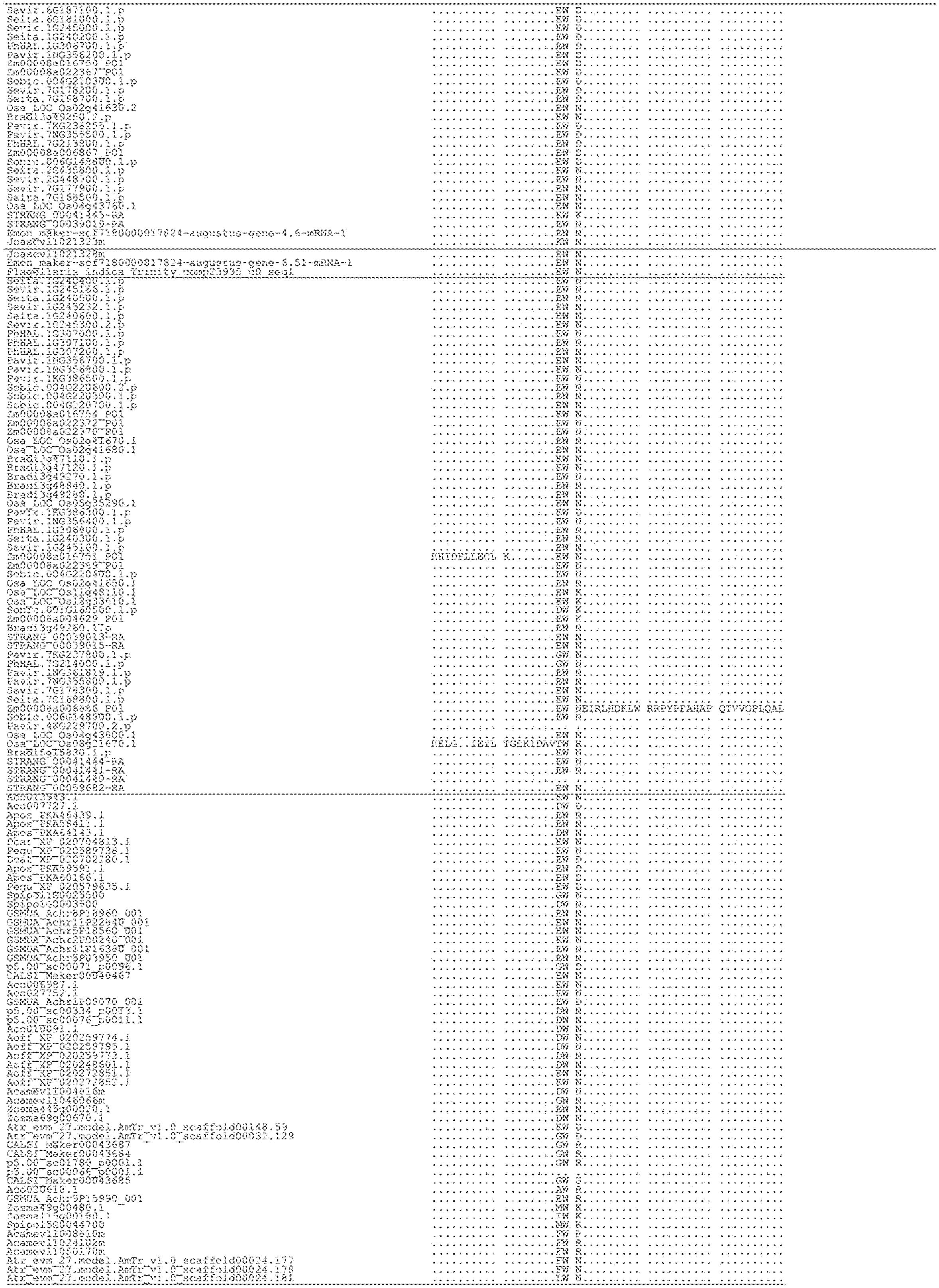

Figure 8(continued)

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Sevir.6G187100.1.p                                      .......... .GKPLPINX. .......... .......... ..........
Seita.6G181000.1.p                                      .......... .GKPLPINX. .......... .......... ..........
Sevir.1G245000.1.p                                      .......... .GKPLPINX. .......... .......... ..........
Seita.1G240200.1.p                                      .......... .GKPLPINX. .......... .......... ..........
PhHAL.1G306700.1.p                                      .......... .GKPLPINX. .......... .......... ..........
Pavir.1NG356200.1.p                                     .......... .GKPLPINX. .......... .......... ..........
Zm00008a016750_P01                                      .......... .GKPLPININ X......... .......... ..........
Zm00008a022367_P01                                      .......... .GKPLPINVX X......... .......... ..........
Sobic.004G220300.1.p                                    .......... .GKPLPINVV NX........ .......... ..........
Sevir.7G178200.1.p                                      .......... .GKPLPICX. .......... .......... ..........
Seita.7G168700.1.p                                      .......... .GKPLPICX. .......... .......... ..........
Osa_LOC_Os02g41630.2                                    .......... .GEPLPINX. .......... .......... ..........
Bradi3g49250.2.p                                        .......... .GEPLPINVV X......... .......... ..........
Pavir.7KG238255.1.p                                     .......... .GKPLPICX. .......... .......... ..........
Pavir.7NG355500.1.p                                     .......... .GKPLPICX. .......... .......... ..........
PhHAL.7G213800.1.p                                      .......... .GKPLPICX. .......... .......... ..........
Zm00008a006867_P01                                      .......... .GEPLPICX. .......... .......... ..........
Sobic.006G148800.1.p                                    .......... .GKPLPICX. .......... .......... ..........
Seita.2G435800.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Sevir.2G448300.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Sevir.7G177900.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Seita.7G168500.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Osa_LOC_Os04g43760.1                                    .......... .GEPLPICX. .......... .......... ..........
STRANG_00041445-RA                                      .......... .GEPLPIC.. .......... .......... ..........
STRANG_00039019-RA                                      .......... .GEPLPIC.. .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1    .......... .GEPLPIC.. .......... .......... ..........
Joascv11021323m                                         .......... .GEPLPICX. .......... .......... ..........
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Joascv11021328m                                         .......... .GEPLPICX. .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1   .......... .GEPLPIC.. .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1            .......... .GEPLPIC.. .......... .......... ..........
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Seita.1G240400.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Sevir.1G245166.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Seita.1G240500.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Sevir.1G245232.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Seita.1G240600.1.p                                      .......... .GEPLPISX. .......... .......... ..........
Sevir.1G245300.2.p                                      .......... .GEPLPISX. .......... .......... ..........
PhHAL.1G307000.1.p                                      .......... .GEPLPICX. .......... .......... ..........
PhHAL.1G307100.1.p                                      .......... .GEPLPICX. .......... .......... ..........
PhHAL.1G307200.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Pavir.1NG356700.1.p                                     .......... .GEPLPICX. .......... .......... ..........
Pavir.1NG356800.1.p                                     .......... .GEPLPICX. .......... .......... ..........
Pavir.1KG386500.1.p                                     .......... .GEPLPICX. .......... .......... ..........
Sobic.004G220600.2.p                                    .......... .GEPLPICX. .......... .......... ..........
Sobic.004G220500.1.p                                    .......... .GEPLPICX. .......... .......... ..........
Sobic.004G220700.1.p                                    .......... .GEPLPICX. .......... .......... ..........
Zm00008a016754_P01                                      .......... .GEPLPICX. .......... .......... ..........
Zm00008a022372_P01                                      .......... .GEPLPICX. .......... .......... ..........
Zm00008a022370_P01                                      .......... .GEPLPICX. .......... .......... ..........
Osa_LOC_Os02g41670.1                                    .......... .GAPLPICX. .......... .......... ..........
Osa_LOC_Os02g41680.1                                    .......... .GEPLPICX. .......... .......... ..........
Bradi3g47110.1.p                                        .......... .GSPLPICX. .......... .......... ..........
Bradi3g47120.1.p                                        .......... .GSPLPICX. .......... .......... ..........
Bradi3g49270.1.p                                        .......... .GEPLPICX. .......... .......... ..........
Bradi3g48840.1.p                                        .......... .GEPLPICX. .......... .......... ..........
Bradi3g49280.1.p                                        .......... .GEPLPICX. .......... .......... ..........
Osa_LOC_Os05g35290.1                                    .......... .GAPLPICX. .......... .......... ..........
Pavir.1KG386300.1.p                                     .......... .GKPLPINX. .......... .......... ..........
Pavir.1NG356400.1.p                                     .......... .GEPLPLCX. .......... .......... ..........
PhHAL.1G306800.1.p                                      .......... .GEPLPLCX. .......... .......... ..........
Seita.1G240300.1.p                                      .......... .GEPLPLCX. .......... .......... ..........
Sevir.1G245100.1.p                                      .......... .GEPLPLCX. .......... .......... ..........
Zm00008a016751_P01                                      .......... .GEPLPLCX. .......... .......... ..........
Zm00008a022369_P01                                      .......... .GAPLPLCX. .......... .......... ..........
Sobic.004G220400.1.p                                    .......... .GEPLPLCX. .......... .......... ..........
Osa_LOC_Os02g41650.1                                    .......... .GAPLPLCX. .......... .......... ..........
Osa_LOC_Os11g48110.1                                    .......... .GAPLPLSKM SMSINGVSPS PQSFRPPTLP LPVEEENPFC
Osa_LOC_Os12g33610.1                                    .......... .GAPLPLNX. .......... .......... ..........
Sobic.001G160500.1.p                                    .......... .GAPLRATX. .......... .......... ..........
Zm00008a004629_P01                                      .......... .GAPLPIIX. .......... .......... ..........
Bradi3g49260.1.p                                        .......... .GEPLPLCX. .......... .......... ..........
STRANG_00039013-RA                                      .......... .GKPLPIC.. .......... .......... ..........
STRANG_00039015-RA                                      .......... .GEPLPIC.. .......... .......... ..........
Pavir.7KG237800.1.p                                     .......... .GSPLPICX. .......... .......... ..........
PhHAL.7G214000.1.p                                      .......... .GEPLPICX. .......... .......... ..........
Pavir.1NG361819.1.p                                     .......... .GEPMEMTTD PAP....... .......... ..........
Pavir.7NG355800.1.p                                     .......... .GEPLPICX. .......... .......... ..........
Sevir.7G178300.1.p                                      .......... .GEPLSICX. .......... .......... ..........
Seita.7G168800.1.p                                      .......... .GEPLSICX. .......... .......... ..........
Zm00008a006866_P01                                      LVFLPRRCTD ESSPGTVCIP PQAPGG.... ......RVIP ..........
Sobic.006G148900.1.p                                    .......... .GEPLPICX. .......... .......... ..........
Pavir.4KG229700.2.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                    .......... .GEPLPICX. .......... .......... ..........
Osa_LOC_Os08g21670.1                                    .......... .GCEQGVPRH EPG.SG.... .......... ..........
Bradi5g15830.1.p                                        .......... .GEPLPLCX. .......... .......... ..........
STRANG_00041444-RA                                      .......... .GEPLPIC.. .......... .......... ..........
STRANG_00041441-RA                                      .......... .......... .......... .......... ..........
STRANG_00041440-RA                                      .......... .......... .......... .......... ..........
STRANG_00059682-RA                                      .......... .GEPLSICRT .......... .......... ..........
------------------------------------------------------------------------------------------------------
Aco013943.1                                             .......... .GEPLPICX. .......... .......... ..........
Aco007727.1                                             .......... .GAPLPICX. .......... .......... ..........
Apos_PKA46439.1                                         .......... .GTPLPIC.. .......... .......... ..........
Apos_PKA58411.1                                         .......... .GVPLPIC.. .......... .......... ..........
Apos_PKA64143.1                                         .......... .GSPLPIS.. .......... .......... ..........
Dcat_XP_020704813.1                                     .......... .GAPLPIC.. .......... .......... ..........
Pequ_XP_020589738.1                                     .......... .GAPLPIC.. .......... .......... ..........
Dcat_XP_020702380.1                                     .......... .GAPLPIC.. .......... .......... ..........
Apos_PKA59591.1                                         .......... .GAPLPIC.. .......... .......... ..........
Apos_PKA60166.1                                         .......... .GAPLPIC.. .......... .......... ..........
Pequ_XP_020579635.1                                     .......... .GAPLPIC.. .......... .......... ..........
Spipo31G0025500                                         .......... .GSPVPICX. .......... .......... ..........
Spipo1G0003500                                          .......... .GAPVPICX. .......... .......... ..........
GSMUA_Achr8P18960_001                                   .......... .GAPLPICX. .......... .......... ..........
GSMUA_Achr11P22840_001                                  .......... .GAPLPICX. .......... .......... ..........
GSMUA_Achr5P18560_001                                   .......... .GAPLPICX. .......... .......... ..........
GSMUA_Achr2P00240_001                                   .......... .GAPLPICX. .......... .......... ..........
GSMUA_Achr11P16380_001                                  .......... .GVPLPNCX. .......... .......... ..........
GSMUA_Achr5P03950_001                                   .......... .GAPLPICX. .......... .......... ..........
p5.00_sc00071_p0096.1                                   .......... .GAPLPLHX. .......... .......... ..........
CALSI_Maker00040467                                     .......... .GAPLPLCX. .......... .......... ..........
Aco006987.1                                             .......... .GAPLPLCX. .......... .......... ..........
Aco027752.1                                             .......... .GAPLPLCX. .......... .......... ..........
GSMUA_Achr1P09070_001                                   .......... .GAPIPICX. .......... .......... ..........
p5.00_sc00334_p0073.1                                   .......... .GAPLPICX. .......... .......... ..........
p5.00_sc00076_p0011.1                                   .......... .GAPLPICX. .......... .......... ..........
Aco010091.1                                             .......... .GAPLPISX. .......... .......... ..........
Aoff_XP_020259774.1                                     .......... .GAPLPIC.. .......... .......... ..........
Aoff_XP_020259795.1                                     .......... .GAPLPIC.. .......... .......... ..........
Aoff_XP_020259773.1                                     .......... .GAPLPIC.. .......... .......... ..........
Aoff_XP_020248601.1                                     .......... .GAPLPIC.. .......... .......... ..........
Aoff_XP_020272851.1                                     .......... .GAPIPIC.. .......... .......... ..........
Aoff_XP_020272852.1                                     .......... .GAPIPIC.. .......... .......... ..........
Acamev11004816m                                         .......... .GAPIPICX. .......... .......... ..........
Acamev11046066m                                         .......... .GAPIPICX. .......... .......... ..........
Zosma445g00020.1                                        .......... .GAPIPICX. .......... .......... ..........
Zosma69g00670.1                                         .......... .GSPLPISX. .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59             .......... .GTPLPICX. .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129            .......... .GAPLPICX. .......... .......... ..........
CALSI_Maker00043687                                     .......... .GSAGPFTPR PDV....... .......... ..........
CALSI_Maker00043684                                     .......... .GSAGPFTPR PNV....... .......... ..........
p5.00_sc01789_p0001.1                                   .......... .GSAGPFTPR PEV....... .......... ..........
p5.00_sc00066_p0001.1                                   .......... .....PLSX. .......... .......... ..........
CALSI_Maker00043685                                     .......... .GLA...... .......... .......... ..........
Aco020618.1                                             .......... .GTPGPFTPR PEV....... .......... ..........
GSMUA_Achr9P15990_001                                   .......... .GSAGPFTPR PEA....... .......... ..........
Zosma79g00480.1                                         .......... .GMAGPFSPR PDL....... .......... ..........
Zosma115g00180.1                                        .......... .GNTGPFTPR PEL....... .......... ..........
Spipo15G0044700                                         .......... .GSAGPFTPR PEV....... .......... ..........
Acamev11008610m                                         .......... .GSAGPFTPR PAA....... .......... ..........
Acamev11024102m                                         .......... .GSAGPFTPR PTA....... .......... ..........
Acamev11050170m                                         .......... .GSAGPFTPR PAG....... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177            .......... .GLAGPFTPH SVP....... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178            .......... .GLAGPFTPH SVP....... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181            .......... .GLAGPFTPR PVP....... .......... ..........
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Figure 8(continued)

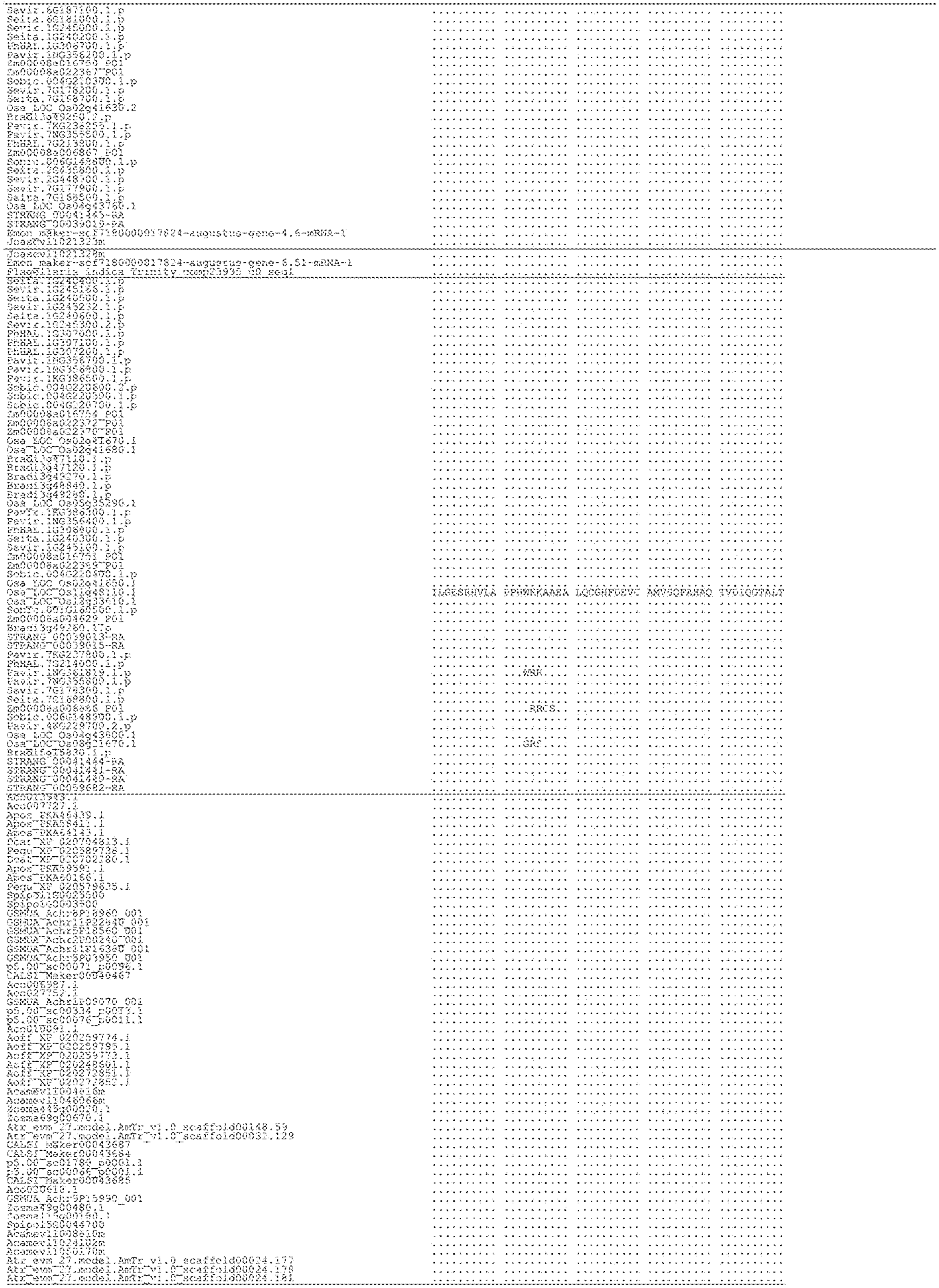

Figure 8(continued)

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Sevir.6G187100.1.p                                      .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                      .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                      .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                     .......... .......... .......... .......... ..........
Zm00008a016750_P01                                      .......... .......... .......... .......... ..........
Zm00008a022367_P01                                      .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                    .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                      .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                      .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                    .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                        .......... .......... .......... .......... ..........
Pavir.7KG238255.1.p                                     .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                     .......... .......... .......... .......... ..........
PhHAL.7G213900.1.p                                      .......... .......... .......... .......... ..........
Zm00008a006867_P01                                      .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                    .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                      .......... .......... .......... .......... ..........
Sevir.2G448300.1.p                                      .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                      .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                      .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                    .......... .......... .......... .......... ..........
STRANG_00041445-RA                                      .......... .......... .......... .......... ..........
STRANG_00039019-RA                                      .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1    .......... .......... .......... .......... ..........
Joascv11021323m                                         .......... .......... .......... .......... ..........
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Joascv11021328m                                         .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1   .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1            .......... .......... .......... .......... ..........
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Seita.1G240400.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                      .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                      .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                      .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                      .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                      .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                     .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                     .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                    .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                    .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                    .......... .......... .......... .......... ..........
Zm00008a016754_P01                                      .......... .......... .......... .......... ..........
Zm00008a022372_P01                                      .......... .......... .......... .......... ..........
Zm00008a022370_P01                                      .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                    .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                    .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                        .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                        .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                        .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                        .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                        .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                    .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                      .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                      .......... .......... .......... .......... ..........
Zm00008a016751_P01                                      .......... .......... .......... .......... ..........
Zm00008a022369_P01                                      .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                    .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                    VAQVTALAPG DHVRVALDEA AARGRVTRSA DWVAENISPG TDTYGVTTSF
Osa_LOC_Os12g33610.1                                    .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                    .......... .......... .......... .......... ..........
Zm00008a004629_P01                                      .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                        .......... .......... .......... .......... ..........
STRANG_00039013-RA                                      .......... .......... .......... .......... ..........
STRANG_00039015-RA                                      .......... .......... .......... .......... ..........
Pavir.7KG227800.1.p                                     .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                     .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                     .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                      .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                      .......... .......... .......... .......... ..........
Zm00008a006866_P01                                      .......... .......... .......... .......... ......SSSL
Sobic.006G148900.1.p                                    .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                    .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                    .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                        .......... .......... .......... .......... ..........
STRANG_00041444-RA                                      .......... .......... .......... .......... ..........
STRANG_00041441-RA                                      .......... .......... .......... .......... ..........
STRANG_00041440-RA                                      .......... .......... .......... .......... ..........
STRANG_00059682-RA                                      .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------------------
Aco013943.1                                             .......... .......... .......... .......... ..........
Aco007727.1                                             .......... .......... .......... .......... ..........
Apos_PKA46439.1                                         .......... .......... .......... .......... ..........
Apos_PKA58411.1                                         .......... .......... .......... .......... ..........
Apos_PKA54143.1                                         .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                     .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                     .......... .......... .......... .......... ..........
Dcat_XP_020702280.1                                     .......... .......... .......... .......... ..........
Apos_PKA59591.1                                         .......... .......... .......... .......... ..........
Apos_PKA60166.1                                         .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                     .......... .......... .......... .......... ..........
Spipo11G0025500                                         .......... .......... .......... .......... ..........
Spipo1G0003500                                          .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr11P16380_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                   .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                   .......... .......... .......... .......... ..........
CALSI_Maker00040467                                     .......... .......... .......... .......... ..........
Aco006987.1                                             .......... .......... .......... .......... ..........
Aco027752.1                                             .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                   .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                   .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                   .......... .......... .......... .......... ..........
Aco010091.1                                             .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                     .......... .......... .......... .......... ..........
Acamev11004816m                                         .......... .......... .......... .......... ..........
Acamev11046066m                                         .......... .......... .......... .......... ..........
Zosma445g00020.1                                        .......... .......... .......... .......... ..........
Zosma69g00670.1                                         .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59             .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129            .......... .......... .......... .......... ..........
CALSI_Maker00043687                                     .......... .......... .......... .......... ..........
CALSI_Maker00043684                                     .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                   .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                   .......... .......... .......... .......... ..........
CALSI_Maker00043685                                     .......... .......... .......... .......... ..........
Aco020618.1                                             .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                   .......... .......... .......... .......... ..........
Zosma79g00480.1                                         .......... .......... .......... .......... ..........
Zosma115g00180.1                                        .......... .......... .......... .......... ..........
Spipo15G0044700                                         .......... .......... .......... .......... ..........
Acamev11008610m                                         .......... .......... .......... .......... ..........
Acamev11024102m                                         .......... .......... .......... .......... ..........
Acamev11050170m                                         .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177            .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178            .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181            .......... .......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                    .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                    .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                   .......... .......... .......... .......... ..........
Zm00008a016750_P01                                    .......... .......... .......... .......... ..........
Zm00008a022367_P01                                    .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                  .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                    .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                  .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                      .......... .......... .......... .......... ..........
Pavir.7KG232255.1.p                                   .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                   .......... .......... .......... .......... ..........
PhHAL.7G213800.1.p                                    .......... .......... .......... .......... ..........
Zm00008a006867_P01                                    .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                  .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                    .......... .......... .......... .......... ..........
Sevir.2G448700.1.p                                    .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                    .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                  .......... .......... .......... .......... ..........
STRANG_00041445-RA                                    .......... .......... .......... .......... ..........
STRANG_00039019-RA                                    .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1  .......... .......... .......... .......... ..........
Joasevl1021323m                                       .......... .......... .......... .......... ..........
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Joasevl1021328m                                       .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1 .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1          .......... .......... .......... .......... ..........
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Seita.1G240400.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                    .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                    .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                    .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                   .......... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                   .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                   .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                  .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                  .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                  .......... .......... .......... .......... ..........
Zm00008a016754_P01                                    .......... .......... .......... .......... ..........
Zm00008a022372_P01                                    .......... .......... .......... .......... ..........
Zm00008a022370_P01                                    .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                  .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                  .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                      .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                      .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                      .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                      .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                      .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                  .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                   .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                   .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                    .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                    .......... .......... .......... .......... ..........
Zm00008a016751_P01                                    .......... .......... .......... .......... ..........
Zm00008a022369_P01                                    .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                  .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                  .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                  GATSHRRTNK TADLQTELIR FLRAGVISKE TLPASFSKAA MLVRAFTLMQ
Osa_LOC_Os12g33610.1                                  .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                  .......... .......... .......... .......... ..........
Zm00008a004629_P01                                    .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                      .......... .......... .......... .......... ..........
STRANG_00039013-RA                                    .......... .......... .......... .......... ..........
STRANG_00039015-RA                                    .......... .......... .......... .......... ..........
Pavir.7KG237800.1.p                                   .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                   .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                   .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                    .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                    .......... .......... .......... .......... ..........
Zm00008a006866_P01                                    GA...RR... .......... .......... .......... ..........
Sobic.006G148900.1.p                                  .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                   .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                  .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                  .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                      .......... .......... .......... .......... ..........
STRANG_00041444-RA                                    .......... .......... .......... .......... ..........
STRANG_00041441-RA                                    .......... .......... .......... .......... ..........
STRANG_00041440-RA                                    .......... .......... .......... .......... ..........
STRANG_00059682-RA                                    .......... .......... .......... .......... ..........
-----------------------------------------------------------------------------------------------------------
Aco013943.1                                           .......... .......... .......... .......... ..........
Aco007727.1                                           .......... .......... .......... .......... ..........
Apos_PKA46439.1                                       .......... .......... .......... .......... ..........
Apos_PKA58411.1                                       .......... .......... .......... .......... ..........
Apos_PKA64143.1                                       .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                   .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                   .......... .......... .......... .......... ..........
Dcat_XP_020702380.1                                   .......... .......... .......... .......... ..........
Apos_PKA59591.1                                       .......... .......... .......... .......... ..........
Apos_PKA60166.1                                       .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                   .......... .......... .......... .......... ..........
Spipo11G0023500                                       .......... .......... .......... .......... ..........
Spipo1G0003500                                        .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr11P16380_001                                .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                 .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                 .......... .......... .......... .......... ..........
CALSI_Maker00040467                                   .......... .......... .......... .......... ..........
Aco006987.1                                           .......... .......... .......... .......... ..........
Aco027752.1                                           .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                 .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                 .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                 .......... .......... .......... .......... ..........
Aco010091.1                                           .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                   .......... .......... .......... .......... ..........
Acamevl1004816m                                       .......... .......... .......... .......... ..........
Acamevl1046066m                                       .......... .......... .......... .......... ..........
Zosma445g00020.1                                      .......... .......... .......... .......... ..........
Zosma69g00670.1                                       .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129          .......... .......... .......... .......... ..........
CALSI_Maker00043687                                   .......... .......... .......... .......... ..........
CALSI_Maker00043684                                   .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                 .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                 .......... .......... .......... .......... ..........
CALSI_Maker00043685                                   .......... .......... .......... .......... ..........
Aco020610.1                                           .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                 .......... .......... .......... .......... ..........
Zosma79g00480.1                                       .......... .......... .......... .......... ..........
Zosma115g00180.1                                      .......... .......... .......... .......... ..........
Spipo15G0044700                                       .......... .......... .......... .......... ..........
Acamevl1008610m                                       .......... .......... .......... .......... ..........
Acamevl1024102m                                       .......... .......... .......... .......... ..........
Acamevl1050170m                                       .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177          .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178          .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181          .......... .......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                     .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                    .......... .......... .......... .......... ..........
Zm00008a016750_P01                                     .......... .......... .......... .......... ..........
Zm00008a022367_P01                                     .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                   .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                   .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                       .......... .......... .......... .......... ..........
Pavir.7KG232255.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                    .......... .......... .......... .......... ..........
PhHAL.7G213800.1.p                                     .......... .......... .......... .......... ..........
Zm00008a006867_P01                                     .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                   .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                     .......... .......... .......... .......... ..........
Sevir.2G448700.1.p                                     .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                   .......... .......... .......... .......... ..........
STRANG_00041445-RA                                     .......... .......... .......... .......... ..........
STRANG_00039019-RA                                     .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1   .......... .......... .......... .......... ..........
Joascv11021323m                                        .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------
Joascv11021328m                                        .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1  .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1           .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356900.1.p                                    .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                    .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                   .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                   .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                   .......... .......... .......... .......... ..........
Zm00008a016754_P01                                     .......... .......... .......... .......... ..........
Zm00008a022372_P01                                     .......... .......... .......... .......... ..........
Zm00008a022370_P01                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                   .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                       .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                       .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                       .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                       .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                       .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                   .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                     .......... .......... .......... .......... ..........
Zm00008a016751_P01                                     .......... .......... .......... .......... ..........
Zm00008a022369_P01                                     .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                   .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                   GYSGIRWEIL EAMARLINLN LIPKLPLRGT ITASGDLVPL SYIAGVLTGR
Osa_LOC_Os12g33610.1                                   .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                   .......... .......... .......... .......... ..........
Zm00008a004629_P01                                     .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                       .......... .......... .......... .......... ..........
STRANG_00039013-RA                                     .......... .......... .......... .......... ..........
STRANG_00039015-RA                                     .......... .......... .......... .......... ..........
Pavir.7KG227800.1.p                                    .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                    .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                     .......... .......... .......... .......... ..........
Zm00008a006866_P01                                     .......... .......... ..PYPPAPAP QTATG...PL QALLVFLPG.
Sobic.006G148900.1.p                                   .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                   .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                       .......... .......... .......... .......... ..........
STRANG_00041444-RA                                     .......... .......... .......... .......... ..........
STRANG_00041441-RA                                     .......... .......... .......... .......... ..........
STRANG_00041440-RA                                     .......... .......... .......... .......... ..........
STRANG_00059682-RA                                     .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------
Aco013943.1                                            .......... .......... .......... .......... ..........
Aco007727.1                                            .......... .......... .......... .......... ..........
Apos_PKA46439.1                                        .......... .......... .......... .......... ..........
Apos_PKA58411.1                                        .......... .......... .......... .......... ..........
Apos_PKA54143.1                                        .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                    .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                    .......... .......... .......... .......... ..........
Dcat_XP_020702280.1                                    .......... .......... .......... .......... ..........
Apos_PKA59591.1                                        .......... .......... .......... .......... ..........
Apos_PKA60166.1                                        .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                    .......... .......... .......... .......... ..........
Spipo11G0025500                                        .......... .......... .......... .......... ..........
Spipo1G0003500                                         .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P16380_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                  .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                  .......... .......... .......... .......... ..........
CALSI_Maker00040467                                    .......... .......... .......... .......... ..........
Aco006987.1                                            .......... .......... .......... .......... ..........
Aco027752.1                                            .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                  .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                  .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                  .......... .......... .......... .......... ..........
Aco010091.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                    .......... .......... .......... .......... ..........
Acamev1I004816m                                        .......... .......... .......... .......... ..........
Acamev1I046066m                                        .......... .......... .......... .......... ..........
Zosma445g00020.1                                       .......... .......... .......... .......... ..........
Zosma69g00670.1                                        .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59            .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129           .......... .......... .......... .......... ..........
CALSI_Maker00043687                                    .......... .......... .......... .......... ..........
CALSI_Maker00043684                                    .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                  .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                  .......... .......... .......... .......... ..........
CALSI_Maker00043685                                    .......... .......... .......... .......... ..........
Aco020610.1                                            .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                  .......... .......... .......... .......... ..........
Zosma79g00480.1                                        .......... .......... .......... .......... ..........
Zosma115g00180.1                                       .......... .......... .......... .......... ..........
Spipo15G0044700                                        .......... .......... .......... .......... ..........
Acamev1I008610m                                        .......... .......... .......... .......... ..........
Acamev1I024102m                                        .......... .......... .......... .......... ..........
Acamev1I050170m                                        .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181           .......... .......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                       .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                       .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                       .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                       .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                      .......... .......... .......... .......... ..........
Zm00008a016750_P01                                       .......... .......... .......... .......... ..........
Zm00008a022367_P01                                       .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                     .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                       .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                       .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                     .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                         .......... .......... .......... .......... ..........
Pavir.7KG238255.1.p                                      .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                      .......... .......... .......... .......... ..........
PhHAL.7G213900.1.p                                       .......... .......... .......... .......... ..........
Zm00008a006867_P01                                       .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                     .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                       .......... .......... .......... .......... ..........
Sevir.2G448300.1.p                                       .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                       .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                       .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                     .......... .......... .......... .......... ..........
STRANG_00041445-RA                                       .......... .......... .......... .......... ..........
STRANG_00039019-RA                                       .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1     .......... .......... .......... .......... ..........
Joascv11021328m                                          .......... .......... .......... .......... ..........
--------------------------------------------------------------------------------------------------------------
Joascv11021328m                                          .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1    .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1             .......... .......... .......... .......... ..........
--------------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                       .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                       .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                       .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                       .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                       .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                       .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                      .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                      .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                     .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                     .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                     .......... .......... .......... .......... ..........
Zm00008a016754_P01                                       .......... .......... .......... .......... ..........
Zm00008a022372_P01                                       .......... .......... .......... .......... ..........
Zm00008a022370_P01                                       .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                     .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                         .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                         .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                         .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                         .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                         .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                     .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                      .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                       .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                       .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                       .......... .......... .......... .......... ..........
Zm00008a016751_P01                                       .......... .......... .......... .......... ..........
Zm00008a022369_P01                                       .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                     .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                     HNSKVVTPEG ESTTAMEALK RAGIEAPFQL QAKEGLALVN GTAVGSAVAA
Osa_LOC_Os12g33610.1                                     .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                     .......... .......... .......... .......... ..........
Zm00008a004629_P01                                       .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                         .......... .......... .......... .......... ..........
STRANG_00039013-RA                                       .......... .......... .......... .......... ..........
STRANG_00039015-RA                                       .......... .......... .......... .......... ..........
Pavir.7KG237800.1.p                                      .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                       .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                      .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                      .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                       .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                       .......... .......... .......... .......... ..........
Zm00008a006866_P01                                       .......... .......... .......... .......... ..........
Sobic.006G148900.1.p                                     .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                      .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                     .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                     .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                         .......... .......... .......... .......... ..........
STRANG_00041444-RA                                       .......... .......... .......... .......... ..........
STRANG_00041441-RA                                       .......... .......... .......... .......... ..........
STRANG_00041440-RA                                       .......... .......... .......... .......... ..........
STRANG_00059682-RA                                       .......... .......... .......... .......... ..........
--------------------------------------------------------------------------------------------------------------
Aco013943.1                                              .......... .......... .......... .......... ..........
Aco007727.1                                              .......... .......... .......... .......... ..........
Apos_PKA46439.1                                          .......... .......... .......... .......... ..........
Apos_PKA58411.1                                          .......... .......... .......... .......... ..........
Apos_PKA54143.1                                          .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                      .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                      .......... .......... .......... .......... ..........
Dcat_XP_020702180.1                                      .......... .......... .......... .......... ..........
Apos_PKA59591.1                                          .......... .......... .......... .......... ..........
Apos_PKA60166.1                                          .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                      .......... .......... .......... .......... ..........
Spipo11G0025500                                          .......... .......... .......... .......... ..........
Spipo1G0003500                                           .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                    .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                    .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                    .......... .......... .......... .......... ..........
GSMUA_Achr11P16360_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                    .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                    .......... .......... .......... .......... ..........
CALSI_Maker00040467                                      .......... .......... .......... .......... ..........
Aco006987.1                                              .......... .......... .......... .......... ..........
Aco027752.1                                              .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                    .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                    .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                    .......... .......... .......... .......... ..........
Aco010091.1                                              .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                      .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                      .......... .......... .......... .......... ..........
Acamev11004816m                                          .......... .......... .......... .......... ..........
Acamev11046066m                                          .......... .......... .......... .......... ..........
Zosma445g00020.1                                         .......... .......... .......... .......... ..........
Zosma69g00670.1                                          .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59              .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129             .......... .......... .......... .......... ..........
CALSI_Maker00043687                                      .......... .......... .......... .......... ..........
CALSI_Maker00043684                                      .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                    .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                    .......... .......... .......... .......... ..........
CALSI_Maker00043685                                      .......... .......... .......... .......... ..........
Aco020610.1                                              .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                    .......... .......... .......... .......... ..........
Zosma79g00480.1                                          .......... .......... .......... .......... ..........
Zosma115g00180.1                                         .......... .......... .......... .......... ..........
Spipo15G0044700                                          .......... .......... .......... .......... ..........
Acamev11008610m                                          .......... .......... .......... .......... ..........
Acamev11024102m                                          .......... .......... .......... .......... ..........
Acamev11050170m                                          .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177             .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178             .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181             .......... .......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                    .......... .......... .......... .......... ..........
Seita.6G181800.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                    .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                   .......... .......... .......... .......... ..........
Zm00008a016750_P01                                    .......... .......... .......... .......... ..........
Zm00008a022367_P01                                    .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                  .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                    .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                  .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                      .......... .......... .......... .......... ..........
Pavir.7KG232255.1.p                                   .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                   .......... .......... .......... .......... ..........
PhHAL.7G213900.1.p                                    .......... .......... .......... .......... ..........
Zm00008a006867_P01                                    .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                  .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                    .......... .......... .......... .......... ..........
Sevir.2G448300.1.p                                    .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                    .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                  .......... .......... .......... .......... ..........
STRANG_00041445-RA                                    .......... .......... .......... .......... ..........
STRANG_00039019-RA                                    .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1  .......... .......... .......... .......... ..........
Joascv11021323m                                       .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------
Joascv11021328m                                       .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1 .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1          .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                    .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                    .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                    .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                   .......... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                   .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                   .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                  .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                  .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                  .......... .......... .......... .......... ..........
Zm00008a016754_P01                                    .......... .......... .......... .......... ..........
Zm00008a022372_P01                                    .......... .......... .......... .......... ..........
Zm00008a022370_P01                                    .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                  .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                  .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                      .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                      .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                      .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                      .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                      .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                  .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                   .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                   .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                    .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                    .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                    .......... .......... .......... .......... ..........
Zm00008a016751_P01                                    .......... .......... .......... .......... ..........
Zm00008a022369_P01                                    .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                  .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                  .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                  TVCFDANILG LLAEPKQDRY ALRTSPQWLG PQIEVIRMAT HSIEREINSV
Osa_LOC_Os12g33610.1                                  .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                  .......... .......... .......... .......... ..........
Zm00008a004629_P01                                    .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                      .......... .......... .......... .......... ..........
STRANG_00039013-RA                                    .......... .......... .......... .......... ..........
STRANG_00039015-RA                                    .......... .......... .......... .......... ..........
Pavir.7KG227800.1.p                                   .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                   .......... .......... .TEASTE... .......... ..........
Pavir.7NG355800.1.p                                   .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                    .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                    .......... .......... .......... .......... ..........
Zm00008a006866_P01                                    .......... .......... ATRLTPP... .......... ..........
Sobic.006G148200.1.p                                  .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                   .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                  .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                  .......... .......... ...EKP.... .......... ..........
Bradi5g15830.1.p                                      .......... .......... .......... .......... ..........
STRANG_00041444-RA                                    .......... .......... .......... .......... ..........
STRANG_00041441-RA                                    .......... .......... .......... .......... ..........
STRANG_00041440-RA                                    .......... .......... .......... .......... ..........
STRANG_00059682-RA                                    .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------
Acc013943.1                                           .......... .......... .......... .......... ..........
Acc007727.1                                           .......... .......... .......... .......... ..........
Apos_PKA46439.1                                       .......... .......... .......... .......... ..........
Apos_PKA58411.1                                       .......... .......... .......... .......... ..........
Apos_PKA54143.1                                       .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                   .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                   .......... .......... .......... .......... ..........
Dcat_XP_020702180.1                                   .......... .......... .......... .......... ..........
Apos_PKA59591.1                                       .......... .......... .......... .......... ..........
Apos_PKA60166.1                                       .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                   .......... .......... .......... .......... ..........
Spipo31G0025500                                       .......... .......... .......... .......... ..........
Spipo1G0003500                                        .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr11P16360_001                                .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                 .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                 .......... .......... .......... .......... ..........
CALSI_Maker00040467                                   .......... .......... .......... .......... ..........
Acc006987.1                                           .......... .......... .......... .......... ..........
Acc027752.1                                           .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                 .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                 .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                 .......... .......... .......... .......... ..........
Acc010091.1                                           .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                   .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                   .......... .......... .......... .......... ..........
Acamev11004816m                                       .......... .......... .......... .......... ..........
Acamev11046066m                                       .......... .......... .......... .......... ..........
Zosma445g00020.1                                      .......... .......... .......... .......... ..........
Zosma69g00670.1                                       .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129          .......... .......... .......... .......... ..........
CALSI_Maker00043687                                   .......... .......... ...SSP.... .......... ..........
CALSI_Maker00043684                                   .......... .......... ...SSP.... .......... ..........
p5.00_sc01789_p0001.1                                 .......... .......... ...SSP.... .......... ..........
p5.00_sc00066_p0001.1                                 .......... .......... .......... .......... ..........
CALSI_Maker00043685                                   .......... .......... .......... .......... ..........
Acc020618.1                                           .......... .......... ...ASP.... .......... ..........
GSMUA_Achr9P15990_001                                 .......... .......... ...SSP.... .......... ..........
Zosma79g00480.1                                       .......... .......... ...MSP.... .......... ..........
Zosma115g00180.1                                      .......... .......... ...MSP.... .......... ..........
Spipo15G0044700                                       .......... .......... ...TSP.... .......... ..........
Acamev11008610m                                       .......... .......... ...GSP.... .......... ..........
Acamev11024102m                                       .......... .......... ...GSP.... .......... ..........
Acamev11050170m                                       .......... .......... ...GSP.... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177          .......... .......... ...ASP.... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178          .......... .......... ...ASP.... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181          .......... .......... ...ASP.... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                     .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                    .......... .......... .......... .......... ..........
Zm00008a016750_P01                                     .......... .......... .......... .......... ..........
Zm00008a022367_P01                                     .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                   .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                   .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                       .......... .......... .......... .......... ..........
Pavir.7KG238255.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                    .......... .......... .......... .......... ..........
PhHAL.7G213900.1.p                                     .......... .......... .......... .......... ..........
Zm00008a006867_P01                                     .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                   .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                     .......... .......... .......... .......... ..........
Sevir.2G448300.1.p                                     .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                   .......... .......... .......... .......... ..........
STRANG_00041445-RA                                     .......... .......... .......... .......... ..........
STRANG_00039019-RA                                     .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1   .......... .......... .......... .......... ..........
Joasev11021323m                                        .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------------------------
Joasev11021328m                                        .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1  .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1           .......... .......... .......... .......... ..........
-----------------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                    .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                    .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                   .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                   .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                   .......... .......... .......... .......... ..........
Zm00008a016754_P01                                     .......... .......... .......... .......... ..........
Zm00008a022372_P01                                     .......... .......... .......... .......... ..........
Zm00008a022370_P01                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                   .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                       .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                       .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                       .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                       .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                       .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                   .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                     .......... .......... .......... .......... ..........
Zm00008a016751_P01                                     .......... .......... .......... .......... ..........
Zm00008a022369_P01                                     .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                   .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                   MDNPLIDVSR DLALRGGNFQ GIPIGVSMDN LRIAIAAIGK LMFAQFSELV
Osa_LOC_Os12g33610.1                                   .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                   .......... .......... .......... .......... ..........
Zm00008a004629_P01                                     .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                       .......... .......... .......... .......... ..........
STRANG_00039013-RA                                     .......... .......... .......... .......... ..........
STRANG_00039015-RA                                     .......... .......... .......... .......... ..........
Pavir.7KG227800.1.p                                    .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                    .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                     .......... .......... .......... .......... ..........
Zm00008a006866_P01                                     .......... .......... .......... .......... ..........
Sobic.006G148900.1.p                                   .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                   .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                       .......... .......... .......... .......... ..........
STRANG_00041444-RA                                     .......... .......... .......... .......... ..........
STRANG_00041441-RA                                     .......... .......... .......... .......... ..........
STRANG_00041440-RA                                     .......... .......... .......... .......... ..........
STRANG_00059682-RA                                     .......... .......... .......... .......... ..........
-----------------------------------------------------------------------------------------------------------------
Aco013943.1                                            .......... .......... .......... .......... ..........
Aco007727.1                                            .......... .......... .......... .......... ..........
Apos_PKA46439.1                                        .......... .......... .......... .......... ..........
Apos_PKA58411.1                                        .......... .......... .......... .......... ..........
Apos_PKA54143.1                                        .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                    .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                    .......... .......... .......... .......... ..........
Dcat_XP_020702380.1                                    .......... .......... .......... .......... ..........
Apos_PKA59591.1                                        .......... .......... .......... .......... ..........
Apos_PKA60166.1                                        .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                    .......... .......... .......... .......... ..........
Spipo11G0025500                                        .......... .......... .......... .......... ..........
Spipo1G0003500                                         .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P16380_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                  .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                  .......... .......... .......... .......... ..........
CALSI_Maker00040467                                    .......... .......... .......... .......... ..........
Aco006987.1                                            .......... .......... .......... .......... ..........
Aco027752.1                                            .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                  .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                  .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                  .......... .......... .......... .......... ..........
Aco010091.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                    .......... .......... .......... .......... ..........
Acamev11004816m                                        .......... .......... .......... .......... ..........
Acamev11046066m                                        .......... .......... .......... .......... ..........
Zosma445g00020.1                                       .......... .......... .......... .......... ..........
Zosma69g00670.1                                        .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59            .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129           .......... .......... .......... .......... ..........
CALSI_Maker00043687                                    .......... .......... .......... .......... ..........
CALSI_Maker00043684                                    .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                  .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                  .......... .......... .......... .......... ..........
CALSI_Maker00043685                                    .......... .......... .......... .......... ..........
Aco020618.1                                            .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                  .......... .......... .......... .......... ..........
Zosma79g00480.1                                        .......... .......... .......... .......... ..........
Zosma115g00180.1                                       .......... .......... .......... .......... ..........
Spipo15G0044700                                        .......... .......... .......... .......... ..........
Acamev11008610m                                        .......... .......... .......... .......... ..........
Acamev11024102m                                        .......... .......... .......... .......... ..........
Acamev11050170m                                        .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181           .......... .......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                             .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                             .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                             .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                             .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                             .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                            .......... .......... .......... .......... ..........
Zm00008a016750_P01                                             .......... .......... .......... .......... ..........
Zm00008a022367_P01                                             .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                           .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                             .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                             .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                           .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                               .......... .......... .......... .......... ..........
Pavir.7KG238255.1.p                                            .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                            .......... .......... .......... .......... ..........
PhHAL.7G213900.1.p                                             .......... .......... .......... .......... ..........
Zm00008a006867_P01                                             .......... .......... .......... .......... ..........
Sobic.006G148500.1.p                                           .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                             .......... .......... .......... .......... ..........
Sevir.2G448300.1.p                                             .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                             .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                             .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                           .......... .......... .......... .......... ..........
STRANG_00041445-RA                                             .......... .......... .......... .......... ..........
STRANG_00039019-RA                                             .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1           .......... .......... .......... .......... ..........
Joasev11021323m                                                .......... .......... .......... .......... ..........
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Joasev11021328m                                                .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1          .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1                   .......... .......... .......... .......... ..........
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Seita.1G240400.1.p                                             .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                             .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                             .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                             .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                             .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                             .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                             .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                             .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                             .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                            .......... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                            .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                            .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                           .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                           .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                           .......... .......... .......... .......... ..........
Zm00008a016754_P01                                             .......... .......... .......... .......... ..........
Zm00008a022372_P01                                             .......... .......... .......... .......... ..........
Zm00008a022370_P01                                             .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                           .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                           .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                               .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                               .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                               .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                               .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                               .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                           .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                            .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                            .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                             .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                             .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                             .......... .......... .......... .......... ..........
Zm00008a016751_P01                                             .......... .......... .......... .......... ..........
Zm00008a022369_P01                                             .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                           .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                           .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                           CDYYNGGLPS NLSGGENPSL DYGFKGAEIA MAAYCGELQY LANLVTTHVQ
Osa_LOC_Os12g33610.1                                           .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                           .......... .......... .......... .......... ..........
Zm00008a004629_P01                                             .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                               .......... .......... .......... .......... ..........
STRANG_00039013-RA                                             .......... .......... .......... .......... ..........
STRANG_00039015-RA                                             .......... .......... .......... .......... ..........
Pavir.7KG237800.1.p                                            .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                             .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                            .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                            .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                             .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                             .......... .......... .......... .......... ..........
Zm00008a006866_P01                                             .......... .......... .......... .......... ..........
Sobic.006G148900.1.p                                           .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                            .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                           .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                           .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                               .......... .......... .......... .......... ..........
STRANG_00041444-RA                                             .......... .......... .......... .......... ..........
STRANG_00041441-RA                                             .......... .......... .......... .......... ..........
STRANG_00041440-RA                                             .......... .......... .......... .......... ..........
STRANG_00059682-RA                                             .......... .......... .......... .......... ..........
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Aco013943.1                                                    .......... .......... .......... .......... ..........
Aco007727.1                                                    .......... .......... .......... .......... ..........
Apos_PKA46439.1                                                .......... .......... .......... .......... ..........
Apos_PKA58411.1                                                .......... .......... .......... .......... ..........
Apos_PKA64143.1                                                .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                            .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                            .......... .......... .......... .......... ..........
Dcat_XP_020702380.1                                            .......... .......... .......... .......... ..........
Apos_PKA59591.1                                                .......... .......... .......... .......... ..........
Apos_PKA60166.1                                                .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                            .......... .......... .......... .......... ..........
Spipo11G0025500                                                .......... .......... .......... .......... ..........
Spipo1G0003500                                                 .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                          .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                         .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                          .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                          .......... .......... .......... .......... ..........
GSMUA_Achr11P16380_001                                         .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                          .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                          .......... .......... .......... .......... ..........
CALSI_Maker00040467                                            .......... .......... .......... .......... ..........
Aco006987.1                                                    .......... .......... .......... .......... ..........
Aco027752.1                                                    .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                          .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                          .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                          .......... .......... .......... .......... ..........
Aco010091.1                                                    .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                            .......... .......... .......... .......... ..........
Acamev1I004816m                                                .......... .......... .......... .......... ..........
Acamev1I046066m                                                .......... .......... .......... .......... ..........
Zosma445g00020.1                                               .......... .......... .......... .......... ..........
Zosma69g00670.1                                                .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59                    .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129                   .......... .......... .......... .......... ..........
CALSI_Maker00043687                                            .......... .......... .......... .......... ..........
CALSI_Maker00043684                                            .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                          .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                          .......... .......... .......... .......... ..........
CALSI_Maker00043685                                            .......... .......... .......... .......... ..........
Aco020610.1                                                    .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                          .......... .......... .......... .......... ..........
Zosma79g00480.1                                                .......... .......... .......... .......... ..........
Zosma115g00180.1                                               .......... .......... .......... .......... ..........
Spipo15G0044700                                                .......... .......... .......... .......... ..........
Acamev1I008610m                                                .......... .......... .......... .......... ..........
Acamev1I024102m                                                .......... .......... .......... .......... ..........
Acamev1I050170m                                                .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177                   .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178                   .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181                   .......... .......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                      .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                      .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                      .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                     .......... .......... .......... .......... ..........
Zm00008a016750_P01                                      .......... .......... .......... .......... ..........
Zm00008a022367_P01                                      .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                    .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                      .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                      .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                    .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                        .......... .......... .......... .......... ..........
Pavir.7KG232255.1.p                                     .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                     .......... .......... .......... .......... ..........
PhHAL.7G213800.1.p                                      .......... .......... .......... .......... ..........
Zm00008a006867_P01                                      .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                    .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                      .......... .......... .......... .......... ..........
Sevir.2G448300.1.p                                      .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                      .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                      .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                    .......... .......... .......... .......... ..........
STRANG_00041445-RA                                      .......... .......... .......... .......... ..........
STRANG_00039019-RA                                      .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1    .......... .......... .......... .......... ..........
Joascv11021323m                                         .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------
Joascv11021328m                                         .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1   .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1            .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                      .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                      .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                      .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                      .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                      .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                     .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                     .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                    .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                    .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                    .......... .......... .......... .......... ..........
Zm00008a016754_P01                                      .......... .......... .......... .......... ..........
Zm00008a022372_P01                                      .......... .......... .......... .......... ..........
Zm00008a022370_P01                                      .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                    .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                    .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                        .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                        .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                        .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                        .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                        .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                    .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                      .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                      .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                      .......... .......... .......... .......... ..........
Zm00008a016751_P01                                      .......... .......... .......... .......... ..........
Zm00008a022369_P01                                      .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                    .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                    SAEQHNQDVN SLGLISARKS AEAVEIINLM SATYMVALCQ AVDLRHLEEN
Osa_LOC_Os12g33610.1                                    .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                    .......... .......... .......... .......... ..........
Zm00008a004629_P01                                      .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                        .......... .......... .......... .......... ..........
STRANG_00039013-RA                                      .......... .......... .......... .......... ..........
STRANG_00039015-RA                                      .......... .......... .......... .......... ..........
Pavir.7KG227800.1.p                                     .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                      .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                     .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                     .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                      .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                      .......... .......... .......... .......... ..........
Zm00008a008866_P01                                      .......... .......... .......... .........Q ALD.......
Sobic.006G148900.1.p                                    .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                    .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                    .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                        .......... .......... .......... .......... ..........
STRANG_00041444-RA                                      .......... .......... .......... .......... ..........
STRANG_00041441-RA                                      .......... .......... .......... .......... ..........
STRANG_00041440-RA                                      .......... .......... .......... .......... ..........
STRANG_00059682-RA                                      .......... .......... .......... .......... ..........
------------------------------------------------------------------------------------------------------------
Aco013943.1                                             .......... .......... .......... .......... ..........
Aco007727.1                                             .......... .......... .......... .......... ..........
Apos_PKA46439.1                                         .......... .......... .......... .......... ..........
Apos_PKA58411.1                                         .......... .......... .......... .......... ..........
Apos_PKA64143.1                                         .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                     .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                     .......... .......... .......... .......... ..........
Dcat_XP_020702280.1                                     .......... .......... .......... .......... ..........
Apos_PKA59591.1                                         .......... .......... .......... .......... ..........
Apos_PKA60166.1                                         .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                     .......... .......... .......... .......... ..........
Spipo11G0023500                                         .......... .......... .......... .......... ..........
Spipo1G0003500                                          .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                   .......... .......... .......... .......... ..........
GSMUA_Achr11P16380_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                   .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                   .......... .......... .......... .......... ..........
CALSI_Maker00040467                                     .......... .......... .......... .......... ..........
Aco006987.1                                             .......... .......... .......... .......... ..........
Aco027752.1                                             .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                   .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                   .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                   .......... .......... .......... .......... ..........
Aco010091.1                                             .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                     .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                     .......... .......... .......... .......... ..........
Acamev1I004816m                                         .......... .......... .......... .......... ..........
Acamev1I046066m                                         .......... .......... .......... .......... ..........
Zosma445g00020.1                                        .......... .......... .......... .......... ..........
Zosma69g00670.1                                         .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59             .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129            .......... .......... .......... .......... ..........
CALSI_Maker00043687                                     .......... .......... .......... .......... ..........
CALSI_Maker00043684                                     .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                   .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                   .......... .......... .......... .......... ..........
CALSI_Maker00043685                                     .......... .......... .......... .......... ..........
Aco020610.1                                             .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                   .......... .......... .......... .......... ..........
Zosma79g00480.1                                         .......... .......... .......... .......... ..........
Zosma115g00180.1                                        .......... .......... .......... .......... ..........
Spipo15G0044700                                         .......... .......... .......... .......... ..........
Acamev1I008610m                                         .......... .......... .......... .......... ..........
Acamev1I024102m                                         .......... .......... .......... .......... ..........
Acamev1I050170m                                         .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177            .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178            .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181            .......... .......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                     .......... .......... .......... .......... ..........
Seita.6G181800.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                    .......... .......... .......... .......... ..........
Zm00008a016750_P01                                     .......... .......... .......... .......... ..........
Zm00008a022367_P01                                     .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                   .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                   .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                       .......... .......... .......... .......... ..........
Pavir.7KG232253.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                    .......... .......... .......... .......... ..........
PhHAL.7G213800.1.p                                     .......... .......... .......... .......... ..........
Zm00008a006867_P01                                     .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                   .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                     .......... .......... .......... .......... ..........
Sevir.2G448700.1.p                                     .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                   .......... .......... .......... .......... ..........
STRANG_00041445-RA                                     .......... .......... .......... .......... ..........
STRANG_00039019-RA                                     .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1   .......... .......... .......... .......... ..........
Joascv11021323m                                        .......... .......... .......... .......... ..........
----------------------------------------------------------------------------------------------------------------
Joascv11021328m                                        .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1  .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1           .......... .......... .......... .......... ..........
-----------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                    .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                    .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                   .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                   .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                   .......... .......... .......... .......... ..........
Zm00008a016754_P01                                     .......... .......... .......... .......... ..........
Zm00008a022372_P01                                     .......... .......... .......... .......... ..........
Zm00008a022370_P01                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                   .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                       .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                       .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                       .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                       .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                       .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                   .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                     .......... .......... .......... .......... ..........
Zm00008a016751_P01                                     .......... .......... .......... .......... ..........
Zm00008a022369_P01                                     .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                   .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                   MREVVKHLIT QVARKTLNTD SDGTLLESRF CSKELQQVVE NLPVPSYIDD
Osa_LOC_Os12g33610.1                                   .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                   .......... .......... .......... .......... ..........
Zm00008a004629_P01                                     .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                       .......... .......... .......... .......... ..........
STRANG_00039013-RA                                     .......... .......... .......... .......... ..........
STRANG_00039015-RA                                     .......... .......... .......... .......... ..........
Pavir.7KG227800.1.p                                    .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                    .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                     .......... .......... .......... .......... ..........
Zm00008a006866_P01                                     .......... .......... .......... .......... ..........
Sobic.006G148900.1.p                                   .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                   .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                       .......... .......... .......... .......... ..........
STRANG_00041444-RA                                     .......... .......... .......... .......... ..........
STRANG_00041441-RA                                     .......... .......... .......... .......... ..........
STRANG_00041440-RA                                     .......... .......... .......... .......... ..........
STRANG_00059682-RA                                     .......... .......... .......... .......... ..........
-----------------------------------------------------------------------------------------------------------
Aco013943.1                                            .......... .......... .......... .......... ..........
Aco007727.1                                            .......... .......... .......... .......... ..........
Apos_PKA46439.1                                        .......... .......... .......... .......... ..........
Apos_PKA58411.1                                        .......... .......... .......... .......... ..........
Apos_PKA54143.1                                        .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                    .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                    .......... .......... .......... .......... ..........
Dcat_XP_020702280.1                                    .......... .......... .......... .......... ..........
Apos_PKA59591.1                                        .......... .......... .......... .......... ..........
Apos_PKA60166.1                                        .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                    .......... .......... .......... .......... ..........
Spipo11G0023500                                        .......... .......... .......... .......... ..........
Spipo1G0003500                                         .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P16360_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                  .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                  .......... .......... .......... .......... ..........
CALSI_Maker00040467                                    .......... .......... .......... .......... ..........
Aco006987.1                                            .......... .......... .......... .......... ..........
Aco027752.1                                            .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                  .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                  .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                  .......... .......... .......... .......... ..........
Aco010091.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                    .......... .......... .......... .......... ..........
Acamev1I004816m                                        .......... .......... .......... .......... ..........
Acamev1I046066m                                        .......... .......... .......... .......... ..........
Zosma445g00020.1                                       .......... .......... .......... .......... ..........
Zosma69g00670.1                                        .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59            .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129           .......... .......... .......... .......... ..........
CALSI_Maker00043687                                    .......... .......... .......... .......... ..........
CALSI_Maker00043684                                    .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                  .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                  .......... .......... .......... .......... ..........
CALSI_Maker00043685                                    .......... .......... .......... .......... ..........
Aco020618.1                                            .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                  .......... .......... .......... .......... ..........
Zosma79g00480.1                                        .......... .......... .......... .......... ..........
Zosma115g00190.1                                       .......... .......... .......... .......... ..........
Spipo15G0044700                                        .......... .......... .......... .......... ..........
Acamev1I008610m                                        .......... .......... .......... .......... ..........
Acamev1I024102m                                        .......... .......... .......... .......... ..........
Acamev1I050170m                                        .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181           .......... .......... .......... .......... ..........
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Figure 8(continued)

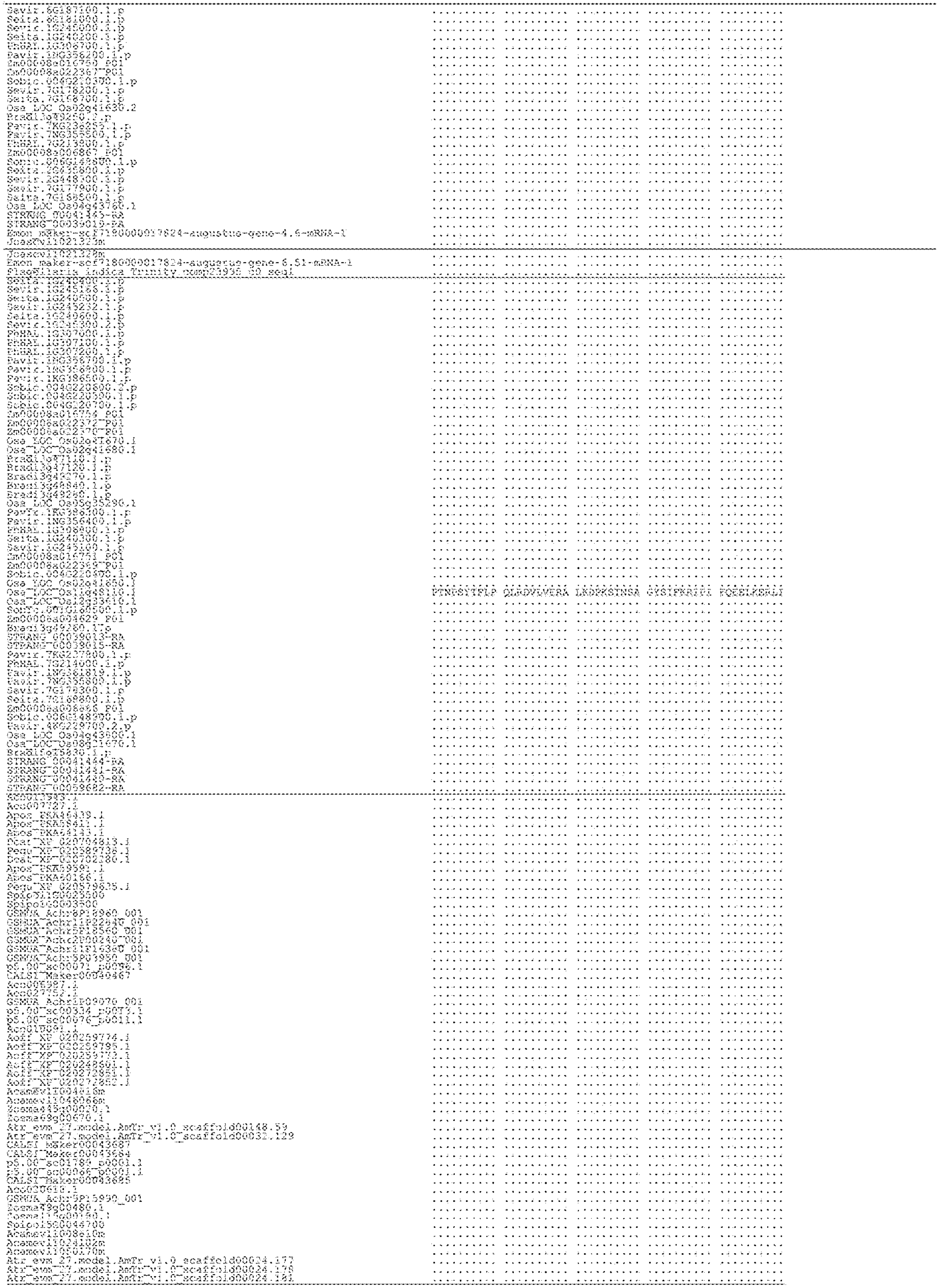

Figure 8(continued)

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---------------------------------------------------------------------------------------------------------
Sevir.6G187100.1.p                                     .......... .......... .......... .......... ..........
Seita.6G181000.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245000.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240200.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G306700.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356200.1.p                                    .......... .......... .......... .......... ..........
Zm00008a016750_P01                                     .......... .......... .......... .......... ..........
Zm00008a022367_P01                                     .......... .......... .......... .......... ..........
Sobic.004G220300.1.p                                   .......... .......... .......... .......... ..........
Sevir.7G178200.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168700.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41630.2                                   .......... .......... .......... .......... ..........
Bradi3g49250.2.p                                       .......... .......... .......... .......... ..........
Pavir.7KG232253.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355500.1.p                                    .......... .......... .......... .......... ..........
PhHAL.7G213800.1.p                                     .......... .......... .......... .......... ..........
Zm00008a006867_P01                                     .......... .......... .......... .......... ..........
Sobic.006G148800.1.p                                   .......... .......... .......... .......... ..........
Seita.2G435800.1.p                                     .......... .......... .......... .......... ..........
Sevir.2G448300.1.p                                     .......... .......... .......... .......... ..........
Sevir.7G177900.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168500.1.p                                     .......... .......... .......... .......... ..........
Osa_LOC_Os04g43760.1                                   .......... .......... .......... .......... ..........
STRANG_00041445-RA                                     .......... .......... .......... .......... ..........
STRANG_00039019-RA                                     .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1   .......... .......... .......... .......... ..........
Joasev11021323m                                        .......... .......... .......... .......... ..........
---------------------------------------------------------------------------------------------------------
Joasev11021328m                                        .......... .......... .......... .......... ..........
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1  .......... .......... .......... .......... ..........
Flagellaria_indica_Trinity_comp23935_c0_seq1           .......... .......... .......... .......... ..........
---------------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245166.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240500.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245232.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240600.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245300.2.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307000.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307100.1.p                                     .......... .......... .......... .......... ..........
PhHAL.1G307200.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG356700.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356800.1.p                                    .......... .......... .......... .......... ..........
Pavir.1KG386500.1.p                                    .......... .......... .......... .......... ..........
Sobic.004G220600.2.p                                   .......... .......... .......... .......... ..........
Sobic.004G220500.1.p                                   .......... .......... .......... .......... ..........
Sobic.004G220700.1.p                                   .......... .......... .......... .......... ..........
Zm00008a016754_P01                                     .......... .......... .......... .......... ..........
Zm00008a022372_P01                                     .......... .......... .......... .......... ..........
Zm00008a022370_P01                                     .......... .......... .......... .......... ..........
Osa_LOC_Os02g41670.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os02g41680.1                                   .......... .......... .......... .......... ..........
Bradi3g47110.1.p                                       .......... .......... .......... .......... ..........
Bradi3g47120.1.p                                       .......... .......... .......... .......... ..........
Bradi3g49270.1.p                                       .......... .......... .......... .......... ..........
Bradi3g48840.1.p                                       .......... .......... .......... .......... ..........
Bradi3g49280.1.p                                       .......... .......... .......... .......... ..........
Osa_LOC_Os05g35290.1                                   .......... .......... .......... .......... ..........
Pavir.1KG386300.1.p                                    .......... .......... .......... .......... ..........
Pavir.1NG356400.1.p                                    .......... .......... .......... .......... ..........
PhHAL.1G306800.1.p                                     .......... .......... .......... .......... ..........
Seita.1G240300.1.p                                     .......... .......... .......... .......... ..........
Sevir.1G245100.1.p                                     .......... .......... .......... .......... ..........
Zm00008a016751_P01                                     .......... .......... .......... .......... ..........
Zm00008a022369_P01                                     .......... .......... .......... .......... ..........
Sobic.004G220400.1.p                                   .......... .......... .......... .......... ..........
Osa_LOC_Os02g41650.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os11g48110.1                                   EEISKAREEP DNGDPEIPNR IKKCRTYPIY GFVPKEVGTK LLSGENKVSP
Osa_LOC_Os12g33610.1                                   .......... .......... .......... .......... ..........
Sobic.001G160500.1.p                                   .......... .......... .......... .......... ..........
Zm00008a004629_P01                                     .......... .......... .......... .......... ..........
Bradi3g49260.1.p                                       .......... .......... .......... .......... ..........
STRANG_00039013-RA                                     .......... .......... .......... .......... ..........
STRANG_00039015-RA                                     .......... .......... .......... .......... ..........
Pavir.7KG227800.1.p                                    .......... .......... .......... .......... ..........
PhHAL.7G214000.1.p                                     .......... .......... .......... .......... ..........
Pavir.1NG361819.1.p                                    .......... .......... .......... .......... ..........
Pavir.7NG355800.1.p                                    .......... .......... .......... .......... ..........
Sevir.7G178300.1.p                                     .......... .......... .......... .......... ..........
Seita.7G168800.1.p                                     .......... .......... .......... .......... ..........
Zm00008a008866_P01                                     .......... DGG....... .......... .......... ..........
Sobic.006G148900.1.p                                   .......... .......... .......... .......... ..........
Pavir.4KG229700.2.p                                    .......... .......... .......... .......... ..........
Osa_LOC_Os04g43800.1                                   .......... .......... .......... .......... ..........
Osa_LOC_Os08g21670.1                                   .......... .......... .......... .......... ..........
Bradi5g15830.1.p                                       .......... .......... .......... .......... ..........
STRANG_00041444-RA                                     .......... .......... .......... .......... ..........
STRANG_00041441-RA                                     .......... .......... .......... .......... ..........
STRANG_00041440-RA                                     .......... .......... .......... .......... ..........
STRANG_00059682-RA                                     .......... .......... .......... .......... ..........
---------------------------------------------------------------------------------------------------------
Aco013943.1                                            .......... .......... .......... .......... ..........
Aco007727.1                                            .......... .......... .......... .......... ..........
Apos_PKA46439.1                                        .......... .......... .......... .......... ..........
Apos_PKA58411.1                                        .......... .......... .......... .......... ..........
Apos_PKA64143.1                                        .......... .......... .......... .......... ..........
Dcat_XP_020704813.1                                    .......... .......... .......... .......... ..........
Pequ_XP_020589738.1                                    .......... .......... .......... .......... ..........
Dcat_XP_020702380.1                                    .......... .......... .......... .......... ..........
Apos_PKA59591.1                                        .......... .......... .......... .......... ..........
Apos_PKA60166.1                                        .......... .......... .......... .......... ..........
Pequ_XP_020579635.1                                    .......... .......... .......... .......... ..........
Spipo11G0025500                                        .......... .......... .......... .......... ..........
Spipo1G0003500                                         .......... .......... .......... .......... ..........
GSMUA_Achr8P18960_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P22840_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P18560_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr2P00240_001                                  .......... .......... .......... .......... ..........
GSMUA_Achr11P16380_001                                 .......... .......... .......... .......... ..........
GSMUA_Achr5P03950_001                                  .......... .......... .......... .......... ..........
p5.00_sc00071_p0096.1                                  .......... .......... .......... .......... ..........
CALSI_Maker00040467                                    .......... .......... .......... .......... ..........
Aco006987.1                                            .......... .......... .......... .......... ..........
Aco027752.1                                            .......... .......... .......... .......... ..........
GSMUA_Achr1P09070_001                                  .......... .......... .......... .......... ..........
p5.00_sc00334_p0073.1                                  .......... .......... .......... .......... ..........
p5.00_sc00076_p0011.1                                  .......... .......... .......... .......... ..........
Aco010091.1                                            .......... .......... .......... .......... ..........
Aoff_XP_020259774.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259795.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020259773.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020248601.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020272851.1                                    .......... .......... .......... .......... ..........
Aoff_XP_020272852.1                                    .......... .......... .......... .......... ..........
Acamev11004816m                                        .......... .......... .......... .......... ..........
Acamev11046066m                                        .......... .......... .......... .......... ..........
Zosma445g00020.1                                       .......... .......... .......... .......... ..........
Zosma69g00670.1                                        .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59            .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129           .......... .......... .......... .......... ..........
CALSI_Maker00043687                                    .......... .......... .......... .......... ..........
CALSI_Maker00043684                                    .......... .......... .......... .......... ..........
p5.00_sc01789_p0001.1                                  .......... .......... .......... .......... ..........
p5.00_sc00066_p0001.1                                  .......... .......... .......... .......... ..........
CALSI_Maker00043685                                    .......... .......... .......... .......... ..........
Aco020610.1                                            .......... .......... .......... .......... ..........
GSMUA_Achr9P15990_001                                  .......... .......... .......... .......... ..........
Zosma79g00480.1                                        .......... .......... .......... .......... ..........
Zosma115g00180.1                                       .......... .......... .......... .......... ..........
Spipo15G0044700                                        .......... .......... .......... .......... ..........
Acamev11008610m                                        .......... .......... .......... .......... ..........
Acamev11024102m                                        .......... .......... .......... .......... ..........
Acamev11050170m                                        .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178           .......... .......... .......... .......... ..........
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181           .......... .......... .......... .......... ..........
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Figure 8(continued)

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Sevir.6G187100.1.p                                           .......... .......... .......... .....
Seita.6G181000.1.p                                           .......... .......... .......... .....
Sevir.1G245000.1.p                                           .......... .......... .......... .....
Seita.1G240200.1.p                                           .......... .......... .......... .....
PhHAL.1G306700.1.p                                           .......... .......... .......... .....
Pavir.1NG356200.1.p                                          .......... .......... .......... .....
Zm00008a016750_P01                                           .......... .......... .......... .....
Zm00008a022367_P01                                           .......... .......... .......... .....
Sobic.004G220300.1.p                                         .......... .......... .......... .....
Sevir.7G178200.1.p                                           .......... .......... .......... .....
Seita.7G168700.1.p                                           .......... .......... .......... .....
Osa_LOC_Os02g41630.2                                         .......... .......... .......... .....
Bradi3g49250.2.p                                             .......... .......... .......... .....
Pavir.7KG238255.1.p                                          .......... .......... .......... .....
Pavir.7NG355500.1.p                                          .......... .......... .......... .....
PhHAL.7G213900.1.p                                           .......... .......... .......... .....
Zm00008a006867_P01                                           .......... .......... .......... .....
Sobic.006G148800.1.p                                         .......... .......... .......... .....
Seita.2G435800.1.p                                           .......... .......... .......... .....
Sevir.2G448300.1.p                                           .......... .......... .......... .....
Sevir.7G177900.1.p                                           .......... .......... .......... .....
Seita.7G168500.1.p                                           .......... .......... .......... .....
Osa_LOC_Os04g43760.1                                         .......... .......... .......... .....
STRANG_00041445-RA                                           .......... .......... .......... .....
STRANG_00039019-RA                                           .......... .......... .......... .....
Emon_maker-scf7180000017824-augustus-gene-4.6-mRNA-1         .......... .......... .......... .....
Joasev1i021323m                                              .......... .......... .......... .....
-------------------------------------------------------------------------------------------------
Joasev1i021328m                                              .......... .......... .......... .....
Emon_maker-scf7180000017824-augustus-gene-6.51-mRNA-1        .......... .......... .......... .....
Flagellaria_indica_Trinity.comp23935_c0_seq1                 .......... .......... .......... .....
-------------------------------------------------------------------------------------------------
Seita.1G240400.1.p                                           .......... .......... .......... .....
Sevir.1G245166.1.p                                           .......... .......... .......... .....
Seita.1G240500.1.p                                           .......... .......... .......... .....
Sevir.1G245232.1.p                                           .......... .......... .......... .....
Seita.1G240600.1.p                                           .......... .......... .......... .....
Sevir.1G245300.2.p                                           .......... .......... .......... .....
PhHAL.1G307000.1.p                                           .......... .......... .......... .....
PhHAL.1G307100.1.p                                           .......... .......... .......... .....
PhHAL.1G307200.1.p                                           .......... .......... .......... .....
Pavir.1NG356700.1.p                                          .......... .......... .......... .....
Pavir.1NG356800.1.p                                          .......... .......... .......... .....
Pavir.1KG386500.1.p                                          .......... .......... .......... .....
Sobic.004G220600.2.p                                         .......... .......... .......... .....
Sobic.004G220500.1.p                                         .......... .......... .......... .....
Sobic.004G220700.1.p                                         .......... .......... .......... .....
Zm00008a016754_P01                                           .......... .......... .......... .....
Zm00008a022372_P01                                           .......... .......... .......... .....
Zm00008a022370_P01                                           .......... .......... .......... .....
Osa_LOC_Os02g41670.1                                         .......... .......... .......... .....
Osa_LOC_Os02g41680.1                                         .......... .......... .......... .....
Bradi3g47110.1.p                                             .......... .......... .......... .....
Bradi3g47120.1.p                                             .......... .......... .......... .....
Bradi3g49270.1.p                                             .......... .......... .......... .....
Bradi3g48840.1.p                                             .......... .......... .......... .....
Bradi3g49280.1.p                                             .......... .......... .......... .....
Osa_LOC_Os05g35290.1                                         .......... .......... .......... .....
Pavir.1KG386300.1.p                                          .......... .......... .......... .....
Pavir.1NG356400.1.p                                          .......... .......... .......... .....
PhHAL.1G306800.1.p                                           .......... .......... .......... .....
Seita.1G240300.1.p                                           .......... .......... .......... .....
Sevir.1G245100.1.p                                           .......... .......... .......... .....
Zm00008a016751_P01                                           .......... .......... .......... .....
Zm00008a022369_P01                                           .......... .......... .......... .....
Sobic.004G220400.1.p                                         .......... .......... .......... .....
Osa_LOC_Os02g41650.1                                         .......... .......... .......... .....
Osa_LOC_Os11g48110.1                                         GEDIEKPNPE YWGWPEKLRS PSSASNGRVN WDRLX
Osa_LOC_Os12g33610.1                                         .......... .......... .......... .....
Sobic.001G160500.1.p                                         .......... .......... .......... .....
Zm00008a004629_P01                                           .......... .......... .......... .....
Bradi3g49260.1.p                                             .......... .......... .......... .....
STRANG_00039013-RA                                           .......... .......... .......... .....
STRANG_00039015-RA                                           .......... .......... .......... .....
Pavir.7KG227800.1.p                                          .......... .......... .......... .....
PhHAL.7G214000.1.p                                           .......... .......... .......... .....
Pavir.1NG361819.1.p                                          ...TAS.... ....SKAVQR X......... .....
Pavir.7NG355800.1.p                                          .......... .......... .......... .....
Sevir.7G178300.1.p                                           .......... .......... .......... .....
Seita.7G168800.1.p                                           .......... .......... .......... .....
Zm00008a006866_P01                                           ...LQTYNCK QHG...SVQH X......... .....
Sobic.006G148900.1.p                                         .......... .......... .......... .....
Pavir.4KG229700.2.p                                          .......... .......... .......... .....
Osa_LOC_Os04g43800.1                                         .......... .......... .......... .....
Osa_LOC_Os08g21670.1                                         ...VFS.... .......... ..GASMGKX. .....
Bradi1g75830.1.p                                             .......... .......... .......... .....
STRANG_00041444-RA                                           .......... .......... .......... .....
STRANG_00041441-RA                                           ...TE..... .......... .......... .....
STRANG_00041440-RA                                           .......... .......... .......... .....
STRANG_00059682-RA                                           .......... .......... .......... .....
-------------------------------------------------------------------------------------------------
Acc013943.1                                                  .......... .......... .......... .....
Acc007727.1                                                  .......... .......... .......... .....
Apos_PKA46439.1                                              .......... .......... .......... .....
Apos_PKA58411.1                                              .......... .......... .......... .....
Apos_PKA54143.1                                              .......... .......... .......... .....
Dcat_XP_020704813.1                                          .......... .......... .......... .....
Pequ_XP_020589738.1                                          .......... .......... .......... .....
Dcat_XP_020702280.1                                          .......... .......... .......... .....
Apos_PKA59591.1                                              .......... .......... .......... .....
Apos_PKA60166.1                                              .......... .......... .......... .....
Pequ_XP_020579635.1                                          .......... .......... .......... .....
Spipo11G0025500                                              .......... .......... .......... .....
Spipo1G0003500                                               .......... .......... .......... .....
GSMUA_Achr8P18960_001                                        .......... .......... .......... .....
GSMUA_Achr11P22840_001                                       .......... .......... .......... .....
GSMUA_Achr5P18560_001                                        .......... .......... .......... .....
GSMUA_Achr2P00240_001                                        .......... .......... .......... .....
GSMUA_Achr11P16380_001                                       .......... .......... .......... .....
GSMUA_Achr5P03950_001                                        .......... .......... .......... .....
p5.00_sc00071_p0096.1                                        .......... .......... .......... .....
CALSI_Maker00040467                                          .......... .......... .......... .....
Acc006987.1                                                  .......... .......... .......... .....
Acc027752.1                                                  .......... .......... .......... .....
GSMUA_Achr1P09070_001                                        .......... .......... .......... .....
p5.00_sc00334_p0073.1                                        .......... .......... .......... .....
p5.00_sc00076_p0011.1                                        .......... .......... .......... .....
Acc010091.1                                                  .......... .......... .......... .....
Aoff_XP_020259774.1                                          .......... .......... .......... .....
Aoff_XP_020259795.1                                          .......... .......... .......... .....
Aoff_XP_020259773.1                                          .......... .......... .......... .....
Aoff_XP_020248601.1                                          .......... .......... .......... .....
Aoff_XP_020272851.1                                          .......... .......... .......... .....
Aoff_XP_020272852.1                                          .......... .......... .......... .....
Acamev1i004816m                                              .......... .......... .......... .....
Acamev1i046066m                                              .......... .......... .......... .....
Zosma445g00020.1                                             .......... .......... .......... .....
Zosma69g00670.1                                              .......... .......... .......... .....
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59                  .......... .......... .......... .....
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129                 .......... .......... .......... .....
CALSI_Maker00043687                                          ...VHR.RPE FWAWFEQGRS P.SATSGRGY WNLX.
CALSI_Maker00043684                                          ...VHK.KPE FWAWFEQGRS P.SATSGRGY WNLX.
p5.00_sc01789_p0001.1                                        ...VHK.KPE YWGWFEQGRS P.SATSGRGY WNLX.
p5.00_sc00066_p0001.1                                        .......... .......... .......... .....
CALSI_Maker00043685                                          .......... .......... ...ANKNRX. .....
Acc020618.1                                                  ...ANR.NPE NWGWFDPVRS P.SATSGRGY WNLX.
GSMUA_Achr9P15990_001                                        ...ALR.NPE NWSWFEQVRS P.SATSGRGY WNLX.
Zosma79g00480.1                                              ...VYK.NPD TWGWFDNMRS P.SSTSGRGF WSKX.
Zosma115g00180.1                                             ...VHK.NPE AWGWFDNLRS P.SSTSGRGY WSKX.
Spipo15G0044700                                              ...AHC.NPE FWSWFDKMRS P.SATSGRGY WNMX.
Acamev1i008610m                                              ...AQH.NPE YWGWFENMRS P.SATSGRGY WNNMX
Acamev1i024102m                                              ...ARR.NP. .......... ....CIGAGL FTX..
Acamev1i050170m                                              ...AQH.NPE YWSWFDNLRS P.SATSGRGY WNNMX
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177                 ...AQG.NPT YWAWFENTRS P.SAISGRGF WNMX.
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178                 ...AQC.NPT YWTWFENTRS P.SATSGRGY WNMX.
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181                 ...AHC.NPT YWAWFENTRS P.SATSGRGY WNLX.
-------------------------------------------------------------------------------------------------
```

Figure 9A

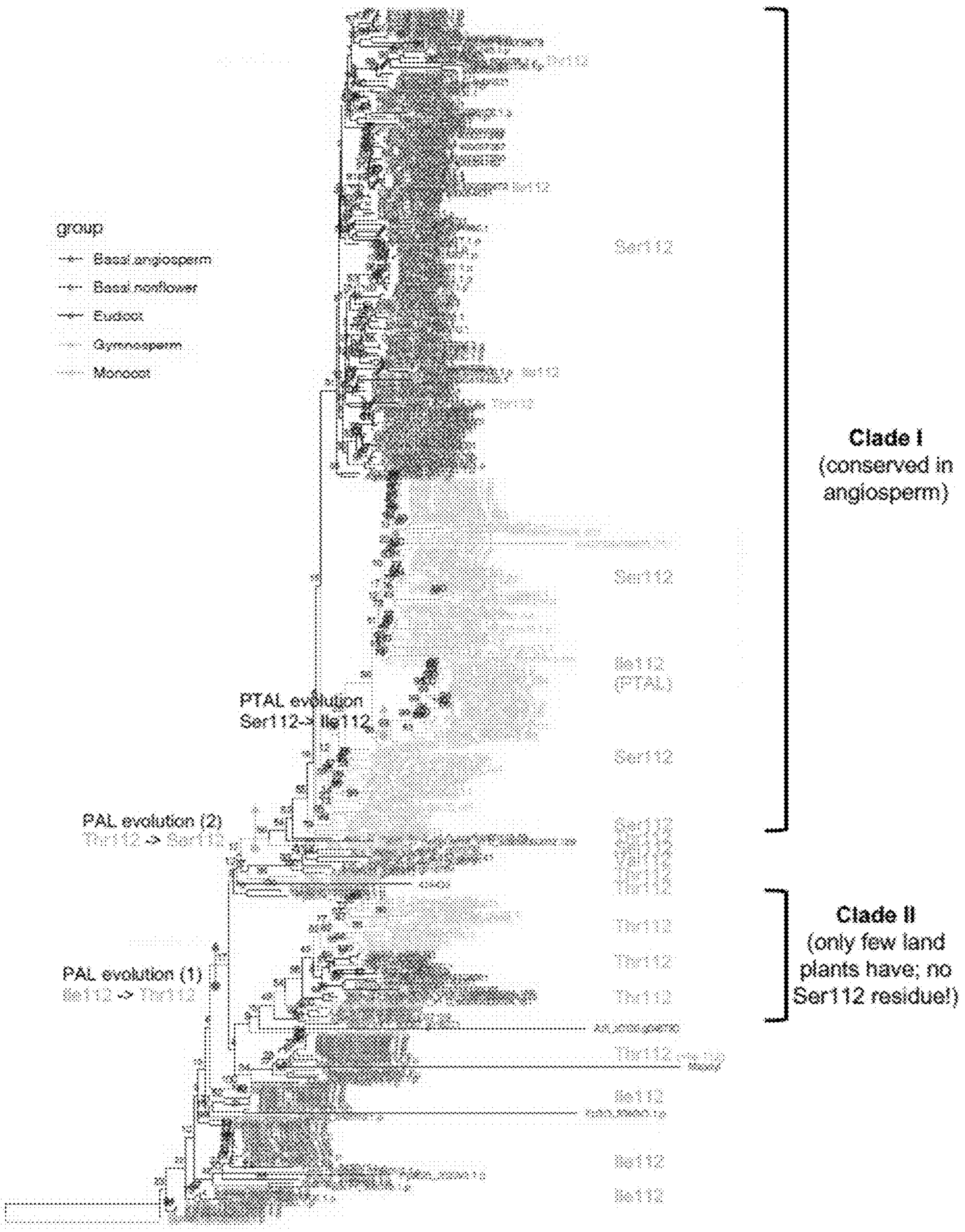
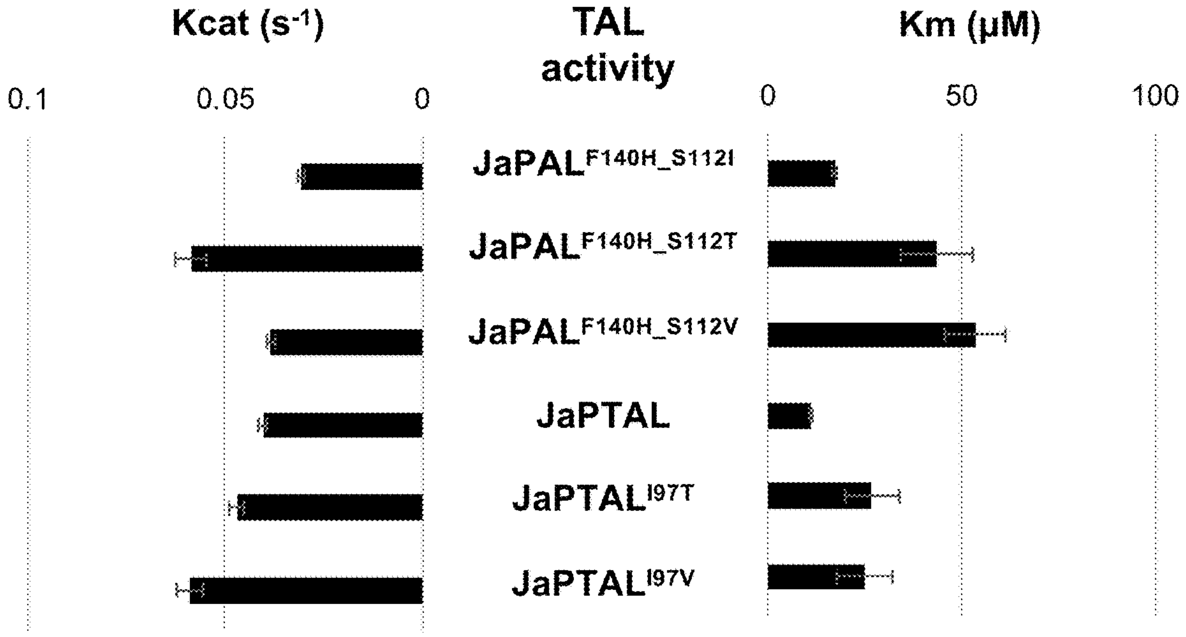
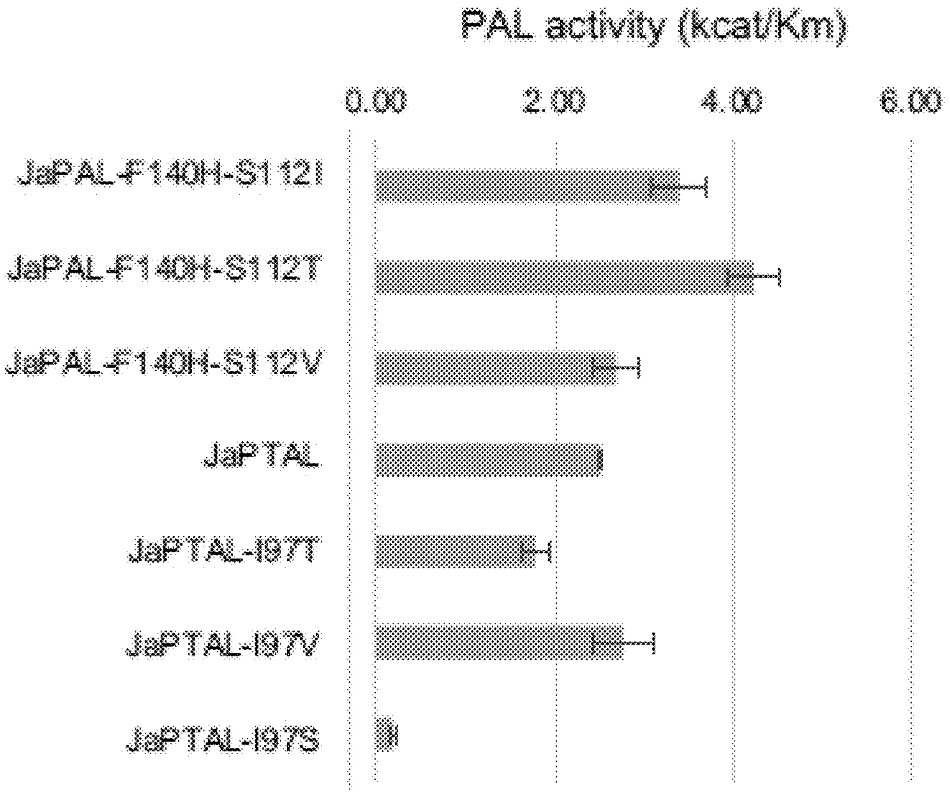

group
Basal angiosperm
Basal nonflower
Eudicot
Gymnosperm
Monocot
Thr112
Ile112
Ser112
Ile112
Thr112
Clade I
(conserved in angiosperm)
Ser112
Ile112
(PTAL)
PTAL evolution
Ser112-> Ile112
Ser112
PAL evolution (2)
Thr112 -> Ser112
Ser112
Thr112
Thr112
Clade II
(only few land plants have; no Ser112 residue!)
Thr112
Thr112
PAL evolution (1)
Ile112 -> Thr112
Thr112
Ile112
Ile112
Ile112

Figure 9B


Kcat (s-1)
TAL activity
Km (μM)
0.1
0.05
0
0
50
100
JaPALF140H_S112I
JaPALF140H_S112T
JaPALF140H_S112V
JaPTAL
JaPTALI97T
JaPTALI97V


PAL activity (kcat/Km)
0.00
2.00
4.00
6.00
JaPAL-F140H-S112I
JaPAL-F140H-S112T
JaPAL-F140H-S112V
JaPTAL
JaPTAL-I97T
JaPTAL-I97V
JaPTAL-I97S

TWO COMBINED MUTATIONS THAT INTRODUCE THE SECOND ENTRY PATHWAY TO SYNTHESIZED LIGNIN FROM TYROSINE IN PLANTS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 63/491,152, filed on Mar. 20, 2023, the contents of which are incorporated by reference in their entireties.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under grant number 1836824 awarded by the National Science Foundation. The government has certain rights in the invention.

SEQUENCE LISTING

[0003] This application includes a sequence listing in XML format titled "960296.04479_ST26.xml", which is 356,334 bytes in size and was created on Mar. 14, 2024. The sequence listing is electronically submitted with this application via Patent Center and is incorporated herein by reference in its entirety.

BACKGROUND

[0004] Lignin is a complex organic polymer that is used as a structural material to support the tissues of land plants. It comprises up to 30% of plant dry mass and is the most abundant aromatic polymer on earth. Engineering the lignin biosynthesis pathway is a potential way to increase carbon sequestration in plants and to enhance the value of plant biomass for use in the production of bioenergy and biomaterials. Accordingly, there is a need in the art for methods of altering this pathway.

SUMMARY

[0005] In a first aspect, the present invention provides engineered phenylalanine ammonia-lyase (PAL) enzymes that have increased tyrosine ammonia-lyase (TAL) activity. These engineered PAL enzymes comprise a first mutation at a position corresponding to residue 112 of SEQ ID NO: 28 and a second mutation at a position corresponding to residue 140 of SEQ ID NO: 28 in a wild-type PAL enzyme and have increased TAL activity relative to the wild-type PAL enzyme.

[0006] In a second aspect, the present invention provides polynucleotides encoding an engineered PAL enzyme described herein.

[0007] In a third aspect, the present invention provides constructs comprising a promoter operably linked to a polynucleotide described herein.

[0008] In a fourth aspect, the present invention provides vectors comprising a polynucleotide or construct described herein.

[0009] In a fifth aspect, the present invention provides cells comprising an engineered PAL enzyme, polynucleotide, construct, or vector described herein.

[0010] In a sixth aspect, the present invention provides seeds comprising an engineered PAL enzyme, polynucleotide, construct, vector, or cell described herein.

[0011] In a seventh aspect, the present invention provides plants grown from a seed described herein and plants comprising an engineered PAL enzyme, polynucleotide, construct, vector, or cell described herein.

[0012] In an eighth aspect, the present invention provides methods of making the plants described herein.

[0013] In a ninth aspect, the present invention provides methods for using the plants described herein to (1) produce a phenylpropanoid-derived product or (3) sequester carbon dioxide. The methods comprise growing the plants. The methods for producing phenylpropanoid-derived products further comprise purifying the phenylpropanoid-derived products produced by the plant.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawings will be provided by the Office upon request and payment of the necessary fee.

[0015] FIGS. **1**A-**1**B show that grasses possess a tyrosine-derived lignin biosynthesis pathway. FIG. **1**A shows a phylogenetic tree of Poales species. The tree was retrieved from Givnish et al. (2010) and Seetharam et al. (2021), with some modifications. FIG. **1**B shows a schematic depiction of the lignin biosynthetic pathway in grasses. While most vascular plants mainly synthesize lignin from phenylalanine (L-Phe) using the enzyme phenylalanine ammonia-lyase (PAL), grasses can also synthesize lignin from tyrosine (L-Tyr) using the enzyme phenylalanine tyrosine ammonia-lyase (PTAL) via an additional shortcut pathway.

[0016] FIGS. **2**A-**2**C show that PTAL enzymes emerged in the common ancestor of grasses and the non-grass graminids *Joinvillea*, just before the emergence of grasses. FIG. **2**A shows a phylogenetic tree of PAL/PTAL genes in monocots, focusing on Poales species. The tree was built using RAxML-ng from the PAL/PTAL orthogroup from Orthofinder in plants. The PAL/PTAL homologs that are characterized in this study are highlighted. FIG. **2**B is a graph showing the Km and kcat of the TAL activity of PTAL/PAL enzymes from the grasses *Sorghum bicolor* (SbPTAL and SbPAL) and *Brachypodium distachion* (BdPTAL and BdPAL) as well as PTAL homologs from *Streptochaeta angustifolia* (SaPTAL-a and SaPTAL-b), *Joinvillea ascendens* (JaPTAL and JaPAL), and *Ecdeiocolea monostachya* (EmoPTAL and EmoPAL). Michaelis-Menten curves for the TAL and PAL assays for JaPTAL and JaPAL are shown below. FIG. **2**C is a graph showing the ratio of TAL and PAL activity (kcat/Km) of PAL and PTAL enzymes from grasses and non-grass graminids.

[0017] FIGS. **3**A-**3**C demonstrate that multiple amino acid residues are critical for the transition from PAL to PTAL. FIG. **3**A is a graph showing the Km and kcat of TAL activity for PTAL/PAL enzymes (i.e., SbPTAL, BdPTAL, SaPTAL-a, SaPTAL-b, EmoPTAL, JaPTAL, JaPAL, EmoPAL, SbPAL, and BdPAL) comprising a mutation at a position corresponding to residue 140 in JaPAL (SEQ ID NO: 28). FIG. **3**B is a partial amino acid sequence alignment highlighting (1) residue His/Phe 140, which has been reported to be critical for recognition of the substrates phenylalanine and tyrosine (*), (2) residues that are highly conserved and distinct between PTAL or PAL enzymes (circle), and residues that are highly conserved among PTAL enzymes but not among PAL enzymes (triangle). A full-length alignment is provided in FIG. **8**.

[0018] FIG. 3C is a set of graphs showing the Km and kcat of TAL and PAL activity for wild-type and mutant JaPTAL and JaPAL enzymes, including JaPAL mutants with mutations at residue 140 (JaPAL^{F140H}) as well as mutants with mutations at the 8 residues highlighted with circles in FIG. **3**A ($\text{JaPAL}^{F140H\_MUT8}$) and mutants with mutations at the 16 residues highlighted with circles and triangles in FIG. **3**A ($\text{JaPAL}^{F140H\_MUT16}$). Different letters indicate a significant difference (ANOVA with post hoc Tukey-Kramer method, $p<0.05$).

[0019] FIGS. **4**A-**4**D demonstrate that the residue Ser 112 is critical for the acquisition of TAL activity. FIG. **4**A is a graph showing the Km and kcat of TAL activity for $\text{JaPAL}^{F140H\_MUT8}$ variants in which one of the eight additional mutations has been reversed. FIG. **4**B is a schematic depiction of a potential TAL reaction mechanism, showing hypothetical roles for the residues His 140 and Ile112 in PTAL enzyme catalysis. Ser/Ile 112 is located next to Tyr113, which is critical for catalysis, and these residues are in the 'inner mobile loop', which has been suggested to function in substrate binding and catalysis. FIG. **4**C is a graph showing the Km and kcat of TAL activity for JaPAL enzymes with mutations at residue 140 (JaPAL^{F140H}), residue 112 (JaPAL^{S112I}), or both residue 140 and residue 112 ($\text{JaPAL}^{F140H\_S112I}$). FIG. **4**D is a graph showing the Km and kcat of TAL activity for *Arabidopsis* AtPAL1 enzymes with a mutation at a position corresponding to residue 140 of JaPAL (AtPAL1^{F144H}), a position corresponding to residue 112 of JaPAL (AtPAL1^{S116I}), or at positions corresponding to both residue 140 and residue 112 of JaPAL ($\text{AtPAL1}^{F144H\_S116I}$). Different letters indicate a significant difference (ANOVA with post hoc Tukey-Kramer method, $p<0.05$).

[0020] FIG. **5** is a phylogenetic tree of PAL/PTAL genes in green plants. The tree was built using RAxML-ng from the PAL/PTAL orthogroup from Orthofinder in plants. Species used as input for the Orthofinder run are listed in Table 1.

[0021] FIG. **6** shows a phylogenetic tree of PAL/PTAL genes in monocots. The tree was built from the PAL/PTAL orthogroup from Orthofinder using monocot species and the basal species *Amborella trichopoda*. Genes from *Amborella* are the outgroup. The PTAL clade includes genes that are known to have PTAL function in grasses, whereas the PAL clade includes genes for which only PAL function is known in grasses. Species used as input for the Orthofinder run are listed in Table 2.

[0022] FIG. **7** shows high-performance liquid chromatography (HPLC) chromatograms for TAL and PAL reaction products produced by PTAL/PAL enzymes from *B. distachyon* and *J. ascendans.*

[0023] FIG. **8** is a full-length alignment of PTAL and PAL protein sequences from monocots (clade I). The sequences shown is the alignment are SEQ ID NO: 1-143, ordered from top to bottom. These sequences are detailed in Table 8. PTAL sequences (SEQ ID NO: 1-27) are shown at the top of each page. PAL sequences are divided into three categories below: basal grass PAL (SEQ ID NO: 28-30), grass PAL (SEQ ID NO: 31-88), and monocot PAL (SEQ ID NO: 89-143). Residues that are required for general aromatic ammonia-lyase activity are denoted with a square. The 16 residues identified by phylogeny-guided alignment analysis are denoted with triangles and circles. These residues include 8 residues that are highly conserved among both PTAL and PAL enzymes but different between them (circles) and 8 residues are highly conserved among PTALs but not among PALs (triangles).

[0024] FIGS. **9**A-**9**B demonstrate that several different substitutions at residue 112 confer TAL activity. FIG. **9**A is a phylogenetic tree of PAL/PTAL genes in green plants. The amino acids Ser and Ile are well conserved at positions corresponding to residue 112 in JaPAL (SEQ ID NO: 28) in angiosperm PAL enzymes, but basal non-flower PAL enzymes possess Ile, Thr, or Val at this position. FIG. **9**B is a set of graphs showing the TAL and PAL activity of JaPAL and JaPTAL enzymes with mutations at residue 112. Substituting the Ile at this position in $\text{JaPAL}^{F140H\_S112I}$ with Thr or Val retains strong TAL activity but substituting it with Ser does not.

DETAILED DESCRIPTION

[0025] The present invention provides engineered phenylalanine ammonia-lyase (PAL) enzymes comprising one or more mutations that increase the enzymes' tyrosine ammonia-lyase (TAL) activity. Also provided are plants comprising the engineered PAL enzymes and methods of using these plants to sequester CO_2 or produce phenylpropanoid-derived products.

[0026] Most vascular plants synthesize lignin from the amino acid phenylalanine using the enzyme phenylalanine ammonia-lyase (PAL). However, grass plants possess a bifunctional enzyme, phenylalanine tyrosine ammonia-lyase (PTAL), that allows them to synthesize lignin and other phenylpropanoids using either phenylalanine or tyrosine as a substrate. To better understand how PTAL enzymes evolved in grasses, the inventors identified orthologs of grass PTAL enzymes in other, closely related plants. Biochemical characterization of these orthologs revealed that PTAL enzymes are found, not only in grasses, but also in the non-grass graminid *Joinvillea ascendans*, which indicates that PTAL enzymes emerged before the evolution of grasses.

[0027] It was previously reported that a particular residue, referred to herein as His/Phe 140, determines whether PAL/PTAL enzymes have TAL activity in bacteria. However, the inventors discovered that both His 140 and an additional residue, Ile112, are required for TAL activity in plants. They demonstrate that introducing Ile 112 and His 140 into the monofunctional PAL enzymes of *J. ascendans* and *Arabidopsis thaliana* converts them into bifunctional PTAL enzymes. Thus, these residues represent novel gene editing targets that can be used to introduce the alternative TAL pathway into plants. Creating genetically engineered plants that can use both phenylalanine and tyrosine to synthesize lignin and phenylpropanoids should increase the carbon flow into these synthesis pathways and increase the amount of carbon sequestered by the plants. Further, it should increase the phenylpropanoid content of the plants, which may increase the value of their plant material, strengthen their disease resistance, and/or improve their nutritional quality.

[0028] While others have previously shown that overexpressing PAL enzymes (*Phytochemistry,* 64: 153-161, 2003) or expressing bacterial TAL enzymes in transgenic plants (*Planta,* 232: 209-218, 2010) have some effect on the production of phenylpropanoid-derived compounds, the inventors predict that engineering the native PAL enzymes of plants to introduce TAL activity will more effectively increase carbon flow into the phenylpropanoid synthesis pathway as compared to PAL overexpression (i.e., because TAL activity is more efficient than PAL activity, see below) while avoiding the need to introduce a transgene from another organism into the plant.

Enzymes:

[0029] Land plants produce a diverse array of phenylpropanoid compounds, which include polymers, such as lignin, suberin, and condensed tannin, as well as soluble metabolites, such as flavonoids, coumarin, stilbenes, and phenylpropenes. In most plants, the first step in the phenylpropanoid biosynthetic pathway is the deamination of the amino acid phenylalanine into trans-cinnamic acid (FIG. **1**B). This reaction is typically catalyzed by the monofunctional enzyme phenylalanine ammonia-lyase (PAL). The second step in this pathway is typically the hydroxylation of trans-cinnamic acid to p-coumaric acid, which is catalyzed by the enzyme cinnamate 4-hydroxylase (C4H). However, plants that express the bifunctional enzyme phenylalanine tyrosine ammonia-lyase (PTAL) can synthesize p-coumarate either (1) from phenylalanine using the same two-step, two-enzyme process, or (2) from tyrosine using a more efficient, one-step process that avoids the rate-limiting C4H step. Thus, in addition to having phenylalanine ammonia-lyase (PAL) activity, PTAL enzymes have tyrosine ammonia-lyase (TAL) activity. As a result, they can use either phenylalanine or tyrosine as a substrate.

[0030] The PAL and PTAL enzymes of the non-grass graminid *Joinvillea ascendens* are used as reference sequences herein. These enzymes are referred to as JaPAL (protein sequence: SEQ ID NO: 28, DNA sequence: SEQ ID NO: 147) and JaPTAL (protein sequence: SEQ ID NO: 27, DNA sequence: SEQ ID NO: 151).

[0031] "Tyrosine ammonia-lyase (TAL) activity" is enzyme activity that converts the amino acid tyrosine into p-coumaric acid via non-oxidative deamination. PAL enzymes naturally lack or have trace levels TAL activity, whereas PTAL enzymes naturally possess strong TAL activity. However, in the Examples, the inventors demonstrate that TAL activity can be introduced into or dramatically increased in PAL enzymes via the introduction of mutations at two specific residues. The TAL activity of an engineered PAL enzyme of the present invention may be increased by 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 11-fold, 12-fold, 13-fold, 14-fold, 15-fold, 16-fold, 17-fold, 18-fold, 19-fold, 20-fold, or more as compared to the TAL activity of the corresponding wild-type PAL enzyme. The TAL activity of an enzyme can be assessed using TAL activity assays, in which the reaction products formed by the enzyme in the presence of the substrate tyrosine are measured. For example, TAL activity can be assessed by measuring the production of the product p-coumaric acid using high-performance liquid chromatography (HPLC) or by measuring absorbance at 309 nm (e.g., using a plate reader). TAL activity can also be assessed by measuring the release of ammonia from the reaction. See Example 1 for a description of such assays.

[0032] Thus, in a first aspect, the present invention provides engineered phenylalanine ammonia-lyase (PAL) enzymes that have increased tyrosine ammonia-lyase (TAL) activity. An "enzyme" is a protein or RNA molecule that acts as a catalyst in living organism. Enzymes decrease the activation energy required for a chemical reaction to occur by stabilizing the transition state.

[0033] The engineered PAL enzymes described herein may be full-length proteins or may be fragments of full-length proteins. As used herein, a "fragment" is a portion of a protein that is identical in sequence to, but shorter in length than, the full-length protein. For example, a fragment may comprise at least 5, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 150, 250, or 500 contiguous amino acid residues of a full-length protein. Fragments may be preferentially selected from certain regions of a protein. A fragment may comprise an N-terminal truncation, a C-terminal truncation, or both an N-terminal and C-terminal truncation relative to the full-length protein. Preferably, the PAL enzyme fragments used with the present invention are functional fragments. As used herein, the term "functional fragment" refers to a fragment that retains at least 20%, 40%, 60%, 80%, or 100% of the PAL/TAL activity of the corresponding full-length protein.

[0034] The PAL enzymes described herein are "engineered," meaning that they have been altered by the hand of man. Specifically, the PAL enzymes of the present invention have been engineered to comprise one or more mutations. As used herein, the term "mutation" refers to a difference in an amino acid sequence relative to a reference sequence (e.g., the sequence of a wild-type PAL enzyme). Mutations include insertions, deletions, and substitutions of an amino acid relative to a reference sequence. An "insertion" refers to a change in an amino acid sequence that results in the addition of one or more amino acid residues. An insertion may add 1, 2, 3, 4, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, or more amino acid residues to a sequence. A "deletion" refers to a change in an amino acid sequence that results in the removal of one or more amino acid residues. A deletion may remove 1, 2, 3, 4, 5, 10, 20, 50, 100, 200, or more amino acids residues from a sequence. A "substitution" refers to a change in an amino acid sequence in which one amino acid is replaced with a different amino acid. An amino acid substitution may be a conversative replacement (i.e., a replacement with an amino acid that has similar properties) or a radical replacement (i.e., a replacement with an amino acid that has different properties).

[0035] The engineered PAL enzymes of the present invention comprise one or more mutations relative to the corresponding wild-type PAL enzyme. The term "wild-type" is used herein to describe the non-mutated version of an enzyme that is most typically found in nature. Wild-type PAL enzymes comprise a serine at the position corresponding to residue 112 of SEQ ID NO: 28 (Ser112) and comprise a phenylalanine at the position corresponding to residue 140 of SEQ ID NO: 28 (Phe 140), whereas wild-type PTAL enzymes comprise an isoleucine at the position corresponding to residue 112 of SEQ ID NO: 28 (Ile112) and comprise a histidine at the position corresponding to residue 140 of SEQ ID NO: 28 (His140) (see, e.g., FIG. **3**B). The engineered PAL enzymes of the present invention comprise a mutation at a position corresponding to residue 112 of SEQ ID NO: 28, and optionally further comprise a second mutation at a position corresponding to residue 140 of SEQ ID NO: 28.

[0036] For simplicity, throughout this application, we have arbitrarily used the wild-type PAL enzyme of *Joinvillea ascendens* (JaPAL; SEQ ID NO: 28) as a reference sequence and have specified the positions of mutations in various PAL/PTAL enzymes using the residue numbering of this enzyme. Any mutation position can be converted to use the residue numbering of another PAL or PTAL enzyme using a sequence alignment, such as the alignment shown in FIG. **8**. For example, residues 112 and 140 of JaPAL (SEQ ID NO: 28) correspond to residues 116 and 144 of AtPAL1 (SEQ ID NO: 144) and correspond to residues 97 and 125 of JaPTAL (SEQ ID NO: 27), as is demonstrated in FIG. **8**. The use of a PAL enzyme as a reference sequence for a PTAL enzyme is warranted by the high degree of sequence conservation between these enzyme groups. For example, the sequence of JaPAL is 86.9% identical and 92.4% similar to the sequence of JaPTAL. Further, PAL and PTAL enzymes are classified as belonging to the same orthogroup (i.e., set of genes derived from a single gene in the last common ancestor).

[0037] In Example 1, the inventors demonstrate that introducing the mutation S112I into the PAL enzyme of *Joinvillea ascendens* (JaPAL; SEQ ID NO: 28) or introducing the corresponding mutation (i.e., S116I) into the PAL enzyme of the distantly related plant *Arabidopsis thaliana* (AtPAL1; SEQ ID NO: 144) increases the TAL activity of these enzymes (FIGS. **4**C-**4**D). Further, they show that introducing the two mutations S112I and F140H into JaPAL or introducing the corresponding mutations (i.e., S116I and F144H) into AtPAL1 converts these PAL enzymes into bifunctional PTAL enzymes, which are referred to herein as JaPAL^{F140H_S112}I (SEQ ID NO: 145) and AtPALIF^{144H_S116I} (SEQ ID NO: 146), respectively. Thus, in some embodiments, the wild-type PAL enzyme is a PAL enzyme is from *Joinvillea ascendens* or *Arabidopsis thaliana*. In specific embodiments, the wild-type PAL enzyme comprises SEQ ID NO: 28 or SEQ ID NO: 144. In some embodiments, the wild-type PAL enzyme comprises a sequence having at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to SEQ ID NO: 28 or SEQ ID NO: 144.

[0038] As is noted above, the inventors have demonstrated that PAL enzymes from multiple, distantly related plants (i.e., *Joinvillea ascendens* (a monocot) and *Arabidopsis thaliana* (a dicot)) can be converted into bifunctional PTAL enzymes. PAL enzymes (which are found in bacteria, fungi, and plants) are highly conserved across a wide variety of land plants, as is demonstrated in FIG. **8**. Thus, the engineered PAL enzymes of the present invention may be any wild-type PAL enzyme from a land plant into which the necessary mutation(s) (i.e., a mutation at a position corresponding to residue 112 of SEQ ID NO: 28 and, optionally, a second mutation at a position corresponding to residue 140 of SEQ ID NO: 28) have been introduced. For example, the wild-type PAL enzyme may be one of the PAL enzymes included in the sequence alignment of FIG. **8**, i.e., SEQ ID NO: 28-143.

[0039] In some embodiments, the engineered PAL enzymes comprise a polypeptide or a functional fragment thereof having at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to a polypeptide selected from SEQ ID NO: 28-143. "Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window. The aligned sequences may comprise additions or deletions (i.e., gaps) relative to each other for optimal alignment. The percentage is calculated by determining the number of matched positions at which an identical nucleic acid base or amino acid residue occurs in both sequences, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100. Protein and nucleic acid sequence identities can be evaluated using the Basic Local Alignment Search Tool ("BLAST"), which is well known in the art (Karlin and Altschul, Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes. *Proc. Natl. Acad. Sci. USA* (1990) 87: 2267-2268; Altschul et al. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucl. Acids Res. (1997) 25: 3389-3402). The BLAST programs identify homologous sequences by identifying similar segments between a query sequence and a test sequence, which is preferably obtained from a protein or nucleic acid sequence database. The BLAST programs can be used with the default parameters or with modified parameters provided by the user.

[0040] FIG. **3**B and FIG. **8** show amino acid sequence alignments of PAL/PTAL enzymes from a variety of plant species (SEQ ID NO: 1-143). Based on these alignments, it is readily apparent that various amino acid residues may be mutated without substantially affecting the PAL/TAL activity of these enzymes. For example, a person of ordinary skill in the art would appreciate that substitutions in a PAL/PTAL enzyme could be selected based on the alternative amino acid residues that occur at the corresponding position in related PAL/PTAL enzyme from another plant species. For example, the *Joinvillea ascendens* PAL enzyme (SEQ ID NO: 28) has a methionine at position 103 while some of the other enzyme sequences shown in FIG. **3**B have a leucine, threonine, or valine at this position. Thus, exemplary modifications that could be made in the *Joinvillea ascendens* PAL enzyme based on this sequence alignment include M103L, M103T, and M103V substitutions. Similar modifications could be made in any of SEQ ID NO: 1-143 at any position shown in the sequence alignment of FIG. **3**B or FIG. **8**. Additionally, a person of ordinary skill in the art could easily align other PAL/PTAL enzyme sequences with the sequences shown in FIG. **3**B or FIG. **8** to identify additional mutations that could be included in the engineered PAL enzymes of the present invention.

[0041] Regardless of their origin, the engineered PAL enzymes of the present invention comprise a mutation at a position corresponding to residue 112 of JaPAL (SEQ ID NO: 28) and optionally further comprise a second mutation at a position corresponding to residue 140 of JaPAL. As used herein, the phrase "at a position corresponding to" refers to an amino acid position that aligns with an amino acid position in another protein in a protein sequence alignment or a protein structure alignment. For example, the phrase "a position corresponding to residue 112 of SEQ ID NO: 28" refers to an amino acid position in the sequence of protein X that aligns with the 112th amino acid residue of SEQ ID NO: 28 when the sequence of protein X is aligned with SEQ ID NO: 28. To determine whether a particular protein sequence has a mutation at a position "corresponding to" a position disclosed herein, one may align that particular protein sequence with SEQ ID NO: 28 using a conventional sequence alignment method (see, e.g., *Bioinformatics* (2007) 23(7): 802-8) and examine the alignment at the appropriate position.

[0042] In some embodiments, the engineered PAL enzyme comprises a serine to isoleucine mutation at a position corresponding to residue 112 of SEQ ID NO: 28 (e.g., a

S112I mutation). However, in Example 3, the inventors demonstrate that several different substitutions at position 112 retain the TAL activity of the JaPAL$^{F140H\_S112I}$ double mutant. Specifically, they show that substituting the Ile at this position with a valine or threonine retains strong TAL activity but substituting it with a serine does not (FIG. **9**B). Thus, in some embodiments, the mutation is a serine to valine mutation or a serine to threonine mutation.

[0043] In Example 1, the inventors generated a JaPAL enzyme, referred to as JaPAL$^{F140H\_MUT8}$, that has a PTAL-type substitution at residue 140 and at eight additional residues that are highly conserved within both PAL and PTAL enzymes but are distinct between these two groups (i.e., residues 102, 112, 121, 138, 267, 444, 448, and 500). Kinetic assays showed that the catalytic properties of TAL activity (especially tyrosine substrate affinity (Km)) of JaPAL$^{F140H\_MUT8}$ were significantly improved compared to those of wild-type JaPAL and were comparable with those of wild-type JaPTAL (FIG. **3**C; Table 3). Thus, in some embodiments, the engineered PAL enzyme further comprises at least one additional mutation at a position corresponding to residue 102, 121, 138, 267, 444, 448, or 500 of SEQ ID NO: 28. In specific embodiments, the at least one additional mutation includes a valine to isoleucine mutation at a position corresponding to residue 102 of SEQ ID NO: 28, an alanine to glycine mutation at a position corresponding to residue 121 of SEQ ID NO: 28, an isoleucine to lysine mutation at a position corresponding to residue 138 of SEQ ID NO: 28, an alanine to serine mutation at a position corresponding to residue 267 of SEQ ID NO: 28, a proline to threonine mutation at a position corresponding to residue 444 of SEQ ID NO: 28, a serine to alanine mutation at a position corresponding to residue 448 of SEQ ID NO: 28, or an isoleucine to valine mutation at a position corresponding to residue 500 of SEQ ID NO: 28.

Polynucleotides:

[0044] In a second aspect, the present invention provides polynucleotides encoding an engineered PAL enzyme described herein. The terms "polynucleotide," "oligonucleotide," and "nucleic acid" are used interchangeably to refer a polymer of DNA or RNA. A polynucleotide may be single-stranded or double-stranded and may represent the sense or the antisense strand. A polynucleotide may be synthesized or obtained from a natural source. A polynucleotide may contain natural, non-natural, or altered nucleotides, as well as natural, non-natural, or altered internucleotide linkages (e.g., phosphoroamidate linkages, phosphorothioate linkages). The term polynucleotide encompasses constructs, vectors, plasmids, and the like. In some embodiments, the polynucleotide is complementary DNA (cDNA; i.e., synthetic DNA that has been reverse transcribed from a messenger RNA) or genomic DNA (i.e., chromosomal DNA from an organism). Those of skill in the art understand that, due to degeneracy of the genetic code, a variety of polynucleotides can encode the same polypeptide.

[0045] While the polynucleotide sequences disclosed herein are derived from sequences found in plants, any polynucleotide sequence that encodes the desired engineered PAL enzyme may be used with the present invention. For example, in some embodiments, the polynucleotides are codon-optimized for expression in a particular cell (e.g., a plant cell, bacterial cell, or fungal cell). "Codon optimization" is a process used to increase expression of a polynucleotide in a particular host cell by altering the sequence of the polynucleotide to accommodate the codon bias of the host cell. Computer programs for generating codon-optimized sequences for use in a particular host cell are known in the art.

Constructs:

[0046] In a third aspect, the present invention provides constructs comprising a promoter operably linked to one of the polynucleotides described herein. As used herein, the term "construct" refers to a recombinant polynucleotide, i.e., a polynucleotide that was formed by combining at least two polynucleotide components from different sources, natural or synthetic. For example, a construct may comprise the coding region of one gene operably linked to a promoter that is (1) associated with another gene found within the same genome, (2) from the genome of a different species, or (3) synthetic. Constructs can be generated using conventional recombinant DNA methods.

[0047] As used herein, the term "promoter" refers to a DNA sequence that defines where transcription of a polynucleotide beings. RNA polymerase and the necessary transcription factors bind to the promoter to initiate transcription. Promoters are typically located directly upstream (i.e., at the 5' end) of the transcription start site. However, a promoter may also be located at the 3' end, within a coding region, or within an intron of a gene that it regulates. Promoters may be derived in their entirety from a native or heterologous gene, may be composed of elements derived from multiple regulatory sequences found in nature, or may comprise synthetic DNA. A promoter is "operably linked" to a polynucleotide if the promoter is positioned such that it can affect transcription of the polynucleotide.

[0048] The promoter used in the constructs described herein may be a heterologous promoter (i.e., a promoter that is not naturally associated with the wild-type PAL enzyme), an endogenous promoter (i.e., a promoter that is naturally associated with the wild-type PAL enzyme), or a synthetic promoter that is designed to function in a desired manner in a particular host cell. Suitable promoters for use with the present invention include, but are not limited to, constitutive, inducible, temporally regulated, developmentally regulated, chemically regulated, tissue-preferred, and tissue-specific promoters. In some cases, it may be advantageous to use a tissue-specific promoter or a developmental stage-specific promoter to ensure that the construct will drive expression of the engineered enzyme in a particular tissue (e.g., roots, leaves) or during a particular developmental stage (e.g., leaf maturation, seed development, senescence).

[0049] In some embodiments, the promoter is a plant promoter, i.e., a promoter that is active in plant cells. Suitable plant promoters include, without limitation, the 35S promoter of the cauliflower mosaic virus, ubiquitin, the tCUP cryptic constitutive promoter, the Rsyn7 promoter, the maize In2-2 promoter, and the tobacco PR-la promoter.

Vectors:

[0050] In a fourth aspect, the present invention provides vectors comprising one of the polynucleotides or constructs described herein. The term "vector" refers to a DNA molecule that is used to carry a particular DNA segment (i.e., a DNA segment included in the vector) into a host cell. Some vectors are capable of autonomous replication in a host cell (e.g., bacterial vectors that include an origin of replication and episomal mammalian vectors). Other vectors can be integrated into the genome of a host cell such that they are replicated along with the host genome (e.g., viral vectors and transposons). Vectors may include heterologous genetic elements that are necessary for propagation of the vector or for expression of an encoded gene product. Vectors may also include a reporter gene or a selectable marker gene. Suitable vectors include plasmids (i.e., circular double-stranded DNA molecules) and viral vectors.

Cells:

[0051] In a fifth aspect, the present invention provides cells comprising one of the engineered enzymes, polynucleotides, constructs, or vectors described herein. The cells may be eukaryotic or prokaryotic. Preferably, the cell is a type of cell that can be used for large-scale production of phenylpropanoid-derived compounds or for carbon dioxide sequestration. In some embodiments, the cell is a plant cell, a bacterial cell, a fungal cell, or a protist cell.

Seeds:

[0052] In a sixth aspect, the present invention provides seeds comprising one of the engineered enzymes, polynucleotides, constructs, vectors, or cells described herein. A "seed" is an embryonic plant enclosed in a protective outer covering. In embodiments in which the plant comprises a nucleic acid (i.e., a polynucleotide, construct, or vector) described herein, the nucleic acid may either be integrated into the genome of the seed or exist independently from the genome.

Plants:

[0053] In a seventh aspect, the present invention provides plants grown from the seeds described herein and plants comprising one of the engineered PAL enzymes, polynucleotides, constructs, vectors, or cells described herein.

[0054] As used herein, the term "plant" includes both whole plants and plant parts. Examples of plant parts include, without limitation, embryos, pollen, ovules, flowers, glumes, panicles, roots, root tips, anthers, pistils, leaves, stems, seeds, pods, flowers, calli, clumps, cells, protoplasts, germplasm, asexual propagates, and tissue cultures. This term also includes chimeric plants in which only a subset of the plant's cells comprises the engineered PAL enzyme, polynucleotide, construct, or vector.

[0055] The inventors predict that engineering the native PAL enzymes of plants to introduce TAL activity will increase carbon flow into lignin/phenylpropanoid synthesis pathways. Thus, the inventors predict that the plants described herein will: (a) produce a greater quantity of lignin as compared to a control plant; (b) produce a greater quantity of phenylpropanoid-derived compounds as compared to a control plant; and/or (c) sequester a greater quantity of carbon dioxide (CO_2) into aromatic compounds as compared to a control plant.

[0056] Examples of phenylpropanoid compounds and derivatives thereof that could be produced in higher quantities by the plants of the present invention include flavonoids, anthocyanins, lignins, phenolic acids, stilbenes, coumarins, tannins, suberin, cutins, sporopollenin, lignans, and phenylpropenes. These compounds may be useful, for example, for making dyes, colorants, nutraceuticals, pharmaceuticals, and industrial materials. Lignin-derived aromatic monomers can be obtained from plants using microbial (*Curr Opin Biotechnol* 56: 179-186, 2019) or chemical (*Angew Chem Int Ed* 55: 8164-8215, 2016) lignin degradation methods.

[0057] "Carbon sequestration" is a process in which atmospheric CO_2 is captured and stored. It is one method for reducing the amount of CO_2 in the atmosphere (i.e., to reduce global climate change). In some embodiments, the methods further comprise harvesting part of the plant while leaving the roots of the plant in the soil such that the carbon contained in the roots is sequestered therein. Harvestable parts of plants include, without limitation, flowers, pollen, seedlings, tubers, leaves, stems, fruit, seeds, roots, cuttings, and the like.

[0058] As used herein, the term "control plant" refers to a comparable plant (e.g., of the same species, cultivar, and age) that was raised under the same or comparable conditions (e.g., water, sunlight, nutrients) but that does not express an engineered PAL enzyme described herein.

[0059] In some embodiments, the plant produces a greater quantity of lignin and/or phenylpropanoid-derived products or produces these products at a greater rate as compared to a control plant. Suitably, the plant produces at least 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 11-fold, 12-fold, 13-fold, 14-fold, 15-fold, 16-fold, 17-fold, 18-fold, 19-fold, or 20-fold more lignin and/or phenylpropanoid-derived products as compared to the control plant. The amount of lignin produced by a plant may be measured using the thioglycolic acid method (J Agric Food Chem 60(4): 922-8, 2012), which is a standard method for estimating the total lignin content in plant biomass. The amount of a phenylpropanoid-derived product produced by a plant may be measured using liquid chromatography-mass spectrometry (LC-MS).

[0060] In some embodiments, the plant sequesters a greater quantity of CO_2 or sequesters CO_2 at a greater rate as compared to a control plant. Suitably, the CO_2 sequestration of the plant is at least 2%, 5%, 10%, 20%, 30%, 40%, 50%, or 60% greater than that of a control plant. CO_2 sequestration may be quantified by measuring the gas exchange activity of the plant. For example, CO_2 assimilation may be measured using an LI-6400XT photosynthesis system equipped with the 6400-40 leaf chamber (LI-COR). Alternatively, labeled $^{13}CO_2$ can be fed to plants and the rate of ^{13}C incorporation into plants can be measured over time.

[0061] The plants of the present invention may be of any species. In some embodiments, the plant is a land plant that comprises a native PAL enzyme. PAL enzymes are expressed broadly in plants. In some embodiments, the plant is selected from Acorus *americanus, Amborella trichopoda, Ananas comosus, Apostasia shenzhenica, Asparagus officinalis, Brachypodium distachyon, Calamus simplicifolius, Dendrobium catenatum, Ecdeiocolea monostachya, Elaeis guineensis, Flagellaria indica, Joinvillea ascendens, Musa acuminata, Oryza sativa, Panicum hallii, Panicum virgatum, Phalaenopsis equestris, Setaria italica, Setaria viridis, Sorghum bicolor, Spirodela polyrhiza, Streptochaeta angustifolia, Zea mays*, and *Zostera marina*. Protein sequences of PAL enzymes found in these plants are provided as SEQ ID NO: 28-143, and these sequences are aligned in FIG. **8**. In some embodiments, the plant is a bioenergy crop (i.e., a plant that can be used to produce bioenergy). In other embodiments, the plant is a plant that produces a useful phenylpropanoid-derived compound, such as a flavonoid, vanillin, lignan, stilbene, coumarin, or phenylpropene. For example, introducing the tyrosine-derived phenylpropanoid pathway in vanilla may result in increased production of vanillin and introducing this pathway in the legume *Medicago truncatula* may result in increased production of phenylpropanoids.

[0062] In some embodiments, the engineered PAL enzyme is encoded by the genome of the plant. In some embodiments, the plant is a plant that naturally expresses a PAL enzyme, and the gene encoding the native PAL enzyme was modified via gene editing to encode a mutation at a position corresponding to residue 112 of SEQ ID NO: 28. In other embodiments, a polynucleotide encoding an engineered version of a PAL enzyme that is not natively expressed by the plant is introduced into the genome of the plant. In other embodiments, the plant comprises a polynucleotide encoding an engineered PAL enzyme that exists independently of the genome. Methods of genetically engineering plants using recombinant biology or gene editing, such as CRISPR/Cas based gene editing, are known to those of skill in the art.

[0063] In some embodiments, the plants further comprise additional mutations that affect how they absorb and utilize atmospheric carbon. The inventors have previously identified mutations in *Arabidopsis thaliana* that deregulate the first step of the shikimate pathway, i.e., a pathway that connects central carbon metabolism to the pathway for aromatic amino acid biosynthesis in plants. See Yokoyama et al., Science Advances 8(23): eabo3416 (2022), which is hereby incorporated by reference in its entirety. These mutations map to genomic loci that encode the three *Arabidopsis* isoforms of the enzyme 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (DHS), which catalyzes the first reaction of the shikimate pathway. The inventors discovered that these mutations reduce inhibition by tyrosine/tryptophan-associated compounds and that plants that express DHS enzymes comprising these mutations produce greater quantities of aromatic amino acids and assimilate greater quantities of CO_2. Thus, in some embodiments, the plants of the present invention further comprise an engineered DHS enzyme that comprises one or more of these mutations, i.e., one or more mutation at a position corresponding to residue 109, 114, 159, 240, 244, 245, 247, 248, 319, 322, or 348 of the *Arabidopsis thaliana* DHS1 enzyme (SEQ ID NO: 152). Plants that further comprise such engineered DHS enzymes (i.e., in addition an engineered PAL enzyme) are expected to produce even higher levels of phenylpropanoids.

[0064] Additionally, the inventors have previously identified an active site residue (i.e., residue 220 of the *Medicago truncatula* PDH enzyme) that determines the substrate specificity (i.e., for prephenate or arogenate) and level of tyrosine feedback inhibition of TyrA family enzymes, which are the key regulatory enzymes of tyrosine biosynthesis. See U.S. Pat. No. 11,136,559, which is hereby incorporated by reference in its entirety. These mutations may be used to enhance the production of tyrosine and tyrosine-derived products in plants. Thus, in some embodiments, the plants of the present invention further comprise an engineered TyrA enzyme. In some embodiments, the engineered TyrA enzyme is an engineered arogenate dehydrogenase (ADH) enzyme comprising a non-acidic amino acid residue at a position corresponding to residue 220 of the *Medicago truncatula* ADH enzyme (e.g., SEQ ID NO: 153, which comprises a D220C mutation). These engineered ADH enzymes have increased prephenate dehydrogenase (PDH) activity and relaxed tyrosine sensitivity as compared to the corresponding wild-type ADH enzyme. In other embodiments, the engineered TyrA enzyme is an engineered PDH enzyme comprising an aspartic acid or glutamic acid at a position corresponding to residue 220 of the *Medicago truncatula* PDH enzyme (e.g., SEQ ID NO: 154, which comprises a C220D mutation). These engineered PDH enzymes have increased ADH activity and increased tyrosine sensitivity as compared to the corresponding wild-type PDH enzyme. Plants that further comprise such engineered TyrA enzymes (i.e., in addition an engineered PAL enzyme) are expected to produce even higher levels of phenylpropanoids.

Methods for Making Plants:

[0065] In an eighth aspect, the present invention provides methods of making the plants described herein. In some embodiments, the methods comprise introducing one of the engineered PAL enzymes, polynucleotides, constructs, or vectors described herein into the plant. As used herein, "introducing" describes a process by which exogenous polypeptides or polynucleotides are introduced into a recipient cell. Suitable introduction methods include, without limitation, *Agrobacterium*-mediated transformation, the floral dip method, bacteriophage or viral infection, electroporation, heat shock, lipofection, microinjection, and particle bombardment.

[0066] In other embodiments, the plant comprises a native gene encoding a PAL enzyme, and the methods comprise editing the native gene to encode an engineered PAL enzyme described herein. "Gene editing" describes a process by which mutations (i.e., deletions, insertions, and substitutions) are introduced into a native gene within an organism's genome. Gene editing can be performed using several different nucleases, including zinc finger nucleases (ZFN), transcription activator-like effector nucleases (TALENs), and CRISPR/Cas endonucleases. Site-directed mutagenesis (e.g., homologous recombination) may also be used to edit a gene.

[0067] In specific embodiments, the methods comprise using a RNA-guided endonuclease (e.g., Cas9) to edit the native gene to have a mutation at a position corresponding to residue 112 of SEQ ID NO: 28. This can be accomplished by using the endonuclease to specifically edit the codon of the gene encoding the residue corresponding to residue 112 of SEQ ID NO: 28. In some embodiments, the methods further comprise using the endonuclease to edit the native gene to have a mutation at a position corresponding to residue 140 of SEQ ID NO: 28.

Methods for Using Plants:

[0068] In a ninth aspect, the present invention provides methods for using the plants described herein to (1) produce a phenylpropanoid-derived product or (2) sequester CO_2. The methods comprise growing the plants described herein or plants genetically engineered to produce the engineered PAL enzymes described herein. The methods for producing phenylpropanoid-derived products further comprise purifying the phenylpropanoid-derived products produced by the plant.

[0069] The present disclosure is not limited to the specific details of construction, arrangement of components, or method steps set forth herein. The compositions and methods disclosed herein are capable of being made, practiced, used, carried out and/or formed in various ways that will be apparent to one of skill in the art in light of the disclosure that follows. The phraseology and terminology used herein is for the purpose of description only and should not be regarded as limiting to the scope of the claims. Ordinal indicators, such as first, second, and third, as used in the description and the claims to refer to various structures or method steps, are not meant to be construed to indicate any specific structures or steps, or any particular order or configuration to such structures or steps. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to facilitate the disclosure and does not imply any limitation on the scope of the disclosure unless otherwise claimed. No language in the specification, and no structures shown in the drawings, should be construed as indicating that any non-claimed element is essential to the practice of the disclosed subject matter. The use herein of the terms "including," "comprising," or "having," and variations thereof, is meant to encompass the elements listed thereafter and equivalents thereof, as well as additional elements. Embodiments recited as "including," "comprising," or "having" certain elements are also contemplated as "consisting essentially of" and "consisting of" those certain elements.

[0070] Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. For example, if a concentration range is stated as 1% to 50%, it is intended that values such as 2% to 40%, 10% to 30%, or 1% to 3%, etc., are expressly enumerated in this specification. These are only examples of what is specifically intended, and all possible combinations of numerical values between and including the lowest value and the highest value enumerated are to be considered to be expressly stated in this disclosure. Use of the word "about" to describe a particular recited amount or range of amounts is meant to indicate that values very near to the recited amount are included in that amount, such as values that could or naturally would be accounted for due to manufacturing tolerances, instrument and human error in forming measurements, and the like. All percentages referring to amounts are by weight unless indicated otherwise.

[0071] No admission is made that any reference, including any non-patent or patent document cited in this specification, constitutes prior art. In particular, it will be understood that, unless otherwise stated, reference to any document herein does not constitute an admission that any of these documents forms part of the common general knowledge in the art in the United States or in any other country. Any discussion of the references states what their authors assert, and the applicant reserves the right to challenge the accuracy and pertinence of any of the documents cited herein. All references cited herein are fully incorporated by reference, unless explicitly indicated otherwise. The present disclosure shall control in the event there are any disparities between any definitions and/or description found in the cited references.

[0072] The following examples are meant only to be illustrative and are not meant as limitations on the scope of the invention or of the appended claims.

EXAMPLES

Example 1

[0073] In the following example, the inventors describe their discovery of a novel mutation that is necessary to convert monofunctional phenylalanine ammonia-lyase (PAL) enzymes into bifunctional phenylalanine tyrosine ammonia-lyase (PTAL) enzymes.

BACKGROUND

[0074] Acquisition of the ability to synthesize lignin was one of the most important events that allowed vascular plants to migrate from water to land and adapt to the harsh environment. Lignin is essential in land plants for providing mechanical strength, facilitating water transportation, and strengthening the physical barrier against biotic and abiotic stresses. In addition to cellulose and hemicelluloses, lignin is one of the major components of plant secondary cell walls, and up to 30% of photosynthetically fixed carbon is utilized to produce lignin. Lignin hinders the efficient use of cell wall polysaccharides as a source of pulp, paper, and bioethanol. However, lignin is the only abundant, renewable feedstock that comprises aromatics. Thus, it has potential for use in the production of sustainable, value-added aromatic materials and high-energy-density solid fuels.

[0075] The monocot grass plant group is one of the most widely distributed plant groups on earth and contains 780 genera and about 12,000 species. These plants succeeded in expanding their habitat from forest to harsh open land by developing a series of morphological, physiological, and biochemical features. This plant group contains a substantial number of economically important crops. For example, grass cereal crops (e.g., rice, wheat, and corn) comprise a major portion of most people's diets, and grass straws are used as livestock feeds. This plant group also contains several crops with superior biomass productivity (e.g., switchgrass, sorghum, and *Miscanthus*) that have potential for use in the production of plant-based energy and materials. Grasses are classified as Poales, a large order of flowering, monocotyledonous plants that contains around 21,000 species of great diversity that evolved within a relatively short evolutionary timescale (Givnish et al., 2010; McKain et al., 2016) (FIG. **1**A).

[0076] Although lignin is an indispensable component of vascular plants, the biosynthesis and structure of lignin differ not only among plant species but also across the organ and cell types of individual plants (Renault et al., 2019; Vanholme et al., 2019). In all vascular plants, lignin is composed of the monomeric units guaiacyl (G), syringyl unit (S), and p-hydroxyphenyl (H), which are produced via polymerization of coniferyl alcohol, sinapyl alcohol, and p-hydroxyphenyl alcohol, respectively. In addition to these three monomers, grass lignin uniquely incorporates γ-acylated (p-coumarylated and feruloylated) monomers and flavone tricin (FIG. **1**B). The G/S/H lignin monomers are synthesized from the aromatic amino acid phenylalanine (L-Phe) through the phenylpropanoid pathway (FIG. **1**B). In the first step of this pathway, L-Phe is deaminated by the enzyme phenylalanine ammonia-lyase (PAL) to produce cinnamic acid, which is then hydroxylated by the enzyme cinnamate 4-hydroxylase (C4H) to produce p-coumaric acid (FIG. **1**B). In addition to this highly conserved PAL-C4H pathway, grasses possess an additional entry pathway that produces p-coumaric acid and lignin from tyrosine (L-Tyr) using the tyrosine ammonia-lyase (TAL) activity of the bifunctional enzyme phenylalanine tyrosine ammonia-lyase (PTAL) (Rosler et al., 1997; Barros et al., 2016). Since this TAL pathway does not require catalysis by the enzyme C4H, it is considered more efficient than the conserved PAL-C4H pathway (Maeda, 2016).

[0077] TAL activity has been detected in plant extracts of a wide range of grass species, including species classified in both the BOP and PACMAD clades (FIG. **1**A), i.e., bamboo, rice, barley, wheat, sugarcane, maize, and oat (Young and Neish, 1966; Higuchi and Shimada, 1969; Havir et al., 1971; Jangaard, 1974). Although there are several reports suggesting that TAL activity is also present in other plant lineages such as legume (Jangaard, 1974; Beaudoin-Eagan and Thorpe, 1985; Giebel, 1973; Khan et al., 2003), the detection of TAL activity in grass extract is more consistent in the literature than in other lineages. Rosler et al. (1997) demonstrated that a PAL isoform from *Zea mays* can utilize both L-Tyr and L-Phe as a substrate by expressing it as a recombinant protein. Later, this bifunctional PTAL enzyme was also identified in *Brachypodium distachyon* via in vivo transgenic down-regulation (Cass et al., 2015; Barros et al., 2016) and in vitro enzyme assays (Barros et al., 2016). In these papers, eight PAL genes were identified in *B. distachyon*, and one of them was demonstrated to have bifunctional PTAL activity. The fact that PTAL genes are highly expressed in vascular organs (Cass et al., 2015; Barros et al., 2016) and that around half of all lignin is produced from L-Tyr (Barros et al., 2016) suggest that the PTAL pathway has a significant physiological role. However, the details regarding the evolutionary emergence of the PTAL enzyme are unknown.

[0078] The residue His 140, which is located in the substrate binding pocket of TAL enzymes, was previously proposed to be a key residue for the acquisition of TAL activity (Dixon and Barros, 2019). This residue was shown to be critical for recognition of the substrate tyrosine based on the crystal structure of the bacterial TAL enzyme (Watts et al. 2006). PAL enzymes have a highly conserved Phe 140 at this position (Louie et al. 2006; Watts et al. 2006). When a His 140 to Phe (H140F) mutation was introduced into the bacterial TAL enzyme, the TAL enzyme (which previously had a high substrate specificity for L-Tyr) was essentially converted into a PAL enzyme with a high specificity for L-Phe (Watts et al. 2006). However, in previous studies, introducing a Phe 140 to His (F140H) mutation into the *Arabidopsis* PAL enzyme failed to convert it into a bifunctional PTAL enzyme (Watts et al. 2006). Further, introducing a H140F mutation into the *Sorghum bicolor* PTAL enzyme produced an enzyme with kinetic properties that were noticeably different from other *S. bicolor* PAL enzymes (Jun et al., 2018). Thus, in addition to His140, other unidentified residue(s) are thought to be necessary for the acquisition of TAL activity (Barros and Dixon, 2020).

[0079] To elucidate the evolutionary history of the emergence of the PTAL enzyme in Poales, we obtained PAL/PTAL homolog sequences from 45 monocot species, including basal-grasses and non-grass graminids, whose genomes were sequenced only recently. We found that PAL orthologs from non-grass graminids nested directly into the grass PTAL clade and were distinct from the PAL clade. Biochemical characterization of recombinant PAL/PTAL homologs demonstrated that PTAL enzymes emerged in the common ancestor of the non-grass graminid *Joinvillea ascendens* and grasses, just before the emergence of grasses. A combined approach using phylogeny-guided sequence comparison and site-directed mutagenesis identified an additional mutation, Ser112 to Ile (S112I), that is essential for the transition from a monofunctional PAL enzyme to a bifunctional PTAL enzyme. We found that introduction of S112I and F140H mutations into PAL enzymes from *J. ascendans* and *Arabidopsis thaliana* conferred significant TAL activity to these enzymes.

Results:

PTAL Evolved in a Common Ancestor of Grasses and the Non-Grass Graminid *Joinvillea*

[0080] To determine when PTAL enzymes emerged in grasses, we obtained the genome sequences of 44 species of green plants, identified their PAL family enzymes using the PTAL orthogroup from OrthoFinder (Table 1), and generated a large-scale phylogenetic tree of plant PAL and PTAL enzymes. The angiosperm PAL family was divided into two distinct clades: clades I and II. Clade I includes well-characterized angiosperm PAL enzymes (e.g., from *Arabidopsis thaliana*, Cochrane et al., 2004) and both PAL and PTAL enzymes from grasses, such as *Zea mays* (Rosler et al., 1997), *Sorghum bicolor* (Jun et al., 2018), and *Brachypodium distachyon* (Barros et al., 2016) (FIG. **5**). The clade II enzymes have not been characterized. We built a detailed phylogenetic tree of the clade I monocot PAL/PTAL family enzymes by identifying another orthogroup that includes 45 monocot species. In our analysis, we included several sister lineages to the core grasses, whose genome sequences became available only recently (FIG. **1**B; Table 2), including a grass that diverged at the base of Poaceae (*Streptochaeta angustifolia*) and two non-grass graminid species (i.e., *Joinvillea ascendens* and *Ecdeiocolea monostachya*) (FIG. **1**B). We found that PAL orthologs from *S. angustifolia, J. ascendens*, and *E. monostachya* nested directly into the PTAL clade of core grasses and were separate from the PAL clade of the remaining grasses (FIG. **2**A; FIG. **6**). This result suggests that monocot PAL enzymes diverged at a common ancestor of the non-grass graminids and that PTAL enzymes subsequently emerged under the selective pressure (FIG. **2**A; FIG. **6**).

[0081] The residue His 140, which is located in the substrate binding pocket of TAL enzymes, was previously shown to be critical for the recognition of the substrate tyrosine based on the crystal structure of the bacterial enzyme (Watts et al. 2006). In contrast, PAL enzymes have highly conserved Phe 140 at this position (Louie et al. 2006, Watts et al. 2006). When the His residue of a bacterial TAL enzyme was mutated to Phe, the TAL enzyme was essentially converted to a PAL enzyme (Watts et al. 2006). To predict the functionality of the PAL/PTAL orthologs from *S. angustifolia, J. ascendens*, and *E. monostachya* (which are labeled in FIG. **2**A), we compared their protein sequences to those of the PTAL enzymes from the core grass clade and

PAL enzymes in the grass and monocot clades (FIG. **2**A). Both of the *S. angustifolia* enzymes (i.e., STRANG_00039019-RA and STRANG_00041445-RA) and one of enzyme from each of *J. ascendens* (i.e., Joascv11021323m) and *E. monostachya* (i.e., Emon_augustus_masked-scf718000019722) possessed the His 140 residue that is critical for tyrosine recognition in the bacterial TAL enzyme (Watts et al. 2006) (FIG. **2**B), suggesting that these proteins are bifunctional PTAL enzymes. To test this hypothesis, we cloned, expressed, and purified recombinant PAL/PTAL orthologs from *S. angustifolia, J. ascendens*, and *E. monostachya* as well as PAL and PTAL enzymes from *Sorghum bicolor* (i.e., SbPAL and SbPTAL) and *Brachypodium distachyon* (i.e., BdPAL and BdPTAL) as positive controls (Barros et al., 2016; Jun et al., 2018). These purified enzymes were mixed with the substrate, Phe or Tyr, at 1 mM and the production of cinnamic acid (CA) or p-coumaric acid (pCA) was analyzed by high-performance liquid chromatography to detect PAL or TAL activity. All ten of the tested enzymes showed detectable PAL and TAL activities as compared to negative controls (i.e., reactions that included boiled enzyme or no substrate) (FIG. **7**). All enzymes produced similar levels of CA from Phe, whereas the production of pCA from Tyr was much higher (50-fold) in the reaction mixtures containing SbPTAL, BdPTAL, STRANG_00039019-RA, STRANG_00041445-RA, Emon_augustus_masked-scf718000019722, and Joascv11021323m than those containing Joascv11021328m, Emon_augustus_masked-scf718000017824, BdPAL, and SbPAL (FIG. **7**). These results suggest that only the PAL/PTAL orthologs that comprise His 140 are bifunctional PTAL enzymes that have both TAL and PAL activity. Therefore, we tentatively named the enzymes with His 140 SaPTAL-a, SaPTAL-b, EmoPTAL, and JaPTAL, and named the enzymes with Phe140 EmoPAL and JaPAL.

[0082] To further examine the TAL activities of these PAL (i.e., JaPAL, EmoPAL, BdPAL, and SbPAL) and PTAL (i.e., SbPTAL, BdPTAL, SaPTAL-a, SaPTAL-b, EmoPTAL, and JaPTAL) enzymes, we determined the kinetic parameters of reactions using various concentrations of the substrate Tyr (FIG. **2**B; Table 3). The apparent Km of the PAL enzymes ranged from 3449 to 6211 µM and the apparent Km of the PTAL enzymes ranged from 11 to 19 µM (Table 3). The kcat values of the PAL enzymes ranged from 0.02 to 0.04 s^{-1} and the kcat values of the PTAL enzymes ranged from 0.04 to 0.09 s^{-1} (Table 3). Consequently, the kcat/Km values of the PTAL enzymes (3.32 to 7.96 s^{-1} μM^{-1}) were calculated to be much higher (485-fold on average) than those of the PAL enzymes (0.01 s^{-1} μM^{-1}) (FIG. **2**C). JaPTAL and JaPAL (which has a sequence similarity of 92.4%) were found to be distinct with regards to both the presence of TAL activity and the level of PAL activity. The PAL activity (kcal/Km) of JaPTAL (6.8 s^{-1} μM^{-1}) was lower than that of JaPAL (78.8 s^{-1} μM^{-1}) with significant differences in both k_{cat} (0.5 s^{-1} and 1.9 s^{-1}) and Km (66 µM and 24 µM) (FIG. **2**B; Table 3). The PAL/PTAL enzymes from other species showed similar kinetics to the PAL activity of JaPAL/JaPTAL, but higher Km values were observed with grass PTAL enzymes (150-227 µM) as compared to non-grass graminid PTAL enzymes (66-69 µM) (Table 3). Consequently, the TAL/PAL activity ratios (kcal/Km) for grass PTAL enzymes were higher than those of non-grass graminid PTAL enzymes (2.7-fold on average) (FIG. **2**C). These quantitative data further support the hypothesis that *S. angustifolia, E. monostachya*, and *J. ascendens* have at least one enzyme having strong TAL activity. These results suggest that the bifunctional PTAL enzymes emerged within a common ancestor of grasses and the non-grass graminid *J. ascendens*, just before the emergence of grasses.

Additional Amino Acids are Involved in the Transition from PAL to PTAL

[0083] To experimentally test the role of His 140 in the acquisition of TAL activity, we next conducted site-directed mutagenesis on the PAL and PTAL enzymes of grasses and non-grass graminids characterized above and analyzed their effects on TAL activity. For the PAL enzymes, the residue corresponding to Phe 140 was converted to His to generate JaPAL^{F140H} EmoPAL^{F134H}, BdPAL^{F137H}, and SbPAL^{F135H}. A detailed kinetic analysis showed that, compared to the corresponding wild-type PAL enzymes, all these mutants exhibited increased overall TAL activity (kcat/Km; 9.7-fold on average) with significantly reduced Km values for Tyr (0.04-fold on average) (Table 3). For the PTAL enzymes, the residue corresponding to His 140 was converted to Phe to generate SbPTAL^{H123F}, BdPTAL^{H123F}, SaPTAL-a^{H118F}, SaPTAL-b^{H126F}, EmoPTAL^{H127F}, and JaPTAL^{H125F}. Compared to the corresponding wild-type PTAL enzymes, all these mutants exhibited decreased TAL activity (0.01-fold on average) and significantly increased Km for Tyr (13.2-fold on average) (FIG. **3**A; Table 3). These results further support the role of His140 as a critical residue for the recognition of Tyr substrate in PTAL enzymes, consistent with prior studies (Watts et al., 2006; Louie et al., 2006; Jun et al., 2018). However, the Km values for TAL activity were still much higher in PAL^{F140H} mutants (222-450 µM) than in wild-type PTALs (11-19 µM) and lower in PTAL^{H140F} mutants (531-765 µM) than in wild-type PALs (3448-6211 µM) (Table 3). As a result, the TAL activity of the PAL^{F140H} mutants was much weaker (~19% on average) than that of the wild-type PTAL enzymes, and PTAL^{H140F} mutants still showed higher TAL activity than that of the wild-type PAL enzymes (FIG. **3**A). The PAL activity of the PAL^{F140H} and PTAL^{H140F} mutants showed much higher (35-fold on average) and lower (0.04-fold on average) Km values, respectively, toward Phe compared with the corresponding wild-type enzymes as expected, but an unexpected reduction in the kcat of the PTAL^{H140F} mutant was observed (0.25-fold on average) (Table 3). Thus, unlike in the bacterial TAL enzyme (Watts et al., 2006), other residues besides the His 140 are likely important for the acquisition of strong TAL activity in the PTAL enzymes of grasses and closely-related non-grass graminids.

Introduction of Eight Additional Mutations Besides F140H Converts PAL into PTAL

[0084] To identify the additional residues critical for the transition of PAL to PTAL in this plant lineage, we conducted a phylogeny-guided sequence comparison (Maeda, 2019) utilizing the phylogenetic distribution of the functional PAL and PTAL enzymes (FIG. **2**A). In the amino acid sequence alignment of monocot PAL and PTAL enzymes (FIG. **3**B, FIG. **8**), we identified 16 residues that are highly conserved in PTAL enzymes. These highly conserved residues include 8 residues (denoted using circles in FIG. **3**B) that are highly conserved within PAL and PTAL groups but are distinct between these two groups, as well as 8 residues (denoted using triangles in FIG. **3**B) that are highly conserved among PTAL enzymes but are variable among PAL enzymes (FIG. **3**B; Table 4). To determine the position of these residues within the PAL/PTAL protein structures, we generated a homology model of JaPAL from *J. ascendens* using the well-characterized parsley PAL structure as a template (PDB:6F6T, Bata et al., 2021). We found that most of the 16 highly conserved residues are located near the active center, with the exception of a few peripheral triangle residues (FIG. **3**B).

[0085] To investigate the potential role of these residues in TAL activity, we generated two JaPAL mutant enzymes, one with PTAL-type substitutions in the 8 circle residues and the other with PTAL-type substitutions in both the circle and triangle residues (Table 4) in addition to the F140H mutation (JaPAL$^{F140H\_MUT8}$ and JaPAL$^{F140H\_MUT16}$, respectively). Kinetic assays showed that the apparent Km value of JaPAL$^{F140H\_MUT8}$ (17.9 μM) was significantly improved compared to that of the JaPAL^{F140H} single mutant (222.7 μM) and closely approached that of wild-type JaPTAL with similar kcat values (FIG. **3**C; Table 3). JaPAL$^{F140H\_MUT8}$ had a 2-fold higher Km for Phe as compared to wild-type JaPTAL with comparable kcat values (FIG. **3**C). JaPAL$^{F140H\_MUT16}$ also showed significantly improved Km (42.2 μM) for TAL activity as compared to JaPAL^{F140H} (and wild-type JaPAL) but, unexpectedly, to a lesser extent than JaPAL$^{F140H\_MUT8}$ (FIG. **3**C). Thus, these results demonstrate that some of the 8 circle residues are involved in TAL activity in PTAL enzymes from non-grass graminids and suggest that the overall configuration of the active site may be critical for the acquisition of bifunctional PTAL activity.

S112I is Critical for Gaining the TAL Activity in Graminid PTALs

[0086] To determine which of the 8 circle residues are essential in the conversion of PAL enzymes to PTAL enzymes (FIG. **3**C), we mutated, one by one, each one of these 8 residues back to the PAL type in JaPAL$^{F140H\_MUT8}$ and determined their effects on catalytic efficiency. The substitution of seven out of eight residues had no to minor impacts on the overall TAL and PAL activity of the mutant enzymes (FIG. **4**A). In contrast, when the I112S substitution was introduced to JaPAL$^{F140H\_MUT8}$ (JaPAL$^{F140H\_MUT8\_I112S}$), both TAL and PAL activities were significantly decreased due to an increase of Km value and decrease of kcat value (FIG. **4**A; Table 3). Therefore, the Ile 112 residue of the PTAL enzyme appears to be crucial for TAL activity.

[0087] We generated homology model structures of JaPAL and JaPTAL proteins using the parsley PAL and sorghum PTAL enzymes, respectively, as templates (FIG. **4**B). We found that the Ser/Ile112 residue does not directly face the substrate but is located next to Tyr113/98 (PAL/PTAL), which is a critical proton acceptor for catalysis (Rother et al., 2002; Jun et al., 2018). These Ser/Ile 112-Tyr113 residues are in the 'inner mobile loop', which has been suggested to be important for substrate binding and catalysis (Rother et al., 2002; Dixon and Barros, 2019). Therefore, we hypothesize that a structural change in the inner-mobile loop affects the structure of the substrate binding pocket, resulting in the different catalytic activities of graminid PAL and PTAL enzymes.

Introduction of F140H and S112I is Sufficient to Change PAL into PTAL

[0088] To test this hypothesis further, the reciprocal S112I mutation was introduced into the JaPAL^{F140H} single mutant to generate the JaPAL$^{F140H\_S112I}$ double mutant. For comparison, a single mutant in which the residue corresponding to Ser112 was converted to Ile (i.e., JaPAL^{S112I}) was generated as well. While kcat was not drastically affected by these mutations, Km of the JaPAL^{F140H_S112}I mutant for TAL activity (17.5 μM) became significantly lower than those of wild-type JaPAL (4859 μM) and the single mutants JaPAL^{F140H} and JaPAL^{S112I} (223 μM and 354 μM, respectively) and reached to the level of wild-type JaPTAL (FIG. **4**C). Thus, we identified an additional residue, Ile 112, which is essential for TAL activity, and our data demonstrate that the introduction of the S112I and F140H mutations is nearly enough to convert monofunctional PAL enzymes into bifunctional PTAL enzymes.

[0089] To test whether two amino acid substitutions equivalent to F140H and S112I can also confer TAL activity in distantly related PAL enzymes, we introduced these mutations into a recombinant *Arabidopsis* PAL1 enzyme that has higher PAL activity and weak TAL activity (Cochrane et al., 2004; Watts et al., 2006) (Table 3). AtPAL1$^{F144H\_S116I}$ showed a drastic reduction in its Km towards Tyr (20.2 μM) as compared to that of wild-type AtPAL1 (3070 μM) and its single mutants (AtPAL1^{F144H} and AtPAL1^{S116I}) (314 μM and 515 μM, respectively) (FIG. **4**D). Overall, the kinetics behavior of the AtPALIF$^{144H\_S116I}$ and JaPAL$^{H140F\_I112S}$ double mutants were similar (FIGS. **4**C-**4**D). Thus, these results demonstrate that conversion of monofunctional PAL enzymes into bifunctional PTAL enzymes can be achieved via introduction of two mutations in distantly related plant PAL enzymes.

[0090] The protein sequences of the JaPAL and AtPAL1 enzymes tested in this example are outlined in Table 6, and the DNA sequences of the JaPAL and AtPAL1 enzymes tested in this example are outlined in Table 7.

Tables:

[0091]

TABLE 1

List of sequence data used to build the green plant phylogenetic tree

File name	Species	Gene starts with	Label	Division/ clade	Common name
Atrichopoda__291__v1.0.protein__ primaryTranscriptOnly.fa.mod.fa	*Amborella trichopoda*	evm__27.model. AmTr__v1.0	basal-angiosperm	Angiosperms	Amborella
Ppatens__318__v3.3.protein__ primaryTranscriptOnly.fa.mod.fa	*Physcomitrella patens*	Pp	basal-nonflower	Bryophyta	moss
Sfallax__522__v1.1.protein__ primaryTranscriptOnly.fa.mod.fa	*Sphagnum fallax*	Sphfalx	basal-nonflower	Bryophyta	flat-topped bogmoss
Smoellendorffii__91__v1.0.protein__ primaryTranscriptOnly.fa.mod.fa	*Selaginella moellendorffii*¬†	XXXXXX or XXXXX	basal-nonflower	Lycophytes	spike moss

TABLE 1-continued

List of sequence data used to build the green plant phylogenetic tree

File name	Species	Gene starts with	Label	Division/ clade	Common name
Mpolymorpha_320_v3.1.protein_primaryTranscriptOnly.fa.mod.fa	*Marchantia polymorpha¬†*	Mapoly	basal-nonflower	Marchantiophyta	liverwort
Azolla_filiculoides.protein.highconfidence_v1.1.fasta	*Azolla filiculoides*	Azfi_	basal-nonflower	Polypodiophyta	fern
Salvinia_cucullata.protein.highconfidence_v1.2.fasta	*Salvinia cucullata*	Sacu_v1.1	basal-nonflower	Polypodiophyta	watermoss
Dcarota_388_v2.0.protein_primaryTranscriptOnly.fa.mod.fa	*Daucus carota*	DCAR	dicot	Asterids	wild carrot
GCF_000188115.4_SL3.0_protein.faa.mod.fa	*Solanum lycopersicum*	NP_ or XP_	dicot	Asterids	tomato
Mguttatus_256_v2.0.protein_primaryTranscriptOnly.fa.mod.fa	*Mimulus guttatus*	Migut	dicot	Asterids	monkey flower
Stuberosum_448_v4.03.protein_primaryTranscriptOnly.fa.mod.fa	*Solanum_tuberosum*	PGSC	dicot	Asterids	potato
Ahypochondriacus_459_v2.1.protein_primaryTranscriptOnly.fa.mod.fa	*Amaranthus hypochondriacus*	AH	dicot	Eudicot	Prince-of-Wales feather
Acoerulea_322_v3.1.protein_primaryTranscriptOnly.fa.mod.fa	*Aquilegia coerulea*	Aqcoe	dicot	Eudicot	blue colombine
Athaliana_167_TAIR10.protein_primaryTranscriptOnly.fa.mod.fa	*Arabidopsis thaliana*	AT	dicot	Rosid	Arabidopsis
Boleraceacapitata_446_v1.0.protein_primaryTranscriptOnly.fa.mod.fa	*Brassica oleracea capitata*	Bol	dicot	Rosid	cabbage
BrapaFPsc_277_v1.3.protein_primaryTranscriptOnly.fa.mod.fa	*Brassica rapa*	Brara	dicot	Rosid	turnip
Csativus_122_v1.0.protein_primaryTranscriptOnly.fa.mod.fa	*Cucumis sativus*	Cucsa	dicot	Rosid	cucumber
Egrandis_297_v2.0.protein_primaryTranscriptOnly.fa.mod.fa	*Eucalyptus grandis*	Eucgr	dicot	Rosid	rose gum
Fvesca_501_v2.0.a2.protein_primaryTranscriptOnly.fa.mod.fa	*Fragaria vesca*	gene	dicot	Rosid	wild strawberry
Graimondii_221_v2.1.protein_primaryTranscriptOnly.fa.mod.fa	*Gossypium raimondii*	Gorai	dicot	Rosid	cotton
Mtruncatula_285_Mt4.0v1.protein_primaryTranscriptOnly.fa.mod.fa	*Medicago truncatula*	Medtr	dicot	Rosid	legume
Ptrichocarpa_210_v3.0.protein_primaryTranscriptOnly.fa.mod.fa	*Populus trichocarpa*	Potri	dicot	Rosid	poplar/black cottonwood
Pvulgaris_442_v2.1.protein_primaryTranscriptOnly.fa.mod.fa	*Phaseolus vulgaris*	Phvul	dicot	Rosid	common bean
Rcommunis_119_v0.1.protein_primaryTranscriptOnly.fa.mod.fa	*Ricinus communis*	2, 3, 4, 5, or 6+ XXXX.mXXXXX	dicot	Rosid	castor bean
Tcacao_233_v1.1.protein_primaryTranscriptOnly.fa.mod.fa	*Theobroma cacao*	Thecc	dicot	Rosid	cocoa
Vvinifera_145	*Vitis vinifera*	GSVIV	dicot	Rosid	grape
Kfedtschenkoi_382_v1.1.protein_primaryTranscriptOnly.fa.mod.fa	*Kalanchoe fedtschenkoi¬†*	Kaladp	dicot	Eudicot	formerly Bryophyllum fedtschenkoi
Creinhardtii_281_v5.6.protein_primaryTranscriptOnly.fa.mod.fa	*Chlamydomonas reinhardtii*	Cre	greenalgae	Chlorophyta	green algae
Pabies1.01.0-HC-pep.faa.mod.fa	*Picea abies*	MA_	gymnosperm	Pinophyta	norway spruce
Aamericanusv1.1.primaryTrs.pep.fa.mod.fa	*Acorus americanus*	Aca	monocot	Monocot	American sweet flag/wetland plant
Spolyrhiza_290_v2.protein_primaryTranscriptOnly.fa.mod.fa	*Spirodela polyrhiza*	Spipo	monocot	Monocot	duckweed
Zmarina_324_v2.2	*Zostera marina*	Zosma	monocot	Monocot	sea grass
Jascendensv1.1.primaryTrs.pep.fa.mod.fa	*Joinvillea ascendens*	Joasc	monocot	Commelinids	Joinvillea
Macuminata_304_v1.protein_primaryTranscriptOnly.fa.mod.fa	*Musa acuminata*	GSMUA	monocot	Commelinids	banana
proteome.all_transcripts.calsi.fasta.mod.fa	*Calamus simplicifolius*	CALSI	monocot	Commelinids	rattan palm
proteome.all_transcripts.egu.fasta.mod.fa	*Elaeis guineensis*	p5.00_sc	monocot	Commelinids	oil palm
Bdistachyon_556_v3.2.protein_primaryTranscriptOnly.fa.mod.fa	*Brachypodium distachyon*	Bradi	monocot	Commelinids	purple false brome
Osativa_323_v7.0.protein_primaryTranscriptOnly.fa.mod.fa	*Oryza sativa*	LOC_Os	monocot	Commelinids	rice
Pvirgatum_516_v5.1.protein_primaryTranscriptOnly.fa.mod.fa	*Panicum virgatum*	Pavir	monocot	Commelinids	switchgrass

TABLE 1-continued

List of sequence data used to build the green plant phylogenetic tree

File name	Species	Gene starts with	Label	Division/ clade	Common name
Sitalica_312_v2.2.protein_primaryTranscriptOnly.fa.mod.fa	*Setaria italica*	Seita	monocot	Commelinids	fostail millet
Streptochaeta_maker_max_proteins_V1.fasta.mod.fa	*Streptochaeta angustifolia*	STRANG_	monocot	Commelinids	Streptochaeta
Sviridis_500_v2.1.protein_primaryTranscriptOnly.fa.mod.fa	*Setaria viridis*	Sevir	monocot	Commelinids	green foxtail
ZmaysPH207_443_v1.1	*Zea mays*	Zm	monocot	Commelinids	maize
Acomosus_321_v3.protein_primaryTranscriptOnly.fa.mod.fa	*Ananas comosus*	Aco	monocot	Commelinids	pineapple

TABLE 2

List of genome sequence data used to build the monocot phylogenetic tree

File name	Species	Gene starts with	Clade	Common name	Ref
Atrichopoda_291_v1.0.protein_primaryTranscriptOnly.fa.mod.fa	*Amborella trichopoda*	evm_27.model.AmTr_V1.0	Angiosperm	Amborella	ncbi
Aamericanusv1.1.primaryTrs.pep	*Acorus americanus*	Acame	monocot	wetland plant	phytozome
Zmarina_324_v2.2	*Zostera marina*	Zosma	monocot	sea grass	phytozome
Spolyrhiza_290_v2	*Spirodela polyrhiza*	Spipo	monocot	duckweed	phytozome
GCA_002076135.1_ASM207613v1	*Xerophyta viscosa*	Xer_vis_	monocot		ncbi
GCF_001876935.1_Asparagusof.V1_protein.faa	*Asparagus officinalis*	Aoff_	monocot	asparagus	ncbi
GCA_002786265.1_ApostasiaASM278626v1_protein.faa	*Apostasia shenzhenica*	Apos_	monocot	orchid	ncbi
GCF_001263595.1_Pequestris_ASM126359v1_protein.faa	*Phalaenopsis equestris*	Pequ_	monocot		ncbi
GCF_001605985.2_Dendrobium_catASM160598v2_protein.faa	*Dendrobium catenatum*	Dcat_	monocot		ncbi
Garlic.pep.fa.mod.fa	*Allium sativum*	Allium_Sat	monocot	garlic	ncbi
Dioscorea_rotundata_TDr96_F1_v1.0.protein_20170801.fasta.mod.fa	*Dioscorea rotundata*	Dio_Rot_v1	monocot	white yam	DNA Databank of Japan (DDBJ)
Macuminata_304_v1	*Musa acuminata*	GSMUA_	monocot	banana	phytozome
calsi_proteome.sel	*Calamus simplicifolius*	CALSI_	monocot	rattan palm	plaza_v4.5_monocots
egu_proteome.sel	*Elaeis guineensis*	p5.00_	monocot	oil palm	ncbi
Cocos_GCA_008124465.1_ASM812446v1_protein.faa	*Cocos nucifera*	Coc_Nuc	monocot	coconut palm	Ncbi
Phoenix_GCF_009389715.1_palm_55x_up_171113_PBpolish2nd_filt_p_protein.faa	*Phoenix dactylifera*	Phoe_Dac	monocot	date palm	Ncbi
Carex_littledalei_GCA_011114355.1 ASM1111435v1_protein.faa.mod.fa	*Carex littledalei*	Car_Lil	monocot		Ncbi
Acomosus_321_v3	*Ananas comosus*	Aco	monocot	pineapple	phytozome
Jascendensv1.1.primaryTrs.pep.fa.mod	*Joinvillea ascendens*	Joascv	monocot		phytozome
Emo_MaSuRCA_v1_v0.all.MERGE.proteins	*Ecdeiocolea monostachya*	Emon_	monocot		Matthew Moscou
Streptochaeta	*Streptochaeta angustifolia*	STRANG_	monocot	basal grass	phytozome
Platifoliusv1.1.primaryTrs.pep [coge genome (not annotated)]	*Pharus latifolius*	Pha_lat	monocot		
Othomaeum_386_v1.0.protein_primaryTranscriptOnly.fa	*Oropetium thomaeum*	Oropetium	monocot	resurrection plant	phytozome
Sbicolor_454_v3.1.1.protein_primaryTranscriptOnly.fa	*Sorghum bicolor*	Sobic	monocot	cereal grass	phytozome
ZmaysPH207_443_v1.1	*Zea mays*	Zm	monocot	maize	phytozome
Sviridis_500_v2.1	*Setaria viridis*	Sevir	monocot	green foxtail	phytozome
Sitalica_312_v2.2.protein_primaryTranscriptOnly.fa	*Setaria italica*	Seita	monocot	foxtail millet	phytozome

TABLE 2-continued

List of genome sequence data used to build the monocot phylogenetic tree

File name	Species	Gene starts with	Clade	Common name	Ref
Pvirgatum__516__v5.1	*Panicum virgatum*	Pavir	monocot	switchgrass	phytozome
PhalliiHAL__496__v2.1.protein__primaryTranscriptOnly.fa	*Panicum hallii*	PhHAL	monocot	Hall's panicgrass	phytozome
Osativa__323__v7.0	*Oryza sativa*	Osa__LOC__	monocot	rice	phytozome
Bstacei__316__v1.1.protein__primaryTranscriptOnly.fa	*Brachypodium stacei*	Brast	monocot	grass	phytozome
Bsylvaticum__490__v1.1.protein__primaryTranscriptOnly.fa	*Brachypodium sylvaticum*	Brasy	monocot	grass	phytozome
Bdistachyon__556__v3.2	*Brachypodium distachyon*	Bradi	monocot	grass	phytozome
Hvulgare__462__r1.protein__primaryTranscriptOnly.fa.mod.fa	*Hordeum vulgare*	Hor__Vul	monocot	barley	JGI

TABLE 3

Kinetic parameters of recombinant PTAL orthologs with or without mutations

	TAL assay			PAL assay		
Protein	Km (μM)	kcat (s^{-1})	kcat/Km (s^{-1} mM^{-1})	Km (μM)	kcat (s^{-1})	kcat/Km (s^{-1} mM^{-1})
SbPTAL	10.8 ± 2.2	0.09 ± 0.00	7.96 ± 1.18	150.1 ± 14.4	0.69 ± 0.01	4.63 ± 0.49
BdPTAL	19.1 ± 2.4	0.09 ± 0.00	4.78 ± 0.36	216.6 ± 10.3	1.05 ± 0.05	4.84 ± 0.11
SaPTAL-a	13.3 ± 1.0	0.04 ± 0.00	3.32 ± 0.13	154.5 ± 3.7	0.39 ± 0.01	2.51 ± 0.03
SaPTAL-b	16.2 ± 0.5	0.06 ± 0.00	3.57 ± 0.07	227.4 ± 1.5	0.56 ± 0.02	2.46 ± 0.10
EmoPTAL	16.3 ± 1.2	0.04 ± 0.0	2.55 ± 0.16	64.1 ± 3.1	0.48 ± 0.00	7.54 ± 0.39
JaPTAL	11.0 ± 0.4	0.04 ± 0.00	3.68 ± 0.22	65.6 ± 1.4	0.45 ± 0.02	6.80 ± 0.18
JaPAL	4859.1 ± 2350.1	0.03 ± 0.01	0.01 ± 0.00	24.4 ± 0.1	1.92 ± 0.01	78.60 ± 0.00
EmoPAL	4226.2 ± 150.6	0.03 ± 0.00	0.01 ± 0.00	27.7 ± 1.9	1.23 ± 0.02	44.70 ± 2.39
BdPAL	3448.6 ± 1045.4	0.02 ± 0.01	0.01 ± 0.00	21.3 ± 2.1	0.86 ± 0.03	40.74 ± 2.68
SbPAL	5347.8 ± 1284.4	0.04 ± 0.01	0.01 ± 0.00	43.9 ± 2.7	0.97 ± 0.02	22.05 ± 1.08
SbPTAL^{H123F}	750.7 ± 36.8	0.03 ± 0.00	0.04 ± 0.00	3.8 ± 2.0	0.10 ± 0.00	30.97 ± 13.70
BdPTAL^{H123F}	765.2 ± 65.8	0.03 ± 0.00	0.04 ± 0.00	6.0 ± 1.4	0.17 ± 0.00	29.92 ± 6.75
SaPTAL-a^{H118F}	531.0 ± 13.2	0.03 ± 0.00	0.06 ± 0.00	6.0 ± 0.8	0.20 ± 0.00	33.60 ± 5.10
SaPTAL-b^{H126F}	723.6 ± 54.8	0.05 ± 0.00	0.06 ± 0.01	6.3 ± 0.5	0.23 ± 0.00	37.05 ± 2.12
EmoPTAL^{H127F}	613.5 ± 18.1	0.04 ± 0.0	0.07 ± 0.01	3.6 ± 0.5	0.12 ± 0.00	32.62 ± 2.12
JaPTAL^{H125F}	535.4 ± 80.5	0.02 ± 0.00	0.04 ± 0.00	6.8 ± 0.7	0.08 ± 0.00	12.28 ± 0.71
JaPAL^{F140H}	222.7 ± 13.5	0.03 ± 0.00	0.13 ± 0.01	697.0 ± 169.2	0.60 ± 0.04	0.89 ± 0.18
EmoPAL^{F134H}	450.1 ± 14.2	0.02 ± 0.00	0.05 ± 0.00	1305.3 ± 25.6	0.42 ± 0.01	0.32 ± 0.01
BdPAL^{F137H}	371.3 ± 15.4	0.04 ± 0.00	0.11 ± 0.01	1082.0 ± 58.1	0.75 ± 0.01	0.70 ± 0.03
SbPAL^{F135H}	412.8 ± 6.5	0.04 ± 0.00	0.10 ± 0.00	1051.6 ± 58.5	0.88 ± 0.05	0.84 ± 0.02
JaPAL$^{F140H\_MUT8}$	17.9 ± 2.0	0.03 ± 0.00	1.81 ± 0.18	141.0 ± 6.3	0.60 ± 0.01	4.25 ± 0.22
JaPAL$^{F140H\_MUT16}$	42.2 ± 2.1	0.02 ± 0.00	0.56 ± 0.02	454.9 ± 4.6	0.46 ± 0.01	1.01 ± 0.0
JaPAL$^{F140H\_MUT8\_I102V}$	24.5 ± 1.4	0.04 ± 0.00	1.67 ± 0.08	231.7 ± 3.5	0.74 ± 0.01	3.19 ± 0.08
JaPAL$^{F140H\_MUT8\_I122S}$	282.3 ± 29.0	0.02 ± 0.00	0.07 ± 0.00	2290.9 ± 344.4	0.29 ± 0.04	0.31 ± 0.00
JaPAL$^{F140H\_MUT8\_G121A}$	12.6 ± 0.6	0.03 ± 0.00	2.12 ± 0.07	58.1 ± 3.4	0.57 ± 0.02	9.88 ± 0.31
JaPAL$^{F140H\_MUT8\_L138I}$	18.3 ± 0.6	0.05 ± 0.00	2.50 ± 0.02	74.3 ± 1.1	0.66 ± 0.01	8.86 ± 0.01
JaPAL$^{F140H\_MUT8\_S267A}$	43.1 ± 1.5	0.04 ± 0.00	0.96 ± 0.03	316.9 ± 6.6	0.85 ± 0.04	2.67 ± 0.06
JaPAL$^{F140H\_MUT8\_T444P}$	25.3 ± 2.4	0.04 ± 0.00	1.61 ± 0.09	191.9 ± 3.6	0.90 ± 0.05	4.70 ± 0.22
JaPAL$^{F140H\_MUT8\_A448S}$	23.3 ± 1.0	0.04 ± 0.00	1.62 ± 0.04	167.7 ± 11.3	0.80 ± 0.03	4.79 ± 0.43
JaPAL$^{F140H\_MUT8\_V500I}$	25.1 ± 3.2	0.05 ± 0.00	1.82 ± 0.14	150.7 ± 3.7	0.82 ± 0.02	5.45 ± 0.14
JaPAL^{S112I}	353.5 ± 45.0	0.05 ± 0.00	0.13 ± 0.01	2.6 ± 0.5	0.21 ± 0.04	79.80 ± 0.00
JaPAL$^{F140H\_S112I}$	17.2 ± 0.7	0.03 ± 0.00	1.79 ± 0.10	67.3 ± 2.5	0.77 ± 0.01	11.46 ± 0.21
AtPAL1	3069.8 ± 433.4	0.05 ± 0.00	0.02 ± 0.00	52.2 ± 3.1	1.42 ± 0.07	27.31 ± 0.85
AtPAL1^{S114I}	515.4 ± 54.3	0.02 ± 0.00	0.04 ± 0.00	10.1 ± 1.9	0.23 ± 0.00	23.71 ± 4.63
AtPAL1^{F144H}	313.9 ± 13.9	0.01 ± 0.00	0.03 ± 0.00	1198.9 ± 21.1	1.58 ± 0.04	1.32 ± 0.02
AtPAL1$^{F144H\_S114I}$	20.2 ± 0.2	0.02 ± 0.00	1.05 ± 0.02	87.3 ± 2.9	0.88 ± 0.01	10.07 ± 0.44
JaPTAL$^{H125F\_I97S}$	Only trace activity detected.			9.42 ± 0.8	0.02 ± 0.00	1.66 ± 0.12

TABLE 4

Residues potentially involved in the transition from PAL to PTAL in graminids. Residue numbering is based on JaPAL (SEQ ID NO: 28).

Residue No.	Identity in PAL	Identity in PTAL	Mutated in JaPAL$^{F140H\_MUT16}$	Mutated in JaPAL$^{F140H\_MUT8}$
70	A (S)	G	x	
102	V	I	x	x
110	T (V/G)	G	x	
112	S	I	x	x
121	A	G	x	x
129	E (Q/K)	D	x	
135	R (K/Q/A)	V	x	
138	I	L	x	x
267	A	S	x	x
271	G (A)	A	x	
279	E (D)	D	x	
334	Y (F)	F	x	
444	P	T	x	x
448	S	A	x	x
500	I	V	x	x
502	S (A)	A	x	

TABLE 5

Primers used in this study

Sequence (5′ to 3′)	Purpose	Template	Lab ID
Nested PCR and in-fusion cloning			
CGCGCGGCAGCCATATGATGGCGTTCCA GAACGAC (SEQ ID NO: 155)	in-fusion cloning of JaPTAL into pET28a	*Joinvillea ascendens* cDNA	pHM1810
GCTCGAATTCGGATCCTCAGCAGATTGG CAGGGG (SEQ ID NO: 156)	in-fusion cloning of JaPTAL into pET28a	*Joinvillea ascendens* cDNA	pHM1811
CAATTGCAGGGAGATCGAGC (SEQ ID NO: 157)	nested PCR for JaPAL	*Joinvillea ascendens* cDNA	pHM1869
TGCTGTTGTAAGGTGGGGAT (SEQ ID NO: 158)	nested PCR for JaPAL	*Joinvillea ascendens* CDNA	pHM1870
CGCGCGGCAGCCATATGATGGAGTGCGA GAACGGC (SEQ ID NO: 159)	in-fusion cloning of JaPAL into pET28a	*Joinvillea ascendens* CDNA	pHM1812
GCTCGAATTCGGATCCTCAGCAGATTGG CAGGGG (SEQ ID NO: 160)	in-fusion cloning of JaPAL into pET28a	*Joinvillea ascendens* CDNA	pHM1813
TCTTCTTCCACACCAAACG (SEQ ID NO: 161)	nested PCR for SaPTAL-a	*Streptochaeta angustifolia* cDNA	pHM1851
GCACAAGAAGGATGCTAGAAAC (SEQ ID NO: 162)	nested PCR for SaPTAL-a	*Streptochaeta angustifolia* CDNA	pHM1852
CGCGCGGCAGCCATATGATGGCGAGCCA GAGGGAC (SEQ ID NO: 163)	in-fusion cloning of SaPTAL-a into pET28a	*Streptochaeta angustifolia* CDNA	pHM1814
GCTCGAATTCGGATCCTTAGCAGATGGG CAGGGG (SEQ ID NO: 164)	in-fusion cloning of SaPTAL-a into pET28a	*Streptochaeta angustifolia* cDNA	pHM1815
ATGGTGGCCCAGAGCGAC (SEQ ID NO: 165)	nested PCR for SaPTAL-b	*Streptochaeta angustifolia* cDNA	pHM1841
TTAGCAGATTGGAAGGGGC (SEQ ID NO: 166)	nested PCR for SaPTAL-b	*Streptochaeta angustifolia* CDNA	pHM1842
CGCGCGGCAGCCATATGATGGTGGCCCA GAGCGAC (SEQ ID NO: 167)	in-fusion cloning of SaPTAL-b into pET28a	*Streptochaeta angustifolia* CDNA	pHM1816

TABLE 5-continued

Primers used in this study

Sequence (5′ to 3′)	Purpose	Template	Lab ID
GCTCGAATTCGGATCCTTAGCAGATTGG AAGGGGC (SEQ ID NO: 168)	in-fusion cloning of SaPTAL-b into pET28a	*Streptochaeta angustifolia* CDNA	pHM1817
CAAGAAGAGCACGCCAACTC (SEQ ID NO: 169)	nested PCR for SbPTAL	*Sorghum bicolor* RTx430 CDNA	pHM2009
GCCACACACACATACGGATC (SEQ ID NO: 170)	nested PCR for SbPTAL	*Sorghum bicolor* RTx430 CDNA	pHM2010
GCGCGGCAGCCATATGATGGCGGGCAAC GGCGCC (SEQ ID NO: 171)	in-fusion cloning of SbPTAL into pET28a	*Sorghum bicolor* RTx430 CDNA	pHM2011
GCTCGAATTCGGATCCTTAGTTGACGAC GTTGAT (SEQ ID NO: 172)	in-fusion cloning of SbPTAL into pET28a	*Sorghum bicolor* RTx430 CDNA	pHM2012
CCACTGTCAGTCACGCAATT (SEQ ID NO: 173)	nested PCR for SbPAL	*Sorghum bicolor* RTx430 CDNA	pHM2066
TGCAACAGCCAAGAACATGC (SEQ ID NO: 174)	nested PCR for SbPAL	*Sorghum bicolor* RTx430 cDNA	pHM2067
GCGCGGCAGCCATATGATGGAGTGCGAG ACGGGT (SEQ ID NO: 175)	in-fusion cloning of SbPAL into pET28a	*Sorghum bicolor* RTx430 cDNA	pHM2068
GCTCGAATTCGGATCCTCAGCAGAGCGG CAGTGG (SEQ ID NO: 176)	in-fusion cloning of SbPAL into pET28a	*Sorghum bicolor* RTx430 cDNA	pHM2069
CTCTGCAATTCGACGAGCTC (SEQ ID NO: 177)	nested PCR for BdPAL	*Brachypodium distachyon* BL31 cDNA	pHM2072
AGTTCTACTGGCTGCCTACC (SEQ ID NO: 178)	nested PCR for BdPAL	*Brachypodium distachyon* BL31 cDNA	pHM2073
GCGCGGCAGCCATATGATGGAGTACGAG AACGGG (SEQ ID NO: 179)	in-fusion cloning of BdPAL into pET28a	*Brachypodium distachyon* BL31 cDNA	pHM2074
GCTCGAATTCGGATCCTCAGCAGAGAGG CAGGGG (SEQ ID NO: 180)	in-fusion cloning of BdPAL into pET28a	*Brachypodium distachyon* BL31 cDNA	pHM2075
AGCTCCTATCTTCTTTCTTTCT (SEQ ID NO: 181)	nested PCR for AtPAL1	*Arabidopsis thaliana* CDNA	pHM2536
AACCACTTCACAGACAATCA (SEQ ID NO: 182)	nested PCR for AtPAL1	*Arabidopsis thaliana* CDNA	pHM2537
CGCGCGGCAGCCATATGATGGAGATTAA CGGGGCACAC (SEQ ID NO: 183)	in-fusion cloning of AtPAL1 into pET28a	*Arabidopsis thaliana* CDNA	pHM2522
GCTCGAATTCGGATCCTTAACATATTGGA ATGGGAGCTCCG (SEQ ID NO: 184)	in-fusion cloning of AtPAL1 into pET28a	*Arabidopsis thaliana* cDNA	pHM2523
Sequencing analysis			
CGACTCACTATAGGGGAATTGTG (SEQ ID NO: 185)	sequencing of pET28a vectors	All of the pET28a construct generated	pHM1826
GCTAGTTATTGCTCAGCGGTG (SEQ ID NO: 186)	sequencing of pET28a vectors	All of the pET28a construct generated	pHM1827
CATTCAAGATCGCCGGCATC (SEQ ID NO: 187)	sequencing of JaPTAL-pET28a	JaPTAL-pET28a	pHM1828
CTAACATCGAACTTGGCCGG (SEQ ID NO: 188)	sequencing of JaPTAL-pET28a	JaPTAL-pET28a	pHM1829
TCTTCCTGGCAGAGACAAGG (SEQ ID NO: 189)	sequencing of JaPTAL-pET28a	JaPTAL-pET28a	pHM1863
TTCCTCAATGCCGGAGTCTT (SEQ ID NO: 190)	sequencing of JaPAL-pET28a	JaPAL-pET28a	pHM1830

TABLE 5-continued

Primers used in this study			
Sequence (5′ to 3′)	Purpose	Template	Lab ID
CTTCTGCGAAGTCATGACCG (SEQ ID NO: 191)	sequencing of JaPAL-DET28a	JaPAL-pET28a	pHM1831
CAACCCAGTGACCAACCATG (SEQ ID NO: 192)	sequencing of JaPAL-pET28a	JaPAL-pET28a	pHM1832
CTACGACGCCAACATTCTCG (SEQ ID NO: 193)	sequencing of SaPTAL-a-pET28a	SaPTAL-a-pET28a	pHM1833
ACATCGGCAAGCTCATGTTC (SEQ ID NO: 194)	sequencing of SaPTAL-a-pET28a	SaPTAL-a-pET28a	pHM1834
TTGATGGCAGGAAGGTGGAT (SEQ ID NO: 195)	sequencing of SaPTAL-b-pET28a	SaPTAL-b-pET28a	pHM1835
ATCGGAAAGCTCATGTTCGC (SEQ ID NO: 196)	sequencing of SaPTAL-b-pET28a	SaPTAL-b-pET28a	pHM1836
CCCCAAGGAAGGTCTGGC (SEQ ID NO: 197)	sequencing of SbPTAL-pET28a	SbPTAL-pET28a	pHM2015
ACATCGGCAAGCTCATGTTC (SEQ ID NO: 198)	sequencing of SbPTAL-pET28a	SbPTAL-pET28a	pHM2016
CATCGTCAATGGCACCTCC (SEQ ID NO: 199)	sequencing of BdPTAL-pET28a	BdPTAL^{H123F}-pET28a	pHM2026
CTCATGTTCGCGCAGTTCTC (SEQ ID NO: 200)	sequencing of BdPTAL-pET28a	BdPTAL^{H123F}-pET28a	pHM2027
GTCTCGCCATGGTCAACG (SEQ ID NO: 201)	sequencing of SbPAL-pET28a	SbPAL-pET28a	pHM2070
CCATCGGCAAGCTCATGTTC (SEQ ID NO: 202)	sequencing of SbPAL-pET28a	SbPAL-pET28a	pHM2071
CCTTGCCATGGTGAACGG (SEQ ID NO: 203)	sequencing of BdPAL-pET28a	BdPAL-pET28a	pHM2076
CAAGCTCATGTTTGCCCAGT (SEQ ID NO: 204)	sequencing of BdPAL-pET28a	BdPAL-pET28a	pHM2077
Site-directed mutagenesis (1)			
CTCAGGTTTCTGAACGCCGGGATCTTC (SEQ ID NO: 205)	site-directed mutagenesis (H123F)	BdPTAL-pET28a	pHM1894
GTTCAGAAACCTGAGGAGCTCGACCTG (SEQ ID NO: 206)	site-directed mutagenesis (H123F)	BdPTAL-pET28a	pHM1895
CTTAGATTCCTCAATGCCGGAATCTT (SEQ ID NO: 207)	site-directed mutagenesis (^{F140H})	JaPTAL-pET28a	pHM1896
ATTGAGGAATCTAAGGAGCTCTATTTG (SEQ ID NO: 208)	site-directed mutagenesis (^{F140H})	JaPTAL-pET28a	pHM1897
AATTAGACACCTCAATGCCGGAGTCTT (SEQ ID NO: 209)	site-directed mutagenesis (H128F)	JaPAL-pET28a	pHM1904
TTGAGGTGTCTAATTAGCTCTCTTTGG (SEQ ID NO: 210)	site-directed mutagenesis (H128F)	JaPAL-pET28a	pHM1905
CTCCGGTTTCTGAATGCTGGAATCTT (SEQ ID NO: 211)	site-directed mutagenesis (H118F)	SaPTAL-a-pET28a	pHM1900

TABLE 5-continued

Primers used in this study

Sequence (5′ to 3′)	Purpose	Template	Lab ID
ATTCAGAAACCGGAGGAGCTCCACCTG (SEQ ID NO: 212)	site-directed mutagenesis (H118F)	SaPTAL-a-pET28a	pHM1901
CTTCGGTTTCTCAATGCCGGAATCTT (SEQ ID NO: 213)	site-directed mutagenesis (H127F)	SaPTAL-b-pET28a	pHM1902
ATTGAGAAACCGAAGGAGCTCCACCTG (SEQ ID NO: 214)	site-directed mutagenesis (H127F)	SaPTAL-b-pET28a	pHM1903
CTCAGGTTTCTCAACGCCGGGATCTTCGGCACC (SEQ ID NO: 215)	site-directed mutagenesis (H125F)	SbPTAL-pET28a	pHM2013
GTTGAGAAACCTGAGCAGCTCGACCTGGAGCGC (SEQ ID NO: 216)	site-directed mutagenesis (H125F)	SbPTAL-pET28a	pHM2014
ATCAGACACCTCAATGCCGGCGCCTTCGGCACC (SEQ ID NO: 217)	site-directed mutagenesis (F135H)	SbPAL-pET28a	pHM2083
ATTGAGGTGTCTGATGAGCTCCCTCTGGAGCGCG (SEQ ID NO: 218)	site-directed mutagenesis (F135H)	SbPAL-pET28a	pHM2084
ATCCGACACCTTAATGCGGGAGCCTTCGGCACC (SEQ ID NO: 219)	site-directed mutagenesis (F138H)	BdPAL-pET28a	pHM2085
ATTAAGGTGTCGGATGAGCTCTCTCTGCAGAGCGC (SEQ ID NO: 220)	site-directed mutagenesis| (F138H)	BdPAL-pET28a	pHM2086
CTTAGATTCCTCAATGCCGGAGTCTTCGGCACC (SEQ ID NO: 221)	site-directed (H140F)	mutagenesis| JaPAL$^{F140H\_MUT8}$-pET28a, JaPAL$^{F140H\_MUT8}$-pET28a	pHM2232
ATTGAGGAATCTAAGTAGCTCTCTTTGGAGAGC (SEQ ID NO: 222)	site-directed mutagenesis (H140F)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2233
ATTGAGGAATCTAAGTAGCTCTACTTGGAGAGC (SEQ ID NO: 223)	site-directed mutagenesis (H140F)	JaPAL$^{F140H\_MUT16}$-pET28a	pHM2234
Site-directed mutagenesis (2)			
GCGACTGGGTCATGAGCAGCATGATGAACGGC (SEQ ID NO: 224)	site-directed mutagenesis (I102V)	JaPAL$^{F140H\_MUT8}$-DET28a	pHM2354
TCATGACCCAGTCGCTGCTGGCCTTGACG (SEQ ID NO: 225)	site-directed mutagenesis (I102V)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2355
ACCGACAGCTACGGTGTCACCACTGG (SEQ ID NO: 226)	site-directed mutagenesis (I112S)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2328
ACCGTAGCTGTCGGTGCCGTTCATCA (SEQ ID NO: 227)	site-directed mutagenesis (I112S)	JaPAL$^{F140H\_MUT8}$-DET28a	pHM2329
CTTTGGAGCCACCTCCCACAGGAGGACC (SEQ ID NO: 228)	site-directed mutagenesis (G121A)	JaPAL$^{F140H\_MUT8}$-DET28a	pHM2356
GAGGTGGCTCCAAAGCCAGTGGTGACACC (SEQ ID NO: 229)	site-directed mutagenesis (G121A)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2357
GAGAGCTAATTAGACACCTCAATGCCGGAGTC (SEQ ID NO: 230)	site-directed mutagenesis (L138I)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2385
GTCTAATTAGCTCTCTTTGGAGAGCACCAC (SEQ ID NO: 231)	|site-directed mutagenesis (L138I)	JaPAL$^{F140H\_MUT8}$-DET28a	pHM2386
CGGCACGGCCGTGGGTTCTGGTCTTG (SEQ ID NO: 232)	site-directed mutagenesis (S267A)	JaPAL$^{F140H\_MUT8}$-DET28a	pHM2334
CCCACGGCCGTGCCGTTCACCATGGC (SEQ ID NO: 233)	site-directed mutagenesis (S267A)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2335
TGGCCTGCCTTCCAACCTGGCCGGTG (SEQ ID NO: 234)	site-directed mutagenesis (T444P)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2336

TABLE 5-continued

Primers used in this study

Sequence (5′ to 3′)	Purpose	Template	Lab ID
TTGGAAGGCAGGCCATTGTTGTAGAAG (SEQ ID NO: 235)	site-directed mutagenesis (T444P)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2337
CAACCTGTCCGGTGGGCGCAACCCGA (SEQ ID NO: 236)	site-directed mutagenesis (A448S)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2338
CCACCGGACAGGTTGGAAGTCAGGCC (SEQ ID NO: 237)	site-directed mutagenesis (A448S)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2339
TGGCCTTATCTCATCCAGGAAGACCG (SEQ ID NO: 238)	site-directed mutagenesis (V500I)	JaPAL$^{F140H\_MUT8}$-pET28a	pHM2340
GATGAGATAAGGCCAAGCGAGTTGAC (SEQ ID NO: 239)	site-directed mutagenesis (V500I)	JaPAL$^{F140H\_MUT8}$-DET28a	pHM2341
Site-directed mutagenesis (3)			
GGAGATAGCTATGGTGTCACCACTGGCTTCG (SEQ ID NO: 240)	site-directed mutagenesis (197S)	JaPTAL^{H128F}-pET28a	pHM2456
ACCATAGCTATCTCCACCGTTCGCCACG (SEQ ID NO: 241)	site-directed mutagenesis (197S)	JaPTAL^{H128F}-pET28a	pHM2457
ACCGACATATACGGTGTCACCACTGGCT (SEQ ID NO: 242)	site-directed mutagenesis (S112I)	JaPAL^{F140H}-pET28a	pHM2458
ACCGTATATGTCGGTGCCGTTCATCA (SEQ ID NO: 243)	site-directed mutagenesis (S112I)	JaPAL^{F140H} pET28a	pHM2459
CACCGACACCTACGGTGTCACCACTGGCT (SEQ ID NO: 244)	site-directed mutagenesis (S112T)	JaPAL^{F140H}-pET28a	pHM2475
CCGTAGGTGTCGGTGCCGTTCATCA (SEQ ID NO: 245)	site-directed mutagenesis (S112T)	JaPAL^{F140H}-pET28a	pHM2476
CACCGACGTCTACGGTGTCACCACTGGC (SEQ ID NO: 246)	site-directed mutagenesis (S112V)	JaPAL^{F140H}-pET28a	pHM2477
CCGTAGACGTCGGTGCCGTTCATCATGC (SEQ ID NO: 247)	site-directed mutagenesis (S112V)	JaPAL^{F140H}-pET28a	pHM2478
TGGAGATGTCTATGGTGTCACCACTGGCTTCG (SEQ ID NO: 248)	site-directed mutagenesis (197V)	JaPTAL^{H128F}-pET28a	pHM2479
CCATAGACATCTCCACCGTTCGCCACG (SEQ ID NO: 249)	site-directed mutagenesis (197V)	JaPTAL^{H128F}-pET28a	pHM2480
TGGAGATACCTATGGTGTCACCACTGGCTTCG (SEQ ID NO: 250)	site-directed mutagenesis (197T)	JaPTAL^{H128F}-pET28a	pHM2481
CCATAGGTATCTCCACCGTTCGCCACG (SEQ ID NO: 251)	site-directed mutagenesis (197T)	JaPTAL^{H128F}-pET28a	pHM2482
ACTGATATATATGGTGTTACTACTGGTTTTGGTG (SEQ ID NO: 252)	site-directed mutagenesis (S116I)	AtPAL1-pET28a	pHM2524
ACCATATATATCAGTGCCTTTGTTCATACTCTC (SEQ ID NO: 253)	site-directed mutagenesis (S116I)	AtPAL1-pET28a	pHM2525
TATTAGACACCTTAACGCCGGAATATTCG (SEQ ID NO: 254)	site-directed mutagenesis F144H)	AtPAL1-pET28a	pHM2526
TTAAGGTGTCTAATAAGTTCCTTCTGAAGTGCG (SEQ ID NO: 255)	site-directed mutagenesis (F144H)	AtPAL1-pET28a	pHM2527
Site-directed mutagenesis (4)			
CATCGCCGCCATCGGCAAGCTCATGTTTG (SEQ ID NO: 256)	site-directed mutagenesis (N407A)	JaPTAL-pET28a	pHM2542
CCGATGGCGGCGATGGCGAGGCGGGTG (SEQ ID NO: 257)	site-directed mutagenesis (N407A)	JaPTAL-pET28a	pHM2543

TABLE 6

Protein sequences of the JaPAL and AtPAL1 enzymes tested in Example 1

Enzyme	Wild-type	S112I/F140H mutant	S112I mutant	F140H mutant
Joinvillea ascendens PAL	JaPAL (SEQ ID NO: 28)	JaPAL$^{F140H\_S112I}$ (SEQ ID NO: 145)	JaPAL^{S112I} (SEQ ID NO: 258)	JaPAL^{F140H} (SEQ ID NO: 259)
Arabidopsis thaliana PAL1	AtPAL1 (SEQ ID NO: 144)	AtPAL1$^{F144H\_S116I}$ (SEQ ID NO: 146)	AtPAL1^{S116I} (SEQ ID NO: 260)	AtPAL1^{F144H} (SEQ ID NO: 261)

TABLE 7

DNA sequences of the JaPAL and AtPAL1 enzymes tested in Example 1

Enzyme	Wild-type	S1121/F140H mutant	S112I mutant	F140H mutant
Joinvillea ascendens PAL	JaPAL (SEQ ID NO: 147)	JaPAL$^{F140H\_S112I}$ (SEQ ID NO: 148)	JaPAL^{S112I} (SEQ ID NO: 262)	JaPAL^{F140H} (SEQ ID NO: 263)
Arabidopsis thaliana PAL1	AtPAL1 (SEQ ID NO: 149)	AtPAL1$^{F144H\_S116I}$ (SEQ ID NO: 150)	AtPAL1^{S116I} (SEQ ID NO: 264)	AtPAL1^{F144H} (SEQ ID NO: 265)

TABLE 8

PTAL and PAL protein sequences aligned FIG. 8

Name	Organism	Sequence
Sevir.6G187100.1.p	*Setaria viridis*	SEQ ID NO: 1
Seita.6G181000.1.p	*Setaria italica*	SEQ ID NO: 2
Sevir.1G245000.1.p	*Setaria viridis*	SEQ ID NO: 3
Seita.1G240200.1.p	*Setaria italica*	SEQ ID NO: 4
PhHAL.1G306700.1.p	*Panicum hallii*	SEQ ID NO: 5
Pavir.1NG356200.1.p	*Panicum virgatum*	SEQ ID NO: 6
Zm00008a016750__P01	*Zea mays*	SEQ ID NO: 7
Zm00008a022367__P01	*Zea mays*	SEQ ID NO: 8
Sobic.004G220300.1.p	*Sorghum bicolor*	SEQ ID NO: 9
Sevir.7G178200.1.p	*Setaria viridis*	SEQ ID NO: 10
Seita.7G168700.1.p	*Setaria italica*	SEQ ID NO: 11
Osa__LOC__Os02g41630.2	*Oryza sativa*	SEQ ID NO: 12
Bradi3g49250.2.p	*Brachypodium distachyon*	SEQ ID NO: 13
Pavir.7KG238255.1.p	*Panicum virgatum*	SEQ ID NO: 14
Pavir.7NG355500.1.p	*Panicum virgatum*	SEQ ID NO: 15
PhHAL.7G213800.1.p	*Panicum hallii*	SEQ ID NO: 16
Zm00008a006867__P01	*Zea mays*	SEQ ID NO: 17
Sobic.006G148800.1.p	*Sorghum bicolor*	SEQ ID NO: 18
Seita.2G435800.1.p	*Setaria italica*	SEQ ID NO: 19
Sevir.2G448300.1.p	*Setaria viridis*	SEQ ID NO: 20
Sevir.7G177900.1.p	*Setaria viridis*	SEQ ID NO: 21
Seita.7G168500.1.p	*Setaria italica*	SEQ ID NO: 22
Osa__LOC__Os04g43760.1	*Oryza sativa*	SEQ ID NO: 23
STRANG__00041445-RA	*Streptochaeta angustifolia*	SEQ ID NO: 24
STRANG__00039019-RA	*Streptochaeta angustifolia*	SEQ ID NO: 25
Emon__maker-scf7180000017824-augustus-gene-4.6-mRNA-1	*Ecdeiocolea monostachya*	SEQ ID NO: 26
Joascv11021323m	*Joinvillea ascendens*	SEQ ID NO: 27
Joascv11021328m	*Joinvillea ascendens*	SEQ ID NO: 28
Emon__maker-scf7180000017824-augustus-gene-6.51-mRNA-1	*Ecdeiocolea monostachya*	SEQ ID NO: 29
*Flagellaria*__*indica*__Trinity__comp23995__c0__seq1	*Flagellaria indica*	SEQ ID NO: 30
Seita.1G240400.1.p	*Setaria italica*	SEQ ID NO: 31
Sevir.1G245166.1.p	*Setaria viridis*	SEQ ID NO: 32
Seita.1G240500.1.p	*Setaria italica*	SEQ ID NO: 33
Sevir.1G245232.1.p	*Setaria viridis*	SEQ ID NO: 34
Seita.1G240600.1.p	*Setaria italica*	SEQ ID NO: 35
Sevir.1G245300.2.p	*Setaria viridis*	SEQ ID NO: 36
PhHAL.1G307000.1.p	*Panicum hallii*	SEQ ID NO: 37
PhHAL.1G307100.1.p	*Panicum hallii*	SEQ ID NO: 38
PhHAL.1G307200.1.p	*Panicum hallii*	SEQ ID NO: 39
Pavir.1NG356700.1.p	*Panicum virgatum*	SEQ ID NO: 40
Pavir.1NG356800.1.p	*Panicum virgatum*	SEQ ID NO: 41
Pavir.1KG386500.1.p	*Panicum virgatum*	SEQ ID NO: 42
Sobic.004G220600.2.p	*Sorghum bicolor*	SEQ ID NO: 43
Sobic.004G220500.1.p	*Sorghum bicolor*	SEQ ID NO: 44

TABLE 8-continued

PTAL and PAL protein sequences aligned FIG. 8

Name	Organism	Sequence
Sobic.004G220700.1.p	*Sorghum bicolor*	SEQ ID NO: 45
Zm00008a016754_P01	*Zea mays*	SEQ ID NO: 46
Zm00008a022372_P01	*Zea mays*	SEQ ID NO: 47
Zm00008a022370_P01	*Zea mays*	SEQ ID NO: 48
Osa_LOC_Os02g41670.1	*Oryza sativa*	SEQ ID NO: 49
Osa_LOC_Os02g41680.1	*Oryza sativa*	SEQ ID NO: 50
Bradi3g47110.1.p	*Brachypodium distachyon*	SEQ ID NO: 51
Bradi3g47120.1.p	*Brachypodium distachyon*	SEQ ID NO: 52
Bradi3g49270.1.p	*Brachypodium distachyon*	SEQ ID NO: 53
Bradi3g48840.1.p	*Brachypodium distachyon*	SEQ ID NO: 54
Bradi3g49280.1.p	*Brachypodium distachyon*	SEQ ID NO: 55
Osa_LOC_Os05g35290.1	*Oryza sativa*	SEQ ID NO: 56
Pavir.1KG386300.1.p	*Panicum virgatum*	SEQ ID NO: 57
Pavir.1NG356400.1.p	*Panicum virgatum*	SEQ ID NO: 58
PhHAL.1G306800.1.p	*Panicum hallii*	SEQ ID NO: 59
Seita.1G240300.1.p	*Setaria italica*	SEQ ID NO: 60
Sevir.1G245100.1.p	*Setaria viridis*	SEQ ID NO: 61
Zm00008a016751_P01	*Zea mays*	SEQ ID NO: 62
Zm00008a022369_P01	*Zea mays*	SEQ ID NO: 63
Sobic.004G220400.1.p	*Sorghum bicolor*	SEQ ID NO: 64
Osa_LOC_Os02g41650.1	*Oryza sativa*	SEQ ID NO: 65
Osa_LOC_Os11g48110.1	*Oryza sativa*	SEQ ID NO: 66
Osa_LOC_Os12g33610.1	*Oryza sativa*	SEQ ID NO: 67
Sobic.001G160500.1.p	*Sorghum bicolor*	SEQ ID NO: 68
Zm00008a004629_P01	*Zea mays*	SEQ ID NO: 69
Bradi3g49260.1.p	*Brachypodium distachyon*	SEQ ID NO: 70
STRANG_00039013-RA	*Streptochaeta angustifolia*	SEQ ID NO: 71
STRANG_00039015-RA	*Streptochaeta angustifolia*	SEQ ID NO: 72
Pavir.7KG237800.1.p	*Panicum virgatum*	SEQ ID NO: 73
PhHAL.7G214000.1.p	*Panicum hallii*	SEQ ID NO: 74
Pavir.1NG361819.1.p	*Panicum virgatum*	SEQ ID NO: 75
Pavir.7NG355800.1.p	*Panicum virgatum*	SEQ ID NO: 76
Sevir.7G178300.1.p	*Setaria viridis*	SEQ ID NO: 77
Seita.7G168800.1.p	*Setaria italica*	SEQ ID NO: 78
Zm00008a006866_P01	*Zea mays*	SEQ ID NO: 79
Sobic.006G148900.1.p	*Sorghum bicolor*	SEQ ID NO: 80
Pavir.4KG229700.2.p	*Panicum virgatum*	SEQ ID NO: 81
Osa_LOC_Os04g43800.1	*Oryza sativa*	SEQ ID NO: 82
Osa_LOC_Os08g21670.1	*Oryza sativa*	SEQ ID NO: 83
Bradi5g15830.1.p	*Brachypodium distachyon*	SEQ ID NO: 84
STRANG_00041444-RA	*Streptochaeta angustifolia*	SEQ ID NO: 85
STRANG_00041441-RA	*Streptochaeta angustifolia*	SEQ ID NO: 86
STRANG_00041440-RA	*Streptochaeta angustifolia*	SEQ ID NO: 87
STRANG_00059682-RA	*Streptochaeta angustifolia*	SEQ ID NO: 88
Aco013943.1	*Ananas comosus*	SEQ ID NO: 89
Aco007727.1	*Ananas comosus*	SEQ ID NO: 90
Apos_PKA46439.1	*Apostasia shenzhenica*	SEQ ID NO: 91
Apos_PKA58411.1	*Apostasia shenzhenica*	SEQ ID NO: 92
Apos_PKA64143.1	*Apostasia shenzhenica*	SEQ ID NO: 93
Dcat_XP_020704813.1	*Dendrobium catenatum*	SEQ ID NO: 94
Pequ_XP_020589738.1	*Phalaenopsis equestris*	SEQ ID NO: 95
Dcat_XP_020702280.1	*Dendrobium catenatum*	SEQ ID NO: 96
Apos_PKA59591.1	*Apostasia shenzhenica*	SEQ ID NO: 97
Apos_PKA60166.1	*Apostasia shenzhenica*	SEQ ID NO: 98
Pequ_XP_020579635.1	*Phalaenopsis equestris*	SEQ ID NO: 99
Spipo11G0025500	*Spirodela polyrhiza*	SEQ ID NO: 100
Spipo1G0003500	*Spirodela polyrhiza*	SEQ ID NO: 101
GSMUA_Achr8P18960_001	*Musa acuminata*	SEQ ID NO: 102
GSMUA_Achr11P22840_001	*Musa acuminata*	SEQ ID NO: 103
GSMUA_Achr5P18560_001	*Musa acuminata*	SEQ ID NO: 104
GSMUA_Achr2P00240_001	*Musa acuminata*	SEQ ID NO: 105
GSMUA_Achr11P16380_001	*Musa acuminata*	SEQ ID NO: 106
GSMUA_Achr5P03950_001	*Musa acuminata*	SEQ ID NO: 107
p5.00_sc00071_p0096.1	*Elaeis guineensis*	SEQ ID NO: 108
CALSI_Maker00040467	*Calamus simplicifolius*	SEQ ID NO: 109
Aco006987.1	*Ananas comosus*	SEQ ID NO: 110
Aco027752.1	*Ananas comosus*	SEQ ID NO: 111
GSMUA_Achr1P09070_001	*Musa acuminata*	SEQ ID NO: 112
p5.00_sc00334_p0013.1	*Elaeis guineensis*	SEQ ID NO: 113
p5.00_sc00076_p0011.1	*Elaeis guineensis*	SEQ ID NO: 114
Aco010091.1	*Ananas comosus*	SEQ ID NO: 115
Aoff_XP_020259774.1	*Asparagus officinalis*	SEQ ID NO: 116
Aoff_XP_020259795.1	*Asparagus officinalis*	SEQ ID NO: 117

TABLE 8-continued

PTAL and PAL protein sequences aligned FIG. 8

Name	Organism	Sequence
Aoff_XP_020259773.1	*Asparagus officinalis*	SEQ ID NO: 118
Aoff_XP_020248601.1	*Asparagus officinalis*	SEQ ID NO: 119
Aoff_XP_020272851.1	*Asparagus officinalis*	SEQ ID NO: 120
Aoff_XP_020272852.1	*Asparagus officinalis*	SEQ ID NO: 121
Acamev11004816m	*Acorus americanus*	SEQ ID NO: 122
Acamev11046066m	*Acorus americanus*	SEQ ID NO: 123
Zosma445g00020.1	*Zostera marina*	SEQ ID NO: 124
Zosma69g00670.1	*Zostera marina*	SEQ ID NO: 125
Atr_evm_27.model.AmTr_v1.0_scaffold00148.59	*Amborella trichopoda*	SEQ ID NO: 126
Atr_evm_27.model.AmTr_v1.0_scaffold00032.129	*Amborella trichopoda*	SEQ ID NO: 127
CALSI_Maker00043687	*Calamus simplicifolius*	SEQ ID NO: 128
CALSI_Maker00043684	*Calamus simplicifolius*	SEQ ID NO: 129
p5.00_sc01789_p0001.1	*Elaeis guineensis*	SEQ ID NO: 130
p5.00_sc00066_p0001.1	*Elaeis guineensis*	SEQ ID NO: 131
CALSI_Maker00043685	*Calamus simplicifolius*	SEQ ID NO: 132
Aco020618.1	*Ananas comosus*	SEQ ID NO: 133
GSMUA_Achr9P15990_001	*Musa acuminata*	SEQ ID NO: 134
Zosma49g00480.1	*Zostera marina*	SEQ ID NO: 135
Zosma115g00180.1	*Zostera marina*	SEQ ID NO: 136
Spipo15G0044700	*Spirodela polyrhiza*	SEQ ID NO: 137
Acamev11008810m	*Acorus americanus*	SEQ ID NO: 138
Acamev11024102m	*Acorus americanus*	SEQ ID NO: 139
Acamev11050170m	*Acorus americanus*	SEQ ID NO: 140
Atr_evm_27.model.AmTr_v1.0_scaffold00024.177	*Amborella trichopoda*	SEQ ID NO: 141
Atr_evm_27.model.AmTr_v1.0_scaffold00024.178	*Amborella trichopoda*	SEQ ID NO: 142
Atr_evm_27.model.AmTr_v1.0_scaffold00024.181	*Amborella trichopoda*	SEQ ID NO: 143

Materials and Methods

Dataset of Genome and Protein Sequences

[0092] We obtained the genome and protein sequence data listed in Table 1 and Table 2 from NCBI, DNA Databank of Japan (DDBJ), phytozome, JGI, and plaza_v4.5_monocots databases. The genome sequence of *Streptochaeta angustifolia* was downloaded from a publication (Seetharam et al., 2021). The genome sequence of *Ecdeiocolea monostachya* was provided by Dr. Matthew Moscou (University of Minnesota, MN).

Phylogenetic Tree Analysis and Identification of Residues Involved in the Transition from PAL to PTAL

[0093] To find PAL homologs, we used OrthoFinder with the protein sequence datasets for green plants (Table 1) and monocots (Table 2) with the options of an MCL inflation parameter of 1.5, DIAMOND for sequence alignment, FastME, MAFFT for multiple sequence alignment, and FastTree for gene trees (Emms and Kelly, 2015). Because many genome sequences had duplicated or truncated sequences annotated as genes, we then ran filter fasta script using the obtained orthogroup sequences to remove duplicate genes and genes shorter than 3× the standard deviation from the mean or a given length (less than 50 amino acids). Using the filtered sequence dataset, we generated an alignment using MAFFT v7.450 (Katoh and Standley, 2013). To determine the best evolutionary model for each PAL tree, we ran ModelTest-NG (Darriba et al. 2020). The best model was JTT+G4+F for the green plant dataset and JTT+I+G4+F for the monocot dataset. The maximum-likelihood phylogenetic tree was generated using RAXML-NG (Alexey et al., 2019).

Cloning of PAL and PTAL Candidate Genes

[0094] Sequences encoding PAL and PTAL candidate enzymes from *S. bicolor, B. distachyon, S. angustifolia*, and *J. ascendens* were amplified from cDNA with gene specific primers and PrimeSTAR® MAX DNA polymerase (Takara Bio) and were cloned into the pET28a vector using the In-Fusion® HD Cloning Kit (Takara Bio). The resulting vectors were submitted for sequence analysis, which confirmed that the coding sequences matched the sequences in the database. Polynucleotides encoding BdPTAL1, EmoPTAL, EmoPAL, JaPAL-MUT9, and JaPAL-MUT17 were synthesized and cloned into pET28a vectors (SynbioTechnologies). For site-directed mutagenesis, 1:100 diluted plasmid was PCR amplified using PrimeSTAR® MAX DNA polymerase (Takara Bio) and mutagenesis primers. The primers used for cloning are shown in Table 5.

Recombinant Protein Expression and Purification

[0095] For recombinant protein expression, the pET28a vectors were transformed into Rosetta-2 (DE3) *E. coli* and cultured in 3 ml of terrific broth (TB) medium containing kanamycin (50 μg/ml), chloramphenicol (34 μg/ml), and 0.1% glucose at 37° C. and 200 rpm overnight. Then, 500 μl of pre-culture solution was added to 50 ml TB medium containing the same antibiotics and further cultured at 27° C. and 200 rpm until the OD_{600} reached 0.5-0.7. The bacterial cultures were then cooled down on ice, isopropyl β-D-1-thiogalactopyranoside (IPTG, 0.5 mM final concentration) was added, and the cultures were incubated at 22° C. and 200 rpm. After 24 hours, the cultures were harvested by centrifugation (5000 g, 5 min, 4° C.) and the pellets were frozen at −30° C. The pellets were thawed and resuspended in lysis buffer containing 50 mM sodium phosphate buffer (pH 8.0), 300 mM NaCl, 10% glycerol, and 0.25 mg lysozyme. After a 30 min incubation on ice, the suspension was sonicated three times for 20 sec and the supernatant was recovered after centrifugation (12500 g, 20 min, 4° C.). The supernatants were added to a new tube containing 100 μl of Ni-NTA beads (Millipore) and the mixture was incubated at

25° C. for 30 min under constant inversion. After unbound proteins were washed away via three washes with washing buffer containing 50 mM sodium phosphate buffer (pH 8.0), 300 mM NaCl, 10% glycerol, and 10 mM imidazole, target proteins were eluted with elution buffer containing 50 mM sodium phosphate buffer (pH 8.0), 300 mM NaCl, 10% glycerol, and 300 mM imidazole. The purified enzyme solutions were desalted using a Sephadex G-50 column (GE Healthcare). The protein concentration was determined using the BioRad protein assay dye (BioRad). The purity was confirmed to be >90% using SDS-PAGE and ImageJ software.

PAL and TAL Enzyme Assays

[0096] All substrate solutions were prepared with 0.01 N NaOH to increase the solubility of L-Tyr. A mixture containing 100 mM Tris-HCl (pH 8.5), 1% glycerol, and purified enzyme in a total volume of 50 μl was preincubated for 3 min at 30° C. PAL and TAL reactions were started by addition of 50 μl of 1 mM substrate (L-Phe or L-Tyr, respectively) and were incubated at 30° C. for 20 min unless otherwise noted. The reactions were terminated by addition of 6N acetic acid (10 μl).

[0097] The reaction products were analyzed using high-performance liquid chromatography (HPLC) (1200 Infinitely Series-Infinitely better, Agilent Technologies) to directly detect products produced by PAL and TAL activity, i.e., cinnamic acid and p-coumaric acid, respectively. Analytical conditions were as follows: column, Neptune T3 C18 column (3 μm, 2.1×150 mm, ES industries); solvent system, solvent A (water including 0.1%[v/v] formic acid) and solvent B (acetonitrile including 0.1%[v/v] formic acid); gradient program: 99% A/1% B at 0 min, 99% A/1% B at 4.5 min, 95% A/5% B at 7.5 min, 85% A/15% B at 12 min, 75% A/25% B at 16.5 min, 70% A/30% B at 21 min, 5% A/95% B at 23 min, 5% A/95% B at 26 min, 99% A/5% B at 26.5 min, and 99% A/5% B at 30 min; flow rate: 0.3 mL/min; DAD: 275 nm for cinnamic acid, 309 nm for p-coumaric acid.

[0098] The kinetic parameters of the recombinant enzymes were determined using HPLC. Reaction mixtures containing 100 mM Tris-HCl (pH 8.5), 1% glycerol, and purified enzyme (0.15 μg for PAL assay and 1 μg for TAL assay) in a 50 μl total volume were preincubated for 3 min at 30° C. PAL and TAL reactions were started by addition of 50 μl substrate solution prepared with 0-4 mM L-Phe and 0-2 mM L-Tyr. After 10 min and 20 min incubations for PAL and TAL assay, respectively, at 30° C., the reaction was terminated by addition of 6N acetic acid (10 μl). Analytical conditions were as follows: column, Atlantis T3 C18 column (3 μm, 2.1×150 mm, Waters); solvent system, solvent A (water including 0.1%[v/v] formic acid) and solvent B (acetonitrile including 0.1%[v/v] formic acid); gradient program: 85% A/15% B at 0 min, 85% A/15% B at 1 min, 70% A/30% B at 3 min, 15% A/95% B at 6.5 min, 15% A/95% B at 7.5 min, 85% A/15% B at 8.5 min, and 85% A/15% B at 10 min; flow rate: 0.4 mL/min; DAD: 275 nm for cinnamic acid, 309 nm for p-coumaric acid. The products were quantified using calibration curves generated using authentic standards. Non-linear hyperbolic regression analyses were conducted using the Excel Solver tool to calculate Km and Vmax values.

Protein Modeling Analysis

[0099] The structures of JaPAL and JaPTAL were generated with SWISS-MODEL (Waterhouse et al., 2018) using a homo-tetrameric PAL structure from parsley 6F6T.pdb (Bata et al., 2021) and a homo-dimeric PTAL structure from sorghum 6AT7.pdb (Sun et al., 2018), respectively, as templates. The sequence identity against each template were 77.3% and 80.5% for JaPAL and JaPTAL, respectively.

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[0129] Watts, K. T., Lee, P. C. and Schmidt-Dannert, C. (2006) Biosynthesis of plant-specific stilbene polyketides in metabolically engineered *Escherichia coli. BMC Biotechnol.,* 6, 22.

[0130] Young, M. R. and Neish, A. C. (1966) Properties of the ammonia-lyases deaminating phenylalanine and related compounds in *Triticum aestivum* and *Pteridium aquilinum. Phytochemistry,* 5, 1121-1132.

Example 2

[0131] In the following example, the inventors describe experiments that demonstrate that several different amino acid substitutions at position 112 in JaPAL retain the TAL activity observed in the JaPAL$^{F140H\_S112I}$ double mutant.

[0132] A phylogenetic analysis revealed that, while the amino acids Ser and Ile are well conserved at positions corresponding to residue 112 in JaPAL in angiosperm PAL enzymes, basal non-flower PAL enzymes possess Ile, Thr, or Val at this position (FIG. **9**A). Also, another group of angiosperm PAL enzymes (clade II in FIG. **9**A), which is not conserved across angiosperms, possess Thr at the corresponding position. Accordingly, we tested the TAL activity of JaPAL and JaPTAL enzymes with and without mutations to these other amino acids at residue 112. We found that substituting the Ile at this position in JaPAL$^{F140H\_S112I}$ with Thr or Val retains strong TAL activity with comparable kcat and Km values but substituting it with Ser does not (FIG. **9**B). Thus, replacing Ser112 with Ile, Val, or Thr together with the F140H mutation could potentially convert a PAL enzyme into a PTAL enzyme.

Example 3

[0133] In the following example, the inventors describe future experiments in which engineered PAL enzymes will be tested in planta.

[0134] To test the effects of the F140H and S112I mutations in plants, we will transiently express recombinant PAL enzymes (e.g., *Arabidopsis* PAL_S112I-F140H) with and without the corresponding mutations in *Nicotiana benthamiana* using *Agrobacterium*-mediated transformation. Soluble metabolites will be extracted from the transformed *Nicotiana* leaves and quantified to determine if the production of any soluble phenylpropanoid compounds was affected by the presence of the recombinant PAL enzymes.

[0135] This experiment will also be conducted in plants that express deregulated TyrA enzymes that we previously discovered, such as *Beta vulgaris* TyrAalpha (Lopez-Nieves et al., *Plant J* 109: 844-855 (2021)). The presence of the deregulated TyrA enzymes should increase the availability of the tyrosine substrate for the TAL activity.

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ITKFEEELRA VLPQEVEAAR VAVAEGTAAV ENRIKDSRSF PLYRFVREEL GCVFLTGEKL  660
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FSKITKFEEE LRAVLPREVE AARVAVAEGT ASVPNRIKDS RSFPLYRFVR EELGCVFLTG  660
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KDASGVAVEL DEEARPRVKA SSEWILDCIA HGGDIYGVTT GFGGTSHRRT KDGPALQVEL  120
LRYSSRTKPH VFVCFFVPVQ YAAPSDHVPA HWQRPVGGCK LQLVSTRLMS VSGSSLTTGA  180
RYVLFSRTCR HLNAGIFGNG SDGHTLPSEV SRAAMLVRIN TLLQGYSGIR FEILEALTKL  240
INTGVSPCLP LRGTITASGD LVPLSYIAGL ITGRPNAQAV TADGRKVDAA EAFKVAGIEG  300
GFFKLNPKEG LAIVNGTSVG SALAAMVCFD ANVLAVLSEV LSAVFCEVMN GKPEYTDHLT  360
HKLKHHPGSI EAAAIMEHIL DGSSFMKHAK EVNAMDPLLK PKQDRYALRT SPQWLGPQIE  420
VIRAATKSIE REVNSVNDNP VIDVHRGKAL HGGNFQGTPI GVSMDNARLA IANIGKLMFA  480
QFSELVNEFY NNGLTSNLAG SRNPSLDYGF KGTEIAMASY CSELQYLANP ITNHVQSAEQ  540
HNQDVNSLGL VSSRKTAEAV DILKLMSSTY MVALCQAVDL RHLEENLKSA VKSCVTAVAR  600
KVLTTSPDGD LHNARFSEKS LLTAIDREAV YGYYDDPCSA NSPLMKKIRA VLVDHALANG  660
EAEKDASASV FSKINKLEEE LREALPREME AARVAFETGT APIANRIEES RSYPLYRFIR  720
QDLGAVYLTG EKLKSPGEEC NKVFLALSEG KLIDPMLECL KEWDGKPLPI C           771

SEQ ID NO: 16         moltype = AA  length = 703
FEATURE               Location/Qualifiers
source                1..703
                      mol_type = protein
                      organism = Panicum hallii
SEQUENCE: 16
MASNTAICES DPLNWGKAAA EMAGSHLDEV KRMVAQFREP LVKIEGSSLR VGQVAAVAAA  60
KDASGVAVEL DEEARPRVKA SSEWILDCIA HGGDIYGVTT GFGGTSHRRT KDGPALQVEL  120
LRHLNAGIFG KGSDGHTLPS EVSRAAMLVR INTLLQGYSG IRFEILEAIT KLINTGVSPC  180
LPLRGTITAS GDLVPLSYIA GLITGRPNAQ AVTVDGRKVD AAEAFKVAGI EGGFFKLNPK  240
EGLAIVNGTS VGSALAAMVC FDANVLAVLS EVLSAVFCEV MNGKPEYTDH LTHKLKHHPG  300
SIEAAAIMEH ILDGSSFMKH AKEVNAMDPL LKPKQDRYAL RTSPQWLGPQ IEVIRSATKS  360
IEREVNSVND NPVIDVHRGK ALHGGNFQGT PIGVSMDNAR LAIANIGKLM FAQFSELVNE  420
FYNNGLTSNL AGSRNPSLDY GFKGTEIAMA SYCSELQYLA NPITNHVQSA EQHNQDVNSL  480
GLVSARKTAE AVDILKLMSS TYMVALCQAV DLRHLEENLK RAVKNCVTTV GRKVLTTSPD  540
GDLHNARFSE KSLLTAIDRE AVYGYYDDPC SANSSLMKKI RAVLVDHALA NGEAEKDASA  600
SVFSKINKFE EELREALPRE MEAARVAFET GTAPIANRIK ESRSYPLYRF IRQDLGAVYL  660
TGEKLKSPGE ECNKVFLALS EGKLIDPMLE CLKEWDGKPL PIC                    703

SEQ ID NO: 17         moltype = AA  length = 709
FEATURE               Location/Qualifiers
source                1..709
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                         mol_type = protein
                         organism = Zea mays
SEQUENCE: 17
MASNTAILES DPLSWGKAAA ELTGSHLDEV KRMVAQFRDP VVKIEGSSLR VGQVAAVAAA  60
KDASGVAVEL DEEARPRVKA SSEWILDCIA HGGDIXSTAS PTAATSTASP PASAAPRTAA  120
PRTGPRSRHL NAGIFGNGSD GHTLPSEVSR AAMLVRINTL LQGYSGIRFE ILEAITKLIN  180
TGVSPCLPLR GTITASGDLV PLSYIAGLIT GRPNAQAVTV DGRKVDAAEA FKAAGIEGGF  240
FKLNPKEGLA IVNGTSVGSA LAAMVCFDAN VLAVLSEVLS AVFCEVMNGK PEYTDHLTHK  300
LKHHPGSIEA AAIMEHILDG SSFMKHAKEV NAMDPLLKPK QDRYALRTSP QWLGPQIEVI  360
RAATKSIERE VNSVNDNPVI DVHRGKALHG GNFQGTPIGV SMDNARLAVA NIGKLMFAQF  420
SELVNEFYNN GLTSNLAGSR NPSLDYGFKG TEIAIASYCS ELQYLANPIT NHVQSAEQHN  480
QDVNSLGLVS ARKTAEAVDI LKLMSSTYMV ALCQAVDLRH LEENLKSAVK SCVMAVARKV  540
LTTSLGGDLH SARFSEKALL TAIDREAVYG YYDDPCSANS PLMKKIRAVL VDHALASGEA  600
EKDASASVFS KINRFEEELR EALPREMEAA RVAFETGAAP IANRIKESRS YPLYRFIRQD  660
LGAVYLTGEK LKSPGEECNK VFLALSEGKL IDPMLDCLKE WDGKPLPIC             709

SEQ ID NO: 18            moltype = AA  length = 703
FEATURE                  Location/Qualifiers
source                   1..703
                         mol_type = protein
                         organism = Sorghum bicolor
SEQUENCE: 18
MASNTAILES DPLSWGKAAA ELTGSHLDEV KRMVAQFRDP VVKIEGSTLR VGQVAAVAAA  60
KDASGVAVEL DEEARPRVKA SSEWILDCIA HGGDIYGVTT GFGGTSHRRT KDGPALQVEL  120
LRHLNAGIFG NGSDGHTLPS EVSRAAMLVR INTLLQGYSG IRFEILEAIT KLLNTGVSPC  180
LPLRGTITAS GDLVPLSYIA GLITGRPNAQ AVTVDGRKVD AAEAFKVAGI QGGFFKLNPK  240
EGLAIVNGTS VGSALAAMVC FDANVLAVLS SVLSAVFCEV MNGKPEYTDH LTHKLKHHPG  300
SIESAAIMEH ILDGSSFMKH AKEVNAMDPL LKPKQDRYAL RTSPQWLGPQ IEVIRAATKS  360
IEREVNSVND NPVIDVHRGK ALHGGNFQGT PIGVSMDNAR LAIANIGKLM FAQFSELVNE  420
FYNNGLTSNL AGSRNPSLDY GFKGTEIAMA SYCSELQYLA NPITNHVQSA EQHNQDVNSL  480
GLVSARKTAE AVDILKLMSS TYMVALCQAV DLRHLEENLK SAVKNCVMAA ARKVLTTSLD  540
GDLHSARFSE KALLTAIDRE AVYGYYDDPC SANSPLMKKI RAVLVDHALA SGEAEKDASA  600
SVFSKINRFE EALREALPRE MEAARVAFET GTAPIGNRIK DSRSYPLYRF IRQDLGAVYL  660
TGEKLKSPGE ECNKVFLALS EGKLIDPMLE CLKEWDGKPL PIC                   703

SEQ ID NO: 19            moltype = AA  length = 703
FEATURE                  Location/Qualifiers
source                   1..703
                         mol_type = protein
                         organism = Setaria italica
SEQUENCE: 19
MACNTAIVTS DPLNWGKAAA ELTGSHLDEV RRMVAQSREP IVRVDGSRLH VGKVAAVAAA  60
KDASGVAVEL DEEARLRVRS SSEWVLSCIE NGGDIYGVTT GFGGNSHRRT KDGHALQVEL  120
LRYLNAGIFG TGSDGHTLPS QVSRAAMLVR INALMQGYSG IRFEILEAIA KLINTGVSPC  180
LPLRGSITAS GDLVPLSYIA GLITGRPNAQ AVTVDGRKVD AAEAFKVAGI KGGFFKLNPK  240
EGLAMVNGTS VGSALAAMVC FDANVLAVLA VVLSAVFCEV MNGKPEYADH LTHKLKHHPG  300
SIEAAAIMEH ILDGSSLMKH AKEVNAMDPL LKPKQDRYAL RTSPQWLGPQ IEVIRAATKA  360
IEREINSVSD NPVIDVNRGK ALHGGNFQGT PIGVSMDNAR LAVASIGRLM FAQFTELVID  420
FYNNGLPSNL AGSRNLSLDF GLKGVEIAMA SYCSELQYLA NPVTNHVQSA EQHTQDVNSL  480
GLISARKTAE AVEILKLMSS TFMIALCQAV DLRHLEENLK SAVKNCVKTV ALKVLTTSPD  540
GEHCSARFSE KTLLAAIDRK AVYSYCDDPC SASSSLMMTI RAVLVDHALA NGEAENEARA  600
PIFSKITKFE EELREALPRE MEKTRVAFET GTAPIGNRIK ESRSYPLYRF IREDLGAVYL  660
TGEKLKSAGE ECNKVFLALS EGKLIDPMLG CLKEWNGEPL PIC                   703

SEQ ID NO: 20            moltype = AA  length = 703
FEATURE                  Location/Qualifiers
source                   1..703
                         mol_type = protein
                         organism = Setaria viridis
SEQUENCE: 20
MACNTAIVTS DPLNWGKAAA ELTGSHLDEV RRMVAQSREP IVRVDGSRLH VGKVAAVAAA  60
KDASGVAVEL DEEARLRVKA SSEWVLSCIE NGGDIYGVTT GFGGNSHRRT KDGHALQVEL  120
LRYLNAGIFG TGSDGHTLPS QVSRAAMLVR INALMQGYSG IRFEILEAIA KLINTGVSPC  180
LPLRGSITAS GDLVPLSYIA GLITGRPNAQ AVTVDGRKVD AAEAFKVAGI KGGFFKLNPK  240
EGLAMVNGTS VGSALAAMVC FDANVLAVLA VVLSAVFCEV MNGKPEYADH LIHKLKHHPG  300
SIEAAAIMEH ILDGSSLMKH AKEVNAMDPL LKPKQDRYAL RTSPQWLGPQ IEVIRAATKA  360
IEREINSVSD NPVIDVNRGK ALHGGNFQGT PIGVSMDNAR LAVASIGRLM FAQFTELVID  420
FYNNGLPSNL AGSRNLSLDF GLKGAEIAMA SYCSELQYLA NPVTNHVQSA EQHTQDVNSL  480
GLISARKTAE AVEILKLMSS TFMIALCQAV DLRHLEENLK SAVKNCVKTV ALKVLTTSPD  540
GEHCSARFSE KALLAAIDRK AVYSYYDDPC SASSSLMMTI RAVLVDHALA NGEAENEARA  600
PIFSKITKFE EELREALPRE MEKTRVAFET GTAPIGNRIK ESRSYPLYRF IREDLGAVYL  660
TGEKLKSAGE ECNKVFLALS EGKLIDPMLG CLKEWNGEPL PIC                   703

SEQ ID NO: 21            moltype = AA  length = 703
FEATURE                  Location/Qualifiers
source                   1..703
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                        mol_type = protein
                        organism = Setaria viridis
SEQUENCE: 21
MACNTAIVTS DPLNWGKAAA ELTGSHLDEV RRMVAQSREP VVRVDGSRLH VGQVAAVAAA  60
KDASGVAVEL DEEARLRVKA SSEWVLSCIE NGGDIYGVTT GFGGNSHRRT KDGHALQVEL  120
LRYLNAGIFG TGSDGHTLPS QVSRAAMLVR INALMQGYSG IRFEILEAIA KLINTGVSPC  180
LPLRGSITAS GDLVPLSYIA GLITGRPNAQ AVTVDGRKVD AAEAFKVAGI EGGFFKLNPK  240
EGLAMVNGTS VGSALAAMVC FDANVLAVLA VVLSAVFCEV MNGKPEYADH LTHKLKHHPG  300
SIEAAAIMEH ILDGSSLMKH AKEVNAMDPL LKPKQDQYAL RTSPQWLGPQ IEVIRAATKA  360
IEREINSVSD NPVIDVHRGK ALHGGNFQGT PIGVSMDNAR LAVASIGRLM FAQFTELVID  420
FYNNGLPSNL AGSRNLSLDF GLKGAEIAMA SYCSELQYLA NPVTNHVQSA EQHTQDVNSL  480
GLISARKTAE AVEILKLMSS TFMIALCQAV DLRHLEENLK SAVKNCVKTV ALKVLTTSPD  540
GEHCSARFSE KALLAAIDRK AVYSYYDDPC SASSSLMMTI RAVLVDHALA NGEAENEAGA  600
PIFSKITKFE EELREALPRE MEKTRVAFET GTAPIGNRIK ESRSYPLYRF IREDLGAVYL  660
TGEKLKSAGE ECNKVFLALS EGKLIDPMLG CLKEWNGEPL PIC                  703

SEQ ID NO: 22           moltype = AA  length = 703
FEATURE                 Location/Qualifiers
source                  1..703
                        mol_type = protein
                        organism = Setaria italica
SEQUENCE: 22
MACSTAIVTS DPLNWGKAAA ELTGSHLDEV RRMVAQSREP VVRVDGSRLH VGQVAAVAAA  60
KDASGVAVEL DEEARLRVKA SSEWVLSCIE NGGDIYGVTT GFGGNSHRRT KDGHALQVEL  120
LRYLNAGIFG TGSDGHTLPS QVSRAAMLVR INALMQGYSG IRFEILEAIA KLINTGVSPC  180
LPLRGSITAS GDLVPLSYIA GLITGRPNAQ AVTVDGRKVD AAEAFKVAGI EGGFFKLNPK  240
EGLAMVNGTS VGSALAAMVC FDANVLAVLA VVLSAVFCEV MNGKPEYADH LTHKLKHHPG  300
SIEAAAIMEH ILDGSSLMKH AKEVNAMDPL LKPKQDQYAL RTSPQWLGPQ IEVIRAATKA  360
IEREINSVSD NPVIDVHRGK ALHGGNFQGT PIGVSMDNAR LAVASIGRLM FAQFTELVID  420
FYNNGLPSNL AGSRNLSLDF GLKGAEIAMA SYCSELQYLA NPVTNHVQSA EQHTQDVNSL  480
GLISARKTAE AVEILKLMSS TFMIALCQAV DLRHLEENLK SAVKNCVKTV ALKVLTTSPD  540
GEHCSARFSE KALLAAIDRK AVYSYYDDPC SASSSLMMTI RAVLVDHALA NGEAENEARA  600
PIFSKITKFE EELREALPRE MEKTRVAFET GTAPIGNRIK ESRSYPLYRF IREDLGAVYL  660
TGEKLKSAGE ECNKVFLALS EGKLIDPMLG CLKEWNGEPL PIC                  703

SEQ ID NO: 23           moltype = AA  length = 707
FEATURE                 Location/Qualifiers
source                  1..707
                        mol_type = protein
                        organism = Oryza sativa
SEQUENCE: 23
MASQTADATG FVASDPLSWG KAALEMTGSH LDEVKRMVAQ SREAVVKIEG SSLRVGQVAA  60
VSAAKDASGV VVELDEEARP RVKASSEWIL NCIAHGGDIY GVTTGFGGTS HRRTKDGQAL  120
QVELLRHLNA GIFGNGSDGN SLPSEVSRAA MLVRINTLLQ GYSGIRFEIL EAITKLINTG  180
VSPCLPLRGT ITASGDLVPL SYIAGLITGR PNAQAVTVDG KKVDAAEAFK IAGIQGGFFR  240
LEPKEGLAIV NGTSVGSALA AMVLYDANVL AVLSEVLSAV FCEVMNGKPE YTDHLTHKLK  300
HHPGSIEAAA IMEHILAGSA FMPHAQKVNE VDPLLKPKQD RYALRTSPQW LGPQIEVIRA  360
ATKSIEREVN SVNDNPVIDV HRGKALHGGN FQGTPIGVSM DNTRLAIANI GKLMFAQFSE  420
LVNEFYNNGL TSNLAGSRNP SLDYGFKGTE IAMASYCSEL QFLANPVTNH VQSAEQHNQD  480
VNSLGLVSAR KTAEAVDILK LMSSTYLVAL CQAVDLRHLE ENLKSAVKNC VTTVAKKVLT  540
TGPAGGLHSA RFSEKALLTA IDREAVYSYA DDPCSANYPL MTKIRAVLVE HALANGPAEK  600
DDGSSVFSKI TAFEEELREA LPREMEAARV AFETGTAPIT NRIKESRSFP LYRFVREELG  660
CVYLTGEKLK SPGEECNKVF LAISERKLID PMLECLKEWN GEPLPIC              707

SEQ ID NO: 24           moltype = AA  length = 706
FEATURE                 Location/Qualifiers
source                  1..706
                        mol_type = protein
                        organism = Streptochaeta angustifolia
SEQUENCE: 24
MVAQSDSAVS ILRDPLNWGK AAEELTGSHF DEVKRMVAQF REPAVTIEGA SLRVGQVASV  60
AAARDGAGAC VELDESARGR VKASSEWILD CIAHGGDIYG VTTGFGGTSH RRTKDGPALQ  120
VELLRHLNAG IFGTGSHGHT LPTEVVRAAM LVRTNTLLQG YSGIRFEILE AITKLLNSGV  180
TPCLPLRGTI TASGDLVPLS YIAGVLTGRP NAEAVTVDGR KVDAAEAFKV AGIEGGFFKL  240
QPKEGLAIVN GTSVGAALAA MVLYDANILA VLSEVMSAVF CEVMNGKPEY TDHLTHKLKH  300
HPGQIEAAAI MEHILDGSSF MKHAKKVNEL DPLLKPKQDR YALRTSPQWL GPQIEVIRAA  360
TKSIEREVNS VNDNPVIDVS RGKALHGGNF QGTPIGVSMD NARLAIASIG KLMFAQFSEL  420
VNEFYNNGLT SNLAGSRNPS LDYGFKGTEI AMASYCSELQ YLGNPITNHV QSAEQHNQDV  480
NSLGLVSARK TAEAIDILKL MSSTYLVALC QAIDLRHLEE NLKNAVKNCV MQVAKKVLTT  540
NPAGDLHNAR FSEKALLTAI DREAVFSYAD DPCSANYPLM QKLRSVLVDH AIANGEDEKE  600
PATSVFAKIT KFEDELRTAL PREMEAARVA VENGTAPTAN RIKESRSYPL YRFIREDLGA  660
VYLTGEKLRS PGEECNKVFV AINQGKLVDP LLECLKEWKG EPLPIC               706

SEQ ID NO: 25           moltype = AA  length = 698
FEATURE                 Location/Qualifiers
source                  1..698
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                        mol_type = protein
                        organism = Streptochaeta angustifolia
SEQUENCE: 25
MASQRDPLNW AAAAAELTGS HLDEVKRMVA QFREPQVKIE GASLRVGQVA AVAAARDAAG  60
ARVELDEAAR GRVKESSEWI LNCIATGGDI YGVTTGFGGT SHRRTKDGPA LQVELLRHLN  120
AGIFGTGSDG HTLPSEVARA AMLVRINTLL QGYSGIRFEI LEAIAKLLNT GVTPCLPLRG  180
TITASGDLVP LSYIAGVITG RPNALAIAPD GRKVDAAEAF KIAGIEGGFF KLQPKEGLAI  240
VNGTSVGAAL AAMVLYDANI LAVLSEVMSA VFCEVMNGKP EYTDHLTHKL KHHPGQIEAA  300
AIMEHILAGS SFMKHAKKVN ELDPLLKPKQ DRYALRTAPQ WLGPQIEVIR AATKSIEREV  360
NSVNDNPVID VKRGKALHGG NFQGTPIGVS MDNARLAIAN IGKLMFAQFS ELVNEFYNNG  420
LTSNLAGSRN PSLDYGFKGT EIAMASYCSE LQFLANPVTN HVQSAEQHNQ DVNSLGLVSA  480
RKTAEAVDIL KLMSSTYLVA LCQAVDLRHL EENLKNAVKN CVTQVAKKVL TTNPTGDLSN  540
ARFSEKALIT SIDREAVFSY ADDPCSANYP LMQKIRAVLV DHAITNGDGE NEPAAAVFAR  600
ITKFEDELRS ALPREMEAAR VAFENGASQT PNRMKDSRSY PLYRFIREDL GAVYLTGEKL  660
RSPGEECNKV FVAISQGKLV DPLLDCLKEW NGEPLPIC                         698

SEQ ID NO: 26           moltype = AA  length = 707
FEATURE                 Location/Qualifiers
source                  1..707
                        mol_type = protein
                        organism = Ecdeiocolea monostachya
SEQUENCE: 26
MACLSSDNVV CIPKDALNWA KAAEELAGSH LEEVKRMVAE FRSPAVRIEG ASLRVGQVAA  60
VAGAEAAAAA KVELDESARA RVKASSDWIV DSVANGGDIY GVTTGFGGTS HRRTRDGPAL  120
QVELLRHLNA GIFGTGKDGH VLPSEVTRAA MVVRINTLLQ GYSGIRFEIL EAITALLNSG  180
VTPCLPLRGT ITASGDLVPL SYIAGLITGR PNAMAVTPDG RKVDAAEAFK VAGIPHGFFK  240
LQPKEGLAMV NGTSVGAALA SMVLFDANIL TVLAVVMSAV FCEVMTGKPE YTDHLTHKLK  300
HHPGQIEAAA IMEHILAGSS FMKLAKKLGE LDPLMKPKQD RYALRTSPQW LGPQIEVIRT  360
ATKSIEREIN SVNDNPVIDV SRGKALHGGN FQGTPIGVSM DNARLAIANI GKLMFAQFSE  420
LVNEFYNNGL TSNLAGSRNP SLDYGFKGAE IAMASYCSEL QFLANPVTNH VQSAEQHNQD  480
VNSLGLVSAR KTAEAIDILK LMSSTYLMAL CQAIDLRHLE ENLKSTVKNC VAQVAKKVLT  540
MSTAGDLHSA RFSEKGLLTA IDREAVFAYA DDPCSPNYPL MQKVRAVLVE HGLANGEAER  600
VTDTSVFAKI TKFEDELRAA LPKEVEAVRA AVENGNAPIP NRVKECRSYP LYRFLREELG  660
TVYLTGEKLR SPGEECNKVF VAINEGKLID PLLECLKEWN GEPLPIC                707

SEQ ID NO: 27           moltype = AA  length = 705
FEATURE                 Location/Qualifiers
source                  1..705
                        mol_type = protein
                        organism = Joinvillea ascendens
SEQUENCE: 27
MAFQNDNVLC IKKDPLNWGK AAEELTGSHL DEVKRMVAES RTPVVKIQGA SLRIGQVAAV  60
AVRETGVAKV ELDESARGRV KASSDWIVNS VANGGDIYGV TTGFGGTSHR RTRDGPALQI  120
ELLRHLNAGI FGTGTDGHVL PSAVTRAAMF VRINTLLQGY SGIRFEILEA IAALLNAGVT  180
PCLPLRGTIT ASGDLIPLSY IAGLITGRPN AVAIAPDGRK VDAAEAFKIA GIPHGFFKLQ  240
PKEGLAIVNG TSVGAALAST VLFDANILAI LAEVLSAVFC EVMTGKPEYT DHLTHRLKHH  300
PGQIEAAAIM EHILEGSSFM KLAKKLGELD PLLKPKQDRY ALRTAPQWLG PQIEVIRAAT  360
KSIEREINSV NDNPIIDVSR GKALHGGNFQ GTPIGVSMDN TRLAIANIGK LMFAQFSELV  420
NDFYNNGLTS NLAGGRNPSL DYGFKGTEIA MASYCSELQF LANPVTNHVQ SAEQHNQDVN  480
SLGLVSARKT AEAVDILKLM SSTFLIALCQ AIDLRHLEEN LKSAVKNCVA QVAKKVLTVN  540
TVGDLHNARF SEKDLLTAID REAVFTYADD PCSPNYPLMQ KVRAVLVEHA LANGEAERVA  600
NTSVFAKITK FEEELRATLP KEVEAARVAV ENRTAPTQNR IKESRSYPLY RFVREDLGTA  660
YLTGEKLRSP GEECNKVFVA INQGKLIDPL LECLKKWNGE PLPIC                  705

SEQ ID NO: 28           moltype = AA  length = 720
FEATURE                 Location/Qualifiers
source                  1..720
                        mol_type = protein
                        organism = Joinvillea ascendens
SEQUENCE: 28
MECENGNVAA VAAVNGGNGL CLQKPQHADP LNWGKAAGEL MGSHLEEVKR MVAEFRAPVV  60
KIEGASLRIA QVAAVAAGEA AAKVELDES SRGRVKASSD WVMSSMMNGT DSYGVTTGFG  120
ATSHRRTKEG GALQRELIRF LNAGVFGTGS DGHVLPAAAT RAAMLVRINT LLQGYSGIRF  180
EILEAITALL NAGVTPCLPL RGTITASGDL VPLSYIAGLI TGRPNSVAVA PDGRKVDAAE  240
AFKIAGIQHG FFELQPKEGL AMVNGTAVGS GLASTVLFEA NILTILAEVL SAVFCEVMTG  300
KPEYTDHLTH KLKHHPGQIE AAAIMEHILE GSSYMKLAKK LGDLDPLMKP KQDRYALRTS  360
PQWLGPQIEV IRASTKSIER EINSVNDNPL IDVSRGKALH GGNFQGTPIG VSMDNTRLAI  420
AAIGKLMFAQ FSELVNDFYN NGLPSNLSGG RNPSLDYGFK GAEIAMASYC SELQFLANPV  480
TNHVQSAEQH NQDVNSLGLI SSRKTAEAVD ILKLMSSTFL IALCQAIDLR HLEENLKSAV  540
KNCVAQVAKK ALTLNTVGDL HNARFSEKDL LTAIDREALF AYADDPCNPN YPLMQKLRAV  600
LVEHALANGE AEHVATTSVF AKITKFEEEL RATLPKEVEA ARVAVENGTA PTPNRIKECR  660
SYPLYRFVRE ELGTEYLTGE KLRSPGEECN KVFVAINQGK LIDPLLECLK EWNGEPLPIC  720

SEQ ID NO: 29           moltype = AA  length = 714
FEATURE                 Location/Qualifiers
source                  1..714
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                        mol_type = protein
                        organism = Ecdeiocolea monostachya
SEQUENCE: 29
MECINGNGAA ANGSGLCLRA GGDPLNWGKA AEEMAGSHLE EVKRMVAEFR APAVRIEGAS  60
LRIAQVAAVA AGGAAKARVE LDEAARGRVQ ASSDWVMSSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGVF GEDSDGHVLP APATRAAMLV RINTLLQGYS GIRFEILEAI  180
TALLNAGVTP CLPLRGTITA SGDLVPLSYI AGLVTGRPNS VAVTPDGRKV NAAEAFKIAG  240
IEHGFFELQP KEGLAMVNGT AVGSGLASIV LFETNILAVL AEVLSAVFCE VMTGKPEYTD  300
HLTHKLKHHP GQIEAAAIME HILDGSSYMK LAKKLGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVSRG KALHGGNFQG TPIGVSMDNT RLAIAAIGKL  420
MFAQFSELVN DFYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL ANPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAVDILKIMS STFLVALCQA IDLRHLEENL KSAIKNCVAQ  540
VAKKALTLNT AGDLHNARFS EKDLLTAIDR EAVFAYADDP CSPNYPLMKK LRSVLVEHAL  600
ANGEAELVAE TSVFAKIAKF EEELRAALPS EVEAAWAAVE NGTAATPNRI KECRSYPLYR  660
FVREELGSGY LTGEKVRSPG EECNRVFVAI NKGKLIDPLL DCLNEWNGEP LPIC        714

SEQ ID NO: 30           moltype = AA  length = 725
FEATURE                 Location/Qualifiers
source                  1..725
                        mol_type = protein
                        organism = Flagellaria indica
SEQUENCE: 30
MECQQNENGI AAAAVANGAA ARETGFCLSD PLNWGKAAEE VKGSHLEEVK RMVAEFRAPV  60
VRLEGASLRI AQVAAVAEGK KAAAGGARVE LDEAARGRVK ASSDWVMDSM TKGTDSYGVT  120
TGFGATSHRR TKEGGALQRE LIRFLNAGIF GSGADSGHVL PTPASRAAML VRINTLLQGY  180
SGIRFEILEA ITALLNAGVT PCLPLRGTIT ASGDLVPLSY IAGLITGRPN AAAIAPDGRK  240
VDAGEAFRIA GIPHGFFELQ PKEGLALVNG TAVGSGLASM VLFEANVLAL LAEVLSALFC  300
EVMTGKPEYT DHLTHKLKHH PGQIEAAAIM EHILEGSSYM KLAKRLGELD PLMKPKQDRY  360
ALRTSPQWLG PQIEVIRAAT KSIEREINSV NDNPLIDVSR SKALHGGNFQ GTPIGVSMDN  420
TRLAIAAIGK LMFAQFSELV NDFYNNGLPS NLSGGRNPSL DYGFKGAEIA MAAYCSELQF  480
LANPVTNHVQ SAEQHNQDVN SLGLISSRKT AEAVDILKLM SSTFMIALCQ AVDLRHLEEN  540
LRSAVKNCVT QVAKKALTMN PVGDLHNARF CEKDLLTAFD REAVFAYADD PCSANYPLMQ  600
KLRAVLVEHA LTNGEAELSQ DTSVFMKIAK FEEELRAALP KEVEAARAAV ESGNAAIPNR  660
IKECRSCPLY QFVREEVGTE YLTGEKTRSP GEECNKVFVA INEGKVIDPL LECLKEWNGE  720
PLPIC                                                              725

SEQ ID NO: 31           moltype = AA  length = 713
FEATURE                 Location/Qualifiers
source                  1..713
                        mol_type = protein
                        organism = Setaria italica
SEQUENCE: 31
MACEKSNVAA NGDGLCMATP RADPLNWGKA AEELMGSHLD EVKRMVADYR QPLVKIEGAS  60
LNIAQVAAVA NGAGEARVEL DESARERVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGTDGHVLPA EATRAAMLVR INTLLQGYSG IRFEILEAIV  180
KLLNANVTPC LPLRGTVTAS GDLVPLSYIA GLVTGRENSV AVAPDGTKVN AAEAFKIAGI  240
QGGFFELQPK EGLAMVNGTA VGSGLASTVL FEANVLAVLA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH ILEGSSYMKL AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVARSK ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQFSELVND YYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AIEILKIMSS TFLIALCQAV DLRHIEENVK SAVKSCVMTV  540
AKKTLSTNST GGLHVARFCE KDLLQEIERE AVFAYADDPC SANYPLMKKL RNVLVERALA  600
NGTAEFNAET SVLAKVAQFE EELRAALPKA VEAARAAVEN GTAAIPIRIT ECRSYPLYRF  660
VREELGAVYL TGEKTRSPGE ELNKVLVAIN LGKHIDPLLE CLKEWNGEPL PIC         713

SEQ ID NO: 32           moltype = AA  length = 713
FEATURE                 Location/Qualifiers
source                  1..713
                        mol_type = protein
                        organism = Setaria viridis
SEQUENCE: 32
MACEKSNVAA NGDGLCMATP RADPLNWGKA AEELMGSHLD EVKRMVADYR QPLVKIEGAS  60
LNIAQVAAVA NGAGEARVEL DESARERVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGTDGHVLPA EATRAAMLVR INTLLQGYSG IRFEILEAIV  180
KLLNANVTPC LPLRGTVTAS GDLVPLSYIA GLVTGRENSV AVAPDGTKVN AAEAFKIAGI  240
QGGFFELQPK EGLAMVNGTA VGSGLASTVL FEANVLAVLA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH ILEGSSYMKL AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVARSK ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQFSELVND YYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AIEILKLMTS TFLIALCQAV DLRHIEENVK SAVKSCVMTV  540
AKKTLSTNST GGLHVARFCE KDLLQEIERE AVFAYADDPC SANYPLMKKL RNVLVERALA  600
NGTAEFNAET SVFAKVAQFE EELRAALPKA VEAARAAVEN GTAAIPIRIT ECRSYPLYRF  660
VREELGAVYL TGEKTRSPGE ELNKVLVAIN QGKHIDPLLE CLKEWNGEPL PIC         713

SEQ ID NO: 33           moltype = AA  length = 713
FEATURE                 Location/Qualifiers
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source                  1..713
                        mol_type = protein
                        organism = Setaria italica
SEQUENCE: 33
MACEKSNVAA NGDGLCMATP RADPLNWGKA AEELMGSHLD EVKRMVADYR QPLVKIEGAS  60
LNIAQVAAVA NGAGEARVEL DESARERVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGTDGHVLPA EATRAAMLVR INTLLQGYSG IRFEILEAIV  180
KLLNANVTPC LPLRGTVTAS GDLVPLSYIA GLVTGRENSV AVAPDGTKVN AAEAFKIAGI  240
QGGFFELQPK EGLAMVNGTA VGSGLASTVL FEANVLAVLA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH ILEGSSYMKL AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVARSK ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQFSELVND YYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AIEILKIMSS TFLIALCQAV DLRHIEENVK SAVKSCVMTV  540
AKKTLSTNST GGLHVARFCE KDLLQEIERE AVFAYADDPC SANYPLMKKL RNVLVERALA  600
NGTAEFNAET SVLAKVAQFE EELRAALPKA VEAARAAVEN GTAAIPIRIT ECRSYPLYRF  660
VREELGAVYL TGEKTRSPGE ELNKVLVAIN QGKHIDPLLE CLKEWNGEPL PIC         713

SEQ ID NO: 34           moltype = AA  length = 713
FEATURE                 Location/Qualifiers
source                  1..713
                        mol_type = protein
                        organism = Setaria viridis
SEQUENCE: 34
MACEKSNVAA NGDGLCMATP RADPLNWGKA AEELMGSHLD EVKRMVADYR QPLVKIEGAS  60
LNIAQVAAVA NGAGEARVEL DESARERVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGTDGHVLPA EATRAAMLVR INTLLQGYSG IRFEILEAIV  180
KLLNANVTPC LPLRGTVTAS GDLVPLSYIA GLVTGRENSV AVAPDGTKVN AAEAFKIAGI  240
QGGFFELQPK EGLAMVNGTA VGSGLASTVL FEANVLAVLA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH ILEGSSYMKL AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVARSK ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQFSELVND YYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AIEILKLMTS TFLIALCQAV DLRHIEENVK SAVKSCVMTV  540
AKKTLSTNST GGLHVARFCE KDLLQEIERE AVFAYADDPC SANYPLMKKL RNVLVERALA  600
NGTAEFNAET SVFAKVAQFE EELRAALPKA VEAARAAVEN GTAAIPIRIT ECRSYPLYRF  660
VREELGAVYL TGEKTRSPGE ELNKVLVAIN QGKHIDPLLE CLKEWNGEPL PIC         713

SEQ ID NO: 35           moltype = AA  length = 714
FEATURE                 Location/Qualifiers
source                  1..714
                        mol_type = protein
                        organism = Setaria italica
SEQUENCE: 35
MECENGRVAA ANGDGLCMAT PRADPLNWGK AAEELMGSHL DEVKRMVADY RQPLVKIEGA  60
SLNIAQVAAV ANGAGEARVE LDESARERVK ASSDWVMNSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGAF GTGTDGHVLP AEATRAAMLV RINTLLQGYS GIRFEILEAI  180
VKLLNANVTP CLPLRGTVTA SGDLVPLSYI AGLVTGRENS VAVAPDGTKV NAAEAFKIAG  240
IQGGFFELQP KEGLAMVNGT AVGSGLASTV LFEANVLAVL AEVLSAVFCE VMNGKPEYTD  300
HLTHKLKHHP GQIEAAAIME HILEGSSYMK LAKKLGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVARS KALHGGNFQG TPIGVSMDNT RLALAAIGKL  420
MFAQFSELVN DYYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL GNPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAIEILKLMT STFLIALCQA VDLRHIEENV KSAVKGCVMT  540
VAKKTLSTNS AGGLHVARFC EKDLLQEIER EAVFAYADDP CSANYPLMKK LRNVLVERAL  600
ANGTAEFNAE TSVLAKVAQF EEELRAALPK AVEAARAAVE NGTAAIPNRI TECRSYPLYR  660
FVREELGAVY LTGEKTRSPG EELNKVLVAI NQGKHIDPLL ECLKEWNGEP LPIS        714

SEQ ID NO: 36           moltype = AA  length = 714
FEATURE                 Location/Qualifiers
source                  1..714
                        mol_type = protein
                        organism = Setaria viridis
SEQUENCE: 36
MECENGRVAA ANGDGLCMAT PRADPLNWGK AAEELMGSHL DEVKRMVADY RQPLVKIEGA  60
SLNIAQVAAV ANGAGEARVE LDESARERVK ASSDWVMNSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGAF GTGTDGHVLP AEATRAAMLV RINTLLQGYS GIRFEILEAI  180
VKLLNANVTP CLPLRGTVTA SGDLVPLSYI AGLVTGRENS VAVAPDGTKV NAAEAFKIAG  240
IQGGFFELQP KEGLAMVNGT AVGSGLASTV LFEANVLAVL AEVLSAVFCE VMNGKPEYTD  300
HLTHKLKHHP GQIEAAAIME HILEGSSYMK LAKKLGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVARS KALHGGNFQG TPIGVSMDNT RLALAAIGKL  420
MFAQFSELVN DYYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL GNPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAIEILKLMT SSFLIALCQA VDLRHIEENV KSAVKGCVMT  540
VAKKTLSTNS AGGLHVARFC EKDLLQEIER EAVFAYADDP CSANYPLMKK LRNVLVERAL  600
ANGTAEFNAD TSVLAKVAQF EEELRAALPN AVEAARAAVE NGTAAIPNRI TECRSYPLYR  660
FVREELGAVY LTGEKTRSPG EELNKVLVAI NQGKHIDPLL ECLKEWNGEP LPIS        714

SEQ ID NO: 37           moltype = AA  length = 713
FEATURE                 Location/Qualifiers
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source                 1..713
                       mol_type = protein
                       organism = Panicum hallii
SEQUENCE: 37
MACEKSNVAA NGDGLCMAKP RADPLNWGKA AEELMGSHLD EVKRMVAEYR QPLVKIEGAS  60
LRIAQVAAVA NGAGEARVEL DESARERVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGTDGHVLPG EATRAAMLVR INTLLQGYSG IRFEILEAIV  180
KLLNANVTPC LPLRGTVTAS GDLVPLSYIA GLVTGRENSV AVAPDGTKVN AAEAFKIAGI  240
QGGFFELQPK EGLAMVNGTA VGSGLASTVL FEANILAVLA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH ILEGSSYMKL AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVARSK ALHGGNFQGT PIGVSMDNTR LALAAIGKLM  420
FAQFSELVND YYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AIEILKLMSS TFLIALCQAV DLRHIEENVK SAVKSCVMTV  540
AKKTLSTNAT GGLHAARFCE KDLLQEIERE AVFAYADDPC SANYPLMKKL RNVLVERALA  600
NGTAEFNAET SVFAKVAQFE EELRAALPKA VEAARAAVEN GTAAIPNRIA ECRSYPLYRF  660
VREELGAVYL TGEKTRSPGE ELNKVLVAIN QGKHIDPLLE CLKEWNGEPL PIC         713

SEQ ID NO: 38          moltype = AA  length = 713
FEATURE                Location/Qualifiers
source                 1..713
                       mol_type = protein
                       organism = Panicum hallii
SEQUENCE: 38
MACEQSNVAA NGDGLCMAKP RADPLNWGKA AEELMGSHLD EVKRMVAEYR QPLVKIEGAS  60
LRIAQVAAVA NGAGEARVEL DESARERVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGTDGHVLPG EATRAAMLVR INTLLQGYSG IRFEILEAIV  180
KLLNANVTPC LPLRGTVTAS GDLVPLSYIA GLVTGRENSV AVAPDGTKVN AAEAFKIAGI  240
QGGFFELQPK EGLAMVNGTA VGSGLASTVL FEANILAVLA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH ILEGSSYMKL AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVARSK ALHGGNFQGT PIGVSMDNTR LALAAIGKLM  420
FAQFSELVND YYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AIEILKLMSS TFLIALCQAV DLRHIEENVK SAVKSCVMTV  540
AKKTLSTNAT GGLHAARFCE KDLLQEIERE AVFAYADDPC SANYPLMKKL RNVLVERALA  600
NGTAEFNAET SVFAKVAQFE EELRAALPKA VEAARAAVEN GTAAIPNRIA ECRSYPLYRF  660
VREELGAVYL TGEKTRSPGE ELNKVLVAIN QGKHIDPLLE CLKEWNGEPL PIC         713

SEQ ID NO: 39          moltype = AA  length = 712
FEATURE                Location/Qualifiers
source                 1..712
                       mol_type = protein
                       organism = Panicum hallii
SEQUENCE: 39
MECENGRVAN GDSLCMATPR GDPLNWGKAA EELMGSHLDE VKRMVAEYRQ PLVKIEGASL  60
RIAQVAAVAN GAGEARVELD ESARERVKAS SDWVMNSMMN GTDSYGVTTG FGATSHRRTK  120
EGGALQRELI RFLNAGAFGT GTDGHVLPGE ATRAAMLVRI NTLLQGYSGI RFEILEAIVK  180
LLNANVTPCL PLRGTVTASG DLVPLSYIAG LVTGRENSVA VAPDGTKVNA AEAFKIAGIQ  240
GGFFELQPKE GLAMVNGTAV GSGLASTVLF EANILAVLAE VLSAVFCEVM NGKPEYTDHL  300
THKLKHHPGQ IEAAAIMEHI LEGSSYMKLA KKLGELDPLM KPKQDRYALR TSPQWLGPQI  360
EVIRAATKSI EREINSVNDN PLIDVARSKA LHGGNFQGTP IGVSMDNTRL ALAAIGKLMF  420
AQFSELVNDY YNNGLPSNLS GGRNPSLDYG FKGAEIAMAS YCSELQFLGN PVTNHVQSAE  480
QHNQDVNSLG LISSRKTAEA IEILKLMSST FLIALCQAVD LRHIEENVKS AVKSCVMTVA  540
KKTLSTNATG GLHAARFCEK DLLQEIEREA VFAYADDPCS ANYPLMKKLR NVLVERALAN  600
GTAEFNAETS VFAKVAQFEE ELRAALPKAV EAARAAVENG TAAIPNRIAE CRSYPLYRFV  660
REELGAVYLT GEKTRSPGEE LNKVLVAINQ GKHIDPLLEC LKEWNGEPLP IC          712

SEQ ID NO: 40          moltype = AA  length = 713
FEATURE                Location/Qualifiers
source                 1..713
                       mol_type = protein
                       organism = Panicum virgatum
SEQUENCE: 40
MACEKSNVAT NGDGLCMATP RADPLNWGKA AEELMGSHLD EVKRMVAEYR QPLVKIEGAS  60
LRIAQVAAVA NGAGEARVEL DESARDRVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGTDGHVLPA EATRAAMLVR INTLLQGYSG IRFEILEAIV  180
KLLNANVTPC LPLRGTVTAS GDLVPLSYIA GLVTGRENSV AVAPDGTKVN AAEAFKIAGI  240
QGGFFELQPK EGLAMVNGTA VGSGLASTVL FEANILAILA EVLSAVFCEI MNGKPEFTDH  300
LTHKLKHHPG QIEAAAIMEH ILEGSSYMKL AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVARSK ALHGGNFQGT PIGVSMDNTR LALAAIGKLM  420
FAQFSELVND YYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AIEILKLMSS TFLIALCQAV DLRHIEENVK SAVKSCVMTV  540
AKKTLSTNAT GGLHVARFCE KDLLQEIERE AVFAYADDPC SANYPLMKKL RNVLVERALA  600
NGAAEFSAET SVFAKVAQFE EELRAALPKA VEAARAAVEN GTAAIPNRIA ECRSYPLYRF  660
VREELGAVYL TGEKTRSPGE ELNKVLVAIN QGKHIDPLLE CLKEWNGEPL PIC         713

SEQ ID NO: 41          moltype = AA  length = 712
FEATURE                Location/Qualifiers
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```
source                 1..712
                       mol_type = protein
                       organism = Panicum virgatum
SEQUENCE: 41
MECENGRGAN GDTLCMATPR ADPLNWGKAA EELMGSHLDE VKRMVAEYRQ PLVKIEGASL  60
RIAQVAAVAN GAGEARVELD ESARDRVKAS SDWVMNSMMN GTDSYGVTTG FGATSHRRTK  120
EGGALQRELI RFLNAGAFGT GTDGHVLPAE ATRAAMLVRI NTLLQGYSGI RFEILEAIVK  180
LLNANVTPCL PLRGTVTASG DLVPLSYIAG LVTGRENSVA VAPDGTKVNA AEAFKIAGIQ  240
GGFFELQPKE GLAMVNGTAV GSGLASTVLF EANILAILAE VLSAVFCEVM NGKPEFTDHL  300
THKLKHHPGQ IEAAAIMEHV LEGSSYMKLA KKLGELDPLM KPKQDRYALR TSPQWLGPQI  360
EVIRAATKSI EREINSVNDN PLIDVARSKA LHGGNFQGTP IGVSMDNTRL ALAAIGKLMF  420
AQFSELVNDY YNNGLPSNLS GGRNPSLDYG FKGAEIAMAS YCSELQFLGN PVTNHVQSAE  480
QHNQDVNSLG LISSRKTAEA IEILKLMSST FLIALCQAVD LRHIEENVKS AVKSCVMTVA  540
KKTLSTNSTG GLHVARFCEK DLLQEIEREA VFAYADDPCS ANYPLMKKLR NVLVERALAN  600
GAAEFSAETS VFAKVAQFEE ELRAALPKAV EAARAAVENG TAAIPNRIAE CRSYPLYRFV  660
REELGAVYLT GEKTRSPGEE LNKVLVAINL GKHIDPLLEC LKEWNGEPLP IC          712

SEQ ID NO: 42          moltype = AA  length = 712
FEATURE                Location/Qualifiers
source                 1..712
                       mol_type = protein
                       organism = Panicum virgatum
SEQUENCE: 42
MECKNGRVAN GDSLCVATPR ADPLNWGKAA EELMGSHLDE VKRMVAEYRQ PLVKIEGASL  60
RIAQVAAVAN GAGEARVELD ESARDRVKAS SDWVMNSMMN GTDSYGVTTG FGATSHRRTK  120
EGGALQRELI RFLNAGAFGT GTDGHVLPAE ATRAAMLVRI NTLLQGYSGI RFEILEAIAK  180
LLNANVTPCL PLRGTITASG DLVPLSYIAG LVTGRENSVA VAPDGSKVNA AEAFKIAGIQ  240
GGFFELQPKE GLAMVNGTAV GSGLASTVLF EANILAILAE VLSAVFCEVM NGKPEFTDHL  300
THKLKHHPGQ IEAAAIMEHI LEGSSYMKHA KKLGELDPLM KPKQDRYALR TSPQWLGPQI  360
EVIRAATKSI EREINSVNDN PLIDVSRGKA LHGGNFQGTP IGVSMDNTRL ALAAIGKLMF  420
AQFSELVNDY YNNGLPSNLS GGRNPSLDYG FKGAEIAMAS YCSELQFLGN PVTNHVQSAE  480
QHNQDVNSLG LISSRKTAEA IEILKLMSST FLIALCQAVD LRHIEENVKS AVKSCVMTVA  540
KRTLSTNSSG GLHVARFCEK DLLQEIEREA VFAYADDPCS ANYPLMKKLR NVLVERALAN  600
GAAEFNAETS VFAKVAQFEE ELRAALPKAV EAARASVENG TAAIPNRIAE CRSYPLYRFV  660
REELGAVYLT GEKARSPGEE LNKVLVAINQ GKHIDPLLEC LKEWNGEPLP IC          712

SEQ ID NO: 43          moltype = AA  length = 714
FEATURE                Location/Qualifiers
source                 1..714
                       mol_type = protein
                       organism = Sorghum bicolor
SEQUENCE: 43
MACENGRVAA TNGDGLCMAT PRADPLNWGK AAEELMGSHL DEVKRMVAEY RQPLVKIEGA  60
SLRIAQVAAV AAGAGEARVE LDESARGRVK ASSDWVMNSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGAF GTGTDGHVLP AEATRAAMLV RINTLLQGYS GIRFEILEAI  180
VKLLNANVTP CLPLRGTVTA SGDLVPLSYI AGLVTGRENS VAVAPDGTKV NAAEAFKIAG  240
IQGGFFELQP KEGLAMVNGT AVGSGLASTV LFEANVLAIL AEVLSAVFCE VMNGKPEYTD  300
HLTHKLKHHP GQIEAAAIME HILEGSSYMK LAKKLGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVARS KALHGGNFQG TPIGVSMDNT RLAIAAIGKL  420
MFAQFSELVN DYYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL GNPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAIEILKLMS STFLIALCQA VDLRHIEENV KSAVKSCVMT  540
VAKKTLSTNS TGGLHVARFC EKDLLQEIER EAVFAYADDP CSANYPLMKK LRNVLVERAL  600
ANGAAEFDAE TSVFAKVAQF EEELRAALPK AVEAARAAVE NGTAAIPNRI TECRSYPLYR  660
FVRQEVGAVY LTGEKTRSPG EELNKVLVAI NQGKHIDPLL ECLKEWNGEP LPIC        714

SEQ ID NO: 44          moltype = AA  length = 714
FEATURE                Location/Qualifiers
source                 1..714
                       mol_type = protein
                       organism = Sorghum bicolor
SEQUENCE: 44
MACENGRVAA TNGDGLCMAT PRADPLNWGK AAEELMGSHL DEVKRMVAEY RQPLVKIEGA  60
SLRIAQVAAV AAGAGEARVE LDESARGRVK ASSDWVMNSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGAF GTGTDGHVLP AEATRAAMLV RINTLLQGYS GIRFEILEAI  180
VKLLNANVTP CLPLRGTVTA SGDLVPLSYI AGLVTGRENS VAVAPDGTKV NAAEAFKIAG  240
IQGGFFELQP KEGLAMVNGT AVGSGLASTV LFEANVLAIL AEVLSAVFCE VMNGKPEYTD  300
HLTHKLKHHP GQIEAAAIME HILEGSSYMK LAKKLGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVARS KALHGGNFQG TPIGVSMDNT RLAIAAIGKL  420
MFAQFSELVN DYYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL GNPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAIEILKLMS STFLIALCQA VDLRHIEENV KSAVKSCVMT  540
VAKKTLSTNS TGGLHVARFC EKDLLQEIER EAVFAYADDP CSANYPLMKK LRNVLVERAL  600
ANGAAEFDAE TSVFAKVAQF EEELRAALPK AVEAARAAVE NGTAAIPNRI TECRSYPLYR  660
FVRQEVGAVY LTGEKTRSPG EELNKVLVAI NQGKHIDPLL ECLKEWNGEP LPIC        714

SEQ ID NO: 45          moltype = AA  length = 714
FEATURE                Location/Qualifiers
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source                1..714
                      mol_type = protein
                      organism = Sorghum bicolor
SEQUENCE: 45
MACDNGRVAA TNGDGLCMAT PRADPLNWGK AAEELMGSHL DEVKRMVAEY RQPLVKIEGA  60
SLRIAQVAAV AAGAGEARVE LDESARGRVK ASSDWVMNSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGAF GTGTDGHVLP AEATRAAMLV RINTLLQGYS GIRFEILEAI  180
VKLLNANVTP CLPLRGTVTA SGDLVPLSYI AGLVTGRENS VAVAPDGTKV NAAEAFKIAG  240
IQGGFFELQP KEGLAMVNGT AVGSGLASTV LFEANVLAIL AEVLSAVFCE VMNGKPEYTD  300
HLTHKLKHHP GQIEAAAIME HILEGSSYMK LAKKLGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVARS KALHGGNFQG TPIGVSMDNT RLAIAAIGKL  420
MFAQFSELVN DYYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL GNPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAIEILKLMS STFLIALCQA VDLRHIEENV KSAVKSCVMT  540
VAKKTLSTNS TGGLHVARFC EKDLLQEIER EAVFAYADDP CSANYPLMKK LRNVLVERAL  600
ANGAAEFDAE TSVFAKVAQF EEELRAALPK AVEAARAAVE NGTAAIPNRI TECRSYPLYR  660
FVRQEVGAVY LTGEKTRSPG EELNKVLVAI NQGKHIDPLL ECLKEWNGEP LPIC        714

SEQ ID NO: 46         moltype = AA  length = 716
FEATURE               Location/Qualifiers
source                1..716
                      mol_type = protein
                      organism = Zea mays
SEQUENCE: 46
MECDNGRVAA TNGDSLCMAL PRAADPLNWG KAAEEMMGSH LDEVKRMVAE YRQPLVKIEG  60
ASLRIAQVAA VAAGAGEARV ELDESARGRV KASSDWVRDS MMNGTDSYGV TTGFGATSHR  120
RTKEGGALQR ELIRFLNAGA FGIGTDAGHV LPAEATRAAM LVRINTLLQG YSGIRFEILE  180
AIVKLLNANV TPCLPLRGTV TASGDLVPLS YIAGLVTGRE NAVAVAPDGT KVNAAEAFRI  240
AGIQSGFFEL QPKEGLAMVN GTAVGSGLAS TVLFEANVLA VLAEVLSAVF CEVMNGKPEY  300
TDHLTHKLKH HPGQIEAAAI MEHILEGSSY MKLAKKLGEL DPLMKPKQDR YALRTSPQWL  360
GPQIEVIRAS TKSIEREINS VNDNPLIDVA RSKALHGGNF QGTPIGVSMD NTRLAVAAIG  420
KLMFAQFSEL VNDYYNNGLP SNLSGGRNPS LDYGFKGAEI AMASYCSELQ FLGNPVTNHV  480
QSAEQHNQDV NSLGLISSRK TAEAIEILKL MSSTFLIALC QAVDLRHIEE NVKSAVKSCV  540
MTVAKKTLST NSTGGLHVAR FCEKDLLQEI EREAVFAYAD DPCSANYPLM KKLRNVLVER  600
ALANGTAEFD AETSVFAKVA QFEEELRTAL PSAVEAARAA VENGTAAIPN RITECRSYPL  660
YRFVREELGA VYLTGEKTRS PGEELNKVLV AINQGKHIDP LLECLKEWNG EPLPIC      716

SEQ ID NO: 47         moltype = AA  length = 714
FEATURE               Location/Qualifiers
source                1..714
                      mol_type = protein
                      organism = Zea mays
SEQUENCE: 47
MECENGRVAA TNSDSLCMAM PRADPLNWGK AAEELMGSHL DEVKRMVAEY RQPLVKIEGA  60
SLSIAQVAAV ATGAGEARVE LDESARSRVK ASSDWVMSSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGAF GTGADGHVLP AEATRAAMLV RINTLLQGYS GIRFEILEAI  180
VKLLNANVTP CLPLRGTVTA SGDLVPLSYI AGLVTGRENS VALAPDGSKI NAAEAFKIAG  240
IQGGFFELQP KEGLAMVNGT AVGSGLASTV LFEANILAIL AEVLSAVFCE VMNGKPEYTD  300
HLTHKLKHHP GQIEAAAIME HILEGSSYMK LAKKLGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVARS KALHGGNFQG TPIGVSMDNT RLAIAAIGKL  420
MFAQFSELVN DYYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL GNPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAIEILKLMS STFLIALCQA VDLRHIEENV KSAVKSCVMT  540
VARKTLSTNS TGGLHVARFC EKDLLQEIER EAVFAYADDP CSANYPLMKK LRNVLVERAL  600
ANGAAEFNAE TSVFAKVAQF EDDLRAALPK AVEAARAAVE NGTAGIPNRI ADCRSYPLYR  660
FVREELGAVY LTGEKTRSPG EELNKVLVAI NQGKHIDPLL ECLKEWNGEP LPIC        714

SEQ ID NO: 48         moltype = AA  length = 714
FEATURE               Location/Qualifiers
source                1..714
                      mol_type = protein
                      organism = Zea mays
SEQUENCE: 48
MATPRADPLN WGKAAEELMG SHLDEVKRMV AEYRQPLVKI EGASLSIAQV AAVAAGAGEA  60
RVELDESARG RVKASSDWVM SSMMNGTDSY GVTTGFGATS HRRTKEGGAL QRELIRFLNA  120
GAFGTGADGH VLPADATRAA MLVRINTLLQ GYSGIRFEIL EAIVKLLNAN VTPCLPLRGT  180
VTASGDLVPL SYIAGLVTGR ENSVAVAPDG SKVNAAEAFK IAGIQGGFFE LQPKEGLAMV  240
NGTAVGSGLA STVLFEANIL AILAEVLSAV FCEVMNGKPE YTDHLTHKLK HHPGQIEAAA  300
IMEHILEGSS YMKLAKKLGE LDPLMKPKQD RYALRTSPQW LGPQIEVIRA ATKSIEREIN  360
SVNDNPLIDV ARSKALHGGN FQGTPIGVSM DNTRLAIAAI GKLMFAQFSE LVNDYYNNGL  420
PSNLSGGRNP SLDYGFKGAE IAMASYCSEL QFLGNPVTNH VQSAEQHNQD VNSLGLISSR  480
KTAEAIEILK LMSSTFLIAL CQAVDLRHIE ENVKSAVKSC VMTVAKKTLS TDSTGGLHVA  540
RFCEKDLLQE IEREAVFAYA DDPCSANYPL MKKLRNVLVE RALANGAAEF NAETSVFAKV  600
AQFEEDLRAA LPKAVEAARA AVENGTAAIP NRITDCRSYP LYRFVREELG AVYLXYPLYR  660
FVREELGAVY LTGEKTRSPG EELNKVLIAI NQGKHIDPLL ECLKEWNGEP LPIC        714

SEQ ID NO: 49         moltype = AA  length = 713
FEATURE               Location/Qualifiers
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source                 1..713
                       mol_type = protein
                       organism = Oryza sativa
SEQUENCE: 49
MACENGQVAA DGINGLCMAA PRADPLNWGK AAEEMSGSHL DEVKRMVAEY RQPLVKIEGA  60
SLRIAQVAAV AAAGEARVEL DESARERVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGTDGHVLSA EATRAAMLVR INTLLQGYSG IRFEILEAIT  180
KLLNANVTPC LPLRGTVTAS GDLVPLSYIA GLVTGRENSV AVAPDGSKVN AAEAFKIAGI  240
QGGFFELQPK EGLAMVNGTA VGSGLASTVL FEANILAVLA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH ILEGSSYMKL AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVSRDK ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQFSELVND YYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AVEILKLMSS TFLVALCQAI DLRQIEENVK SAVKSCVMTV  540
ARKTLSTSAT GGLHAARFCE KDLLQEIDRE AVFAYADDPC SANYPLMKKL RNVLVERALA  600
NGAAEFNAET SVFAKVAQFE EELRAALPAA VLAARAAVEN GTAATPNRIT ECRSYPLYRF  660
VREELGTAYL TGEKTRSPGE ELNKVLVAIN QGKHIDPLLE CLKEWNGAPL PIC         713

SEQ ID NO: 50          moltype = AA  length = 713
FEATURE                Location/Qualifiers
source                 1..713
                       mol_type = protein
                       organism = Oryza sativa
SEQUENCE: 50
MECENGRVSA NGMSGLCVAA PRADPLNWGK ATEEMTGSHL DEVKRMVAEY RQPLVKIEGA  60
SLRIAQVAAV AAAGEARVEL DESARERVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGTDGHVLPA EATRAAMLVR INTLLQGYSG IRFEILEAIA  180
KLLNANVTPC LPLRGTITAS GDLVPLSYIA GLVTGRENAV AVAPDGSKVN AAEAFKIAGI  240
QGGFFELQPK EGLAMVNGTA VGSGLASTVL FEANILAILA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH ILEGSSYMKH AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVSRGK ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQFSELVND FYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTDE AIDILKLMSS TFLIALCQAV DLRHIEENVK SAVKSCVMTV  540
AKKTLSTNST GDLHVARFCE KDLLKEIDRE AVFAYADDPC SHNYPLMKKL RNVLVERALA  600
NGAAEFNADT SVFAKVAQFE EELRATLPGA IEAARAAVEN GTAAIPSRIT ECRSYPLYRF  660
VREELGTKYL TGEKTRSPGE ELNKVLVAIN EGKHIDPLLE CLKEWNGEPL PIC         713

SEQ ID NO: 51          moltype = AA  length = 710
FEATURE                Location/Qualifiers
source                 1..710
                       mol_type = protein
                       organism = Brachypodium distachyon
SEQUENCE: 51
MACENGQVAA NGICTAIQHA DPLNWGKAAE ALTGSHLEEV KRMVAEYRQP VVTIEGASLS  60
IAKVAAVAAA GEAQVQLDES ARERVKASSD WVMDSMANGV DSYGVTTGFG ATSHRRTKEG  120
GALQRELIRF LNAGAFGTGS DGHVLPAGAT RAAMLVRINT LLQGYSGIRF EILEAIAKLL  180
NANVTPCLPL RGTITASGDL VPLSYIAGLV TGRENSVAVA PDGSKVNAAE AFKIAGIHGG  240
FFELQPKEGL AMVNGTAVGS GLASTVLFDA NVLAVMAEVI SAVFCEVMNG KPEFTDHLTH  300
KLKHHPGQIE AAAIMEHILE GSSYMKLAKK LGDLDPLMKP KQDRYALRTS PQWLGPQIEV  360
IRAATKSIER EINSVNDNPL IDVSRGKAIH GGNFQGTPIG VSMDNTRLAL AAIGKLMFAQ  420
FSELVNDFYN NGLPSNLSGG RNPSLDYGFK GAEIAMASYC SELQFLGNPV TNHVQSAEQH  480
NQDVNSLGLI SARKTAEAIE ILKLMTSTFL VALCQAIDLR HIEENVKSAV TSCVRAVAKK  540
TLSTNSAGGL HVARFSEKDL IQEIDREAVF AYADDPCNPN YPLMKKLRGV LVERALANGV  600
AEFDAETSVF AKVARFEEEL RAALPVAVEA ARAAVESGTA EAPNRIAECR SYPLYRFVRQ  660
ELGTVYLTGE KTRSPGEELN KVLVAINQGK HIDPLLECLK EWNGEPLPIC             710

SEQ ID NO: 52          moltype = AA  length = 716
FEATURE                Location/Qualifiers
source                 1..716
                       mol_type = protein
                       organism = Brachypodium distachyon
SEQUENCE: 52
MTMASKNVHV SADGYLILCP ATSQHADPLN WGKAAEALTG SHLEEVKRMV AEYRQPVVTI  60
EGASLSIAKV AAVAAAGEAQ VQLDESARER VKASSDWVMD SMANGVDSYG VTTGFGATSH  120
RRTKEGGALQ RELIRFLNAG AFGTGSDGHV LPAGATRAAM LVRINTLLQG YSGIRFEILE  180
AIAKLLNANV TPCLPLRGTI TASGDLVPLS YIAGLVTGRE NSVAVAPDGS KVNAAEAFKI  240
AGIHGGFFEL QPKEGLAMVN GTAVGSGLAS TVLFDANVLA VMAEVISAVF CEVMNGKPEF  300
TDHLTHKLKH HPGQIEAAAI MEHILEGSSY MKLAKKLGDL DPLMKPKQDR YALRTSPQWL  360
GPQIEVIRAA TKSIEREINS VNDNPLIDVS RGKAIHGGNF QGTPIGVSMD NTRLALAAIG  420
KLMFAQFSEL VNDFYNNGLP SNLSGGRNPS LDYGFKGAEI AMASYCSELQ FLGNPVTNHV  480
QSAEQHNQDV NSLGLISARK TAEAIEILKL MTSTFLVALC QAIDLRHIEE NVKSAVTSCV  540
RAVAKKTLST NSAGGLHVAR FSEKDLIQEI DREAVFAYAD DPCNPNYPLM KKLRGVLVER  600
ALANGVAEFD AETSVFAKVA RFEEELRAAL PVAVEAARAA VESGTAEAPN RIAECRSYPL  660
YRFVRQELGT VYLTGEKTRS PGEELNKVLV AINQGKHIDP LLECLKEWNG EPLPIC      716

SEQ ID NO: 53          moltype = AA  length = 711
FEATURE                Location/Qualifiers
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source                1..711
                      mol_type = protein
                      organism = Brachypodium distachyon
SEQUENCE: 53
MARENARVAA ANGICTAIQH ADPLNWGKAA EELTGSHLDE VKRMVVEYRE PVVTIEGASL  60
SIAKVAAVAA AGEAKVELDE SARERVKASS DWVMNSMANG VDSYGVTTGF GATSHRRTKE  120
GGALQRELIR FLNAGAFGTG SDGHVLPAGA TRAAMLVRIN TLLQGYSGIR FEILEAIAKL  180
LNANVTPCLP LRGTITASGD LVPLSYIAGL VTGRENSVAV APDGRKVNAA EAFKIAGIHG  240
GFFELQPKEG LAMVNGTAVG SGLASTVLFE ANILAVLAEV ISAVFCEVMN GKPEFTDHLT  300
HKLKHHPGQI EAAAIMEHIL EGSSYMKLAK KQGELDPLMK PKQDRYALRT SPQWLGPQIE  360
VIRAATKSIE REINSVNDNP LIDVSRGKAI HGGNFQGTPI GVSMDNTRLA LAAIGKLMFA  420
QFSELVNDLY NNGLPSNLSG GRNPSLDYGL KGAEIAMASY CSELQFLGNP VTNHVQSAEQ  480
HNQDVNSLGL ISSRKTAEAI EILKLMSSTF LVALCQAIDL RHIEENVKSA VKSCVMTVAK  540
KTLSTNSTGD LHVSRFCEKD MLQEIDREAV FAYADDPCNH NYPLMKKLRG VLVESALANG  600
VAEYNVETSV FAKVAQFEEE LRAALPKAVE AARAAVESGT AATPNRITEC RSYPLYRFVR  660
EELGTVFLTG EKTRSPGEEL NKVLMAINQG KHIDPLLECL KEWNGEPLPI C           711

SEQ ID NO: 54         moltype = AA  length = 712
FEATURE               Location/Qualifiers
source                1..712
                      mol_type = protein
                      organism = Brachypodium distachyon
SEQUENCE: 54
MECENGQFAA NGTGLCMATP SADPLNWGKA AEELTGSHLD EVKRMVAEYR KPVVTIEGAT  60
LSIAKVAAVA AAGEAKVELD ESARERIKAS SDWVMNSMMN GTDSYGVTTG FGATSHRRTK  120
EGGALQRELI RFLNAGAFGT GSDGHVLPAG ATRAAMLVRI NTLLQGYSGI RFEILEAIAK  180
LLNANVTPCL PLRGTITASG DLVPLSYIAG LVTGRENSVA VTPDGRKVNA AEAFKLAGIH  240
GGFFELQPKE GLAMVNGTAV GSGLASTVLF EANILAVLAE VISAVFCEVM NGKPEFTDHL  300
THKLKHHPGQ IEAAAIMEHI LEGSSYMKLA KKLGDLDPLM KPKQDRYALR TSPQWLGPQI  360
EVIRAATKSI EREINSVNDN PLIDVSRGKA IHGGNFQGTP IGVSMDNTRL ALAAIGKLMF  420
AQFSELVNDF YNNGLPSNLS GSRNPSLDYG FKGAEIAMAS YCSELQFLGN PVTNHVQSAE  480
QHNQDVNSLG LISSRKTAEA VEILKLMSST FLVALCQAID LRHIEENVKI AVKSCVMTVA  540
KKTLSTNSTG GLHVARFCEK DLLQEIEREA VFAYADDPCS ANYPLMKKLR SVLVERALSN  600
GMAEFNAETS VFAKVAQFEE ELRTVLPKAV EAARAAVESG TAATPNRIKE CRSYPLYRFV  660
REELGTAYLT GEKTRSPGEE LNKVLVAINQ GKHIDPLLEC LKEWNGEPLP IC          712

SEQ ID NO: 55         moltype = AA  length = 712
FEATURE               Location/Qualifiers
source                1..712
                      mol_type = protein
                      organism = Brachypodium distachyon
SEQUENCE: 55
MECENGQFAA NGTGLCMATP RADPLNWGKA AEELTGSHLD EVKRMVAEYR KPVVTIEGAT  60
LSIAKVAAVA AAGEAKVELD ESARERVKAS SDWVMNSMAN GVDSYGVTTG FGATSHRRTK  120
EGGALQRELI RFLNAGAFGT GSDGHVLPAG ATRAAMLVRI NTLLQGYSGI RFEILEAIAK  180
LLNANVTPCL PLRGTITASG DLVPLSYIAG LVTGRENSVA VTPDGRKVNA AEAFKIAGIH  240
GGFFELQPKE GLAMVNGTAV GSGLASTVLF EANILAVLAE VISAVFCEVM NGKPEFTDHL  300
THKLKHHPGQ IEAAAIMEHI LEGSSYMKLA KKLGDLDPLM KPKQDRYALR TSPQWLGPQI  360
EVIRAATKSI EREINSVNDN PLIDVSRGKA IHGGNFQGTP IGVSMDNTRL ALAAIGKLMF  420
AQFSELVNDF YNNGLPSNLS GSRNPSLDYG FKGAEIAMAS YCSELQFLGN PVTNHVQSAE  480
QHNQDVNSLG LISSRKTAEA VEILKLMSST FLVALCQAID LRHIEENVKS AVKSCVMTVA  540
KRTLSTNSTG GLHVARFCEK DLLQEIEREA VFAYADDPCS ANYPLMKKLR GVLVERALSN  600
GKAEFNAETS VFAKVAQFEE ELRTALPKAV EAARSAVESG TAATPNRIKE CRSYPLYRFV  660
REELGTAYLT GEKTRSPGEE LNKVLVAINQ GKHIDPLLEC LKEWNGEPLP IC          712

SEQ ID NO: 56         moltype = AA  length = 716
FEATURE               Location/Qualifiers
source                1..716
                      mol_type = protein
                      organism = Oryza sativa
SEQUENCE: 56
MECETGYVAA AADGGLCMEV PRADPLNWGK AAEEMAGSHL DEVKRMVAEY RQPVVRIEGA  60
SLRIAQVAAV AGAGDGEAAM VELDESARER VKASSDWVMN SMANGTDSYG VTTGFGATSH  120
RRTKEGGALQ RELIRFLNAG AFGTGADGHV LPAGATRAAM LVRINTLLQG YSGIRFEILE  180
AVAKLLNANV TPCLPLRGTI TASGDLVPLS YIAGLVTGRE NSVAVAPDGR KVNAAEAFKI  240
AGIQGGFFEL QPKEGLAMVN GTAVGSGLAS TVLFEANVLA ILAEVLSAVF CEVMNGKPEY  300
TDHLTHKLKH HPGQIEAAAI MEHILEGSSY MKEAKRLGEL DPLMKPKQDR YALRTSPQWL  360
GPQIEVIRAA TKSIEREINS VNDNPLIDVS RGKALHGGNF QGTPIGVSMD NTRLAIAAIG  420
KLMFAQFSEL VNDFYNNGLP SNLSGGRNPS LDYGFKGAEI AMASYCSELQ FLGNPVTNHV  480
QSAEQHNQDV NSLGLISSRK TAEAIDILKL MSSTFLVALC QAIDLRHIEE NVKGAVKTCV  540
MTVAKKTLST NSTGGLHVAR FCEKDLLSEI DREAVFAYAD DPCSANYPLM KKLRSVLVER  600
ALANGAAEFD AETSVLAKVA RFEEELRAAL PRAVEAARAA VESGTAAAPN RIAECRSYPL  660
YRFVREELGT AYLTGEKTRS PGEELNKVLV AINQGKHIDP LLECLKEWNG APLPIC      716

SEQ ID NO: 57         moltype = AA  length = 717
FEATURE               Location/Qualifiers
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source                  1..717
                        mol_type = protein
                        organism = Panicum virgatum
SEQUENCE: 57
MECETGLVRS LHGDGLCAPA PAPRAADPLN WGKAAEDLSG SHLGEVQRMV AEFREPLVRI  60
QGASLSIAQV AAVAAGTGEA RVELDESARG RVKASSDWVM SSMMNGTDSY GVTTGFGATS  120
HRRTKEGGAL QRELIRFLNA GAFGTGADGH VLPAEATRAA MLVRINTLLQ GYSGIRFEIL  180
EAIAKLLNAN VTPCLPLRGT ITASGDLVPL SYIAGLITGR QNSVAVAPDG RKVDAAEAFK  240
IAGIEHGFFE LQPKEGLAMV NGTAVGSGLA STVLFEANVL AVMAEVISAV FCEVMTGKPE  300
FTDHLTHKLK HHPGQIEAAA IMEHILEGSS YMKLAKKLGE LDPLMKPKQD RYALRTSPQW  360
LGPQIEVIRF ATKSIEREIN SVNDNPLIDV SRGKALHGGN FQGTPIGVSM DNTRLALAAI  420
GKLMFAQFSE LVNDYYNNGL PSNLSGGRNP SLDYGFKGAE IAMASYCSEL QFLGNPVTNH  480
VQSAEQHNQD VNSLGLISSR KTAEAIDILK LMTSTFLIAL CQAIDLRHLE ENMKAAVKNC  540
VTQVAKKTLS MNAMGGLHIA RFCEKDLQTA IDREAVFAYA DDPCSPNYPL MQKLRAVLIE  600
HALANGDAER VAETSIFAKI TKFEEELRAV LPREVEAARV AVAEGAAPLP NRIKDSRSFP  660
LYRFVREELG CVFLTGEKLK SPGEECNKVF VGISEGKLVD PMLECLKEWD GKPLPIN     717

SEQ ID NO: 58           moltype = AA  length = 717
FEATURE                 Location/Qualifiers
source                  1..717
                        mol_type = protein
                        organism = Panicum virgatum
SEQUENCE: 58
MECETGLVRS LHGDGLCVPA PAAARADPLN WGKAAEDLSG SHLGEVQRMV AEFREPLVRI  60
QGASLSIAQV AAVAAGAGEA RVELDESARG RVKASSDWVM SSMMNGTDSY GVTTGFGATS  120
HRRTKEGGAL QRELIRFLNA GAFGTGADGH VLPAEATRAA MLVRINTLLQ GYSGIRFEIL  180
EAIAKLLNAN VTPCLPLRGT ITASGDLVPL SYIAGLITGR QNSVAVAPDG RKVDAAEAFK  240
IAGIEHGFFE LQPKEGLAMV NGTAVGSGLA STVLFEANVL AVMAEVISAV FCEVMTGKPE  300
FTDHLTHKLK HHPGQIEAAA IMEHILEGSS YMKLAKKLGE LDPLMKPKQD RYALRTSPQW  360
LGPQIEVIRF ATKSIEREIN SVNDNPLIDV SRGKALHGGN FQGTPIGVSM DNTRLALAAI  420
GKLMFAQFSE LVNDFYNNGL PSNLSGGRNP SLDYGFKGAE IAMASYCSEL QFLGNPVTNH  480
VQSAEQHNQD VNSLGLISSR KTAEAIDILK LMTSTFLIAL CQAIDLRHLE ENMKAAVKNC  540
VTQVAKKTLS MNAMGGLHIA RFCEKDLQTA IDREAVFAYA DDPCSPNYPL MQKLRAVLIE  600
HALANGDAER VVETSIFAKV AEFEQQVRAA LPKGVEAARA AVESGNPMVP NRIKECRSYP  660
LYRFVREELG TEYLTGEKTR SPGEELNKVL VAINQRKHID PLLECLKEWN GEPLPLC     717

SEQ ID NO: 59           moltype = AA  length = 718
FEATURE                 Location/Qualifiers
source                  1..718
                        mol_type = protein
                        organism = Panicum hallii
SEQUENCE: 59
MECETGIVRS LHGDGLCVPA PAAAARADPL NWGKAAEDLS GSHLGEVQRM VAEFREPLVR  60
IQGASLSIAQ VAAVAAGAGE ARVELDESAR ERVKASSDWV MNSMMNGTDS YGVTTGFGAT  120
SHRRTKEGGA LQRELIRFLN AGAFGTGADG HVLPAEATRA AMLVRINTLL QGYSGIRFEI  180
LEAIAKLLNA NVTPCLPLRG TITASGDLVP LSYIAGLITG RQNSVAVAPD GRKVDAAEAF  240
KIAGIEHGFF ELQPKEGLAM VNGTAVGSGL ASTVLFEANV LAIMAEVISA VFCEVMTGKP  300
EFTDHLTHKL KHHPGQIEAA AIMEHILEGS SYMKLAKKLG ELDPLMKPKQ DRYALRTSPQ  360
WLGPQIEVIR FATKSIEREI NSVNDNPLID VSRGKALHGG NFQGTPIGVS MDNTRLALAA  420
IGKLMFAQFS ELVNDFYNNG LPSNLSGGRN PSLDYGFKGA EIAMASYCSE LQFLGNPVTN  480
HVQSAEQHNQ DVNSLGLISS RKTAEAIDIL KLMTSTFLIA LCQAIDLRHL EENMKAAVKN  540
CVTQVAKKTL SMNAMGGLHI ARFCEKDLQT AIDREAVFAY ADDPCSANYP LMQKLRAVLI  600
EHALANGDAE RVVETSIFAK VAEFEQQVRA ALPKEVEAAR AAVESGNPMV PNRIKECRSY  660
PLYRFVREEL GTEYLTGEKT RSPGEELNKV LVAINQRKHI DPLLECLKEW NGEPLPLC    718

SEQ ID NO: 60           moltype = AA  length = 718
FEATURE                 Location/Qualifiers
source                  1..718
                        mol_type = protein
                        organism = Setaria italica
SEQUENCE: 60
MECETGLVRS LHGDGLCMSA QAAAPRADPL NWGKAAEDLS GSHLDEVKRM VAEFREPLVK  60
IQGASLSIAQ VAAVAAGAGE ARVELDESAR ERVKASSDWV MNSMMNGTDS YGVTTGFGAT  120
SHRRTKEGGA LQRELIRFLN AGAFGTGADG HVLPAEATRA AMLVRINTLL QGYSGIRFEI  180
LETIAKLLNA NVTPCLPLRG TITASGDLVP LSYIAGLITG RQNSVAVAPD GRKVDAAEAF  240
KIAGIEHGFF ELQPKEGLAM VNGTAVGSGL ASTVLFEANV LAIMAEVISA VFCEVMTGKP  300
EFTDHLTHKL KHHPGQIEAA AIMEHILEGS SYMKLAKKLG ELDPLMKPKQ DRYALRTSPQ  360
WLGPQIEVIR FATKSIEREI NSVNDNPLID VSRGKALHGG NFQGTPIGVS MDNTRLALAA  420
IGKLMFAQFS ELVNDFYNNG LPSNLSGGRN PSLDYGFKGA EIAMASYCSE LQFLGNPVTN  480
HVQSAEQHNQ DVNSLGLISS RKTAEAIEIL KLMTSTFLIA LCQAIDLRHL EENMKAAVKN  540
CVTQVAKKTL SMNAMGGLHI ARFCEKDLQT AIDREAVFAY ADDPCSPNYP LMQKLRAVLI  600
EHALANGDAE RVVETSIFAK VAEFEQQVRA ALPKEVEAAR AAVESGRPMV PNRIKECRSY  660
PLYRFVREEL GAEYLTGEKT RSPGEELNKV LVAINERKHI DPLLECLKEW NGEPLPLC    718

SEQ ID NO: 61           moltype = AA  length = 718
FEATURE                 Location/Qualifiers
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source                1..718
                      mol_type = protein
                      organism = Setaria viridis
SEQUENCE: 61
MECETGLVRS LHGDGLCMSA QAAAPRADPL NWGKAAEDLS GSHLDEVKRM VAEFREPLVK  60
IQGASLSIAQ VAAVAAGAGE ARVELDESAR ERVKASSDWV MNSMMNGTDS YGVTTGFGAT  120
SHRRTKEGGA LQRELIRFLN AGAFGTGADG HVLPAEATRA AMLVRINTLL QGYSGIRFEI  180
LETIAKLLNA NVTPCLPLRG TITASGDLVP LSYIAGLITG RQNSVAVAPD GRKVDAAEAF  240
KIAGIEHGFF ELQPKEGLAM VNGTAVGSGL ASTVLFEANV LAIMAEVISA VFCEVMTGKP  300
EFTDHLTHKL KHHPGQIEAA AIMEHILEGS SYMKLAKKLG ELDPLMKPKQ DRYALRTSPQ  360
WLGPQIEVIR FATKSIEREI NSVNDNPLID VSRGKALHGG NFQGTPIGVS MDNTRLALAA  420
IGKLMFAQFS ELVNDFYNNG LPSNLSGGRN PSLDYGFKGA EIAMASYCSE LQFLGNPVTN  480
HVQSAEQHNQ DVNSLGLISS RKTAEAIEIL KLMTSTFLIA LCQAIDLRHL EENMKAAVKN  540
CVTQVAKKTL SMNAMGGLHI ARFCEKDLQT AIDREAVFAY ADDPCSPNYP LMQKLRAVLI  600
EHALANGDAE RVVETSIFAK VAEFEQQVRA ALPKEVEAAR AAVESGRPMV PNRIKECRSY  660
PLYRFVREEL GAEYLTGEKT RSPGEELNKV LVAINERKHI DPLLECLKEW NGEPLPLC    718

SEQ ID NO: 62         moltype = AA  length = 728
FEATURE               Location/Qualifiers
source                1..728
                      mol_type = protein
                      organism = Zea mays
SEQUENCE: 62
MECEAGLLVR SSLNGEGLCM PAPRADPLNW GKAAEGLSGS HLDEVKRMVA EFREPLVKIQ  60
GASLSVAQVA AVAVGAGGGE ARVELDESAR ERVRASSDWV MGSMMNGTDS YGVTTGFGAT  120
SHRRTKEGGA LQRELIRFLN AGAFGTGADG HVLPAEATRA AMLVRVNTLL QGYSGIRFEI  180
LEAIAKLLNA NVTPCLPLRG TIXRATSSRS PTSPASSRAA RTPWRKVGAA EAFKIAGIEH  240
GFFELQPKEG LAMVNGTAVG SGLASTVLFE ANVLAVLAEV ISAVFCEVMT GKPEFTDHLT  300
HKLKHHPGQI EAAAVMEHIL EGSSYMKLAK RLGELDPLMK PKQDRYALRT SPQWLGPQIE  360
VIRFATKSIE REINSVNDNP LIDVSRGKAL HGGNFQGTPI GVSMDNTRLA LAAIGKLMFA  420
QFSELVNDYY NNGLPSNLSG GRNPSLDYGF KGAEIAMASY CSELQFLGNP VTNHVQSAEQ  480
HNQDVNSLGL ISSRKTAEAI DILKLMSSTF LIALCQAIDL RHLEENVKAA VKNCVTQVAK  540
KSLSLNARGG LHNARFCEKD LQTAIDREAV FAYADDPCSP NYALMQKLRA VLVEHALANG  600
DAERDVDTSI FAKVAEFEQQ VRAALPKEVE AARAAVENGS PLVPNRIKEC RSYPLYRFVR  660
EEVGTEYLTG EKTRSPGEEL NKVLVAINQR KHIDPLLECL KXAINQRKHI DPLLECLKEW  720
NGEPLPLC                                                          728

SEQ ID NO: 63         moltype = AA  length = 721
FEATURE               Location/Qualifiers
source                1..721
                      mol_type = protein
                      organism = Zea mays
SEQUENCE: 63
MECETGLVRS LNGEGLCMSS SSAAAAPRAD ALNWGKAAED LSGSHLDEVK RMVVEFREPL  60
VRIQGASLSI GQVAAVAAGA GGEARVELDE SARGRVKASS DWVMSSMMNG TDSYGVTTGF  120
GATSHRRTKE GGALQRELIR FLNAGAFGTG ADGHVLPAEA TRAAMLVRIN TLLQGYSGIR  180
FEILEAIAKL LNANVTPCLP LRGTITASGD LVPLSYIAGL ITGRQNSVAV GPDGRKVGAA  240
EAFRIAGIEH GFFELQPKEG LAMVNGTAVG SGLASTVLFE ANVLAVMAEV ISAVFCEVMT  300
GKPEFTDHLT HKLKHHPGQI EAAAIMEHVL EGSSYMKLAK KLGELDPLMK PKQDRYALRT  360
SPQWLGPQIE VIRFATKSIE REINSVNDNP LIDVSRGKAL HGGNFQGTPI GVSMDNTRLA  420
LAAIGKLMFA QFSELVNDYY NNGLPSNLSG GRNPSLDYGF KGAEIAMASY CSELQFLGNP  480
VTNHVQSAEQ HNQDVNSLGL ISSRKTAEAV DILKLMTSTF LIALCQAIDL RHLEENVKAA  540
VKNCVTQVAK KSLSLNARGG LHNARFCEKD LQTAIDREAV FAYADDPCSP NYPLMQKLRA  600
VLVEHALANG DAERAAETSI FAKVAEFEQQ VRAALPKEVE AARAAVESGN PLVPNRIREC  660
RSYPLYRFVR EEVGTEYLTG ERTRSPGEEL NKVLVAINQR KHIDPLLECL KEWNGAPLPL  720
C                                                                 721

SEQ ID NO: 64         moltype = AA  length = 718
FEATURE               Location/Qualifiers
source                1..718
                      mol_type = protein
                      organism = Sorghum bicolor
SEQUENCE: 64
MECETGLVRS LNGDGLCMSA QAAPRGADPL NWGKAAEDLS GSHLEEVKRM VAEFRDPVVK  60
IQGASLSIAQ VAAVAAGAGE ARVELDESAR ERVKASSDWV MSSMMNGTDS YGVTTGFGAT  120
SHRRTKEGGA LQRELIRFLN AGAFGTGADG HVLPAEATRA AMLVRINTLL QGYSGIRFEI  180
LEAIAKLLNA NVTPCLPLRG TITASGDLVP LSYIAGLITG RQNSVAVAPD GRKVDAAEAF  240
KIAGIEHGFF ELQPKEGLAM VNGTAVGSGL ASTVLFEANV LAIMAEVISA VFCEVMTGKP  300
EFTDHLTHKL KHHPGQIEAA AIMEHILEGS SYMKLAKKLG ELDPLMKPKQ DRYALRTSPQ  360
WLGPQIEVIR FATKSIEREI NSVNDNPLID VSRGKALHGG NFQGTPIGVS MDNTRLALAA  420
IGKLMFAQFS ELVNDYYNNG LPSNLSGGRN PSLDYGFKGA EIAMASYCSE LQFLGNPVTN  480
HVQSAEQHNQ DVNSLGLISS RKTAEAIDIL KLMTSTFLIA LCQAIDLRHI EENVKAAVKN  540
CVTQVAKKSL SLNARGGLHN ARFCEKDLQT AIDREAVFAY ADDPCSPNYP LMQKLRAVLI  600
EHALANGDAE RVVETSIFAK VAEFEQQVRA ALPKEVEAAR AAVESGNPLV PNRIKECRSY  660
PLYRFVREEV GTQYLTGEKT RSPGEELNKV LVAINQRKHV DPLLECLKEW NGEPLPLC    718
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SEQ ID NO: 65          moltype = AA  length = 718
FEATURE                Location/Qualifiers
source                 1..718
                       mol_type = protein
                       organism = Oryza sativa
SEQUENCE: 65
MECETGLVRS LNGDGLCMSS VSAPPRADPL NWGKAADELA GSHLDEVKRM VEDFRQPLVK  60
IEGASLTIAQ VAAVAAGAGD ARVELDESAR GRVKASSDWV MNSMMNGTDS YGVTTGFGAT  120
SHRRTKEGGA LQRELIRFLN AGAFGTGTDG HVLPAEATRA AMLVRINTLL QGYSGIRFEI  180
LEAITKLLNA NVTPCLPLRG TITASGDLVP LSYIAGLITG RQNSVAVAPD GRKVTAAEAF  240
KIAGIEHGFF ELQPKEGLAM VNGTAVGSGL ASTVLFEANV LAILAEVLSA VFCEVMTGKP  300
EYTDHLTHKL KHHPGQIEAA AIMEHILEGS SYMKLAKKLG ELDPLMKPKQ DRYALRTSPQ  360
WLGPQIEVIR FATKSIEREI NSVNDNPLID VSRGKALHGG NFQGTPIGVS MDNTRLALAA  420
IGKLMFAQFS ELVNDFYNNG LPSNLSGGRN PSLDYGFKGA EIAMASYCSE LQFLGNPVTN  480
HVQSAEQHNQ DVNSLGLISS RKTAEAIDIL KLMSSTFLIA LCQAIDLRHL EENMKTAVKN  540
CVMQVAKKSL SMNHMGGLHI ARFCEKDLLT AIDREAVFAY ADDPCSANYP LMQKLRAVLI  600
EHALANGDAE RVLETSIFAK VAEFEQHVRA ALPKEVEAAR AAVENGTPLV PNRIKECRSY  660
PLYRFVREEV GTEYLTGEKT RSPGEELNKV LVAINERKHI DPLLECLKEW NGAPLPLC    718

SEQ ID NO: 66          moltype = AA  length = 700
FEATURE                Location/Qualifiers
source                 1..700
                       mol_type = protein
                       organism = Oryza sativa
SEQUENCE: 66
MECETGVNGS GPRGSDPLYW GKAAEGVAGS HLEEVKRMVV EYRAPLVKID GAMLSVAKVA  60
AVAGEAARVQ VVLDESARPR LEASREWVFE STMNGTDTYG VTTGFGGAAH RRTKEFAALQ  120
KELIRYLNAG VFGASRSDGY TLPTEVTRAA MLVRINTLTQ GYSGIRFEIL EAIAKLLNAN  180
VTPCLPLRGT ITASGDLVPL SYIAGLITGR HNSAAVAPDG TKVDAAEAFR MAGIEHGFFA  240
LQPKEGLAIV NGTAVGSGLA AIVLFEANVL AVLAEVLSAV YCEVMAGNPE YTDHLIHALK  300
HHPGQIEAAA IMEHILEGSS YMKKLAKDKE QGQGELDRLT KLKQDRYAIR TAPQWLGPQV  360
EVIRFATKSI EREINSVNDN PVIDVARRKA LHGGNFQGTP VGVSMDNTRL AIAAIGRLMF  420
SQFSELVSSF YSNGLPSNLS GGRNPSLDYG FNGAEVAMAS YCSELQFLAN PVTNHVQTAE  480
QHNQSVNSLG LISSRMTAEA VTILKLMSST FLIALCQAVD LRQLEESIKA AVNKCVTNVA  540
KKSLTLAMDD DDHLLALLGA AIDRVAVFTY AEDPCRSSLP LMQKLRAVLM EHALANNGDI  600
LLAKVAEFEQ QLRAVLPDEV EAARAAVESG TAPNRISDCR SYPLYRFVRK ELGAEYLTGE  660
KTRSPGEEVD KVVIAMNQHK HIHPLLECLS EWKGAPLPLS                       700

SEQ ID NO: 67          moltype = AA  length = 680
FEATURE                Location/Qualifiers
source                 1..680
                       mol_type = protein
                       organism = Oryza sativa
SEQUENCE: 67
MECETGLVDR PLNGDPLYWG KAAEGLAGSH LDEVKRMVVE YRAPLVKIDG AMLSVAKVAA  60
VAGEAARVQV VLDESARPRL EASREWVFDS TMNGTDTYGV TTGFGGAAHR RTKEFAALQK  120
ELIRRSDGYT LPTEVTRAAM LVRINTLTQG YSGIRFEILE AIAKLLNANV TPCLPLRGTI  180
TASGDLVPLS YIAGLITGRQ NSAAVAPDGS KVDAAEAFRI AGIEHGFFAL QPKEGLAIVN  240
GTAVGSGLAA IVLFEANVLA VLAEVLSAVY CEVMAGNPEY TDHLIHALKH HPGQIEAAAI  300
MEHILEGSSY MRLAKEQGEL DRLTKLRQDR YAIRTAPQWL GPQVEVIRFA TKSIEREINS  360
VNDNPVIDVA RRKALHGGNF QGTPIGVSMD NTRLAIAAIG RLMFSQFSEL ASSFYSNGLP  420
SNLSGGRNPS LDYGFNGAEV AMASYCSELQ FLANPVTNHV QTAEQHNQSV NSLGLISSRM  480
TAEAVTILKL MSSTFLIALC QAVDLRQLEE SIKAAVNKCV TNVAKKSLAM DDDDLLALLG  540
AAIDRVAVFT YAEDPCRSSL PLIQKLRAVL MDHALANGDN QLAKVAEFEQ QLRAVLHDEV  600
EAARAAVESG TAPNRITQCR SYPLYRFVRK ELGAEYLTGE KTRSPGEEVD KVVIAMNQHK  660
HINPLLECLS EWKGAPLPLN                                             680

SEQ ID NO: 68          moltype = AA  length = 709
FEATURE                Location/Qualifiers
source                 1..709
                       mol_type = protein
                       organism = Sorghum bicolor
SEQUENCE: 68
MECETGLVDR PRRNGSAGPH VVDDDPLKWG KAAEDLTGSH LDDVRRMVEE YRMPLVKIDG  60
AMLSVAKVAA VAGEATRRVQ VVLDESARPR LEASREWVFD STMNGTDTYG VTTGFGGASH  120
RRTKEFRALQ TELIRYLNAG VFGASSSDGY TLPAEVTRAA MLVRINTLTQ GYSGIRFEIL  180
EAIAKLLNAN VTPCLPLRGS ITASGDLVPL SYIAGLITGR GNSAAVAPDG TKVGAAEAFR  240
IAGIDHGFFA LEPKEGLAIV NGTAVGSGLA AIVLFEANVL AVLAEVLSAV YCEVMAGNPE  300
YTDHLIHALK HHPGQIEAAA IMEHVLEGSS YMKLAREQAE LDPLTKPKQD RYAIRTTPQW  360
LGPQVEVIRF ATKSIEREIN SVNDNPVIDV ARGKALHGGN FQGTPVGVSM DNTRLAVAAI  420
GKLMFAQFTE LVSSFYSNGL PSNLSGGRDP SLDYGFNGAE VAMASYCSEL QFLANPVTNH  480
VQTAEQHNQS VNSLGLISSR MTAEAVTILK LMSSTFLIAL CQAIDLRQLE ESIKAAVKKC  540
VARVAKKCLA MDDDAAAAAA QLLGAVDRVA VFTYAEDPCR PSLPLMQKLR VVLMEHALGA  600
AEGAVETTSI LAKVAEFEQQ LRAVLPDEVE AARAAVESGT APKRIAECRS YPLYRFVREE  660
LGAEYLTGEK TRSPGEEVDK VVIAMNQRKH IDPLLECLSD WKGAPLHAT              709
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SEQ ID NO: 69          moltype = AA  length = 698
FEATURE                Location/Qualifiers
source                 1..698
                       mol_type = protein
                       organism = Zea mays
SEQUENCE: 69
MECETGLVDR PLNSSAPRTG DPLKWGKAAE GLTGSHLDEV KRMVEEYRVP LVKIDGAVLS  60
VAKVAAVAGR VQVALDESAR PRLEASREWV FESTMNGTDT YGVTTGFGGA CHRRTKEFAA  120
LQKELIRYLN AGVFGASSSD GYTLPPEVTR AAMLVRINTL TQGYSGIRFE ILEAIAKLLN  180
ANVTPCLPLR GSITASGDLV PLSYIAGLIT GRKNSVAVAP DGTKVDAVEA FRIAGIEHGF  240
FALQPKEGLA IVNGTAVGSG LAAIVLFEAN ILAVLAEVLS ALYCEVMAGN PEYTDHLIHA  300
LKHHPGQIEA AAIMEHILEG SSYMKLAKEQ GELDPLTKMK QDRYAIRTTP QWLGPQVEVI  360
RFATKSIERE INSVNDNPII DVARRKALHG GNFQGTPVGV SMDNTRLAVA AIGKLMFAQF  420
SELVSSFYSN GLPSNLSGGR NPSLDYGFNG AEVAMASYCS ELQFLANPVT NHVQTAEQHN  480
QSVNSLGLIS SRMTAEAVTI LKLMSSTFLI ALCQAVDLRQ LEESIKAAVK KCVSHVAKKS  540
LAIDDHDLLV AIDRVAVFTY AEDPCRPSYP LMQKLRAVLM EHALINGDSN TERPMETSIL  600
AKVAEFEKQL SAVLPDEVEA ARAAVESGTT PNRITECRSY PLYRFVREEL GAEYLTGEKT  660
RSPGEEVDKV VIAMNQRKHI DPLLQCLSEW KGAPLPII                         698

SEQ ID NO: 70          moltype = AA  length = 717
FEATURE                Location/Qualifiers
source                 1..717
                       mol_type = protein
                       organism = Brachypodium distachyon
SEQUENCE: 70
MECENGLVGS LNGEGLCMSA PPRAAADPLN WAKTAEELAG SHLEEVKKMV AQFRMPLVKI  60
EGATLGIAQV AAVAAGAGEA RVELDESARG RVKESSDWVM NSMMNGTDSY GVTTGFGATS  120
HRRTKEGGAL QRELIRFLNA GAFGTGTDGH VLPAEATRAA MLVRINTLLQ GYSGIRFEIL  180
EAITKLLNAN VTPCLPLRGT ITASGDLVPL SYIAGLITGR QNSVAVAPDG SKVSAAEAFK  240
IAGIEHGFFE LQPKEGLAMV NGTAVGSGLA STVLFEANIQ AILAEVLSAV FCEVMTGKPE  300
FTDHLTHKLK HHPGQIEAAA IMEHILEGSS YMKEAKKQGE LDPLMKPKQD RYALRTSPQW  360
LGPQIEVIRF ATKSIEREIN SVNDNPLIDV SRGKAIHGGN FQGTPIGVSM DNTRLAIAAI  420
GKLMFAQFSE LVNDFYNNGL PSNLSGGRNP SLDYGFKGAE IAMASYCSEL QFLGNPVTNH  480
VQSAEQHNQD VNSLGLISSR KTAEAIDILK IMSSTFLIAL CQAIDLRHLE ENMKTAVRNC  540
VMQVAKKTLS MNAMGGLHIA RFCEKDLLTA IDREAVFAYA DDPCSPNYPL MQKLRAVLIE  600
HALANGDGER ALETSIFAKV AEFEQNLRAA LPKEVEAARA SVENGTPLAP NRIKDCRSYP  660
LYRFVREELG TEYLTGEKTR SPGEELNKVL VAMNQRKHID PLLECLKEWN GEPLPLC    717

SEQ ID NO: 71          moltype = AA  length = 716
FEATURE                Location/Qualifiers
source                 1..716
                       mol_type = protein
                       organism = Streptochaeta angustifolia
SEQUENCE: 71
MECENSQVAA NGNCLCLAKP QADPLNWGKA AEELTGSHLD EVKRMVAEYR EPVVRIEGAG  60
LRIAQVAAVA AAADGGEAAK VELDESARGR VKASSDWVMN SMTKGTDSYG VTTGFGATSH  120
RRTKEGGALQ RELIRFLNAG AFGTGTDGHV LPAAATRAAM LVRINTLLQG YSGIRFEILE  180
AIAALLNVNV TPCLPLRGTI TASGDLVPLS YIAGLVTGRQ NSVAVTTDGR KVNAAEAFKI  240
AGIQHGFFEL QPKEGLAMVN GTAVGSGLAS TVLFEANILA ILSEVLSAVF CEVMNGKPEY  300
TDHLTHKLKH HPGQIEAAAI MEHILEGSSY MKLAKKLGEL DPLMKPKQDR YALRTSPQWL  360
GPQIEVIRAA TKSIEREINS VNDNPLIDVS RGKALHGGNF QGTPIGVSMD NTRLAIAAIG  420
KLMFAQFSEL VNDFYNNGLP SNLSGGRNPS LDYGFKGAEI AMASYCSELQ FLGNPVTNHV  480
QSAEQHNQDV NSLGLISSRK TAEAIDILKL MSSTFLIALC QAIDLRHIEE TVKSAVKNCV  540
MQVAKKVLSM NAAGDLHIAR FCEKDLLTAI DREAVFAYAD DPCSGTYPLM KNLRAVLVEH  600
ALANGEAERN AETSVFAKVA KFEEELRAAL PKAVEAARAS VENGTGPTPN RIKACRSYPL  660
YRFVREELGT EYLSGEKTRS PGEELDKVLV AINQGKHIDP LLECLKEWNG KPLPIC     716

SEQ ID NO: 72          moltype = AA  length = 716
FEATURE                Location/Qualifiers
source                 1..716
                       mol_type = protein
                       organism = Streptochaeta angustifolia
SEQUENCE: 72
MECENVHVAA NGNGLCLAKP HADPLNWGAA ASELTGSHLD EVKRMVAHFR EPVVNIEGAG  60
LRIGQVAAVA AAADGVAAAM VELDESARGR VKASSDWVMN SMTEGTDSYG VTTGFGATSH  120
RRTKEGGALQ RELIRFLNAG AFGTGADGYV LPAPATRAAM LVRINTLLQG YSGIRFEILE  180
AIAKLLNANV TPCLPLRGTI TASGDLVPLS YIAGLVTGRQ NSVAVTLDGR KVNAAEAFKI  240
AGIQHGFFEL QPKEGLAMVN GTAVGSGLAS TVLFEANILA ILAEVLSAVF CEAMNGKPEY  300
TDHLTHKLKH HPGQIEAAAI MEHILEGSSY MKLAKKLGEL DPLMKPKQDR YALRTSPQWL  360
GPQIEVIRAA TKSIEREINS VNDNPLIDVS RGKALHGGNF QGTPIGVSMD NTRLAIAAIG  420
KLMFAQFSEL VNDFYNNGLP SNLSGGRNPS LDYGFKGAEI AMASYCSELQ FLGNPVTNHV  480
QSAEQHNQDV NSLGLISSRK TAEAIDILKL MSSTFLIALC QAIDLRHIEE NVKSAVKNCV  540
MQVSKRVLSL NATGNLHIAR FCEKDLLTAI DREAVFAYAD DPCNASYPLM KNLRAVLVEH  600
ALANGEAERN VDTSVFTKVA EFEQQLRAAL PKEVEAARAA VENGAATVPN RIKECRSYPL  660
YRFAREELGT DYLTGEKARS PGEEVDKVLV AINQGKHIDP LLECLKEWNG EPLPIC     716
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SEQ ID NO: 73           moltype = AA  length = 714
FEATURE                 Location/Qualifiers
source                  1..714
                        mol_type = protein
                        organism = Panicum virgatum
SEQUENCE: 73
MECENGRVAA ATGNGVCLPV PPRADPLNWG KAAENLAGSH LEAVKRMVEE YRRPLVRIEG  60
ASLTVAQVAA VAAAGEARVE LDESARGRVK ASSDWVMSSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGAF GTGDDGHVLP ASATRAAMLV RINTLLQGYS GIRFEILEAI  180
AALLNANVTP CLPLRGTITA SGDLVPLSYI AGLVTGRPNS VAVTPDGRKV DAAEAFKAAG  240
IQHGFFELQP KEGLAMVNGT AVGSGLASPV LFEANVLAVL AEVLSAVFCE VMNGKPEYTD  300
HLTHKLKHHP GQIEAAAIME HILEGSSYMA LAKKLGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVSRG KALHGGNFQG TPIGVSMDNT RLAVAAIGKL  420
MFAQFSELVN DFYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL ANPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAVDILKLMS STFLVALCQA IDLRHLEENL KSAVKSCVMT  540
VAKKTLSTGA TGALHSARFC EKDLLTAIDR EAVFAYADDP CSANYPLMQK MRSVLVEHAL  600
ANGEAEHDPD TSVFAKLATF EEELRAALPR EVDAARAAVE NGTAAIPNRI AECRSYPLYR  660
FVRQELGTEY LTGEKTRSPG EEVNKVFVAM NAGKHIDAVL ECLKGWNGEP LPIC        714

SEQ ID NO: 74           moltype = AA  length = 713
FEATURE                 Location/Qualifiers
source                  1..713
                        mol_type = protein
                        organism = Panicum hallii
SEQUENCE: 74
MECENGHVAA SGNGVCLPVP PRADPLNWGK AAEDLAGSHL EAVKRMVEEY RRPLVKIEGA  60
SLTVAQVAAV AAAGEARVEL DESARGRVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGDDGHVLPA SATRAAMLVR INTLLQGYSG IRFEILETIA  180
ALLNANVTPC LPLRGTITAS GDLVPLSYIA GLVTGRPNSV AVTPDGRKVD AAEAFKVAGI  240
QHGFFELQPK EGLAMVNGTA VGSGLASMVL FEANVLAVLA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEY ILDGSSYMML AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVSRGK ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQFSELVND FYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLA NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AIDILKLMSS TFLIALCQAI DLRHLEENLK SAVKGCVMTV  540
AKKTLSTSAT GALHSARFCE KDLLTAIDRE AVFAYADDPC SANYPLMQKM RSVLVEHALA  600
NGEAERDPDT SVFAKVTAFE EELRAALPRE VDAARAAVES GTAAIPNRIA ECRSYPLYRF  660
VREELGTEYL TGEKTRSPGE EVNKVFVAMN AGKHIDAVLE CLKGWNGEPL PIC         713

SEQ ID NO: 75           moltype = AA  length = 80
FEATURE                 Location/Qualifiers
source                  1..80
                        mol_type = protein
                        organism = Panicum virgatum
SEQUENCE: 75
MTVFAKVATF EEELRAALSR EVDAARGAVI PNRIAECRSY LKTRSFDEEV NKVFVAVNAG  60
KHIDAMLECL KEWNGEPMPM                                              80

SEQ ID NO: 76           moltype = AA  length = 713
FEATURE                 Location/Qualifiers
source                  1..713
                        mol_type = protein
                        organism = Panicum virgatum
SEQUENCE: 76
MECENGHVAA NGNGVCLPVP PRADPLNWGK AAEDLAGSHL EAVRRMVEEY RRPLVKIEGA  60
SLTVAQVAAV AAAAEARVEL DESARGRVKA SSDWVMNSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL VRFLNAGAFG TGDDGHVLPA SATRAAMLVR INTLLQGYSG IRFEILETIA  180
ALLNANVTPC LPLRGTITAS GDLVPLSYIA GLVTGRPNSV AVTPDGRKVD AAEAFKVAGI  240
QHGFFELQPK EGLAMVNGTA VGSGLASIVL FEANVLAVLA EVLSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH ILDGSSYMML AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVSRGK ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQFSELVND FYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQFLA NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AVDILKLMSS TFLIALCQAI DLRHLEENLK SAVKSCVMTV  540
AKKTLSTSAT GALHSARFCE KDLLTAIDRE AVFAYADDPC STNYPLMQKM RSVLVEHALA  600
NGEAERDPDT SVFGKVATFE EELRAALPPE VEASRAGVEK GAAAIPNRIA ECRSYPLYRF  660
VRQELGTEYL TGEKTRSPGE EVNKVFVAMN AGKHIDAVLE CLKEWNGEPL PIC         713

SEQ ID NO: 77           moltype = AA  length = 715
FEATURE                 Location/Qualifiers
source                  1..715
                        mol_type = protein
                        organism = Setaria viridis
SEQUENCE: 77
MECENGHVVA ANGNGVCLPV PPRADPLNWG KAAEDLSGSH LEAVKRMVEE YRRPLVRIEG  60
SSLTVAQVAA VANGAGEARV ELDESARGRV KASSDWVMNS MMNGTDSYGV TTGFGATSHR  120
RTKEGGALQR ELIRFLNAGA FGTGDDGHVL PASATRAAML VRINTLLQGY SGIRFEILET  180
IASLLNANVT PCLPLRGTIT ASGDLVPLSY IAGLVTGRPN SVAVTADGKK VGAAEAFKAA  240
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GIQHGFFELQ PKEGLAMVNG TAVGSGLASM VLFEANVLAV LAEVLSAVFC EVMNGKPEYT  300
DHLTHKLKHH PGQIEAAAIM EHILEGSSYM KLAKKLGELD PLMKPKQDRY ALRTSPQWLG  360
PQIEVIRAAT KSIEREINSV NDNPLIDVSR GKALHGGNFQ GTPIGVSMDN TRLAIAAIGK  420
LMFAQFSELV NDFYNNGLPS NLSGGRNPSL DYGFKGAEIA MASYCSELQF LGNPVTNHVQ  480
SAEQHNQDVN SLGLISSRKT AEAVDILKLM SSTFLIALCQ AIDLRHLEEN LKGAVKSCVM  540
TVAKKTLSTG ATGALHNARF CEKDLLTAID REAVFAYADD SCSANYPLMQ KMRSVLVEHA  600
LANGEAERDP ETSVFAKVAT FEEEIRAALP REVEAARAAV ENGTAAIPNR IAECRSYPLY  660
RFVREELGTQ YLTGEKTRSP GEEVDKVFVA MNLGKHIDAV LECLKEWNGE PLSIC        715

SEQ ID NO: 78          moltype = AA  length = 715
FEATURE                Location/Qualifiers
source                 1..715
                       mol_type = protein
                       organism = Setaria italica
SEQUENCE: 78
MECENGHVVA ANGNGVCLPV PPRADPLNWG KAAEDLSGSH LEAVKRMVEE YRRPLVRIEG  60
SSLTVAQVAA VANGAGEARV ELDESARGRV KASSDWVMNS MMNGTDSYGV TTGFGATSHR  120
RTKEGGALQR ELIRFLNAGA FGTGDDGHVL PASATRAAML VRINTLLQGY SGIRFEILET  180
IASLLNANVT PCLPLRGTIT ASGDLVPLSY IAGLVTGRPN SVAVTADGKK VGAAEAFKAA  240
GIQHGFFELQ PKEGLAMVNG TAVGSGLASM VLFEANVLAV LAEVLSAVFC EVMNGKPEYT  300
DHLTHKLKHH PGQIEAAAIM EHILEGSSYM KLAKKLGELD PLMKPKQDRY ALRTSPQWLG  360
PQIEVIRAAT KSIEREINSV NDNPLIDVSR GKALHGGNFQ GTPIGVSMDN TRLAIAAIGK  420
LMFAQFSELV NDFYNNGLPS NLSGGRNPSL DYGFKGAEIA MASYCSELQF LGNPVTNHVQ  480
SAEQHNQDVN SLGLISSRKT AEAVDILKLM SSTFLIALCQ AIDLRHLEEN LKGAVKSCVM  540
TVAKKTLSTG ATGALHNARF CEKDLLTAID REAVFAYADD SCSANYPLMQ KMRSVLVEHA  600
LANGEAERDP ETSVFAKVAT FEEEIRAALP REVEAARAAV ENGTAAIPNR IAECRSYPLY  660
RFVREELGTQ YLTGEKTRSP GEEVDKVFVA MNLGKHIDAV LECLKEWNGE PLSIC        715

SEQ ID NO: 79          moltype = AA  length = 824
FEATURE                Location/Qualifiers
source                 1..824
                       mol_type = protein
                       organism = Zea mays
SEQUENCE: 79
MECENGHVAA SGNGGVCLAA PRADPLNWVK AAEDLAGSHL DAVKRMVEEY RRPLVKIEGA  60
SLTVAQVAAV AAAGEARVEL DESARGRVKA SSDWVMDSMM NGTDSYGVTT GFGATSHRRT  120
KEGGALQREL IRFLNAGAFG TGDDGHVLPA SATRAAMLVR INTLLQGYSG IRFEILEAIA  180
ALLNANVTPC LPLRGTITAS GDLVPLSYIA GLVTGRPNST AVAPDGRKVG AAEAFEIAGI  240
QHGFFELQPK EGLAMVNGTA VGSGLASMVL FEANVLAVLA EVMSAVFCEV MNGKPEYTDH  300
LTHKLKHHPG QIESAAIMEH ILEGSSYMAL AKKLGELDPL MKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDALHGG NFQGTPIGVS MDNTRLAVAA IGKLMFAQFS  420
ELVNDFYNNG LPSNLSGGRN PSLDYGFKGA EIAMASYCSE LQFLANPVTN HVQSAEQHNQ  480
DVNSLGLISS RKTAEAVDVL KLMSSTFLVA LCQAIDLRHL EENLRSAVKR CVTVVARKTL  540
STGATGALHD ARFCEKDLLT AIEREAVFAY ADDPCSATYP LMQKMRSVLV EHALANGEAE  600
RDPDTSVFAK VATFEEELRA ALPREVDAAR AAVESGTAAI RNRIAECRSY PLYRFVREEL  660
GTEYLTGEKA RSPGEEVDKV FVAMNLGKHI DAVLECLKEW NEIRLHDKLW RRPYPPAHAP  720
QTVVGPLQAL LVFLPRRCTD ESSPGTVCIP PQAPGGRVIP RRCSSSSLGA RRPYPPAPAP  780
QTATGPLQAL LVFLPGATRL TPPQALDDGG LQTYNCKQHG SVQH                   824

SEQ ID NO: 80          moltype = AA  length = 714
FEATURE                Location/Qualifiers
source                 1..714
                       mol_type = protein
                       organism = Sorghum bicolor
SEQUENCE: 80
MECENGHAAG ASGNGVCLAT PRAADPLNWG KAAEDLTGSH LEAVKRMVEE YRRPLVKIEG  60
ASLTVAQVAA VAAAGEARVE LDESARGRVK ASSDWVMNSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGAF GTGDDGHVLP AAATRAAMLV RINTLLQGYS GIRFEILETI  180
AALLNANVTP CLPLRGTITA SGDLVPLSYI AGLVTGRPNS TAVAPDGRKV GAAEAFKIAG  240
IQHGFFELQP KEGLAMVNGT AVGSGLASMV LFEANVLAVL AEVMSAVFCE VMNGKPEYTD  300
HLTHKLKHHP GQIESAAIME HILDGSSYMM LAKKMGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVSRG KALHGGNFQG TPIGVSMDNT RLAVAAIGKL  420
MFAQFSELVN DFYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL ANPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAVDVLKLMS STFLIALCQA VDLRHLEENL KSAVKSCVTT  540
VAKKTLSTSA TGGLHNARFC EKDLLTAIDR EAVFAYADDP CSANYPLMQK MRSVLVEHAL  600
ANGEAERDPE TSVFAKVATF EEELRAALPR EVDAARAAVE NGTAAVPNRI AECRSYPLYR  660
FVREELGTEY LTGEKTRSPG EEVNKVFVAM NLGKHIDAVL ECLKEWNGEP LPIC         714

SEQ ID NO: 81          moltype = AA  length = 418
FEATURE                Location/Qualifiers
source                 1..418
                       mol_type = protein
                       organism = Panicum virgatum
SEQUENCE: 81
MNVTTGFGAT SGFGATSHRR TKEGSALQRE LIRFLNAGAF GTGDDGHVLP AAATHAAMLV  60
RINTLLQGYS GIRFQILEAI AALLNANVTP CFPLRGTITA SGDLVPLSYI AGLVTGRPNS  120
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VAVAPDGRKV GAAEAFGIAG IQHGFFELQP KEGLAMVNGT AVGSGLASIM LFEANVLAVL  180
AEVLSAVFCE AMNGKSEYTD RLTHKLKHHP GQIEAAAIME HILEGSSYMM LAKKLGELDP  240
LMKPNQDRYA LRTSPQWLGP QIEVIRAATK SIEREINSVN DNPLIDVSRG KALHGGNFQG  300
TPIGVSMDNT RLAIAAIGKL MFAQFSELVN DFYNNGLPSN LSGGRNPSLD YGFKGAEIAM  360
ASYCSDLQFL ANPVTNHVQS AEQHNQDVNS LGLISSRKTA EAVEILKLMS STFLIALC    418

SEQ ID NO: 82          moltype = AA  length = 714
FEATURE                Location/Qualifiers
source                 1..714
                       mol_type = protein
                       organism = Oryza sativa
SEQUENCE: 82
MECENGHVAA AANGSSLCVA KPRADPLNWG KAAEELSGSH LDAVKRMVEE YRRPVVTIEG  60
ASLTIAQVAA VASAGAARVE LDESARGRVK ASSDWVMNSM MNGTDSYGVT TGFGATSHRR  120
TKEGGALQRE LIRFLNAGAF GNGDDGHVLP AAATRAAMLV RINTLLQGYS GIRFEILETI  180
ATLLNANVTP CLPLRGTITA SGDLVPLSYI AGLVTGRPNS VAVTPDGRKV DAAEAFKIAG  240
IQHGFFELQP KEGLAMVNGT AVGSGLASMV LFEANVLGVL AEVLSAVFCE VMNGKPEYTD  300
HLTHKLKHHP GQIEAAAIME HILEGSSYMM LAKKLGELDP LMKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVSRG KALHGGNFQG TPIGVSMDNT RLAIAAIGKL  420
MFAQFSELVN DFYNNGLPSN LSGGRNPSLD YGFKGAEIAM ASYCSELQFL ANPVTNHVQS  480
AEQHNQDVNS LGLISSRKTA EAIDVLKLMS STFLIALCQA IDLRHLEENV RSAVKGCVTT  540
VARKTLSTSA TGDLHKARFC EKDLLQAIDR EAVFAYADDP CSANYPLMQK MRAVLIEHAL  600
ANGEAERNVD TSVFAKVATF EEELRVALPR EVEAARAAVE NGTAAKANRI TECRSYPLYR  660
FVREELGTEY LTGEKTRSPG EEVNKVFVAM NQGKHIDALL ECLKEWNGEP LPIC        714

SEQ ID NO: 83          moltype = AA  length = 189
FEATURE                Location/Qualifiers
source                 1..189
                       mol_type = protein
                       organism = Oryza sativa
SEQUENCE: 83
MQKMRTVLIE HALANSEAER NVNTSVFAKV AMFEEKLRAA LPREVEATRA AVENGTAAKA  60
NRITECKSYS LYRFVCKELR TEYLTGKKID AVARSQCSRR SSARRCPGKW RLPRAAVENG  120
TATKANRITE CRSYSLYRFV RKELGIEYLT GEKIDAVTWR GCEQGVRRHE PGSGGRSEKP  180
VFSGASMGR                                                          189

SEQ ID NO: 84          moltype = AA  length = 715
FEATURE                Location/Qualifiers
source                 1..715
                       mol_type = protein
                       organism = Brachypodium distachyon
SEQUENCE: 84
MEYENGHAAT YGDGLCVAAP LAPRADPLNW GKAAEELSGS HLDAVKRMVE EYRRPVVKME  60
GASLTIAQVA AVAAGAEARV ELDESARGRV KESSDWVMNS MMNGTDSYGV TTGFGATSHR  120
RTKEGGALQR ELIRFLNAGA FGTGEDGHVL PAAATRAAML VRVNTLLQGY SGIRFEILET  180
IATLLNANVT PCLPLRGTIT ASGDLVPLSY IAGLVTGRPN SVATAPDGRK VNAAEAFKIA  240
GIQHGFFELQ PKEGLAMVNG TAVGSGLASM VLFEANILGV LAEVLSAVFC EVMNGKPEFT  300
DHLTHKLKHH PGQIEAAAIM EHILEGSSYM MLAKKLGELD PLMKPKQDRY ALRTSPQWLG  360
PQIEVIRAAT KSIEREINSV NDNPLIDVSR GKAIHGGNFQ GTPIGVSMDN TRLAIAAIGK  420
LMFAQFSELV NDFYNNGLPS NLSGGRNPSL DYGFKGAEIA MASYCSELQF LGNPVTNHVQ  480
SAEQHNQDVN SLGLISSRKT AEAIDILKLM SSTFLVALCQ AIDLRHLEEN VRSAVKNCVT  540
TVARKTLSTN VNGHLHNARF CEKDLLLTID REAVFAYADD PCSANYPLMQ KMRAVLVEHA  600
LANGEAERDV ETSVFAKLAA FEQELRAVLP KEVEAARAAV ENGTATKQNR IAECRSYPLY  660
RFVREELGTE YLTGEKTRSP GEEVDKVFVA MNQGKHIDAL LECLKEWNGE PLPLC       715

SEQ ID NO: 85          moltype = AA  length = 715
FEATURE                Location/Qualifiers
source                 1..715
                       mol_type = protein
                       organism = Streptochaeta angustifolia
SEQUENCE: 85
MEFLSCVAAN GNGLCLATPQ ADPLNWGKAA AELTGSHLDE VKRMVAEYRK PVVRIEGANL  60
SIAQVVAVAL AGGAAAAAKV ELDESARGRV KASSDWVMNS MMNDTDSYGV TTGFGATSHR  120
RTKQGGALQR ELIRFLNAGA FGTGEDGHVL PTAATRAAML VRINTLLQGY SGIRFEILEA  180
VAALLNANVT PCVPLRGTIT ASGDLVPLSY IAGLVTGRPN SVAVAPDGRK VDAAEAFKIA  240
GIQHGFFELQ PKEGLAMVNG TAVGSGLAST VLFEANILAV LAEVLSAVFC EVMNGKPEYT  300
DHLTHKLKHH PGQIEAAAIM EHILEGSSYM MLAKKLGELD PLMKPKQDRY ALRTSPQWLG  360
SQIEVIRAAT KSIEREINSV NDNPLIDVSR GKALHGGNFQ GTPIGVSMDN ARLAIAAIGK  420
LMFAQFSELV NDIYNNGLPS NLSGGRNPSL DYGFKGAEIA MASYCSELQF LANPVTNHVQ  480
SAEQHNQDVN SLGLISSRKT AEAIDILKLM SSTYLIALCQ AVDLRHLEEN IKSAVKKCVT  540
AAAKKALNTS TTGDLHIARF CEKDLLTAID REAVFAYADD PCSNNYPLMQ KLREVLVEHA  600
LANGEAERNV ETSVFAKIAM FEEELRAVLP REVEAARAAV ENGAAAKPNR ITECRSYPLY  660
RFVREELGAK YLTGEKTRSP GEEVDKVFVA INQGKHIDPL LECLKEWNGE PLPIC       715

SEQ ID NO: 86          moltype = AA  length = 245
FEATURE                Location/Qualifiers
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source                 1..245
                       mol_type = protein
                       organism = Streptochaeta angustifolia
SEQUENCE: 86
MASYCSKLQF LANPVTDHVK STEQHTQDVN SLGLISSRKT AEAIDIPKLM SSTFLIALCQ  60
AVDLRHVEEN IKSAIKNCVT MVAKKALNIS TTGDLHITRF CKDLLTVIER EAVFTYAGDP  120
CSENYRLMQK LCAMHVEHIL ANGEAKHNGE TTFLAKITMF EEVLPGEVKA IREAMENRAT  180
VMPNRTIECW LYPLYQFMRE KLGVEDLTGE MTWSPDGEVD KVFVAINQGK HIDPLLECLK  240
EWNIE                                                              245

SEQ ID NO: 87          moltype = AA  length = 436
FEATURE                Location/Qualifiers
source                 1..436
                       mol_type = protein
                       organism = Streptochaeta angustifolia
SEQUENCE: 87
LNWGKAAEEL TGSHLDEVKH LVAQYRKPMV RIKGTSLSIA QVKAVASAGG DAAAAKLELD  60
ESTRGRVKAS SDWAMSSMTN DTDTYGVTTA FGANSHRTTK ESGALQRALI RYLHAGVFGT  120
GTGDNVLPAA ATRGAMLVRI NSLLQGYSGI RFEIVEAIVA LLNANVTPCL PLRGTITAKV  180
GAAEACTIAG IQHGFFELQP KEGIALVNGT AVGCGLASAV LFEANILAVL AVVLCAVFCE  240
VMIGKPEYTD HLTHKLKHHL GQIEAVANME HILEGSSYKM LAKKLDELDP LMKPKKDRYA  300
LRTSPQWLGS HVEVIRATTK SIEREINSVN DNPLIDVSRS KALHGGNFQG TPIGVSTDMS  360
LTFAAIGKLM FSQLSELVND CTTMACLPTC PADPKLAAPL ALLMPCRRSG TTARGSACVL  420
PTMPPSAPTC RAPRGY                                                  436

SEQ ID NO: 88          moltype = AA  length = 906
FEATURE                Location/Qualifiers
source                 1..906
                       mol_type = protein
                       organism = Streptochaeta angustifolia
SEQUENCE: 88
MPCFDQRRRT ARQDHLQRRP PTVKWGAAKW NSREVTENEV QRQKIEHLVC VTVHAVGDRA  60
ELEDGRCDGV MGTLAKAGRG RGGGGVVGRG GAGGRGRGGA GVVGRGGAAG RGRGGAGRCG  120
RIGVVRGENM LGEGGAAGRL GGGELVREKK NLQHGGDVAW GEKVLGRASG NEWQVWGRPS  180
MTWVVHRSFG SWRGERESGR VEAYCNGLRL ARPYADPLNW GTAAVELTGS HLEEVKRMVA  240
ESRLPVVTIE GAGLRIAHVA AVATACGGGA AAARVELDES ARGHVKASSD WVMNSMVNGV  300
DTYGITTGFG GTSYRRTKEG GSLQRELIRF LNAGVFGTGA DGHVLPAATT RAAMLVRINT  360
LLQGYSGIRF EILEAIAALL NANVTPRLPL RGTLTASGDV IPLSYIAGLI TGRQNSVAAA  420
PDGRNMDAAE AFKIAGIQHG FFELQPKEGL ALVNGTAVGS GLASMVLFEA NVLALLAEVL  480
AAVFCEVMHG KPEYTDHLTH KLKHHPGQIE AAAIMEHILE GSSYMKLAKE LAELDPLTKP  540
KQDRYALRSS PQWLGPQVEV IRAATKSIER EINSVSDNPL IDVSRDKALH CGNFQGTPIG  600
VSMDNTRLAV AAISRLMFAQ FSELVNDFYN NGLPANLSGG RDPSLDFGFK GADIAIASYC  660
SELQFLANPV TSHVQSAERH NQDINSLGFI SARMTAEAID LLKLMSSTFL VALCQAVDLR  720
HLEENIKSTV KNCVTTAATK TLGTTHTVRF SEDLLTAIDR EAVFAYADDP CSPKYPLMKN  780
LRAVLLERAL ANGEAERDVE TSVLAKLASF EEELHAELPK AVEAARVAVE NGGAPTPNRV  840
KECRSYPLYR FVRDEAGAEY LTGEKARSPG EEVDKVFVAM NLGKHIDPLL DCLKEWNGEP  900
LSICRT                                                             906

SEQ ID NO: 89          moltype = AA  length = 649
FEATURE                Location/Qualifiers
source                 1..649
                       mol_type = protein
                       organism = Ananas comosus
SEQUENCE: 89
MGGGSRPRAA RGRQADGIAV AAVAGAPPAA GAAWPRAPTA YRRHHGFGAT SHRRTKEGAA  60
SRGQLIRFLN AGIFGSGRES GQTLPAAATR AAMLVRINTL LQGYSGIRFE ILESITALLN  120
SHVTPCLPLR GTITASGDLV PLSYIAGILT GRPNSVAVAP DGRSVDAAEA FRLAGIPHGF  180
FELQPKEGLA LVNGTAVGSG LASIVLFEAN ILAVLSEVMS AVFCEVMQGK PEFTDHLTHK  240
LKHHPGQIEA AAIMEHVLEG SSYMKMARKL HELDPLQKPK QDRYALRTSP QWLGPQIEVI  300
RAATISIERE INSVNDNPLI DVSRNKALHG GNFQGTPIGV SMDNTRLAIA AIGKLMFAQL  360
SELVNDFYNN GLPSNLSGGR NPSLDYGFKG AEIAMAAYCS ELQFLANPVT NHVQSAEQHN  420
QDVNSLGLIS ARKTAEAVEI LKLMSSTFLI ALCQAIDLRH LEENLKNAIK NAVSQIAKRV  480
LTMGPNGELH PSRFCEKDLI TVIDREHVFS YADDPCSATY PLMQKLRQVL VEHALGNGEK  540
EKATETSIFQ KIFAFEEELK AQLPKEVEAV RAAVESGSSA IANRIKECRS YPLYRFVREE  600
LGTEYLTGEK VRSPGEEFDK VFVAINEGKL IDPLLECLKE WNGEPLPIC               649

SEQ ID NO: 90          moltype = AA  length = 752
FEATURE                Location/Qualifiers
source                 1..752
                       mol_type = protein
                       organism = Ananas comosus
SEQUENCE: 90
MECDANGVVT DPLGWAAAAA AAAESGSHLE EVKRMVEEFR APAVTLKGVE LKISQVAAVA  60
MAKAVAPGVR VELAEAARGG VEASSEWVME SMARGTDSYG VAAVAMAKAV APGVRVELAE  120
AARGGVEASS EWVMESMARG TDSYGVTTGF GATSHRRTKQ GGALQKELIR FLNAGIFGSG  180
PKSEQTLPAS ATRAAMLVRI NTLLQGYSGI RFEILEAIAA FLNSHITPCL PLRGTITASG  240
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DLVPLSYIAG LLTGRPNSIA VGPDGRSLDA SEAFRLAGIM QGFFDLQPKE GLALVNGTAV  300
GSGLASIVLY EANILAVLSE VLSAIFCEVM QGKPEFTDHL THKLKHHPGQ IEAAAIMEHI  360
LDGSSYMKAA KKLHELDPLQ KPKQDRYALR TSPQWLGPQI EVIRAATKSI EREINSVNDN  420
PLIDVSRNKA LHGGNFQGTP IGVSMDNTRL AIAAIGKLMF AQFSELVNDF YNNGLPSNLS  480
GGRNPSLDYG FKGAEIAMAA YCSELQFLAN PVTNHVQSAE QHNQDVNSLG LISSRKTAEA  540
VEILKLMSST YLIALCQAID LRHLEENLMH AVKNAVSQVA KRVLTMDTAG ELHPARFCVK  600
DLIKVVDCEA AFSYADDPCS PSYLLMQKLR QVLVEHALKN GEKEKNSNSS IFQKITAFEE  660
ELKANLPKEV DAARVAFETG SSAIPNRVKE CRSYPLYRFI REELGTEYLT GERVRSPGEE  720
CDKVFAAING GLLIDPLLEC LKDWDGAPLP IC                                752

SEQ ID NO: 91          moltype = AA  length = 714
FEATURE                Location/Qualifiers
source                 1..714
                       mol_type = protein
                       organism = Apostasia shenzhenica
SEQUENCE: 91
MEHAADNGHL NGKVDDGTFC IQGRRDPLGW RAAAEAVEKS HLDEVKRMVE EFLRPSVKLE  60
GTALTISQVA AVAAGAATTV ELAESSRSGV KASNDWVLES MSRGVDSYGI TTGFGATSHR  120
RTKEVASLQK ELIRFLNAGI FGSGQDNTLP PAATRAAMLV RINTLLQGYS GIRFEVLEAI  180
TALLNSNITP CLPLRGTVTA SGDLVPLSYI AGILIGRPNA KAITADGDNV GAAEALRLAG  240
ISGGFFELQP KEGLAIVNGT AVGSGLASIV LFEANILAVM AEVLSALFCE VMQGKPEFTD  300
HLTHKLKHHP GQIEAAAIME HVLDGSSYMK MAKKIHEMDP LQKPKQDRYA LRTSPQWLGP  360
QIEVIRAATK SIEREINSVN DNPLIDVSRN RALHGGNFQG TPVGVSMDNT RLAIAAIGKL  420
MFAQFSELVN DFYNNGLPSN LSGGRNPSLD YGFKGAEIAM AAYCSELQFL GNPVTNHVES  480
AEQHNQDVNS LGLISSRKTA EAVEILKLMT STFLVGLCQA VDLRHLEENL KNVVKNSVTQ  540
AAKRVLTMGV NGELHPSRFC EKDLIKMIDR EYVFAYADDP CSSTYPLMQK LRQVLVEHAL  600
TNGENEKDPN SSIFQKITAF EEEIKSSLPK ELEAARANVE NGSPAIANRI MECRSYPLYR  660
FVREELGSEF LTGEKVRSPG EEFDKVFNAI CQGKAINPLL ECLKEWNGIP LPIC        714

SEQ ID NO: 92          moltype = AA  length = 713
FEATURE                Location/Qualifiers
source                 1..713
                       mol_type = protein
                       organism = Apostasia shenzhenica
SEQUENCE: 92
MEHAAENGHL NGKVDDGFCI QGRRDPLGWR AAAEAVEKSH LDEVKRMVEE FLRPSVKLEG  60
TALTISQVAA VAAGAAATVE LAESTRSGVK ASNDWVLGSM SRGVDSYGVT TGFGATSHRR  120
TKEVASLQKE LIRFLNAGIF GSGQDNTLPP AATRAAMLVR INTLLQGYSG IRFEILEAIT  180
ALLNSNITPC LPLRGTVTAS GDLVPLSYIA GILIGRPNAK AITADGDNVG AAEALRLAGI  240
SGGFFELQPK EGLAIVNGTA VGSGLASIVL FEANILAVMA EVLSALFCEV MQGKPEFTDH  300
LTHKLKHHPG QIEAAAIMEH VLDGSSYMKM EKKIHEMDPL LKPKHGRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVSRNR ALHGGNFQGT PVGVSMDNTR LAIAAIGKLM  420
FAQFSELVND FYNNGLPSNL SGGRNPSLDY GFKGAEIAMA AYCSELQFLG NPVTNHVEST  480
EQHNQDVNSL GLISSRKTAE AVEILKLMTS TFLVGLCQAV DLRHLEENLK NVVKNSVSQA  540
AKRVLTMGVN GELHPSRFCE KDLIKMIDRE YVFAYADDPC SSTYPLMQKL RQMLVEHALT  600
NGEKEKDPNF SIFQKITAFE EEIKSSLPKE LEAARANVEN GSPAIANRIM LCRSYPLYRF  660
VREELGSEFL TGEKVRSPGE EFDKVFNAIC QGKAINPLLE CLKEWNGVPL PIC         713

SEQ ID NO: 93          moltype = AA  length = 737
FEATURE                Location/Qualifiers
source                 1..737
                       mol_type = protein
                       organism = Apostasia shenzhenica
SEQUENCE: 93
MLQPDPGNSL SDKRRNFSSL NFFFFLLLIS YPPSMEQSRK NEHLKGWPDA LGWVAAAAAM  60
ERSHLSEVKR MVDEFRQPTV KLVGAELKIS QVAAVASGTM SAVELADSTR AGVKASSDWV  120
MESMNRGTDS YGVTTGFGST SHRRTKQGAA LQKELIRFLN AGIFGSRTEN TLPPAAARAA  180
MLVRINTLLQ GYSGIRFEIL EAITALLNSN ITPCLPLRGT ITASGDLVPL SYIAGILTGR  240
PNAKALTSDG STVDAAEAFR LAGISGGFFE LQPKEGLALV NGTAVGSGLA SIVLFEANIL  300
SLMAVVLSAL FCEVMQGKPE FTDHLTHKLK HHPGQIEAAA IMEYVLEGSS YVKMAKKLHE  360
MDPLLKPKQD RYALRTSPQW LGPQIEVIRS ATNSIEREIN SVNDNPLIDV SRNKALHGGN  420
FQGTPVGVSM DNTRLAIAAI GKLMFAQFSE LVNDFYSNGL PSNLSGGRNP SLDYGFKGAE  480
IAMAAYCSEL QFLANPVTNH VQSAEQHNQD INSLGLISAR KTMEAVEILK LMSSTFLVGI  540
CQAVDLRHLE ENLKNAVKNA VSQAAKKVLT TGVNGELHPS RFCEKDLIKV IDREYVFNYA  600
DDPCSSSYPL MQKLRQVLVD HALNNGDKEK DPTSSIFQKI AAFEEEVKNA VTKDVETARA  660
AVENGSPAIS NRIKDCRSYP IYRFVREELG TGFLSGNSVK SPGEEFDKVF DAICEGKAID  720
PLLECLKDWN GSPLPIS                                                 737

SEQ ID NO: 94          moltype = AA  length = 709
FEATURE                Location/Qualifiers
source                 1..709
                       mol_type = protein
                       organism = Dendrobium catenatum
SEQUENCE: 94
MENGHANGIA VMEDLCLKGS DPLGWVAAAK AAEGSHLDEV KRMVEDFRRP VVMLEGAELK  60
ISQVAAVASG AATSVELAES ARAGVKASSD WVLESMNLGG DHYGVTTGFG ATSHRRTKQG  120
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GALQKELIRF LNAGIFGSNP DNTLSPSATR AAMLVRINTL LQGYSGIRFE ILEAIASLLN  180
KNITPCLPLR GTITASGDLV PLSYIAGVLT GRPNAKAITS DGAAIDASEA FRLAGISGGF  240
FELQPKEGLA LVNGTAVGSG LASIVLFEAN ILAVMAEVLS ALFCEVMQGK PEYTDHLTHK  300
LKHHPGQIEA AAIMEHVLEG SSYMKMAKKL HEMDPLQKPK QDRYALRTSP QWLGPQIEVI  360
RAATKSIERE INSVNDNPLI DVSRNKALHG GNFQGTPIGV SMDNTRLAIA AIGKLMFAQI  420
SELVNDFYNN GLPSNLSGGR NPSLDYGFKG AEIAMAAYCS ELQYLANPVT NHVQSAEQHN  480
QDVNSLGLIS SRKTAEAVEI LKLMTSTFLV AICQAIDLRH LEENLKSAVK NAVSLAAKKT  540
LTMGINGELH PSRFCEKDLI TVIEREYVFA YADDPCCPTY PLMKNLRQVL VEHALNNGEK  600
EKDANSSIFQ KITAFEEEIK AVIPKEVEAT RVAFEKGSST IGNRIKECRS YPLYRFVREE  660
LGASFLTGEK VTSPGEEFDK VFEAISKGKA IDPLFECLKE WNGAPLPIC             709

SEQ ID NO: 95          moltype = AA  length = 709
FEATURE                Location/Qualifiers
source                 1..709
                       mol_type = protein
                       organism = Phalaenopsis equestris
SEQUENCE: 95
MENGHANGVA VMEGLCVKGR DPLGWAAAAK AAEGSHLDEV KRMVEEFRQP LVLLGGAELS  60
ISQVAAVASG AAPAVELAES ARAGVKASSD WVLDNTNHGG DYYGVTTGFG ATSHRRTKQA  120
GALQKELIRF LNAGIFGSNP NNTLSPATTR AAMLVRINTL LQGYSGIRFE ILEAIASLLN  180
NKITPCLPLR GTITASGDLV PLSYIAGVLT GRPNAKAVTA DGVAIDAAEA FRLAGISGVF  240
FKLQPKEGLA LVNGTAVGSG LASIVLFEAN ILAVMAEVLS ALFCEVMQGK PEYTDHLTHK  300
LKHHPGQIEA AAIMEHVLEG SSYMKVAKKL HEMDPLQKPK QDRYALRTSP QWLGPQIEVI  360
RSATKSIERE INSVNDNPLI DVSRNKALHG GNFQGTPIGV SMDNTRLAIA AIGKLMFAQI  420
SELVNDFYNN GLPSNLSGGR NPSLDYGFKG AEIAMAAYCS ELQYLANPVT NHVQSAEQHN  480
QDVNSLGLIS SRKTAEAVEI LKLMTSTFLV AICQAIDLRH LEENLKSTVK NAVSLAAKKT  540
LTTGVNGELH PSRFCEKDLI KVIDREYVFA YADDPCSSTY PLMKNLRQVL VEHALNNGEK  600
EKDSTSSIFQ KIAAFEEEIK ATVPKEVEAA RAAFEKGSSA IGNRIKECRS YPLYRFVREE  660
LGAGFLTGEK VRSPGEEFDK VFDAISEGKA IDPLLECLKE WNGAPLPIC             709

SEQ ID NO: 96          moltype = AA  length = 713
FEATURE                Location/Qualifiers
source                 1..713
                       mol_type = protein
                       organism = Dendrobium catenatum
SEQUENCE: 96
MEHVKGNGYA NGAKAMEGLC LKGRDQLGWA AAAKALEGSH LDEVKRMVKE FRSPVVRLEG  60
AELKISQVAA VAAGAASTVE LAESARAGVK ASSDWVMESM DSGGDTYGVT TGFGATSHRR  120
TKQGGALQKE LIRFLNAGIF GSGKDNTLPP AATRAAMLVR INTLLQGYSG IRFEILEAIT  180
NLLNNKITPC LPLRGTITAS GDLVPLSYIA AILTGRPNVK AITAEGATID AAEAFRLAGI  240
SGGFFELQPK EGLALVNGTA VGSGLASTVL FEANILSVMA EVLSAVFCEV MQGKPEYTDH  300
LTHKLKHHPG QIEAAAIMEH VLEGSSYMKV AKKLHEMDPL QKPKQDRYAL RTSPQWLGPQ  360
IEVIRAATKS IEREINSVND NPLIDVSRNI ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQISELVND FYNNGLPSNL SGGRNPSLDY GFKGAEIAMA SYCSELQYLA NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AVEILKLMTS TFLVALCQAI DLRHLEENLK SAVKNTVSQV  540
AKRVLTIGVK GELHPSRFCE KDLIKVIDRE YVFAYADDPC SSTYPLMQNL RQVLVEHALN  600
NGEKEKEADS SIFQKITAFE EELKAVLPKE VEATRLAFEN GTSTIGNRIK DCRSYPIYRF  660
VREELGTSFL TGEEVRSPGE EFDKVFNAIC EGKAIDPLLE CLQEWDGAPL PIC         713

SEQ ID NO: 97          moltype = AA  length = 710
FEATURE                Location/Qualifiers
source                 1..710
                       mol_type = protein
                       organism = Apostasia shenzhenica
SEQUENCE: 97
MDHSKVNGHA NGAMEGLCLR RPDPLNWGAA AEALEGSHLD EVKRMVEEFR RPEVKLEGAD  60
LKISQVAAVA AGDVASVELA ESARAGVKAS SDWVLDSVNR GTDSYGVTTG FGATSHRRTK  120
QGGALQKELI RFLNAGIFGS GKENTLPATA TRAAMLVRIN TLLQGYSGIR FEILEAITSL  180
LNSNVTPCLP LRGTVTASGD LVPLSYIAGI LTGRQNAKAV AADGSVVDAA GAFRLAGISG  240
GFFELQPKEG LALVNGTAVG SGLASIVLFE SNILVLMAEV LSALFCEVMQ GKPEYTDHLT  300
HKLKHHPGQI EAAAIMEHIL DGSSYMKMAK KIHEMDPLQK PKQDRYALRT SPQWLGPQIE  360
VIRAATKSIE REINSVNDNP LIDVSRNKAL HGGNFQGTPI GVSMDNTRLA IAAIGKLMFA  420
QFSELVNDFY NNGLPSNLSG GRNPSLDYGF KGAEIAMASY CSELQFLANP VTNHVQSAEQ  480
HNQDVNSLGL ISSRKTMEAV QILQLMTSTF LVGLCQAVDL RHLEENLKSS VKNAVSQAAK  540
RVLTMGVNGE LHPSRFCEKD LIKVIDREYV FAYADDPCSF SYPLMQKLRQ VLVDHAIGNG  600
EKERDPNTSI FQKILAFEEE LKAVLPKEAE AARAAFDNGS PAIANRIRDC RSYPLYRFVK  660
EVGAGFLTGE KTRSPGEAFD KVFVAISEGK VIDPLLECLK EWDGAPLPIC            710

SEQ ID NO: 98          moltype = AA  length = 711
FEATURE                Location/Qualifiers
source                 1..711
                       mol_type = protein
                       organism = Apostasia shenzhenica
SEQUENCE: 98
MDHVKENGHG NGELNGLCLR APADPLNWGS AAAAMEGSHL DEVKRMVEEF RRPAVRLEGA  60
ALKISQVAAV AAGSGVAVVL SESARAGVKA SSEWVLESMN RGTDSYGVTT GFGATSHRRT  120
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KQGGALQKEL IRFLNAGIFG SGEENQLPAP ATRAAMLVRI NTLLQGYSGI RFEILEAITS  180
LLNSNVTPCL PLRGSITASG DLVPLSYIAG ILIGRPNAKA LTPEGSAVDA AEAFRLAGIP  240
NGFFELQPKE GLALVNGTAV GSGLAALVLF EANILALMAE VLSALFCEVM QGMPEFADHL  300
THKLKHHPGQ IEAAAIMEHI LAGSSYMKAA KKIHETDPLQ KPKQDRYALR TSPQWLGPQI  360
EVIRSATKSI EREINSVNDN PLIDVSRNRA LHGGNFQGTP IGVSMDNTRL AVAAIGKLMF  420
AQFSELVNDS YNNGLPSNLS GGRNPSLDYG FKGAEVAMAA YCSELQFLAN PVTNHVQSAE  480
QHNQDVNSLG LISARKTMEA VQNLKLMTST FLVALCQAVD LRHLEENLKN AVKNAVGQAA  540
KRVLTMGVTG ELHPARFCEK DLIKAIDREH VFAYADDPCS ASYPLMQRLR QVLVEHAIAN  600
GEKEKDSSAS IFQKIVDFEE EVKATVPREV EAARAAVESG SPAIENRIRE CRSYPLYRFV  660
KETGAGFLTG EKARSPGEEF DKVFGAFCEG KVIDPLLECL KEWDGAPLPI C           711

SEQ ID NO: 99          moltype = AA  length = 701
FEATURE                Location/Qualifiers
source                 1..701
                       mol_type = protein
                       organism = Phalaenopsis equestris
SEQUENCE: 99
MDACKVNGLC VQGHDPLNWG AAAAELQGSH LDEVKKMVEE FRRPVVQLEG EXISQAAAVA  60
IGGGGATVEL AESARAGVKA SSDWVLESVD KGTDSYGVTT GFGATSHRRT KQGGALQKEL  120
IRFLNAGIFG SGNSNTLPSS TTRAAMLVRI NTLLQGYSGI RFEILEAIAT LLNTNITPCL  180
PLRGTITASG DLIPLSYIAG ILTGRPNSKA LTPNGSTVDA VTAFHLAGIS TGFFELQPKE  240
GLALVNGTAV GSGLASMVLF ETNILAIMAE VLSALFCEVM QGKPEYTDHL THKLKHHPGQ  300
IEAAAIMEHI LEGSSYMKMA KKLHEMDPLQ KPKQDRYALR TSPQWLGPQI EVIRAATKSI  360
EREINSVNDN PLIDVSRNKA LHGGNFQGTP IGVSMDNTRL AIAAIGKLMF AQFSELVNDF  420
YNNGLPSNLT SGRNPSLDYG FKGAEIAMAS YCSELQALAN PVTNHVQSAE QHNQDVNSLG  480
LISSRKTAES VDILKLMTTT FLVGLCQAVD LRHLEENLKN AVKNTVSQVA KRTLTMGVNG  540
ELHPSRFCEK DLIKVIDREY VFSYADDPCS STYPLMPKLR AVLVEHALNN GDKEKNSSTS  600
IFQKISSFEA ELKAAMPKEV EAARAAFENG SPAIENRIKD CRSYPLYRFV KQVGAGFLTG  660
EKIVSPGEEF DKVYNAICEG KAIDPLLECL KEWDGAPLPI C                      701

SEQ ID NO: 100         moltype = AA  length = 731
FEATURE                Location/Qualifiers
source                 1..731
                       mol_type = protein
                       organism = Spirodela polyrhiza
SEQUENCE: 100
MEAATQVHCN GNGNVKLEAF CLKPAAAAAA PAVAPVSGDP LNWGAAADSL RGSHLDEVKR  60
MVEDFRRPLV RLEGADLKIS QVAAVASGRG TLRVELAESA RERVKASSDW VMDSMNKGTD  120
SYGVTTGFGA TSHRRTKQGG ALQRELIRFL NAGIFGSGDD SANTTLPQSA TRAAMLVRIN  180
TLLQGYSGIR FEIMEAITAL LNHHVTPCLP LRGTITASGD LVPLSYIAGM LTGRPNARAV  240
NAAGEKVSAQ EAFQQAGISG GFFELQPKEG LALVNGTAVG SGLASVVLFE ANILAVLAEV  300
LSAVFCEVMQ GKPEFTDHLT HKLKHHPGQI EAAAIMEHIL EGSSYMKMAK KIHELDPLQK  360
PKQDRYALRT SPQWLGPQVE VLRHATKSIE REINSVNDNP LVDVSRNKAL HGGNFQGTPI  420
GVSMDNARLA LAAIGKLMFA QLSELVNDFY NNGLPSNLSG GRNPSLDYGF KGAEIAMASY  480
CSELQFLGNP VTNHVQSAEQ HNQDVNSLGL ISARKTAEAV EILKLMTSTY LVALCQAVDL  540
RHLEENLKAA VKNTVSQVAK RVLTMGVNGE LHPSRFCEKD LLKVVDREYV FAYADDPCLS  600
TYPLMQKLRQ VLVEHAIANG EKEKDSATSI FQKVTAFEEE LKMALPKEVE AAREAVEKGA  660
PAIPNRIEDC RSYPLYKFVR EELGTAMLTG EKVRSPGEEF DKVFTAISQG KVIDPLFNCL  720
SGWNGSPVPI C                                                       731

SEQ ID NO: 101         moltype = AA  length = 723
FEATURE                Location/Qualifiers
source                 1..723
                       mol_type = protein
                       organism = Spirodela polyrhiza
SEQUENCE: 101
MEAAGQINSN GHSGVLEGFC LKPTIAAGDP LNWGAAAESL SGSHLEEVKR MVEEFRQPLV  60
QLEGADLKIS QVAAVAAAGG GASLRVELAD SARPRVKASS DWVMDSMNRG TDSYGVTTGF  120
GATSHRRTKQ GAALQKELIR FLNAGIFGSG ADSGNTTLPP AATRAAMLVR VNTLLQGYSG  180
IRFEILEAIT ALLNNGVTPC LPLRGTITAS GDLVPLSYIA GMLTGRPNAK AVTAEGKQVS  240
AEEAFRLAGI AGGFFELQPK EGLALVNGTA VGSGLASMVL FEANILAVLA EVLSAVFCEV  300
MQGKPEFTDH LTHKLKHHPG QIEAAAIMEH ILEGSSYMKM AKKLHELDPL QKPKQDRYAL  360
RTSPQWLGPQ VEVLRQATKS IEREINSVND NPLIDVSRGK ALHGGNFQGT PIGVSMDNSR  420
LAIAAIGKLM FAQISELVND FYNNGLPSNL TAGRNPSLDY GFKGAEIAMA AYCSELQFLA  480
NPVTNHVQSA EQHNQDVNSL GLISARKTAE AVEILKLMTS TYLVALCQAV DLRHLEENLK  540
NAVKNTVSQV AKRVLTIGVN GELHPSRFCE KDLIRAVDRE HVFTYADDPC SATYPLMQKL  600
RQVLVEHALT NGEKEKDSNT SIFQKVAAFE EELKMTLPKE VEAVRAAFDN GTAVIPNRIK  660
ECRSYPLYKF VREELGTSLL TGEKVRSPGE EFDKVYVAIS QGKVVDPLFE CLRDWNGAPV  720
PIC                                                                723

SEQ ID NO: 102         moltype = AA  length = 601
FEATURE                Location/Qualifiers
source                 1..601
                       mol_type = protein
                       organism = Musa acuminata
SEQUENCE: 102
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MEVENGVGNG PCIKADPLNW GAAAEAMTRS HLDDVKRMVE EFRQPLVRLE GATLNISQVA  60
AVAMAAHSSA VRVELSESAR DRVSASSEWV MDSMTKGTDS YGVTTGFGAT CHRRTREGGA  120
LQRELIRFLN AGIFGSGWES GHTLPPSAAR AAMLVRINTL LQGYSGIRFE ILEAMASLLN  180
SGITPCIPLR GTITASGDLL PLSYIAALLT GRPNAKAFCP GGETVDAAEA FRRAGIPRGF  240
FELQPKEGLA LVNGTAVGSG LASVVLYEAN VLAVLAEVLS AIFCEVMQGK PEFTDHLTHK  300
LRHHPGQIEA AAIMEHILDG SSYMKMAKNL HEQDPLQKPK QDRYALRTSP QWLGPQIEVI  360
RSATKSIERE INSVNDNPLI DVSRNKALHG GNFQGTPIGV SMDNARLALA TIGKLLFAQF  420
SELDNDLYNN GLPSNLSGGR NPSLDYGFKG AEIAMAAYCS ELQFLANPVT NHVQSAEQHN  480
QDVNSLGLIS SRKTAEAVDI LKLMSATYLV ALCQAIDLRH LEENLKKAVT NTVSQVAKRC  540
RSYPLYRFVR EELGTAYLTG EKVRSPGEEF DKVFAAINRG QLIDPLLECL KEWNGAPLPI  600
C                                                                 601

SEQ ID NO: 103          moltype = AA  length = 655
FEATURE                 Location/Qualifiers
source                  1..655
                        mol_type = protein
                        organism = Musa acuminata
SEQUENCE: 103
MEVENGVHGN GFADGLCVKA DPLNWGAAAE ALTGSHLDEV KRMVEEFRRP LVRLEGATLK  60
ISQVAAVAMA PHSAVRVELS ESAREGVRAS SQWVTDSMTN GTDSYGVTTG FGATSHRRTK  120
EGGALQKELI RFLNAGIFGS GTESAHTLPT PAARAAMLVR VNTLLQGYSG IRFEILEAMA  180
SLLNSGITPC LPLRGTITAS GDLVPLSYIA GVLTGRPNAK AFAPGGEAVD AAEAFRRSGI  240
PHGFFELQPK EGLALVNGTA VGSGLASVVL YEANVLAVLA EVLSAVFCEV MQGKPEFTDH  300
LTHKLKHHPG QIEAAAIMEH ILDGSSYMKM AKKLHEQDPL QKPKQDRYAL RTSPQWLGPQ  360
IEVIRSATKS IEREINSVND NPLIDVSRNK ALHGGNFQGT PIGVSMDNAR LALAAIGKLM  420
FAQFSELVND FYNNGLPSNL SGGRNPSLDY GFKGAEIAMA AYCSELQFLA NPVTNHVQSA  480
EQHNQDVNSL GLISSRKTAE AVDILKLMST TYLVALCQAI DLRHLEENLK QAVKNTVSQV  540
AKRVLTTAAN GELHPSRFCE KDLITVIDRE HVFSYIDDPC SSTYALMPKL RMECRSYPLY  600
RFVRKELGAA YLTGEKVRSP GEEFDKVFAA INKGLLIDPL MECLKEWNGA PLPIC       655

SEQ ID NO: 104          moltype = AA  length = 652
FEATURE                 Location/Qualifiers
source                  1..652
                        mol_type = protein
                        organism = Musa acuminata
SEQUENCE: 104
MENGGVHANG SLCIRTDPLN WGAAAEAVTG SHLEEVKRMV GEFRQPLVRL EGATLKISQV  60
AAVATEPHSA VRVELSESAR EGVRASSQWV MDSMTKGTDS YGVTTGFGAT SHRRTKQGGA  120
LQQELIRFLN AGIFGSGAES GHTLPTPAAR AAMLVRINTL LQGYSGIRFE ILEAMASLLN  180
SGITPCLPLR GTITASGDLV PLSYIAGLLT GRGNAKALAP GGEWVDAAEA FRRAGIPHGF  240
FELQPKEGLA MVNGTAVGSG LASLVLYEVN VLAVLAEALS AVFCEVMQGK PEFTDHLTHK  300
LKHHPGQIEA AAIMEHILDG SSYMKMAKKL HEQDPLQKPK QDRYALRTSP QWLGPQIEVI  360
RASTKSIERE INSVNDNPLI DVSRNKALHG GNFQGTPIGV SMDNTRLAVA AIGKLMFAQF  420
SELVNDFYNN GLPSNLSGGR NPSLDYGFKG AEIAMAAYCS ELQFLANPVT NHVQSAEQHN  480
QDVNSLGLIS SRKTAEAVDI LKLMSATYLV ALCQAIDLRH LEENLKHAVK NTVGQVAKRV  540
LTTGANGELH PSRFCEKDLI MVVDRENVFS YIDDPCSSTY ALMPKLRMVL CRSYPLYRLV  600
REELGVAYLT GEKARSPGEE FDKVFMAVNE GLLIDPLLEC LKEWNGAPLP IC          652

SEQ ID NO: 105          moltype = AA  length = 653
FEATURE                 Location/Qualifiers
source                  1..653
                        mol_type = protein
                        organism = Musa acuminata
SEQUENCE: 105
MEVENGAYTN STTDGLCIKA DALNWATAAE ALSGNHLDEV RRMVEESRRP LVRLEGATLT  60
ISQVAAVATA AAVRVELSES ARDGVRASSQ WVVDSMTKGT DSYGVTTGFG ATSHRRTKEG  120
GALQKELIRF LNAGIFGSGE ESRHTLPASA ARAAMLVRVN TLLQGYSGIR FEILEAMASL  180
LNCGITPCLP LRGTITASGD LVPLSYIAGL LTGRPNAKAL DPAGEAIDAA EAFRRAGIPH  240
GFFELQPKEG LALVNGTAVG SGLASVVLYE ANVLAVLAEV LSAVFCEVML GKPEFTDHLT  300
HKLKHHPGQI EAAAIMEHIL DGSSFMKIAK KLHEQDPLQK PKQDRYALRT SPQWLGPQIE  360
VIRSSTKSIE REINSVNDNP LIDVSRNKAL HGGNFQGTPI GVSMDNTRLA LAAIGKLMFA  420
QFSELVNDFY NNGLPSNLSG GRTPSLDYGF KGAEIAMAAY CSELQFLANP VTNHVQSAEQ  480
HNQDVNSLGL ISSRKTADAV DILKLMSATY LVALCQAIDL RHLEENLKNA VKNTVSQVAK  540
RVLTAGVNGE LQPSRFCEKD LITIVDREHV FSYIDDPCSS TYALMPKLRM ECRSYPLYRF  600
VREELGTACL TGEKVRSPGE EFDKVFVAIN GGSLIDPLLE CLKEWNGAPL PIC         653

SEQ ID NO: 106          moltype = AA  length = 643
FEATURE                 Location/Qualifiers
source                  1..643
                        mol_type = protein
                        organism = Musa acuminata
SEQUENCE: 106
MEVENGAAGG LRVETDPLNW AAAAEALAGS HLDEVRRMTW EFRQPLVKLE GSTLRISQVA  60
AIAAGAHSAV RVELSESARD EVCASSRWVV DSTAKGTNSN GMTAGFGAAS HRRTKEGGAL  120
QKELIRFLNV GIFGSGAESG HTLPPSATRA AMLVRINTLL QGYSGIRFEI LEAMASLLNS  180
GITPCLPLRG TITASGDLVP LSYIAGVLTG RPNAKACDPA GETMDAAEAF RRAGIPHEFF  240
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ELQPKEGLAL VNGTTVGSGL ASVVLYEANV LALLAEVLSA VFCEVMQGNP EFTDHLTHRL  300
KHHPGQIEAA AIMEHILDGS SYMKMAKKLH EQDPLQKPKK DRYALRTSPQ WLGPQIEVIR  360
SSTKSIEREI NSVNDNPLID VARNKTIYGG NFQGTPIGVS MDNARLALAA VGKLMFAQFS  420
ELVNDLYNNG LPSNLSGGRN PSLDYGFKGA EIAMAAYCSE LQFLANPVTN HVQSAEQHNQ  480
DVNSLGFISS RKAAEAVDIL KLMSATYLLA LCQAIDLRHL EENLKNAVKN TVSQVAKRVL  540
TTGAFCEKNL ITVADREHIF GYIDDPCSST YALMPKLRMA LCRSYPLYRF VREELGTEYL  600
TGEKVRSPGE EFDKVFVAID RGLVIDPLLE CLKEWNGVPL PMC                    643

SEQ ID NO: 107         moltype = AA  length = 651
FEATURE                Location/Qualifiers
source                 1..651
                       mol_type = protein
                       organism = Musa acuminata
SEQUENCE: 107
MEFERNGHHA NGGLCIKDPL NWAAAAEALT GSHLDEVKKM VAESRQPLVS LEGTTLKIAH  60
VAAVAGQSGA RVELSESARG RVRASSDWVM DSMTKGTDSY GVTTGFGATS HRRTKQGGAL  120
QKELIRFLNA GIFGSGSDQS GHTLPPPATR AAMLVRINTL LQGYSGIRFE ILEAITSLLN  180
SNITPCLPLR GTITASGDLV PLSYIAGILT GRPNSKAISP AGEAIDAAEA FRLAGIPHGF  240
FELQPKEGLA LVNGTAVGSG LASMVLFDAN ILAVLSEVLS AIFCEVMQGK PEFTDHLTHK  300
LKHHPGQIEA AAIMEHVLEG SSYMKMAKKL HEQDPLQKPK QDRYALRTSP QWLGPQIEVI  360
RSSTKSIERE INSVNDNPLI DVSRNKALHG GNFQGTPIGV SMDNTRLAIA AIGKLMFAQF  420
SELVNDFYNN GLPSNLSGGR NPSLDYGFKG AEIAMAAYCS ELQFLANPVT NHVQSAEQHN  480
QDVNSLGLIS SRKTAEAVDI LKLMSSTYLV ALCQAIDLRH LEENLKNAVK NTVIQVAKKT  540
LTTGVNGELH PSRFCEKDLI TIIDREHVFS YVDDPCSSTY PLMQKLRQEC RSYPLYRFVR  600
AELSTGYLTG EKVRSPGEDF DKIFAAINKG MVIDPLLECL KEWNGAPLPI C           651

SEQ ID NO: 108         moltype = AA  length = 711
FEATURE                Location/Qualifiers
source                 1..711
                       mol_type = protein
                       organism = Elaeis guineensis
SEQUENCE: 108
MESAHESGNA NGAVKGLCIK DPLNWVAAAE ALTGSHFDEV KRMVEEFRQP MVRLEGASLK  60
ISQVAAVAMA ESAARVELSE ASREGVQASS QWVMDSMNNG TDSYGVTTGF GATSHRRTKQ  120
GGALQKELIR FLNAGIFGSS PQSVHTLPPS ATRAAMLVRI NTLLQGYSGI RFEILEAMNR  180
LLNSNITPCV PLRASISASG DLVPLSYIAG ILSGRPNAVA ISPTGQPIDA AEAFRLAGIP  240
HGFFELQPKE GLALVNGTAV GSGLASLVLF EANILALLSE VLSAIFCEVM NGKPEFTDHL  300
THKLKHHPGQ IEAAAIMEHV LEGSSYMKLA KKLHELDPLQ KPKQDRYALR TSPQWLGPQI  360
EVIRSSTKSV EREINSVNDN PLIDVSRKKA LHGGNFQATP VGVSMDNTRL AIAAIGKLMF  420
AQFSELVNDF YNNGLPSNLS GGRDPSLDYG FKGAEIAMAA YCSELQFLGN PVTNHVQSAE  480
QHNQDVNSLG LISARKTQEA VDILKLMSST YLVAICQAID LRHVEENLKN TVKNTVGQVA  540
KRVLTMGVNG ELHPSRFCEK DLIKVIDREY VFSYADDPCS STYTLMEKLR QVLVEHALNN  600
GEKEKDATTS IFQKITAFEQ ELKAVLPKEV EATRVAFENG NLPIENRIKD CRSYPLYRFV  660
RELGTGFLTG EKVRSPGEEF DKVFVAINRG MVIDPLLECL KGWDGAPLPL H           711

SEQ ID NO: 109         moltype = AA  length = 713
FEATURE                Location/Qualifiers
source                 1..713
                       mol_type = protein
                       organism = Calamus simplicifolius
SEQUENCE: 109
MEFGHQNGNG NGAVDGFCIK DPLNWIAAAE SLTGSHLDEV KRMVEEFRQP SVKLEGATLK  60
ISQVAAVAVA ESAVRVELSE ASREGVQASS QWVLDSMDKG TDSYGVTTGF GATSHRRTKQ  120
GGALQRELIR FLNAGIFGSG LESSDHTLPS SATRAAMLVR INTLLQGYSG IRFEILEAIT  180
SLLNSNITPC VPLRGSISAS GDLIPLSYIA GVLSGRPNAV AISPSGQRID ATEAFRLAGI  240
PHNFFELQPK EGLAMVNGTA VGSGLASIVL FEANILAVLS EVLSAIFCEV MNGKPEFTDH  300
LTHKLKHHPG QIEAAAIMEH ILDGSFYMKM AKKLHELDPL QKPKQDRYAL RTSPQWLGPQ  360
IEVIRSSTKS IEREINSVND NPLIDVSRNK ALHGGNFQGT PIGVSMDNTR LAIAAIGKLM  420
FAQFSELVND YYNNGLPSNL SGGPNPSLDY GFKGAEIAMA AYCSELQFLG NPVTNHVQSA  480
EQHNQDVNSL GLISARKTQE AVEILKLMSS TYLVALCQAI DLRHLEENLT ATVKNAVIQV  540
AKRVLTMGVN GELHPSRFCE KDLIKVIDRE YVFSYADDPC SSTYTLMPKL RQVLVEHALN  600
NGERERDAST SIFQKITAFE EELKATLPKE VEAARVAFEN GSLPIENRIK ECRSYPLYRF  660
VREELGAGYL TGEKARSPGE EFNKVFVAIS RGLVIDPLFE CLKEWNGAPL PLC         713

SEQ ID NO: 110         moltype = AA  length = 725
FEATURE                Location/Qualifiers
source                 1..725
                       mol_type = protein
                       organism = Ananas comosus
SEQUENCE: 110
MEFVEGYLCA DEKKQRDPLN WGRAAEAMSG SHLEEVKRMV EEFRRPLVRL EGADLKISQV  60
AAVAMGDFAQ AQAQAQPVPV PVPVPVRVEL SEGARDAVRA SSDWVLASMD KGTDSYGVTT  120
GFGATSHRRT KQGGALQREL IRFLNAGIFG SGRESGQTLP ASATRAAMLV RINTLLQGYS  180
GIRFEILEAI TALLNSRVTP CLPLRGTITA SGDLVPLSYI AGILTGRPNA KAVGPDGEAE  240
LSAAEAFEVA GIGGGFFELQ PKEGLALVNG TAVGSGLASI VLFEANILAV LSEVLSAVFC  300
EVMQGKPEFT DHLTHKLKHH PGQIEAAAIM EHVLEGSSYM RMAKKLHELD PLQKPKQDRY  360
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ALRTSPQWLG PQIEVIRSST RSIEREINSV NDNPLIDVAR NKALHGGNFQ GTPIGVSMDN  420
TRLALAAIGK LMFAQFSELV NDFYNNGLPS NLSGGRNPSL DYGFKGAEIA MAAYCSELQF  480
LGNPVTNHVQ SAEQHNQDVN SLGLISARKT AEAVEILKLM TSTYLVALCQ AIDLRHLEEN  540
LKSAVKNAVG QAAKRVLTVG AGGELHPARF CEKDLIKVVD RDHVFAYADD PCSSTYPLMQ  600
KLRQVLVEQA LGNGEKEKDP NNSIFQKIAA FEEELKAQLP KEVEAARVAF ENGTSAIPNR  660
IQECRSYPLY RFVREELGAG YLTGEKVRSP GEEFNKVFNA ICKGKAIDPM LECLKEWNGA  720
PLPLC                                                              725

SEQ ID NO: 111         moltype = AA  length = 725
FEATURE                Location/Qualifiers
source                 1..725
                       mol_type = protein
                       organism = Ananas comosus
SEQUENCE: 111
MEFVEGYLCA DEKKQRDPLN WGRAAEAMSG SHLEEVKRMV EEFRRPLVRL EGADLKISQV  60
AAVAMGDFAQ AQAQAQAQPV PVPVPVRVEL SEGARDAVRA SSDWVLASMD KGTDSYGVTT  120
GFGATSHRRT KQGGALQREL IRFLNAGIFG SGRESGQTLP ASATRAAMLV RINTLLQGYS  180
GIRFEILEAI TALLNSRVTP CLPLRGTITA SGDLVPLSYI AGILTGRPNA KAVGPDGEAE  240
LSAAEAFEVA GIGGGFFELQ PKEGLALVNG TAVGSGLASI VLFEANVLAV LSEVLSAVFC  300
EVMQGKPEFT DHLTHKLKHH PGQIEAAAIM EHVLEGSSYM RMAKKLHELD PLQKPKQDRY  360
ALRTSPQWLG PQIEVIRSST RSIEREINSV NDNPLIDVAR NKALHGGNFQ GTPIGVSMDN  420
TRLALAAIGK LMFAQFSELV NDFYNNGLPS NLSGGRNPSL DYGFKGAEIA MAAYCSELQF  480
LGNPVTNHVQ SAEQHNQDVN SLGLISARKT AEAVEILKLM TSTYLVALCQ AIDLRHLEEN  540
LKSAVKNAVG QAAKRVLTVG AGGELHPARF CEKDLIKVVD RDHVFAYADD PCSSTYPLMQ  600
KLRQVLVEQA LGNGEKEKDP NNSIFQKIAA FEEELKAQLP KEVEAARVAF ENGTSAIANR  660
IQECRSYPLY RFVREELGAG YLTGEKVRSP GEEFNKVFNA ICKGKAIDPM LECLKEWNGA  720
PLPLC                                                              725

SEQ ID NO: 112         moltype = AA  length = 654
FEATURE                Location/Qualifiers
source                 1..654
                       mol_type = protein
                       organism = Musa acuminata
SEQUENCE: 112
MEFAPKAQVV ENGEAFCLKA DPLNWIKAAE SLTGSHLDEV KRMVEEFRKP QVRLEGATLT  60
ISQVAAVAAA RSPVRVELSE EARDGVRASS EWVMESMNKG TDSYGVTTGF GATSHRRTKQ  120
GGALQKELIR FLNAGIFGSG PESGNTLPSS AAKAAMLVRV NTLLQGYSGI RFEILEAIAS  180
LLNNGITPCL PLRGTITASG DLVPLSYIAG ILTGRPNAKA VGPDGKVIGA AEAFRLAGIA  240
DGFFELQPKE GLALVNGTAV GSGLASMVLF EANVLAVLSE VLSAVFCEVM QGKPEFTDHL  300
THKLKHHPGQ IEAAAIMEHI LEGSSYMKMA QKLHEQDPLQ KPKQDRYALR TSPQWLGPQI  360
EVIRASTKSI EREINSVNDN PLIDVSRSKA LHGGNFQGTP IGVSMDNTRL AVAAIGKLMF  420
AQFSELVNDF YNNGLPSNLS GGRNPSLDYG FKGAEIAMAA YCSELQFLAN PVTNHVQSAE  480
QHNQDVNSLG LISARKTAEA VDILKLMSTT YLVALCQAVD LRHLEENLKS AVKSTVSQVA  540
KRVLTMGANG ELHPARFCEK ELIKVVDREH VFTYVDDPCS ATYPLMQKLR QECRSYPLYR  600
LVREELKTGF LTGEKVTSPG EEFDKVFDAI CQGKVIDPLL ECLKEWDGAP IPIC        654

SEQ ID NO: 113         moltype = AA  length = 704
FEATURE                Location/Qualifiers
source                 1..704
                       mol_type = protein
                       organism = Elaeis guineensis
SEQUENCE: 113
MENCNANGFC LPDPLRWAEA AEELSGSHLD EVKLMVEEYR KPLVRLEGAT LRISQVAAVA  60
TSKSPVTVEL SEAARDGVKA SSVWVMESMS KGTDSYGVTT GFGATYHRRT KQGGALQMEL  120
IRFLNAGIFG AGPESGHALP VSATRAAMLV RINTLLQGYS GIRFEILEAM ARLLNCSVTP  180
CLPLRGTITA SGDLVPLSYI AGLLTGRPNS KATTPDGTAI DASEGFQLAG IAGGFFKLQP  240
KEGLALVNGT AVGSGLASMV LFEANILAVL SEVVSAMFCE VMQGKPEFTD HLTHKLKHHP  300
GQMEAAAIME HILEGSSYVK MAEKLHERDP LQKPKQDRYA LRTSPQWLGP QIEVIRMSTK  360
SIEREINSVN DNPLIDVSRS KALHGGNFQG TPVGVSMDNT RLAIAAIGKL MFAQFSELVN  420
DSYSNGLPSN LSAGRNPSLD YGFKGAEIAM AAYCSELQFL GNPVTNHVQS AELHNQDVNS  480
LGLISARKTA EAVEILKLMS STYLVALCQA IDLRHLEENL KSTVKNTVAQ VSKGVLTMGA  540
DGELHPSRFC EKDLIRVIDG EYVFSYVDDP CSSTYPLIQK LRQVLVEHAL NNGEKEKDPS  600
SSIFQKIAAF EEELRTVLPR EVESARVALE NGRSAIANRI QECRSYPLYR FVREELDTGL  660
LTGEKVRSPG EEFDKVFDAI CEAKVIEPLL ECLKDWNGAP LPTC                   704

SEQ ID NO: 114         moltype = AA  length = 704
FEATURE                Location/Qualifiers
source                 1..704
                       mol_type = protein
                       organism = Elaeis guineensis
SEQUENCE: 114
MENGGAKSFC LPDPLHWAKA AEALTGSHLD EVKHMVEEYR KPLVRLEGAT LKISQVAAVA  60
TSESPVTVEL SEATRDGVKA SSQWVMDSMN KGTDSYGVTT GFGATSHRRT KQGGALQKEL  120
IRFLNAGIFG GGAESGHTLP VSASRAAMLV RINTLLQGYS GIRFEILEAM TNLLNGRITP  180
CLPLRGSISA SGDLVPLSYI AGLLTGRPNS KATTPDGTTV DASEAFQLAG IPSGFFELQP  240
KEGLAIVNGT AVGSGLASMV LFETNILAVL SEVLSAIFCE VMQGKPEFTD HLTHKLKHHP  300
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GQIEAAALME YILEGSSYMK MAKKLHELDP LQKPKQDRYA LRTSPQWLGP QIEVIRMSTK  360
SVEREINSVN DNPLIDVSRS KALHGGNFQG TPVGVSMDNT RLAIAAIGKL MFAQFSELVN  420
DFYNNGLPSN LSGGRNPSLD YGFKGAEIAM AAYCSELQFL GNPVTNHVQS AEQHNQDVNS  480
LGLISARKTA EAVEILKLMS STYLVALCQA IDLRHLEENL KNTVKNTVTQ VAKRVLTIGA  540
NGELHPSRFC EKDLIKVIDR EYVFAYIDDP CSFTYPLMQK LRQVLVEHAL NNGEKEKDPS  600
SSIFQKISVF EEELKTLLPK EVEGARVAFE NGNSAIANRI KECRSYPLYR FVRDELDAGF  660
LTGEKVRSPG EEFNKVFNAI CEGKVIDPLL ECLKDWNGAP LPIC                    704

SEQ ID NO: 115         moltype = AA  length = 709
FEATURE                Location/Qualifiers
source                 1..709
                       mol_type = protein
                       organism = Ananas comosus
SEQUENCE: 115
MERAPSSTKK DLSMEDPLNW AGAAEPTKVS HFDEVKRMVE EFRKPLVRLA GANLTISQVA  60
AVAASEATVT VELSEAARAG VKASSEWVME SIDKGKDSTG ITAGFGAASH RRTEQGAALQ  120
NELIRFLNVG IFGDGLESGH MLPRAATRAA MLVRINSLLQ GYSGIRFEIL EAIASLLNAN  180
VTPCVPLRGS ITASGDLVPL AYIAGLLSGR PNSKAIGPDG MCIDAAEAFQ LARIIGGFFE  240
LRPKEGIALV NGTTVGSGLA SIVLFEANIL AVLSEVLSAV FCEVMQGKPE FTDHLTHKLK  300
HHPGQIEAAA IMEHILEGSS YMKKAKELHE LDPLQKPKKD RYAVCTSPQW LGPQIEVIRS  360
STKSIEREIN SVNDNPLIDV SRDKALHGGN FQGTPIGVSM DNTRLAVAAI GKLMFAQFSE  420
LVNDLYNNGL PSNLSGGRNP SLDYGFKGAE IAMAAYCSEL QFLANPVTTH VQSAEQHNQD  480
VNSLGLISAR KTAEAVDVLK LMSSTYVVAL CQAIDLRHLE ENLKAAVKHT VSQAAKRVLM  540
MGADGGLQPS MFCVEGLIKV IDREHVFSYI DDPCSSAYPL VQKLRQALVE HALSRGEKEK  600
DNDSSTFFLH RITAFEEELS AHLPKDVEAA WVAFGSGKSA IQNRIKECRS YPLYKFVKEE  660
LGTECLTGEK VRSPGEEFDK VFDAICQARM IDPLLECLKD WNGAPLPIS             709

SEQ ID NO: 116         moltype = AA  length = 701
FEATURE                Location/Qualifiers
source                 1..701
                       mol_type = protein
                       organism = Asparagus officinalis
SEQUENCE: 116
MENICMKTKQ ADPLNWGAAA EALTGSHLDE VKRMVEDFRN PVVKLEGADL KISQVAAVAM  60
GEGRVELAEA AREGVKASSD WVMESMGKGT DSDGVTTGFG ATSHRRTKQG GALQKELIRF  120
LNAGIFGSGR ESGNMLSTSA TRAAMLVRIN TLLQGYSGIR FEILEAITSF LNANITPCLP  180
LRGTISSSGD LVPLSYIAGM LTGRPNSKAI GPNGSEIDAA EAFKLAGIPS GFFELQPKEG  240
LALVNGTAVG SALASTVLFE ANILAVLAEI ISAVFCEVMQ GKPEFTDHLT HKLKHHPGQI  300
EAAAIMEHIL EGSSYMQMAK KVHELDPLQK PKQDRYALRT SPQWLGPQIE VIRSSTKSIE  360
REINSVNDNP LIDVSRNKAL HGGNFQGTPI GVSMDNTRLA IAAIGKLMFA QVSELVNDFY  420
NNGLPSNLSG GRNPSLDYGF KGAEIAMASY CSELQYLANP VTNHVESAEQ HNQDVNSLGL  480
ISSRKTAEAV EILKLMTSTF LVALCQAIDL RHLEENLKQA VKNTVSQVSK RVLTTGVNGE  540
LHPSRFCEKE LIKVIDREYV FAYIDDPCSY TYPLMQKVRQ VLVEHALNNG EKERDLNTSI  600
FQKIAVFEEE LKAVLPKEVE AARVAVENGS AAIANRIKEC RSYPLYRFVR EELGTELLTG  660
EKVRSPGEEF DKVFVAISQG KMIDAVLACL KDWNGAPLPI C                       701

SEQ ID NO: 117         moltype = AA  length = 567
FEATURE                Location/Qualifiers
source                 1..567
                       mol_type = protein
                       organism = Asparagus officinalis
SEQUENCE: 117
MLSTSATRAA MLVRINTLLQ GYSGIRFEIL EAITSFLNAN ITPCLPLRGT ISSSGDLVPL  60
SYIAGMLTGR PNSKAIGPNG SEIDAAEAFK LAGIPSGFFE LQPKEGLALV NGTAVGSALA  120
STVLFEANIL AVLAEIISAV FCEVMQGKPE FTDHLTHKLK HHPGQIEAAA IMEHILEGSS  180
YMQMAKKVHE LDPLQKPKQD RYALRTSPQW LGPQIEVIRS STKSIEREIN SVNDNPLIDV  240
SRNKALHGGN FQGTPIGVSM DNTRLAIAAI GKLMFAQVSE LVNDFYNNGL PSNLSGGRNP  300
SLDYGFKGAE IAMASYCSEL QYLANPVTNH VESAEQHNQD VNSLGLISSR KTAEAVEILK  360
LMTSTFLVAL CQAIDLRHLE ENLKQAVKNT VSQVSKRVLT TGVNGELHPS RFCEKELIKV  420
IDREYVFAYI DDPCSYTYPL MQKVRQVLVE HALNNGEKER DLNTSIFQKI AVFEEELKAV  480
LPKEVEAARV AVENGSAAIA NRIKECRSYP LYRFVREELG TELLTGEKVR SPGEEFDKVF  540
VAISQGKMID AVLACLKDWN GAPLPIC                                       567

SEQ ID NO: 118         moltype = AA  length = 701
FEATURE                Location/Qualifiers
source                 1..701
                       mol_type = protein
                       organism = Asparagus officinalis
SEQUENCE: 118
MENICMKTKQ ADPLNWGAAA EALTGSHLDE VKRMVEDFRN PVVKLEGADL KISQVAAVAM  60
GEGRVELAEA AREGVKASSD WVMESMGKGT DSYGVTTGFG ATSHRRTKQG GALQKELIRF  120
LNAGIFGSGR ESGNMLSTSA TRAAMLVRIN TLLQGYSGIR FEILEAITSF LNANITPCLP  180
LRGTISSSGD LVPLSYIAGM LTGRPNSKAI GPNGSEIDAA EAFKLAGIPS GFFELQPKEG  240
LALVNGTAVG SALASTVLFE ANILAVLAEI ISAVFCEVMQ GKPEFTDHLT HKLKHHPGQI  300
EAAAIMEHIL EGSSYMQMAK KVHELDPLQK PKQDRYALRT SPQWLGPQIE VIRSSTKSIE  360
REINSVNDNP LIDVSRNKAL HGGNFQGTPI GVSMDNTRLA IAAIGKLMFA QVSELVNDFY  420
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NNGLPSNLSG GRNPSLDYGF KGAEIAMASY CSELQYLANP VTNHVESAEQ HNQDVNSLGL  480
ISSRKTAEAV EILKLMTSTF LVALCQAIDL RHLEENLKQA VKNTVSQVSK RVLTTGVNGE  540
LHPSRFCEKE LIKVIDREYV FAYIDDPCSY TYPLMQKVRQ VLVEHALNNG EKERDLNTSI  600
FQKIAVFEEE LKAVLPKEVE AARVAVENGS AAIANRIKEC RSYPLYRFVR EELGTELLTG  660
EKVRSPGEEF DKVFVAISQG KMIDAVLACL KDWNGAPLPI C                      701

SEQ ID NO: 119         moltype = AA  length = 613
FEATURE                Location/Qualifiers
source                 1..613
                       mol_type = protein
                       organism = Asparagus officinalis
SEQUENCE: 119
MGEGRVELAE AAREGVKASS DWVMESMGKG TDSYGVTTGF GATSHRRTKQ GGALQKELIR  60
FLNAGIFSSG KXNPTIEAIT SFLNTNITPC LPLRGTISSS GDLVPLSYIA GMLTGRPNSK  120
AISPDGTHID AAEAFKLAGI PSGFFELQPK EGLALVNGTA VGSGLASTVL FEANILAVLS  180
EIISAVFCEV MQGKPEFTDH LTHKLKHHPG QIEAAAIMEH ILDGSSYMQM AKKVHELDPL  240
QKPKQDRYAL RTSPQWLGPQ IEVIRSSTKS IEREINSVND NPLIDVSRNK ALHGGNFQGT  300
PIGVSMDNTR LAIAAIGKLM FAQLSELVND FYNNGLPSNL SGGRNPSLDY GFKGAEIAMA  360
SYCSELQYLA NPVTNHVQSA EQHNQDVNSL GLISSRKTAE AVEILKLMTS TFLVALCQAI  420
DLRHLEENLK QAVKNTVSQV SKRVLTTGVN GELHPSRFCE LELIKMIDRE YVFAYIDEPC  480
SYNYPLMQKL RQVLVEHALN NGEKEKDVKT SIFQKIAAFE EELKAVLPKE VEAARVAVEA  540
GNAQIGNRIK ECRSYPLYKF VREELGTGLL TGEKVRSPGE EFDKVFVAIS EGKVIDPMLE  600
CLRDWNGAPL PIC                                                    613

SEQ ID NO: 120         moltype = AA  length = 705
FEATURE                Location/Qualifiers
source                 1..705
                       mol_type = protein
                       organism = Asparagus officinalis
SEQUENCE: 120
MSHVNGNGVC VAADPLNWGA AAQSLSGSHL DEVKKMVKDY REGPVRIEGA TLKVAHVAAV  60
AAGEATARVE LDESARARVK ASSDWVMESM GKGTDSYGVT TGFGATSHRR TKEGGALQKE  120
LIRFLNAGIF GSGPESGNTL PAPATRAAML VRINTLLQGY SGIRFEILEA ITRLLNSNIT  180
PVLPLRGTIS SSGDLVPLSY IAGMLTGRPN SKAVAPDGRT VDATEAFKLA GIDGGFFELQ  240
PKEGLALVNG TAVGSGLAST VLFDANVLLV LSEVLSAMFC EVMQGKPEYT DHLTHKLKHH  300
PGQIEAAAIM EHILDGSSYM KMAKKLHEQD PLQKPKQDRY ALRTSPQWLG PLTEVIRAAT  360
KSIEREINSV NDNPLIDVSR NKALHGGNFQ GTPIGVSMDN TRLAIAAIGK LMFAQFSELV  420
NDFYNNGLPS NLSGGRNPSL DYGFKGAEIA MASYCSELQF LANPVTNHVE SAEQHNQDVN  480
SLGLISSRKT AEAVQILKLM SSTFLVGLCQ AINLRHLEEN LRSTVKNTVS QVAKRILTVG  540
VNGELHPSRF CELDLIKVVE REPVFAYIDD PCSATYPLMQ KLRQVLVEHA LTNGDKEKPV  600
NTSIFHRIEE FEDELKALLP KEVEGVRMAF ENGRLSIPNR IKECRSYPLY RLVREELGAE  660
YLTGERVRSP GEEFDKVFNA ICGGKLIDPL LECLSEWNGA PIPIC                 705

SEQ ID NO: 121         moltype = AA  length = 705
FEATURE                Location/Qualifiers
source                 1..705
                       mol_type = protein
                       organism = Asparagus officinalis
SEQUENCE: 121
MSHVNGNGVC VAADPLNWGA AAQSLSGSHL DEVKKMVKDY REGPVRIEGA TLKVAHVAAV  60
AAGEATARVE LDESARARVK ASSDWVMESM GKGTDSYGVT TGFGATSHRR TKEGGALQKE  120
LIRFLNAGIF GSGPESGNTL PAPATRAAML VRINTLLQGY SGIRFEILEA ITRLLNSNIT  180
PVLPLRGTIS SSGDLVPLSY IAGMLTGRPN SKAVAPDGRT VDATEAFKLA GIDGGFFELQ  240
PKEGLALVNG TAVGSGLAST VLFDANVLLV LSEVLSAMFC EVMQGKPEYT DHLTHKLKHH  300
PGQIEAAAIM EHILDGSSYM KMAKKLHEQD PLQKPKQDRY ALRTSPQWLG PLTEVIRAAT  360
KSIEREINSV NDNPLIDVSR NKALHGGNFQ GTPIGVSMDN TRLAIAAIGK LMFAQFSELV  420
NDFYNNGLPS NLSGGRNPSL DYGFKGAEIA MASYCSELQF LANPVTNHVE SAEQHNQDVN  480
SLGLISSRKT AEAVQILKLM SSTFLVGLCQ AINLRHLEEN LRSTVKNTVS QVAKRILTVG  540
VNGELHPSRF CELDLIKVVE REPVFAYIDD PCSATYPLMQ KLRQVLVEHA LTNGDKEKPV  600
NTSIFHRIEE FEDELKALLP KEVEGVRMAF ENGRLSIPNR IKECRSYPLY RLVREELGAE  660
YLTGERVRSP GEEFDKVFNA ICGGKLIDPL LECLSEWNGA PIPIC                 705

SEQ ID NO: 122         moltype = AA  length = 707
FEATURE                Location/Qualifiers
source                 1..707
                       mol_type = protein
                       organism = Acorus americanus
SEQUENCE: 122
MENGFCMKKE EEVVDPLNWA KSAEPLMGSH LEEVKRMVEE FRNPLVCLEG ADLKISQVAA  60
VAAEGGGHVR VELSEAARPR VKASSDWVME SMNKGTDSYG VTTGFGATSH RRTKQGGALQ  120
KELIRFLNAG IFGSSNDSSN TLPPPATRAA MLVRTNTLLQ GYSGIRFEIL ESITALLNTG  180
VTPCLPLRGT ITASGDLVPL SYIAGMLTGR PNAKAIGPDG RTIDATEAFR AAGIQTGFFE  240
LQPKEGLALV NGTAVGSGLA SMVLYEANVL SLLAEVLSAV FCEVMQGKPE YTDHLTHKLK  300
HHPGQIEAAA IMEHILDGSS YMKLAQKLHE QDPLQKPKQD RYALRTSPQW LGPQIEVIRA  360
ATQSIQREIN SVNDNPLIDV SRNKALHGGN FQGTPIGVSM DNTRLAIAAI GKLMFAQFSE  420
LVNDFYNNGL PSNLSGGRNP SLDYGFKGAE IAMAAYCSEL QFLGNPVTNH VQSAEQHNQD  480
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VNSLGLISSR KTAEAVEILK LMSATYLVGL CQAIDLRHLE EILRNTVRNT VMQVAKRVLT  540
MGGNGELHPS RFCEKDLIKV VDRESVYAYV DEPCSATYPL MQKLRQVLVE HAINNGEKER  600
EVGTSIFQKI GVFEEEIKAV LPKEVEAARV AYEAGNASVG NRIAECRSYP LYRFVREELK  660
TGLLTGEKVR SPGEEFDKVF VAISEGRVID PLLECLSDWN GAPIPIC                707

SEQ ID NO: 123          moltype = AA  length = 720
FEATURE                 Location/Qualifiers
source                  1..720
                        mol_type = protein
                        organism = Acorus americanus
SEQUENCE: 123
MEHSLNGFTN GSVNQNGLCL KKEAASTDPL NWAKSTEPLM GSHLEEVKKM VEEFRNPLVS  60
LEGADLKISQ VAAVAAGGGE GVRVQLSETA RPRVKASSDW VMDSMSKGTD SYGVTTGFGA  120
TSHRRTKQGG ALQKELIRFL NAGIFGASND TGNTLPPPAT RAAMLVRINT LLQGYSGIRF  180
EILESITAFL NTGITPCLPL RGTITASGDL VPLSYIAGML TGRPNSKAIG PDGQTIDATE  240
AFRLSGIQTG FFELQPKEGL ALVNGTAVGS GLASMVLYEA NILSVLAEVI SAVFCEVMQG  300
KPEYTDHLTH KLKHHPGQIE AAAIMEHILD GSSYMKLAQK LHEQDPLQKP KQDRYALRTS  360
PQWLGPQIEV IRSATQSIQR EINSVNDNPL IDVSRNKALH GGNFQGTPIG VSMDNTRLAI  420
AAIGKLMFAQ FSELVNDFYN NGLPSNLSGG RNPSLDYGFK GAEIAMAAYC SELQFLGNPV  480
TNHVQSAEQH NQDVNSLGLI SSRKTAEAVE ILKLMSATYL VGLCQAIDLR HLEEIMRNTV  540
RNTVSQVAKR TLTMGVNGEL HPSRFCEKDL IKVIDREYVF AYVDDPCSAT YPLMQKLRQV  600
LVEHALNNGE KEKEWSTSIF QKISLFEEEL KAVLPKEVEA ARAAYEAGNS SVSNRIEECR  660
SYPLYKFVRE ELKTGLLTGE KVRSPGEEFD KVFVAISQGK VIDPLLECLS GWNGAPIPIC  720

SEQ ID NO: 124          moltype = AA  length = 712
FEATURE                 Location/Qualifiers
source                  1..712
                        mol_type = protein
                        organism = Zostera marina
SEQUENCE: 124
MDAMDLCQVK LSNGATNGIT DADPLNWGAA AEELTGSHLQ EVKRMVEDFN NPLVKIEGAT  60
LKISQVAAVA TASAEVQLSE TARERVTASS HWVMDSMNKG TDSYGVTTGF GATSHRRTKQ  120
GGALQKELIR FLNAGIFGGS KDTANTLPSA TTRAAMLVRA NTLLQGYSGI RFEILEAMTK  180
FLNGNITPCL PLRGTITASG DLVPLSYIAG FLTGRTNSKA IGPDGKQITS SEAFAIAGIQ  240
EGFFQLQPKE GLALVNGTAV GSGLASMVLF DANILALSAE VLSAVFCEVM QGKPEFTDHL  300
THKLKHHPGQ IEAAAIMEHI LDGSSYMKMA AKIHEQDPLQ KPKQDRYALR TSPQWLGPQV  360
EVIRASTKSI EREINSVNDN PLIDVSRNKA LHGGNFQGTP IGVSMDNTRL AIAAIGKLMF  420
AQFSELVNDF YNNGLPSNLS GGRNPSLDYG FKGGEIAMAS YCSELQFLAN PVTNHVQSAE  480
QHNQDVNSLG LISARKTAES IEILKLMTST FLVGICQAID LRHMEENLKA SVKNTVSQVA  540
KRVLTMTANG ELHPSRFCEK DLLKVVDREY VFSYIDDPCS ATYPLMQKLR SVLVDHALNN  600
GDKEKDEAMS IFQKIAVFEE ELIAALPKEV EAARLAVEAG KPAIANRIEE CRSYPLYKFV  660
REELRTGLLT GEKVRSPGEE FDKVFVAINE GELVGPLMEC LKEWNGAPIP IC          712

SEQ ID NO: 125          moltype = AA  length = 694
FEATURE                 Location/Qualifiers
source                  1..694
                        mol_type = protein
                        organism = Zostera marina
SEQUENCE: 125
MGADPLKWEE AAEGMKGSHV AEVKQMIEDF RNPLVVLEGK NLKIAHVAAV AGDSSGSVGV  60
VVSQENRVVV AASSDWIMES MNKGTDSYGV TTGFGATSHR RTKQGGALQA ELIRFLNAGI  120
FSSGNSDSCN MLPASTTRAA MLVRINSLLQ GYSGIRFEIL EALTDFLNHN ITPCLPLRGS  180
ITASGDLIPL SYIVGLLIGR PNSKAIAPDG TQITAEKAFS LAGIHSGFFE LQPKEGLALV  240
NGTTVGSGLA STVLFDANIL SILAEVLSAV FCEVMAGKPE FTDHLTHKLK HHPGQIEAAA  300
IMEHILDGSS YMKNVNEHDP LQKPKQDRYA LRTSPQWLGP QIEVIRASTK SIEREINSVN  360
DNPLIDVKRG KAIHGGNFQG TPIGVSMDNT RLAIAAIGKL VFAQFSELVN HFYNNGLPSN  420
LSGGSNPSLD YGFKGGEIAM ASYCSELQFL GNPVTNHVQS AEQHNQDVNS LGLISARKTA  480
ESVEILKMMS ATFLVALVQA VNLRHLEENM KRTVKNVVGQ VAKRVLTLGV NSELHPSRFC  540
EKDLIKVIDR EQVFDYIDDP CNATYPLMEK LRGVLVDHAL GNWEKETDVS TSIFQKIPTF  600
EAELKLTLPK EVDAARLAHE NGNSVVGNRI KDCRSYPLYR FVTEELGVGL LTGEKIRSPG  660
EEFDKVFAAI NRGELIDPLF HCLADWNGSP LPIS                              694

SEQ ID NO: 126          moltype = AA  length = 710
FEATURE                 Location/Qualifiers
source                  1..710
                        mol_type = protein
                        organism = Amborella trichopoda
SEQUENCE: 126
MEFSAHQSHS NGKLDGLCVS DPLNWTAMAE TFKGSHLEEV KKMVSEFQKP LVKLEGHSLS  60
IAKVAAVARK EHDVSVELSH EARPRVQASS NWVMDSMTKG TDSYGVTTGF GATSHRRTRN  120
GEALQKELIR FLNAGIFGDN SDLTLPRSTT RAAMLVRVNT LLQGFSGIRF EILEAIAALL  180
NKGISPCLPL RGTITASGDL VPLSYIAGLL TGRPNAKAIG PNGQVMSSEE ALNLAGVQSG  240
PFELQPKEGL ALVNGTAVGS GLASTVLFDA NILAILAEVL SAIFCEVMQG KLEFTDHLTH  300
KLKHHPGQIE AAALMEHILA GSYYMKEAAR IHEFDPLQKP KQDRYALRTS PQWLGPQIEV  360
IRAATKSIER EINSVNDNPI IDVSRNKALH GGNFQGTPIG VSMDNTRLAL AAIGKLMFAQ  420
FSELVNDFYN NGLPSNLSGG RNPSLDYGFK GAEIAMASYT SELQFLANPV TNHVQSAEQH  480
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NQDVNSLGLI SSRKTAEAIE ILQLMSATFI SALCQAIDLR QLEENLKAAV KLAVGQAVKK  540
VLTMRENGEL LPSRFCEKDL LNVVEREYVF AYADDPCSSN YPLMQKLRGV LVEHALASGE  600
KEKEMGSSIF ERIGLFEQEL KAILPKEVET ARASVEKGDS AIPKRIKECR SYPIYKFVRS  660
VLGTELLSGE RQRSPGEEFD KVFEAIRGGR IIEPLLDCVK EWDGTPLPIC             710

SEQ ID NO: 127         moltype = AA  length = 690
FEATURE                Location/Qualifiers
source                 1..690
                       mol_type = protein
                       organism = Amborella trichopoda
SEQUENCE: 127
MKSVSTDPLN WGSFAEGSHL SLVKKLVDEF RCRTISLSGT DLSIAHVAAV SSGAPNSGPR  60
VDLSSESMSN VSASCQWITE SSTKGADTYG VTTGFGASSH RRTNQADSLQ RELIRFLNAG  120
IINADNPALP VSATRAAMIV HTNTLMKGYS GIRWKILRAL VALLNSGVTP LVPLRGTITA  180
SGDLVPLSYI AGVLICRPNA QAIAPDGSIV GAKQALEMAN TSDGPFELGP KEGVALVNGT  240
SVGAGLASLV LFDANILAVL SEVLSAIFCE AMGGKPEFCD HLVHKLKHHP GQIEAGAIME  300
HILAGSSYMN RVAKFHGTSP SQKPKKDRYA MVTSPQWLGP QIEVIRAATE TIQKEINSVN  360
DNPLIDVSRN KTIQGGNFQG TAIGVAMDNT RLALAAIGKL MFAQFTELVN DFYNNGLPSN  420
LSGGPNPSLD FGFKGAEVAM ASYMSELGFL ANPVTNHVQS AEQHNQDVNS LGLISARKTN  480
EAVEILKLMS STYLVALCQA IDLRHIEENL QGAVNRAVSR VARQVLDATI EGELSGSNLC  540
EELLRVVEAE YAFSYIDDPC NPNYPLIQKL RGVLFGRVMA AKKEVGILVL QKIEDFELEL  600
KNHLPKEVEL TREAIEKGNS MIPNRIRECR SYPLYRFVRS ELEVGFLSGE RTVSPGEEFN  660
KVSIAINKGK LIDPLLECLH GWDGAPLPIC                                  690

SEQ ID NO: 128         moltype = AA  length = 737
FEATURE                Location/Qualifiers
source                 1..737
                       mol_type = protein
                       organism = Calamus simplicifolius
SEQUENCE: 128
MASPDAPSHF IRDLRPPTLP IPIDGVNPIA VSGTSYVPHP PHWKKAAEAL DCAHFNEVHR  60
MISQFSSVSS VKIEGTTLTI ADVAAVARRA AVFVELDAAA ARTRVDCSVN WVAETVKRGT  120
DTYGVTTGFG ATSHYRTKKF AELQTELIRF LNAGVIGREP LSSTYAKAAM LVRINTLMQG  180
YSGIRWELLE AITKLMNHNL IPKLPLRGTI TASGDLVPLS YIAGLLTGRH NSRVITPEGD  240
EITSTEALKR VGIDRPFDLQ AKEGLALVNG TAVGSAVAAT VCYDANILAI LSVILSAMFC  300
EAMQGNPEFA DPLTHELKHH PGQIESAAIM EYLLDGSDYM KEALLRHEKE PLTKPKQDRY  360
ALRTSPQWLG PQIEVIRMAT HSIEREINSV NDNPLIDVAR DIALHGGNFQ GTPVGVSMDN  420
LRIALAAIGK LVFAHSPSSL DYGLKGAEIA MAAYCSELQY LANPVTTHVQ SAEQHNQDVN  480
SLGLISARKS AEAVEILKLM MATYMVGLCQ AIDLRQLEEN LKEVVKHAVM QAARKALFVA  540
EDGSLLETRF CEKDLIQVVE KQPVFSYIDD PANPAYALML QLREVLVEKA LEGSEEGMVM  600
FKRTPKFQEE LKERLREEVG RARERFEKGD FIVGNRIRKC RTYPVYQLVR EELGTELLTG  660
KKKVSPGEHI EKVYQAIVEG KVGSVVVKCV EGWRGSAGPF TPRPDVSSPV HRRPEFWAWF  720
EQGRSPSATS GRGYWNL                                                737

SEQ ID NO: 129         moltype = AA  length = 729
FEATURE                Location/Qualifiers
source                 1..729
                       mol_type = protein
                       organism = Calamus simplicifolius
SEQUENCE: 129
MASPDGPVRS IRNLRPPTLP IPADGINPIA VSGTSYVPHP PHWKKAAEAL DCAHFDEVHR  60
MISQFSSVSS VKIEGTALTV ADVAAVARCA AVSVELDAAA ARARVDRSAA WVAEKIDSGT  120
DTYGVTTGFG ATSHRRTKKT ADLQTELIRF LNAGVIGTEA LPSKYAKAAM LVRTNTLMQG  180
YSGIRWELLE TIVKFMNHNL IPKLPLRGTI TASGDLVPLS YIAGLLTGRH NSRVITPEGD  240
EIASTEALKR VGIDRPFDLQ AKEGLALVNG TAVGSAVAAT VCYDANILVI LSVILSAMFC  300
EAMQGKPEFT DPLTHELKHH PGQIESAAIM EYLLDGSDYM KEALLRHEKE PLTKPKQDRY  360
ALRTSPQWLG PQIEVIRMAT HSIEREINSV NDNPLIDVAR DIALHGGNFQ GTPIGVSMDN  420
LRIALAAIGK LVFAQFSELV CDYYNDGLPS NLCAGADPSL DYGLKGAEIA MAAYCSELQY  480
LANPVTTHVQ SAEQHNQDVN SLGHRFEAVG GEPERGGEAR GDASCEESPV RGRGRELLET  540
RFCEKDLIQV VEKQPVFSYI DDPANPAYAL MLQLREVLVE KALEGSEEGM VMFKRVPKFQ  600
EELKERLREE VGRARERFEK GDFIVGNRIR KCRTYPVYQL VREELGTELL TGEKKVSPGE  660
YIEKVYQAIG EGKVGSVVVK CVEGWRGSAG PFTPRPNVSS PVHKKPEFWA WFEQGRSPSA  720
TSGRGYWNL                                                         729

SEQ ID NO: 130         moltype = AA  length = 757
FEATURE                Location/Qualifiers
source                 1..757
                       mol_type = protein
                       organism = Elaeis guineensis
SEQUENCE: 130
MASPNTPFRS IRALRPPTLP VPADGINPIA VSGTSYVPNP PHWKKAAEAL DCAHFDEVHR  60
MISQFSSLSS VKIEGTTLTV AAVAAIARRA AVSVELDAAS AQSRVDRSAA WVAENIERGT  120
DTYGVTTGFG ATSHRRTKKT ADLQTELIRF LNAGVIGTEP LPSSYAKAAM LVRTNTLLQG  180
YSGIRWELLE TIAKLMNHNL IPRLPLRGTI TASGDLVPLS YIAGVLTGRH NSRVITPEGD  240
EIAATEALKR VDINRPFDLQ AKEGLALVNG TAVGAAVAAT VCYDANILAV LSVILSAMFC  300
EAMQGKPEFT DPLTHELKHH PGQIESAAIM EYLLDGSDYM KEAQLRHERE PLTKPKQDRY  360
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ALRTSPQWLG PQIEVIRMAT HSIEREINSV NDNPLIDVAR GIALHGGNFQ GTPIGVSMDN  420
LRIALAAIGK LVFAQFSELV CDYYNDGLPS NLSAGADPSL DYGLKGAEIA MAAYCSELQY  480
LANPVTTHVQ SAEQHNQDVN SLGLISARKS AEAVEILKLM IATYMVALCQ AIDLRQLEEN  540
LKEVVKHSVM QAARKALFVA EDGSLLETRF CEKDLIQVVE KQPVFSYIDD PGNPAYALML  600
QLREVLVEKA LEGSEAGMAM FKRIPEFQEE LRQRLREEVG KARERFGKGD FMVGNRIKKC  660
RTCPVYRFVR EELGTELLTG EKKVSPGEYI EKVYQAIGEG KVGSVVVECV EGWRGSAGPF  720
TPRPEVSSPV HKKPEYWGWF EQGRSPSATS GRGYWNL                           757

SEQ ID NO: 131          moltype = AA  length = 698
FEATURE                 Location/Qualifiers
source                  1..698
                        mol_type = protein
                        organism = Elaeis guineensis
SEQUENCE: 131
MAFPGKPSEP NVCIHSHPIA DSASAYISDP YHWKKAAETL SSAYFDEVRR MITQFSELTS  60
ICLQGTTSLT VAQVAAITRR SSVTVTLDAA TARARVDRSA AWVAEHSNTA GFGASSHRRT  120
NKTGDLQAEL IRFLNAGVIG ADPFPSSYTK AAMLVRTNTL MQGYSGVRWE LLEAMSKLMN  180
QNLIPKIPLR GSICELLPLS YIAGVLIGRD NSLVTTLEGR EITSMEALKR VGIDRPFELH  240
SREGIALVNG TALGSAVAAA ACYDANILAI LAVILSAIFC EAMRGRPEFG DPLTHELKHH  300
LGQIESAAIM KYLLEGSDYM KEAELRRGRE PPTKPKQDRY ALRTSPQWLG PQIELIRMAT  360
HSIEREINSV DDNPLVDISR GVFLRGGNFQ GTPIDVSMDS LRIALAAIGK LIFAQFSELV  420
CDYYNDGLPS NLSAGADPSL DYGFKGAEIA MAAYCSELQY LANPVTAHVQ SAEQNNQDVN  480
SLGLIAARKS VEAVEILRLM MATYMVALCQ AIDLRQLEEN LREVVKQAVV EAARKVLDSA  540
EDGSLSEARF WEKDLIQVVE RLPVYSYIDD PGNAKNALMQ QLREALVEKA LEGNEEGRVV  600
FKRISEFQEE ARQRSREEVE RARERFRKGD FVIGSRINKC RTYPMYKFVR EEVGTELLTG  660
EKKVSPGEYI EKVYEAMKER RFFYYHIVYI MSVIHPLS                          698

SEQ ID NO: 132          moltype = AA  length = 661
FEATURE                 Location/Qualifiers
source                  1..661
                        mol_type = protein
                        organism = Calamus simplicifolius
SEQUENCE: 132
MAFPRKPSES TVCDSQATFI SDPDPWKKAA ETLSSTYFDE ASRMITQFSE LTSICLQGTP  60
LTVAQVAAIT SRPSVAVTLD AATAHARVDD SAAWVAERSN TTAGFGASSH RGTNKTADLQ  120
AELIRFLNAG VVGADPLPAS YTKAAMLVRT NTLMQGYSGV RWELLEAMTK LMNHNLIPKI  180
PLRGSICELL PLSYIAGVLI GRHNSLVITP EGDEITSVEA LKRAGIDRPF ELHSREGIAL  240
VNGTALGSAV AAAVCFDANI LALLSVVLSA MFCEAMQGRP EFAHPLTHEL KHHPGQIESA  300
AIMKYLLDGS DYMKEAELRR DREPITKPKQ DRYALRTSPQ WLGPHIELIR MATHSIEREI  360
NSVDDNPLID VSRGVFLRGG NFQGTPIDVS MDSLRIALAA IGKLVFAQFS ELVCDYYNNG  420
LPSNLSAGAD PSLDYGLKGR RSRWQPRKSV EAVEILRLMM ATYIVALCQA IDLRQWEENL  480
REVVKQAVVQ AASKALDSAE DGRSSEARFW EKDLIQVVER LPVYSYIDDP ANAKYALMQQ  540
LREVLVEKAL QGGEEERVVF KSIPKFQEEV RERLKEEVGR ARERFGKGDF VIGNRISKCR  600
TYPVYKFVRE EVGTELLTGE KKVSPGEYIE KVCKAMKEKR VGEVIVECIE GWSGLAANKN  660
R                                                                  661

SEQ ID NO: 133          moltype = AA  length = 686
FEATURE                 Location/Qualifiers
source                  1..686
                        mol_type = protein
                        organism = Ananas comosus
SEQUENCE: 133
MASPNPKGST RPIRRPRPPT LPVPTDGINP IAVSGTSYVP DPPHWAAAAD ALRCTHFDDV  60
HRMVAQFSSV ASVDLEGTAL TVAQVAAVAR RPAVSVALDA AAARARGYSG IRWELLEAMA  120
KLMNHNLIPK MPLRGTITAS GDLVPLSYIA GVLTGRHNVR VLAPDGGEIS AAEALARAGV  180
GPAFELQAKE GLALVNSTAV GAAVAATVCY DANVLAVLSV VLSAMFCEAM NGKPEFADPL  240
THELKHHPGQ IESAAIMEFL LDGSDYVSEA KLRHEREPLT KPKQDRYALR TSPQWLGPQI  300
EVIRTATHSV EREINSVNDN PLIDVARDMA LHGGNFQGTP IGVSMDNLRI ALAAVGKLVF  360
AQFSELVCDY YNDGLPSNLS AGEDPSLDYG LKGAEIAMAA YCSELQYLAN PVTTHVQSAE  420
QHNQDVNSLG LISARKSAEA VDILKLMMAT HMVGLCQAVD LRRLEELLLE AVKRAVARAA  480
RKALYVADDG ALSEARFCEK ELLQVVERQP VFSYIDDPAN PNYALMLQLR EVLVEKALGG  540
SEEGMAAFKR IPQFQEELKR VLKEEVGKTR EEFTSKKDET LKSRIEKCRT YPVYRFVRAE  600
VGTEMLTGEK RASPGEHIEK VYAAMGEKGR IGEVVVECVG AWRGTPGPFT PRPEVASPAN  660
RNPENWGWFD PVRSPSATSG RGYWNL                                       686

SEQ ID NO: 134          moltype = AA  length = 703
FEATURE                 Location/Qualifiers
source                  1..703
                        mol_type = protein
                        organism = Musa acuminata
SEQUENCE: 134
MDSPGSYIRP IRCFRPPTLP VPTDGINPIA VSGTSYVPDP PHWKKAAEAL SCAHFDEVHR  60
MITQFSTLSS VDLEGTTLTV AQVAAVSRRL TVSVVLDADT ARERVDRSAA WTELIRFLNA  120
GVVGKEFLPS SYAKAAMLVR TNTLMQGYSG IRWELLEAIA KLMNCNMIPK LPLRGTITAS  180
GDLVPLSYIA GLLTGRHNSR VVTPEGDEIT SVEALKRVGI GAPFELQAKE GLALVNGTAV  240
GSAVAATVCY DANILALLSV ILSAMFCEAM QGKPEFTDPL THELKHHPGQ IESAAIMEFL  300
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LDGSDYMKEA KLRHEREPLT KPKQDRYALR TSPQWLGPQI EVIRTATHSI EREINSVNDN  360
PLIDVARDIA LHGGNFQGTP IGVSMDNLRV ALAAIGKLVF AQFSELVCDY YNDGLPSNLS  420
AGADPSLDYG LKGAEIAMAA YCSELQYLAN PVTTHVQSAE QHNQDINSLG LISARKSAEA  480
VEILKLMMAT YMIALCQAID LRHLEENLRE VVKHVLLQSA RKSLYVAEDG RLTEARFCEK  540
ELIQVAERQP VFSYIDDPAN PSYALMLQLR EVLVEKALEG TEEGMAAFKR IPKFQEELGS  600
ALNEEIAKAR ERFGRGDFIV GSRIKKCRTY PVYNFVREEV GTELLTGEKK VVVKCVGEWR  660
GSAGPFTPRP EASSPALRNP ENWSWFEQVR SPSATSGRGY WNL                    703

SEQ ID NO: 135         moltype = AA  length = 741
FEATURE                Location/Qualifiers
source                 1..741
                       mol_type = protein
                       organism = Zostera marina
SEQUENCE: 135
MALAKKFSIN VPATQTDEAS KTSHWTKASE AIQSNHFDEV RRMISQFSNS ESVNIEGASL  60
TVAQVSAIAR NSSRPVTLDA SAARERVDRS ANWVADNIAR GTDTYGVTTG FGSTSHRRTK  120
KTSDLQAELI RFLNAGVIGK DYLPINFAKA AMLVRTNTLM QGYSGIRWEV LEAMEKLMNK  180
NLIPKLPLRG TITASGDLVP LSYIAGFLTG RHNSSAVTSD GEVISSQEAL KRIGIDEPFE  240
LQAKEGLAIC NGTAVGSAVA ATVCYDANIL GYLAVTLSAM FCEAMQGKSE FTDPLTHKLK  300
HHPGQIEAAA IMEYILDGSD LLKEAKARND REPLTKPKQD RYALRTSPQW LGPQLEVIRM  360
ATHSIEREIN SVNDNPIIDV DRDIALHGGN FQGTPIGVSM DNIRIAIAAI GKLMFAQFSE  420
LVCDYYNNGL PSNLPGGKDP SLDYGLKGAE IAMASYCSEI QYLANPVTTH VQSAEQHNQD  480
VNSLGLISAR KSAEAIEILK LMSSTYMVGL CQAIDLRHLE ENLREVVKHS VLQTARKTLY  540
TTEDGSLSST RFCEKELLQV VECQPVFSYI DDPANTSYAL LLQLREVLVE KSLTSEEDKD  600
GYFVFKKITE FTNDLKVRVA KDVEVAREKF EKGEYLVGKR IGKCRTNGVY QLVRNVAQTE  660
ILTGEKKVSP GECIEKVYDC ILQGKLEDVL VKCLSMWKGM AGPFSPRPDL MSPVYKNPDT  720
WGWFDNMRSP SSTSGRGFWS K                                            741

SEQ ID NO: 136         moltype = AA  length = 744
FEATURE                Location/Qualifiers
source                 1..744
                       mol_type = protein
                       organism = Zostera marina
SEQUENCE: 136
MANSTKSAMI RSITVPAVSE NAPAQHWKKA SEAIQSNHFD EVRQMITQFS QSQSVNIEGT  60
SLTVAQVAAI TRRADVRVTL DADAARARVS RSATWVSDNI ARGTDTYGVT TGFGSTSHRR  120
TNKTSDLQAE LIRFLNAGVI GKDHLPLSYS KAAMLVRTNT LMQGYSGIRW EVLQGMEKLM  180
NKNVIPKLPL RGTITASGDL VPLSYIAGLL TGRHNSRAVT AEGEVLTSLE ALKHAGIDGP  240
FELQAKEGLA LVNGTAVGSA VAATVCYDAN IIGYLAVILS AMFCEAMQGK PEFTDPLTHA  300
LKHHPGQIEA AAIMEFILDG SDFMKEAKAR NEREPLTKPK QDRYALRTSP QWLGPQLEVI  360
RMATHSIERE INSVNDNPII DVDRDIALHG GNFQGTPIGV SMDNIRIALA AIGKLMFAQF  420
SEMVCDYYNN GLPSNLPGGK DPSLDYGLKG AEIAMASYCS ELQYLANPVT THVQSAEQHN  480
QDVNSLGLIS ARKSAEAIEI LKLMSSTYMV GLCQAIDLRQ MEENLREVVK HSILQSIKKT  540
LYMSEGDSDL ARTRFCEKEL LQVVECQPVF SYIDDPSNSS YALLLQLREV LVEESLKSSK  600
EEVGYSAFKK ITVFEEDLKE RVVKDVAVAR EEIEKGVYMV GNRIRKCRTK SVYDLVRKVA  660
QTEILTGEKK ISPGECIEKV YEVFEQGKVE DALLQCLDIW KGNTGPFTPR PELMSPVHKN  720
PEAWGWFDNL RSPSSTSGRG YWSK                                         744

SEQ ID NO: 137         moltype = AA  length = 758
FEATURE                Location/Qualifiers
source                 1..758
                       mol_type = protein
                       organism = Spirodela polyrhiza
SEQUENCE: 137
MAAQTNGLVR PTEAFRPPTL PLPKDGINPI FVSGDSYIPD PPHWKKAAEA LQCTHFEEVR  60
RMISQFQSTQ TVDLQGTTLT VAQVAAVSRR QEVAVRLNEP VARDRVDRSA KWVADNIARG  120
TDTYGVTTGF GATSHRRTKK VTDLQTELIR FLNAGVIGKD FLPTSYSKAA MLVRTNTLMQ  180
GYSGIRWEVL EAVTKLMNQN VIPKLPLRGT ITASGDLVPL SYIAGLLTGR HNSRAVTPEG  240
EELTSSEALK RVGILCPFEL QAKEGLALVN GTAVGSAVAA TVCFDANVLA LLSVVLSALF  300
CEAMQGKPEF ADPLTHELKH HPGQIESAAI MEFLLDGSDY MREAKLRNER EPLTKPKQDR  360
YALRTSPQWL GPQIEVIRMA THAIEREINS VNDNPLIDVA RDIALHGGNF QGTPVGVSMD  420
NLRIAIAAIG KLVFAQFSEL VCDYYNNGLP SNLSGGEDPS LDYGLKGAEI AMAAYCSELQ  480
YLANPVTTHV QSAEQHNQDV NSLGLISARK SAEAVEILKL MMSTYMVGLC QALDLRHLEE  540
NLREVVKHAV TEAARKTLYT AEDGTMLESR FCEKDLLQVV ECQPIFSYID DPANPSYALL  600
LQLREVLVEK SLNKSEDGYA VFTRIPVFQE ELKARLSEEV PQARQRFEKG DFLVPHRARR  660
CRTYPIYKLV RSVAGAEFLT GEKKISPGEC IEKVVDAIDE GKLGDALSAC LAMWRGSAGP  720
FTPRPEVTSP AHCNPEFWSW FDKMRSPSAT SGRGYWNN                           758

SEQ ID NO: 138         moltype = AA  length = 762
FEATURE                Location/Qualifiers
source                 1..762
                       mol_type = protein
                       organism = Acorus americanus
SEQUENCE: 138
MASTEAFTRP IESLRPPTLP LPTAGKNPIS VSGNSYVSNP PHWQKASEAL LCTHFDEVRK  60
MVDQYRNSPS VDLTGTSLTV AQVAAITRRP EVSVALDAAA AKARVARSAQ WVADNIARGT  120
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DTYGVTTGFG ATSHRRTNKT ADLQAELIRF LNAGVIGKEH LPASYAKAAM LVRTNTLMQG  180
YSGIRWELLE AMEKLMNHNL IPKMPLRGTI TASGDLVPLS YIAGLLTGRH NSVAVATETG  240
ELVKATEALK RIGVNTPFEL QAKEGLALVN GTAVGSAVAA TVCYDSNVLA LLAEVLSAAF  300
CEAMHGKPEF TDPLTHELKH HPGQIESAAI MEYLLDGSDL IKAAQARHEK DPLTKPKQDR  360
YALRTSPQWL GPQIEVIRAA THSIAREINS VNDNPIIDCD RDMALHGGNF QGTPIGVSMD  420
NLRIAIAAIG KLVFAQFSEL VCDYYNNGLP SNLSGGPNPS LDYGLKGAEI AMASYCSELQ  480
YLANPVTTHV QSAEQHNQDV NSLGLISARK SAEAVDILKL MMSTYMVGLC QAFDLRHLEE  540
NMREVVKHVV LKTAKKTLYC EESDGTLLES RFCEKELLMV VEHQPVFSYI DDPANPSYAL  600
LLQLREVLVE KALKDLKDDT SSVVFKRIPL FQEELKKRLT EEVLKARERF DEGDFPVPNR  660
AKKGRTSAVY EFVRGEVGTE LLTGEKKTSP GEQIEKVYEA MMEGKVEGVL MRCLSFWRGS  720
AGPFTPRPAA GSPAQHNPEY WGWFENMRSP SATSGRGYWN NM                    762

SEQ ID NO: 139         moltype = AA  length = 730
FEATURE                Location/Qualifiers
source                 1..730
                       mol_type = protein
                       organism = Acorus americanus
SEQUENCE: 139
MASTEAITRP IESLRPPILP LPTAGDNPIS VSGNSYVSNP PHWKKASEAL LCTHFDEVRK  60
MVDQYRNSPD VSLTGTSLTV AQVAAVTRRP TVSVTLDGAA AKSRVARSAQ WVADNSLRDT  120
NGITTGFGAT SHRRTNKTAD LQEELIRFLN AGVIGKDNLP ASYAKAAMLV RTNTLMQGYS  180
GIRWELLEAM EKLMNHNLIP KLPLRGTITA SGDLIPLAYI AGLLTGRHNS VAVATDTGEL  240
VKATEALKRI GVESPFELQA KEGLALVNGT AVGSAVAATV CYDANVLALL AEVLSAAFCE  300
VMHGKPEFTD PLTHELKHHP GQIESAAIME YLFDGSDLIK AGQARHENDP LTKPDRYALR  360
TSPQWLGPQI EVIRAATHSI EREINSVNDN PIIDCDRDMA LHGGNFQGTP IGVSMDNLRI  420
AIAAIGKLVF AQFSELVCDY HNNGLPSNLS GGPNPSLDYG LKGAEIAMAS YCSELQYLAN  480
PVTTHVQSAE QHNQDVNSLG LISARKSAEA VDILKLKMST YMVGLCQAFD LRHLEENMRE  540
VVKHIVLKTA KTLYGEECEK ELLMVVEHQP VFSYIEDPVN PSYALLLQLR EVLVEKALKD  600
LNDPSSVVFK RIPLFEEELK KRLSEEVAKA RERFDEGDFL VPNRAKKGRT YPVYEFVRGE  660
VGTELLTGEK KTSPGEQIEK VYEATMEGKV EEVLMRCLSF WRGSAGPFTP RPTAGSPAHH  720
NPCTGAGLIT                                                        730

SEQ ID NO: 140         moltype = AA  length = 763
FEATURE                Location/Qualifiers
source                 1..763
                       mol_type = protein
                       organism = Acorus americanus
SEQUENCE: 140
MASSTEGLSR PIESLRPPTL PLPTGGKNPI SVSGNSYVSN PPHWKKAAEA LLCTHFDEVR  60
KMVHQYRNSS SVDLTGTTLT VAQVAAIARR PKVSVALDAA SAKARVARSA QWVADNIARG  120
TDTYGITTGF GATSHRRTNK AEDLQAELIR FLNAGVIGKE YLPTSYAKAA MLVRTNTLMQ  180
GYSGIRWELL EAMESLMNHN LIPKMPLRGT ITASGDLVPL SYIAGLLTGR HNSVAVATET  240
GELVKATEAL KRIGVGSPFE LQAKEGLALV NGTAVGSAVA ATVCYDANVL ALLSEVLSAA  300
FCEAMQGKPE FTDPLTHELK HHPGQIESAA IMEYLLDGSD HIKACAARQE KDPLTKPKQD  360
RYALRTSPQW LGPQIEVIRA ATHSIAREIN SVNDNPIIDC DRDLALHGGN FQGTPIGVSM  420
DNLRIAIAAI GKLVFAQFSE LVCDYYNNGL PSNLSGGPNP SLDYGLKGAE IAMASYCSEL  480
QYLANPVTTH VQSAEQHNQD VNSLGLISAR KSAEAVDILK LMLSTYMIGL CQAFDLRHLE  540
ENMREVVKHV VLQAAKKTLY TEADGTLLDT RFCEKELLQV VEHQPVFSYI DDPTNPSYAL  600
LLQLREVLVE RALKNINEEN GHGKVLKMIP VFQEELKRRL SEEVPKARER FDKGDFPVPN  660
RANKCRTYPL YQFVRGEVGT ELLTGEKKTS PGEYIEKVYE AMKEGKVEDV LMKCLTFWRG  720
SAGPFTPRPA GGSPAQHNPE YWSWFDNLRS PSATSGRGYW NNM                   763

SEQ ID NO: 141         moltype = AA  length = 736
FEATURE                Location/Qualifiers
source                 1..736
                       mol_type = protein
                       organism = Amborella trichopoda
SEQUENCE: 141
MAENGPQAIE SCRPATLPLP IKSTSTICSN GFHSTVTPPP HWKKASEALE ISHFQEVSKM  60
ISQFNQAQTV TLQGTSFTVA QVTAITRRAH VSVDLDEHTA RARVAESANW VRENIARGTD  120
TYGVTTGFGA TSHRRTTKTS ELQTELIRFL NAGVIGKEHL PVTYARAAMA VRTNTLMQGY  180
SGIRWEILEA MAKLISLNLI PKIPLRGTIT ASEGGEEIAA LEALRRAGIE NPFELQAKEG  240
LALVNGTAVG AAVASSVCFD ANLLALLAEV LSALFCEVMQ GKPEFTDPLT HQLKHHPGQI  300
EAAAVMEFLL DQSDYMNEAK IKHEKDPLSK PKQDRYALRT SPQWLGPQIE VIRMATHSIE  360
REINSVNDNP LIDVARDMAL HGGNFQGTPI GVSMDNLRIA IAAIGKLMFA QFSELVCDYY  420
NNGLPSNLSG GPNPSLDYGM KGAEIAMAAY TSELQYLANP VTTHVQSAEQ HNQDVNSLGL  480
ISARKSAEAI EILKLMSATF LVALCQAVDL RHLEENMREI VKHVVMQTAR KTLYMEEDSG  540
SLLDTRFYEK ELLQVVDHQP VFSYLDDPAN PSYALLLQLR EVLVEKSLES EKEGDGFSIF  600
KRIGVFQEEL KARLREEIPK ARERFDAGDF PVPNRIKGCR TYPVYKFVRS EMGTALLSGT  660
TKVSPGEEIE KVYEGISEGK LGNVLLQCLS FWNGLAGPFT PHSVPASPAQ GNPTYWAWFE  720
NTRSPSAISG RGFWNM                                                 736

SEQ ID NO: 142         moltype = AA  length = 755
FEATURE                Location/Qualifiers
source                 1..755
                       mol_type = protein
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                       organism = Amborella trichopoda
SEQUENCE: 142
MAETAESCRP PSLLLPMKTT SIICSNGLHS NVTPPPHWKK ASEALETSHF HEVSEMISQF  60
NQAHTVTLQG TSLTVAQVTA ITRRANISVH LDEPTARARV AESSNWVREN IARGTHINGV  120
TSGFGATSHS RTNKTTELQA ELIRFLNVGV MGKEHLSVTY ARAAMAVRTN TLMQGYSGIR  180
WEILEAMAKL TSLNLIPKIP LRGTITASGD LVPLSYIAGL LTNRPNSRVL TEGGEEIAAL  240
EALRRAGIEN PFDLQAKEGL ALVNGTAVGA AVASSVCFDA NLLALLAEVL SALFCEVMQG  300
KPEFTDPLTH QLKHHPGQIE AAAVMEFLLD QSDYMNEAKI KHKKDPLSKP KQDRYALRTS  360
PQWLGPQIEV IRMATHSIER EINSVNDNPL IDVARDMALH GGNFQGTPIG VSMDNLRIAI  420
AAIGKLMFAQ FSELVCDYYN NGLPSHLSGG PNPSLDYGMK GAEIAMAAYT SELQYLANPV  480
TTHVQSAEQH NQDVNSLGLI SARKSAEAIE ILKLMSATFL VALCQAVDLR HLEENMREIV  540
KHVVMQTARK TLYMEEDSGS LLDTRFDEKE LLQVVDHQPV FSYLDDPANP SYALLLQLRE  600
VLVEKSLKSE KEGDGFSIFK RIGVFQEELK ARLTEEIPKA RERFDAGDFP VPNRIKRCRT  660
YPVYKFVRSE MGTALLRGTK KVSPGEEIEK VYEGISEGKL GNVLLQCLSF WNGLAGPFTP  720
HSVPASPAQC NPTYWTWFEN TRSPSATSGR GYWNM                             755

SEQ ID NO: 143         moltype = AA  length = 759
FEATURE                Location/Qualifiers
source                 1..759
                       mol_type = protein
                       organism = Amborella trichopoda
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ISQFNQAQTV TLQGTSLTVA QVTAITRQTG VSVNLDEHTA RARVARSADW VRENIARGTD  120
TYGVTTGFGA TSHRRTSKTT DLQTELIRFL NAGVISKEHL PVAYARASMA VRTNTLMQGY  180
SGIRWEILEA LAKLISLNLI PKIPLRGTIT ASGDLVPLSY IAGLLTNRPN SRVLTKDGEE  240
ISALEALKRS GIETPFELQA KEGLALVNGT AVGAAVASSV CFDANLLALL AEVLSALFCE  300
VMQGKPEFTD PLTHQLKHHP GQIEAAAVME FLLDQSDYMN EAKIKHEKDP LTKPKQDRYA  360
LRTSPQWLGP QIEVIRMATH SIEREINSVN DNPLIDVDRD MALHGGNFQG TPIGVSMDNL  420
RIAIAAIGKL MFAQFSELVC DYYNNGLPSN LSGGPNPSLD YGMKGAEIAM AAYTSELQYL  480
ANPVTTHVQS AEQHNQDVNS LGLISARKSA EAIEILKLMS ATFLVALCQA VDLRHLEENM  540
REIVKHVVLQ TAKKTLYMEE DNGSLLDTRF YEKELLQVVD HQPVFSYLDD PSNPSYALML  600
QLREVLVEKS LKSNTEADGF SIFKRIGVFQ EELKVRLSEE IPKARERFDA GDFPVPNRIK  660
KCRTYPIYKF VRNEMGTALL SGTKQISPGE EIEKVYEGIS EGKLGKVLLQ CLSLWNGLAG  720
PFTPRPVPAS PAHCNPTYWA WFENTRSPSA TSGRGYWNL                         759

SEQ ID NO: 144         moltype = AA  length = 725
FEATURE                Location/Qualifiers
source                 1..725
                       mol_type = protein
                       organism = Arabidopsis thaliana
SEQUENCE: 144
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RKPVVNLGGE TLTIGQVAAI STIGNSVKVE LSETARAGVN ASSDWVMESM NKGTDSYGVT  120
TGFGATSHRR TKNGVALQKE LIRFLNAGIF GSTKETSHTL PHSATRAAML VRINTLLQGF  180
SGIRFEILEA ITSFLNNNIT PSLPLRGTIT ASGDLVPLSY IAGLLTGRPN SKATGPNGEA  240
LTAEEAFKLA GISSGFFDLQ PKEGLALVNG TAVGSGMASM VLFETNVLSV LAEILSAVFA  300
EVMSGKPEFT DHLTHRLKHH PGQIEAAAIM EHILDGSSYM KLAQKLHEMD PLQKPKQDRY  360
ALRTSPQWLG PQIEVIRYAT KSIEREINSV NDNPLIDVSR NKAIHGGNFQ GTPIGVSMDN  420
TRLAIAAIGK LMFAQFSELV NDFYNNGLPS NLTASRNPSL DYGFKGAEIA MASYCSELQY  480
LANPVTSHVQ SAEQHNQDVN SLGLISSRKT SEAVDILKLM STTFLVAICQ AVDLRHLEEN  540
LRQTVKNTVS QVAKKVLTTG VNGELHPSRF CEKDLLKVVD REQVYTYADD PCSATYPLIQ  600
KLRQVIVDHA LINGESEKNA VTSIFHKIGA FEEELKAVLP KEVEAARAAY DNGTSAIPNR  660
IKECRSYPLY RFVREELGTE LLTGEKVTSP GEEFDKVFTA ICEGKIIDPM MECLNEWNGA  720
PIPIC                                                              725

SEQ ID NO: 145         moltype = AA  length = 720
FEATURE                Location/Qualifiers
source                 1..720
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 145
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KIEGASLRIA QVAAVAAGEA AAAKVELDES SRGRVKASSD WVMSSMMNGT DIYGVTTGFG  120
ATSHRRTKEG GALQRELIRH LNAGVFGTGS DGHVLPAAAT RAAMLVRINT LLQGYSGIRF  180
EILEAITALL NAGVTPCLPL RGTITASGDL VPLSYIAGLI TGRPNSVAVA PDGRKVDAAE  240
AFKIAGIQHG FFELQPKEGL AMVNGTAVGS GLASTVLFEA NILTILAEVL SAVFCEVMTG  300
KPEYTDHLTH KLKHHPGQIE AAAIMEHILE GSSYMKLAKK LGDLDPLMKP KQDRYALRTS  360
PQWLGPQIEV IRASTKSIER EINSVNDNPL IDVSRGKALH GGNFQGTPIG VSMDNTRLAI  420
AAIGKLMFAQ FSELVNDFYN NGLPSNLSGG RNPSLDYGFK GAEIAMASYC SELQFLANPV  480
TNHVQSAEQH NQDVNSLGLI SSRKTAEAVD ILKLMSSTFL IALCQAIDLR HLEENLKSAV  540
KNCVAQVAKK ALTLNTVGDL HNARFSEKDL LTAIDREALF AYADDPCNPN YPLMQKLRAV  600
LVEHALANGE AEHVATTSVF AKITKFEEEL RATLPKEVEA ARVAVENGTA PTPNRIKECR  660
SYPLYRFVRE ELGTEYLTGE KLRSPGEECN KVFVAINQGK LIDPLLECLK EWNGEPLPIC  720

SEQ ID NO: 146         moltype = AA  length = 725
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source                 1..725
                       mol_type = protein
                       organism = synthetic construct
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TGFGATSHRR TKNGVALQKE LIRHLNAGIF GSTKETSHTL PHSATRAAML VRINTLLQGF  180
SGIRFEILEA ITSFLNNNIT PSLPLRGTIT ASGDLVPLSY IAGLLTGRPN SKATGPNGEA  240
LTAEEAFKLA GISSGFFDLQ PKEGLALVNG TAVGSGMASM VLFETNVLSV LAEILSAVFA  300
EVMSGKPEFT DHLTHRLKHH PGQIEAAAIM EHILDGSSYM KLAQKLHEMD PLQKPKQDRY  360
ALRTSPQWLG PQIEVIRYAT KSIEREINSV NDNPLIDVSR NKAIHGGNFQ GTPIGVSMDN  420
TRLAIAAIGK LMFAQFSELV NDFYNNGLPS NLTASRNPSL DYGFKGAEIA MASYCSELQY  480
LANPVTSHVQ SAEQHNQDVN SLGLISSRKT SEAVDILKLM STTFLVAICQ AVDLRHLEEN  540
LRQTVKNTVS QVAKKVLTTG VNGELHPSRF CEKDLLKVVD REQVYTYADD PCSATYPLIQ  600
KLRQVIVDHA LINGESEKNA VTSIFHKIGA FEEELKAVLP KEVEAARAAY DNGTSAIPNR  660
IKECRSYPLY RFVREELGTE LLTGEKVTSP GEEFDKVFTA ICEGKIIDPM MECLNEWNGA  720
PIPIC                                                              725

SEQ ID NO: 147         moltype = DNA  length = 2163
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source                 1..2163
                       mol_type = genomic DNA
                       organism = Joinvillea ascendens
SEQUENCE: 147
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ctcaatgccg gagtcttcgg caccggctcc gacggccacg tgctgccggc cgcggcaaca  480
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SEQ ID NO: 148         moltype = DNA  length = 2163
FEATURE                Location/Qualifiers
source                 1..2163
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 148
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tga                                                                2163

SEQ ID NO: 149          moltype = DNA  length = 2178
FEATURE                 Location/Qualifiers
source                  1..2178
                        mol_type = genomic DNA
                        organism = Arabidopsis thaliana
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SEQ ID NO: 150          moltype = DNA  length = 2178
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                       mol_type = other DNA
                       organism = synthetic construct
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atcgccggac ttctcaccgg tcgtcccaat tccaaagcta ctggtcccaa cggtgaagct  720
ttaacagcag aggaagcttt caaattagca ggaatcagct ccggattctt tgatctccag  780
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gctcttcgta cttctcctca atggttaggt cctcaaatcg aagtgatccg ttacgcaacg  1140
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aaagaagtgg aagcagcaag agcagcctac gataacggaa catcggctat cccgaacagg  1980
atcaaggaat gtaggtcgta tccattgtat agattcgtga gggaagagct tggaacagag  2040
cttttgaccg gagagaaagt gacgtcgcct ggagaagagt tcgacaaggt tttcacggcg  2100
atttgtgaag gtaaaatcat tgatccgatg atggaatgtc tcaacgagtg gaacggagct  2160
cccattccaa tatgttaa                                                 2178

SEQ ID NO: 151         moltype = DNA  length = 2118
FEATURE                Location/Qualifiers
source                 1..2118
                       mol_type = genomic DNA
                       organism = Joinvillea ascendens
SEQUENCE: 151
atggcgttcc agaacgacaa tgtcctttgc ataaagaagg accccctaaa ctgggggaaa  60
gcggcggagg agctgacggg gagccacctc gacgaggtga agaggatggt ggcggagtcc  120
cggacgccag tggttaagat ccagggcgcc agcctgagga tcgggcaggt ggcggcggtg  180
gcggtccgcg agacgggcgt cgccaaggtg gagcttgacg agtcagcccg cggccgcgtc  240
aaggccagca gcgactggat cgtgaacagc gtggcgaacg gtggagatat atatggtgtc  300
accactggct tcggaggcac ctctcacagg aggaccaggg acggtcctgc gctccaaata  360
gagctcctta gacacctcaa tgccggaatc ttcggcaccg gcaccgacgg ccacgtcctg  420
ccgtcggcgg tgacacgtgc tgccatgttc gtccgtatca acactttgct ccagggctac  480
tccggcatcc gctttgagat cctcgaggcg atcgctgcac tgctgaatgc tggcgtcacg  540
ccgtgcctgc cactccgcgg caccatcacc gcgtccggag acctcatccc cttgtcctac  600
attgcgggcc tcattaccgg ccgaccgaac gcagtggcga tcgcccccga tggcaggaag  660
gtggacgccg ccgaggcatt caagatcgcc ggcatcccgc acggcttctt caagctgcag  720
cccaaggaag gtcttgccat agtgaacggc acatccgtag ggctgccct ggcatccacg  780
gtgctcttcg acgcgaatat tcttgccatc cttgccgagg tcttgtctgc tgtgttctgc  840
gaggtcatga ccggcaagcc ggagtacacc gaccacctga cacacaggct gaagcaccac  900
ccaggacaga tagaggccgc ggccatcatg gagcacatct tggaaggcag ctcgttcatg  960
aagctggcga agaagctcgg ggagctcgac cctctgctga agccgaagca ggaccggtac  1020
gcgctacgca cggcgccgca gtggctcggc ccccagatcg aggtcatacg cgccgccacc  1080
aagtcgatcg agcgcgagat caactctgtc aatgacaacc caatcatcga cgtctcccgc  1140
ggcaaggcgc tccatggcgg caacttccaa ggcaccccca tcggcgtgtc catggacaac  1200
acccgcctcg ccatcgccaa catcggcaag ctcatgtttg cgcagttctc cgagctcgtg  1260
aacgacttct acaacaatgg cctaacatcg aacttggccg gcgggcgcaa cccgagcttg  1320
gactacggtt tcaagggtac cgagatcgcc atggcctcgt actgctctga gctccagttc  1380
ttggccaacc ccgtgactaa ccatgtccag agtgccgagc agcacaacca ggatgtcaac  1440
tcgcttggcc ttgtctctgc caggaagact gccgaggcag tggacatact gaagctcatg  1500
tcgtcgacgt tcttgattgc actgtgccag gccatcgacc tgcgccacct cgaggagaac  1560
ctcaagagtg cagtcaagaa ctgcgtggcg caggtggcca agaaggtgct gaccgtgaac  1620
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acagtcgggg acctgcacaa tgcgcgcttc agcgagaagg acctgctcac ggcgatcgac  1680
cgcgaggcag tgttcactta cgcagatgac ccctgcagcc ccaactatcc gctgatgcag  1740
aaggtgcgcg ctgtgctcgt tgagcacgcc ctcgccaatg gcgaggctga gcgcgtggcc  1800
aacacgtccg tgtttgccaa gatcaccaag ttcgaggagg agttgcgagc gacactgccc  1860
aaggaagtcg aggcggcccg ggtggccgtg gagaatcgca ctgcgccaac ccagaaccgg  1920
atcaaggaat cacggtcata cccactgtac cgtttcgtgc gtgaggacct cgggacggcg  1980
tacttgaccg gagagaagct gcggtctcct ggcgaggagt gcaacaaggt gtttgtggcc  2040
atcaaccagg gcaagcttat tgacccactg ctggagtgcc tcaagaagtg gaacggtgag  2100
cccctgccaa tctgctga                                                2118

SEQ ID NO: 152          moltype = AA  length = 525
FEATURE                 Location/Qualifiers
source                  1..525
                        mol_type = protein
                        organism = Arabidopsis thaliana
SEQUENCE: 152
MALSNASSLS TRSIYGGDLS HRPSNRQSSF TFHPAVNTKP KSVNLVTAVH AAEPARNAVS  60
VKESVASSSS GALKWTPESW KLKKALQLPD YPNANELESV LKTIEAFPPI VFAGEARNLE  120
ERLADAAVGK AFLLQGGDCA ESFKEFNATN IRDTFRVLLQ MSIVLTFGGQ VPVIKVGRMA  180
GQFAKPRSDA FEEKDGVKLP SYKGDNINGD TFDEKSRIPD PNRMIRAYTQ SAATLNLLRA  240
FATGGYAAIQ RVTQWNLDFV EQSEQADRYQ ELANRVDEAL GFMSACGLGT DHPLMTTTDF  300
YTSHECLLLP YEQSLTRLDS TSGLYYDCSA HMVWCGERTR QLDGAHVEFL RGIANPLGIK  360
VSNKMDPFEL VKLVEILNPN NKPGRITVIV RMGAENMRVK LPHLIRAVRR SGQIVTWVCD  420
PMHGNTIKAP CGLKTRAFDS ILAEVRAFLD VHEQEGSHAG GIHLEMTGQN VTECIGGSRT  480
VTYDDLSSRY HTHCDPRLNA SQSLELAFIV AERLRKRRTG SQRVS                  525

SEQ ID NO: 153          moltype = AA  length = 266
FEATURE                 Location/Qualifiers
source                  1..266
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 153
MSNSPSLKIG IVGFGSFGQF LAKTMIKQGH TLTATSRTDY SHTCLQLGIQ FFRDVGTFIE  60
ANNDVILICT SIMSFTKVLS SMPLACLKKP TTLFVDVLSV KEHPREVLLR VLPEESDILC  120
THPMFGPESG KNGWKDLNFM YDKVRIHDEA TCSNFLHIFA SEGCKMLQMS CEEHDKIAAK  180
SQFITHTIGR TLAEMDIEST PIDTKGFQTL TQLKNTTMRC SFDLYSGLFV HNRFAKQELE  240
NLQRALDRVK EMLVQRMREE LGPEKD                                       266

SEQ ID NO: 154          moltype = AA  length = 268
FEATURE                 Location/Qualifiers
source                  1..268
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 154
MSSSSKSLKI GIVGFGTFGQ FLANTMIKQG HTLTATSRTD YSQLCDQMGI HFFRDITAFL  60
DADMDVILLC TSISSLSEVV GSMPLACLKR PTLFVDVLSV KEHPKNLLLK VLPEESDILC  120
THPMFGPVSG KNGWQNLTFM FDKVRIKDEV TCSKFLQIFA SEGCKMVEMS CEEHDKAAAK  180
SQFITHTIGR TLAEMDIKST PIDTKGFQTL VELKKPVMGD SFDLYSGLFV YNRFARQELE  240
NLEHALHKVK EMLVQRIDEG QNPERTES                                     268

SEQ ID NO: 155          moltype = DNA  length = 35
FEATURE                 Location/Qualifiers
source                  1..35
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 155
cgcgcggcag ccatatgatg gcgttccaga acgac                             35

SEQ ID NO: 156          moltype = DNA  length = 34
FEATURE                 Location/Qualifiers
source                  1..34
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 156
gctcgaattc ggatcctcag cagattggca gggg                              34

SEQ ID NO: 157          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 157
caattgcagg gagatcgagc                                              20

SEQ ID NO: 158          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
```

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```
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 158
tgctgttgta aggtggggat                                            20

SEQ ID NO: 159         moltype = DNA  length = 35
FEATURE                Location/Qualifiers
source                 1..35
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 159
cgcgcggcag ccatatgatg gagtgcgaga acggc                           35

SEQ ID NO: 160         moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 160
gctcgaattc ggatcctcag cagattggca gggg                            34

SEQ ID NO: 161         moltype = DNA  length = 19
FEATURE                Location/Qualifiers
source                 1..19
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 161
tcttcttcca caccaaacg                                             19

SEQ ID NO: 162         moltype = DNA  length = 22
FEATURE                Location/Qualifiers
source                 1..22
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 162
gcacaagaag gatgctagaa ac                                         22

SEQ ID NO: 163         moltype = DNA  length = 35
FEATURE                Location/Qualifiers
source                 1..35
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 163
cgcgcggcag ccatatgatg gcgagccaga gggac                           35

SEQ ID NO: 164         moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 164
gctcgaattc ggatccttag cagatgggca gggg                            34

SEQ ID NO: 165         moltype = DNA  length = 18
FEATURE                Location/Qualifiers
source                 1..18
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 165
atggtggccc agagcgac                                              18

SEQ ID NO: 166         moltype = DNA  length = 19
FEATURE                Location/Qualifiers
source                 1..19
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 166
ttagcagatt ggaaggggc                                             19

SEQ ID NO: 167         moltype = DNA  length = 35
FEATURE                Location/Qualifiers
source                 1..35
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 167
```

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```
cgcgcggcag ccatatgatg gtggcccaga gcgac                        35

SEQ ID NO: 168         moltype = DNA  length = 35
FEATURE                Location/Qualifiers
source                 1..35
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 168
gctcgaattc ggatccttag cagattggaa ggggc                        35

SEQ ID NO: 169         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 169
caagaagagc acgccaactc                                         20

SEQ ID NO: 170         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 170
gccacacaca catacggatc                                         20

SEQ ID NO: 171         moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 171
gcgcggcagc catatgatgg cgggcaacgg cgcc                         34

SEQ ID NO: 172         moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 172
gctcgaattc ggatccttag ttgacgacgt tgat                         34

SEQ ID NO: 173         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 173
ccactgtcag tcacgcaatt                                         20

SEQ ID NO: 174         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 174
tgcaacagcc aagaacatgc                                         20

SEQ ID NO: 175         moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 175
gcgcggcagc catatgatgg agtgcgagac gggt                         34

SEQ ID NO: 176         moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 176
gctcgaattc ggatcctcag cagagcggca gtgg                         34

SEQ ID NO: 177         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
```

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```
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 177
ctctgcaatt cgacgagctc                                      20

SEQ ID NO: 178         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 178
agttctactg gctgcctacc                                      20

SEQ ID NO: 179         moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 179
gcgcggcagc catatgatgg agtacgagaa cggg                      34

SEQ ID NO: 180         moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 180
gctcgaattc ggatcctcag cagagaggca gggg                      34

SEQ ID NO: 181         moltype = DNA  length = 22
FEATURE                Location/Qualifiers
source                 1..22
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 181
agctcctatc ttctttcttt ct                                   22

SEQ ID NO: 182         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 182
aaccacttca cagacaatca                                      20

SEQ ID NO: 183         moltype = DNA  length = 38
FEATURE                Location/Qualifiers
source                 1..38
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 183
cgcgcggcag ccatatgatg gagattaacg gggcacac                  38

SEQ ID NO: 184         moltype = DNA  length = 41
FEATURE                Location/Qualifiers
source                 1..41
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 184
gctcgaattc ggatccttaa catattggaa tgggagctcc g              41

SEQ ID NO: 185         moltype = DNA  length = 23
FEATURE                Location/Qualifiers
source                 1..23
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 185
cgactcacta taggggaatt gtg                                  23

SEQ ID NO: 186         moltype = DNA  length = 21
FEATURE                Location/Qualifiers
source                 1..21
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 186
```

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```
gctagttatt gctcagcggt g                                      21

SEQ ID NO: 187          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 187
cattcaagat cgccggcatc                                        20

SEQ ID NO: 188          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 188
ctaacatcga acttggccgg                                        20

SEQ ID NO: 189          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 189
tcttcctggc agagacaagg                                        20

SEQ ID NO: 190          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 190
ttcctcaatg ccggagtctt                                        20

SEQ ID NO: 191          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 191
cttctgcgaa gtcatgaccg                                        20

SEQ ID NO: 192          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 192
caacccagtg accaaccatg                                        20

SEQ ID NO: 193          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 193
ctacgacgcc aacattctcg                                        20

SEQ ID NO: 194          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 194
acatcggcaa gctcatgttc                                        20

SEQ ID NO: 195          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 195
ttgatggcag gaaggtggat                                        20

SEQ ID NO: 196          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
```

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```
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 196
atcggaaagc tcatgttcgc                                          20

SEQ ID NO: 197         moltype = DNA  length = 18
FEATURE                Location/Qualifiers
source                 1..18
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 197
ccccaaggaa ggtctggc                                            18

SEQ ID NO: 198         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 198
acatcggcaa gctcatgttc                                          20

SEQ ID NO: 199         moltype = DNA  length = 19
FEATURE                Location/Qualifiers
source                 1..19
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 199
catcgtcaat ggcacctcc                                           19

SEQ ID NO: 200         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 200
ctcatgttcg cgcagttctc                                          20

SEQ ID NO: 201         moltype = DNA  length = 18
FEATURE                Location/Qualifiers
source                 1..18
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 201
gtctcgccat ggtcaacg                                            18

SEQ ID NO: 202         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 202
ccatcggcaa gctcatgttc                                          20

SEQ ID NO: 203         moltype = DNA  length = 18
FEATURE                Location/Qualifiers
source                 1..18
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 203
ccttgccatg gtgaacgg                                            18

SEQ ID NO: 204         moltype = DNA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 204
caagctcatg tttgcccagt                                          20

SEQ ID NO: 205         moltype = DNA  length = 27
FEATURE                Location/Qualifiers
source                 1..27
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 205
```

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```
ctcaggtttc tgaacgccgg gatcttc                                          27

SEQ ID NO: 206          moltype = DNA  length = 27
FEATURE                 Location/Qualifiers
source                  1..27
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 206
gttcagaaac ctgaggagct cgacctg                                          27

SEQ ID NO: 207          moltype = DNA  length = 26
FEATURE                 Location/Qualifiers
source                  1..26
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 207
cttagattcc tcaatgccgg aatctt                                           26

SEQ ID NO: 208          moltype = DNA  length = 27
FEATURE                 Location/Qualifiers
source                  1..27
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 208
attgaggaat ctaaggagct ctatttg                                          27

SEQ ID NO: 209          moltype = DNA  length = 27
FEATURE                 Location/Qualifiers
source                  1..27
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 209
aattagacac ctcaatgccg gagtctt                                          27

SEQ ID NO: 210          moltype = DNA  length = 27
FEATURE                 Location/Qualifiers
source                  1..27
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 210
ttgaggtgtc taattagctc tctttgg                                          27

SEQ ID NO: 211          moltype = DNA  length = 26
FEATURE                 Location/Qualifiers
source                  1..26
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 211
ctccggtttc tgaatgctgg aatctt                                           26

SEQ ID NO: 212          moltype = DNA  length = 27
FEATURE                 Location/Qualifiers
source                  1..27
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 212
attcagaaac cggaggagct ccacctg                                          27

SEQ ID NO: 213          moltype = DNA  length = 26
FEATURE                 Location/Qualifiers
source                  1..26
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 213
cttcggtttc tcaatgccgg aatctt                                           26

SEQ ID NO: 214          moltype = DNA  length = 27
FEATURE                 Location/Qualifiers
source                  1..27
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 214
attgagaaac cgaaggagct ccacctg                                          27

SEQ ID NO: 215          moltype = DNA  length = 33
FEATURE                 Location/Qualifiers
```

-continued

```
source                 1..33
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 215
ctcaggtttc tcaacgccgg gatcttcggc acc                              33

SEQ ID NO: 216         moltype = DNA  length = 33
FEATURE                Location/Qualifiers
source                 1..33
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 216
gttgagaaac ctgagcagct cgacctggag cgc                              33

SEQ ID NO: 217         moltype = DNA  length = 33
FEATURE                Location/Qualifiers
source                 1..33
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 217
atcagacacc tcaatgccgg cgccttcggc acc                              33

SEQ ID NO: 218         moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 218
attgaggtgt ctgatgagct ccctctggag cgcg                             34

SEQ ID NO: 219         moltype = DNA  length = 33
FEATURE                Location/Qualifiers
source                 1..33
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 219
atccgacacc ttaatgcggg agccttcggc acc                              33

SEQ ID NO: 220         moltype = DNA  length = 35
FEATURE                Location/Qualifiers
source                 1..35
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 220
attaaggtgt cggatgagct ctctctgcag agcgc                            35

SEQ ID NO: 221         moltype = DNA  length = 33
FEATURE                Location/Qualifiers
source                 1..33
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 221
cttagattcc tcaatgccgg agtcttcggc acc                              33

SEQ ID NO: 222         moltype = DNA  length = 33
FEATURE                Location/Qualifiers
source                 1..33
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 222
attgaggaat ctaagtagct ctctttggag agc                              33

SEQ ID NO: 223         moltype = DNA  length = 33
FEATURE                Location/Qualifiers
source                 1..33
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 223
attgaggaat ctaagtagct ctacttggag agc                              33

SEQ ID NO: 224         moltype = DNA  length = 32
FEATURE                Location/Qualifiers
source                 1..32
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 224
```

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```
gcgactgggt catgagcagc atgatgaacg gc                              32

SEQ ID NO: 225         moltype = DNA  length = 29
FEATURE                Location/Qualifiers
source                 1..29
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 225
tcatgaccca gtcgctgctg gccttgacg                                  29

SEQ ID NO: 226         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 226
accgacagct acggtgtcac cactgg                                     26

SEQ ID NO: 227         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 227
accgtagctg tcggtgccgt tcatca                                     26

SEQ ID NO: 228         moltype = DNA  length = 28
FEATURE                Location/Qualifiers
source                 1..28
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 228
ctttggagcc acctcccaca ggaggacc                                   28

SEQ ID NO: 229         moltype = DNA  length = 29
FEATURE                Location/Qualifiers
source                 1..29
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 229
gaggtggctc caaagccagt ggtgacacc                                  29

SEQ ID NO: 230         moltype = DNA  length = 32
FEATURE                Location/Qualifiers
source                 1..32
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 230
gagagctaat tagacacctc aatgccggag tc                              32

SEQ ID NO: 231         moltype = DNA  length = 30
FEATURE                Location/Qualifiers
source                 1..30
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 231
gtctaattag ctctctttgg agagcaccac                                 30

SEQ ID NO: 232         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 232
cggcacggcc gtgggttctg gtcttg                                     26

SEQ ID NO: 233         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 233
cccacggccg tgccgttcac catggc                                     26

SEQ ID NO: 234         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
```

-continued

```
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 234
tggcctgcct tccaacctgg ccggtg                                       26

SEQ ID NO: 235         moltype = DNA  length = 27
FEATURE                Location/Qualifiers
source                 1..27
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 235
ttggaaggca ggccattgtt gtagaag                                      27

SEQ ID NO: 236         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 236
caacctgtcc ggtgggcgca acccga                                       26

SEQ ID NO: 237         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 237
ccaccggaca ggttggaagt caggcc                                       26

SEQ ID NO: 238         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 238
tggccttatc tcatccagga agaccg                                       26

SEQ ID NO: 239         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 239
gatgagataa ggccaagcga gttgac                                       26

SEQ ID NO: 240         moltype = DNA  length = 31
FEATURE                Location/Qualifiers
source                 1..31
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 240
ggagatagct atggtgtcac cactggcttc g                                 31

SEQ ID NO: 241         moltype = DNA  length = 28
FEATURE                Location/Qualifiers
source                 1..28
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 241
accatagcta tctccaccgt tcgccacg                                     28

SEQ ID NO: 242         moltype = DNA  length = 28
FEATURE                Location/Qualifiers
source                 1..28
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 242
accgacatat acggtgtcac cactggct                                     28

SEQ ID NO: 243         moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 243
```

-continued

```
accgtatatg tcggtgccgt tcatca                                     26

SEQ ID NO: 244          moltype = DNA  length = 29
FEATURE                 Location/Qualifiers
source                  1..29
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 244
caccgacacc tacggtgtca ccactggct                                  29

SEQ ID NO: 245          moltype = DNA  length = 25
FEATURE                 Location/Qualifiers
source                  1..25
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 245
ccgtaggtgt cggtgccgtt catca                                      25

SEQ ID NO: 246          moltype = DNA  length = 28
FEATURE                 Location/Qualifiers
source                  1..28
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 246
caccgacgtc tacggtgtca ccactggc                                   28

SEQ ID NO: 247          moltype = DNA  length = 28
FEATURE                 Location/Qualifiers
source                  1..28
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 247
ccgtagacgt cggtgccgtt catcatgc                                   28

SEQ ID NO: 248          moltype = DNA  length = 32
FEATURE                 Location/Qualifiers
source                  1..32
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 248
tggagatgtc tatggtgtca ccactggctt cg                              32

SEQ ID NO: 249          moltype = DNA  length = 27
FEATURE                 Location/Qualifiers
source                  1..27
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 249
ccatagacat ctccaccgtt cgccacg                                    27

SEQ ID NO: 250          moltype = DNA  length = 32
FEATURE                 Location/Qualifiers
source                  1..32
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 250
tggagatacc tatggtgtca ccactggctt cg                              32

SEQ ID NO: 251          moltype = DNA  length = 27
FEATURE                 Location/Qualifiers
source                  1..27
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 251
ccataggtat ctccaccgtt cgccacg                                    27

SEQ ID NO: 252          moltype = DNA  length = 34
FEATURE                 Location/Qualifiers
source                  1..34
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 252
actgatatat atggtgttac tactggtttt ggtg                            34

SEQ ID NO: 253          moltype = DNA  length = 33
FEATURE                 Location/Qualifiers
```

-continued

```
source                 1..33
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 253
accatatata tcagtgcctt tgttcatact ctc                           33

SEQ ID NO: 254         moltype = DNA  length = 29
FEATURE                Location/Qualifiers
source                 1..29
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 254
tattagacac cttaacgccg gaatattcg                                29

SEQ ID NO: 255         moltype = DNA  length = 33
FEATURE                Location/Qualifiers
source                 1..33
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 255
ttaaggtgtc taataagttc cttctgaagt gcg                           33

SEQ ID NO: 256         moltype = DNA  length = 29
FEATURE                Location/Qualifiers
source                 1..29
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 256
catcgccgcc atcggcaagc tcatgtttg                                29

SEQ ID NO: 257         moltype = DNA  length = 27
FEATURE                Location/Qualifiers
source                 1..27
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 257
ccgatggcgg cgatggcgag gcgggtg                                  27

SEQ ID NO: 258         moltype = AA  length = 720
FEATURE                Location/Qualifiers
source                 1..720
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 258
MECENGNVAA VAAVNGGNGL CLQKPQHADP LNWGKAAGEL MGSHLEEVKR MVAEFRAPVV  60
KIEGASLRIA QVAAVAAGEA AAAKVELDES SRGRVKASSD WVMSSMMNGT DIYGVTTGFG  120
ATSHRRTKEG GALQRELIRF LNAGVFGTGS DGHVLPAAAT RAAMLVRINT LLQGYSGIRF  180
EILEAITALL NAGVTPCLPL RGTITASGDL VPLSYIAGLI TGRPNSVAVA PDGRKVDAAE  240
AFKIAGIQHG FFELQPKEGL AMVNGTAVGS GLASTVLFEA NILTILAEVL SAVFCEVMTG  300
KPEYTDHLTH KLKHHPGQIE AAAIMEHILE GSSYMKLAKK LGDLDPLMKP KQDRYALRTS  360
PQWLGPQIEV IRASTKSIER EINSVNDNPL IDVSRGKALH GGNFQGTPIG VSMDNTRLAI  420
AAIGKLMFAQ FSELVNDFYN NGLPSNLSGG RNPSLDYGFK GAEIAMASYC SELQFLANPV  480
TNHVQSAEQH NQDVNSLGLI SSRKTAEAVD ILKLMSSTFL IALCQAIDLR HLEENLKSAV  540
KNCVAQVAKK ALTLNTVGDL HNARFSEKDL LTAIDREALF AYADDPCNPN YPLMQKLRAV  600
LVEHALANGE AEHVATTSVF AKITKFEEEL RATLPKEVEA ARVAVENGTA PTPNRIKECR  660
SYPLYRFVRE ELGTEYLTGE KLRSPGEECN KVFVAINQGK LIDPLLECLK EWNGEPLPIC  720

SEQ ID NO: 259         moltype = AA  length = 720
FEATURE                Location/Qualifiers
source                 1..720
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 259
MECENGNVAA VAAVNGGNGL CLQKPQHADP LNWGKAAGEL MGSHLEEVKR MVAEFRAPVV  60
KIEGASLRIA QVAAVAAGEA AAAKVELDES SRGRVKASSD WVMSSMMNGT DSYGVTTGFG  120
ATSHRRTKEG GALQRELIRH LNAGVFGTGS DGHVLPAAAT RAAMLVRINT LLQGYSGIRF  180
EILEAITALL NAGVTPCLPL RGTITASGDL VPLSYIAGLI TGRPNSVAVA PDGRKVDAAE  240
AFKIAGIQHG FFELQPKEGL AMVNGTAVGS GLASTVLFEA NILTILAEVL SAVFCEVMTG  300
KPEYTDHLTH KLKHHPGQIE AAAIMEHILE GSSYMKLAKK LGDLDPLMKP KQDRYALRTS  360
PQWLGPQIEV IRASTKSIER EINSVNDNPL IDVSRGKALH GGNFQGTPIG VSMDNTRLAI  420
AAIGKLMFAQ FSELVNDFYN NGLPSNLSGG RNPSLDYGFK GAEIAMASYC SELQFLANPV  480
TNHVQSAEQH NQDVNSLGLI SSRKTAEAVD ILKLMSSTFL IALCQAIDLR HLEENLKSAV  540
KNCVAQVAKK ALTLNTVGDL HNARFSEKDL LTAIDREALF AYADDPCNPN YPLMQKLRAV  600
LVEHALANGE AEHVATTSVF AKITKFEEEL RATLPKEVEA ARVAVENGTA PTPNRIKECR  660
SYPLYRFVRE ELGTEYLTGE KLRSPGEECN KVFVAINQGK LIDPLLECLK EWNGEPLPIC  720
```

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```
SEQ ID NO: 260         moltype = AA  length = 725
FEATURE                Location/Qualifiers
source                 1..725
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 260
MEINGAHKSN GGGVDAMLCG GDIKTKNMVI NAEDPLNWGA AAEQMKGSHL DEVKRMVAEF  60
RKPVVNLGGE TLTIGQVAAI STIGNSVKVE LSETARAGVN ASSDWVMESM NKGTDIYGVT  120
TGFGATSHRR TKNGVALQKE LIRFLNAGIF GSTKETSHTL PHSATRAAML VRINTLLQGF  180
SGIRFEILEA ITSFLNNNIT PSLPLRGTIT ASGDLVPLSY IAGLLTGRPN SKATGPNGEA  240
LTAEEAFKLA GISSGFFDLQ PKEGLALVNG TAVGSGMASM VLFETNVLSV LAEILSAVFA  300
EVMSGKPEFT DHLTHRLKHH PGQIEAAAIM EHILDGSSYM KLAQKLHEMD PLQKPKQDRY  360
ALRTSPQWLG PQIEVIRYAT KSIEREINSV NDNPLIDVSR NKAIHGGNFQ GTPIGVSMDN  420
TRLAIAAIGK LMFAQFSELV NDFYNNGLPS NLTASRNPSL DYGFKGAEIA MASYCSELQY  480
LANPVTSHVQ SAEQHNQDVN SLGLISSRKT SEAVDILKLM STTFLVAICQ AVDLRHLEEN  540
LRQTVKNTVS QVAKKVLTTG VNGELHPSRF CEKDLLKVVD REQVYTYADD PCSATYPLIQ  600
KLRQVIVDHA LINGESEKNA VTSIFHKIGA FEEELKAVLP KEVEAARAAY DNGTSAIPNR  660
IKECRSYPLY RFVREELGTE LLTGEKVTSP GEEFDKVFTA ICEGKIIDPM MECLNEWNGA  720
PIPIC                                                              725

SEQ ID NO: 261         moltype = AA  length = 725
FEATURE                Location/Qualifiers
source                 1..725
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 261
MEINGAHKSN GGGVDAMLCG GDIKTKNMVI NAEDPLNWGA AAEQMKGSHL DEVKRMVAEF  60
RKPVVNLGGE TLTIGQVAAI STIGNSVKVE LSETARAGVN ASSDWVMESM NKGTDSYGVT  120
TGFGATSHRR TKNGVALQKE LIRHLNAGIF GSTKETSHTL PHSATRAAML VRINTLLQGF  180
SGIRFEILEA ITSFLNNNIT PSLPLRGTIT ASGDLVPLSY IAGLLTGRPN SKATGPNGEA  240
LTAEEAFKLA GISSGFFDLQ PKEGLALVNG TAVGSGMASM VLFETNVLSV LAEILSAVFA  300
EVMSGKPEFT DHLTHRLKHH PGQIEAAAIM EHILDGSSYM KLAQKLHEMD PLQKPKQDRY  360
ALRTSPQWLG PQIEVIRYAT KSIEREINSV NDNPLIDVSR NKAIHGGNFQ GTPIGVSMDN  420
TRLAIAAIGK LMFAQFSELV NDFYNNGLPS NLTASRNPSL DYGFKGAEIA MASYCSELQY  480
LANPVTSHVQ SAEQHNQDVN SLGLISSRKT SEAVDILKLM STTFLVAICQ AVDLRHLEEN  540
LRQTVKNTVS QVAKKVLTTG VNGELHPSRF CEKDLLKVVD REQVYTYADD PCSATYPLIQ  600
KLRQVIVDHA LINGESEKNA VTSIFHKIGA FEEELKAVLP KEVEAARAAY DNGTSAIPNR  660
IKECRSYPLY RFVREELGTE LLTGEKVTSP GEEFDKVFTA ICEGKIIDPM MECLNEWNGA  720
PIPIC                                                              725

SEQ ID NO: 262         moltype = DNA  length = 2163
FEATURE                Location/Qualifiers
source                 1..2163
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 262
atggagtgcg agaacggcaa tgttgcagct gttgccgccg tcaacggcgg caatggcctg  60
tgcttgcaga agccgcagca cgccgacccc ctgaactggg ggaaggcggc gggggagctg  120
atggggagcc atcttgagga ggtgaagagg atggtggcgg agttccgggc gccggtggtg  180
aagatcgagg gcgccagcct gaggatcgcg caggtggcgg ccgttgcggc cggcgaggcg  240
gccgcggcca aggtggagct cgatgagtcc tcccgcggcc gcgtcaaggc cagcagcgac  300
tgggtcatga gcagcatgat gaacggcacc gacatatacg gtgtcaccac tggctttgga  360
gccacctccc acaggaggac caaggagggt ggtgctctcc aaagagagct aattagattc  420
ctcaatgccg gagtcttcgg caccggctcc gacggccacg tgctgccggc cgcggcaaca  480
agggcggcaa tgctcgtccg catcaacacc ctcctccagg gctactctgg aatccgcttc  540
gagatccttg aggcgatcac tgcgctgctc aacgccggcg tcacgccgtg cctgcctctc  600
cgtggcacga tcaccgcgtc gggagacctg gtcccgctgt cctacattgc cggcctcatt  660
accggccgcc cgaactccgt ggcagtcgcc cccgacggca ggaaggtgga cgccgctgag  720
gcgttcaaga tcgctggcat ccagcacggc ttcttcgagc tgcagccaaa ggaaggtctg  780
gccatggtga acggcacggc cgtgggttct ggtcttgcat ccacagtgct cttcgaggcg  840
aacattctta ccattcttgc ggaggtcttg tcggcagtct tctgcgaagt catgaccggc  900
aagccggagt acaccgacca cctgacacac aagctgaagc accaccccgg acagatagag  960
gccgcggcca tcatggagca catcttggaa ggaagctcgt acatgaagct ggcgaagaag  1020
ctcggcgacc ttgacccgct gatgaagccg aagcaggacc ggtacgcact ccgcacatcg  1080
ccacagtggc tcggccccca gatcgaggtc atccgtgcct ccaccaagtc aattgagcgt  1140
gagatcaact ccgtcaacga caacccgctc atcgatgtct cccgtggcaa ggcgctccac  1200
ggcggcaact tccagggcac tcccatcggt gtgtccatgg acaatacccg cctcgccatc  1260
gcggccattg gcaagctcat gtttgcgcag ttctcagagc tcgttaacga cttctacaac  1320
aatggcctgc cttccaacct gtccggtggg cgcaacccga gcttggacta tggtttcaag  1380
ggtgccgaga tcgccatggc ctcatactgc tctgagctcc agttcttggc caacccagtg  1440
accaaccatg tccagagcgc tgagcagcac aaccaggatg tcaactcgct tggccttatc  1500
tcatccagga agaccgccga ggcagtggac atactgaagc tcatgtcgtc gacgttcttg  1560
atcgcattgt gccaggccat tgacctgcgc caccttgagg agaacctcaa gagcgcagtc  1620
aagaactgcg tggcgcaggt tgccaagaag gcgctgacct tgaacacagt cggggacctc  1680
cacaacgcac gcttcagcga gaaggaccta ctcacagcga tcgaccgtga ggcgttgttc  1740
gcgtacgcgg acgacccgtg caaccccaac tacccgctga tgcagaaact gcgcgcggta  1800
```

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ctcgtcgagc atgccctcgc caacggcgag gctgagcacg tggccaccac ctccgtgttt 1860
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gcccgggtgg ccgtggagaa cggcaccgcg cctacaccga accggatcaa ggaatgccgg 1980
tcataccctc tgtaccggtt cgtgcgcgag gagcttggga cagagtactt gaccggggag 2040
aaactgcggt ctcctggtga ggagtgcaac aaggtgtttg tggccatcaa ccagggcaag 2100
ctcattgacc cactgctgga gtgcctcaag gagtggaacg gtgagcccct gccaatctgc 2160
tga 2163

SEQ ID NO: 263 moltype = DNA length = 2163
FEATURE Location/Qualifiers
source 1..2163
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 263
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tgcttgcaga agccgcagca cgccgacccc ctgaactggg ggaaggcggc gggggagctg 120
atggggagcc atcttgagga ggtgaagagg atggtggcgg agttccgggc gccggtggtg 180
aagatcgagg gcgccagcct gaggatcgcg caggtggcgg ccgttgcggc cggcgaggcg 240
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agggcggcaa tgctcgtccg catcaacacc ctcctccagg gctactctgg aatccgcttc 540
gagatccttg aggcgatcac tgcgctgctc aacgccggcg tcacgccgtg cctgcctctc 600
cgtggcacga tcaccgcgtc gggagacctg gtcccgctgt cctacattgc cggcctcatt 660
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gcgttcaaga tcgctggcat ccagcacggc ttcttcgagc tgcagccaaa ggaaggtctg 780
gccatggtga acggcacggc cgtgggttct ggtcttgcat ccacagtgct cttcgaggcg 840
aacattctta ccattcttgc ggaggtcttg tcggcagtct tctgcgaagt catgaccggc 900
aagccggagt acaccgacca cctgacacac aagctgaagc accaccccgg acagatagag 960
gccgcggcca tcatggagca catcttggaa ggaagctcgt acatgaagct ggcgaagaag 1020
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ccacagtggc tcggccccca gatcgaggtc atccgtgcct ccaccaagtc aattgagcgt 1140
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aaactgcggt ctcctggtga ggagtgcaac aaggtgtttg tggccatcaa ccagggcaag 2100
ctcattgacc cactgctgga gtgcctcaag gagtggaacg gtgagcccct gccaatctgc 2160
tga 2163

SEQ ID NO: 264 moltype = DNA length = 2178
FEATURE Location/Qualifiers
source 1..2178
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 264
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gcagcggagc aaatgaaagg tagccatttg gatgaagtga agagaatggt tgctgagttt 180
aggaagccag ttgtgaatct tggtggtgag actctgacca ttggacaagt ggctgcgatc 240
tcaactattg gtaacagtgt gaaggtggag ctatcggaga cagctagagc cggtgtgaat 300
gctagtagtg attgggttat ggagagtatg aacaaaggca ctgatatata tggtgttact 360
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cttattagat tccttaacgc cggaatattc ggaagcacga aagaaacaag ccacacattg 480
ccacactccg ccacaagagc cgccatgctt gtacgaatca acactctcct ccaaggattt 540
tccggtatcc gatttgagat tctcgaagca attaccagtt tcctcaacaa caacatcact 600
ccatctctcc ccctccgtgg tacaatcacc gcctccggag atctcgttcc tctctcctac 660
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cctaaggaag gtctcgcgct agtcaatggc acggcggttg gatctggaat ggcgtcaatg 840
gtgttattcg aaacgaatgt tctctctgtt ttggctgaga ttttgtcggc ggttttcgca 900
gaggtgatga gtggtaagcc tgagttcacc gatcatctca ctcacagact taaacatcat 960
cccggtcaaa tcgaagcggc ggcgataatg gagcatatcc tcgacggaag ctcgtacatg 1020
aaattagctc agaagcttca cgagatggat ccgttacaga aacctaaaca agatcgttac 1080

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aacaaggcga ttcacggtgg taacttccaa ggaacaccaa tcggagtttc aatggataac  1260
acgagattgg cgatagcagc gattggtaaa ctcatgtttg ctcaattctc agagcttgtg  1320
aatgatttct acaacaatgg tttaccctcg aatctaaccg cttcgaggaa tccaagtttg  1380
gattatggat tcaagggagc tgagattgca atggcttctt attgttcaga gcttcaatac  1440
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SEQ ID NO: 265         moltype = DNA  length = 2178
FEATURE                Location/Qualifiers
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                       mol_type = other DNA
                       organism = synthetic construct
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cccattccaa tatgttaa                                                2178
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What is claimed:

1. An engineered phenylalanine ammonia-lyase (PAL) enzyme comprising a mutation relative to a wild-type PAL enzyme, wherein the mutation is at a position corresponding to residue 112 of SEQ ID NO: 28, and wherein the engineered PAL enzyme has increased TAL activity relative to the wild-type PAL enzyme.

2. The engineered PAL enzyme of claim **1**, wherein the mutation is a serine to isoleucine mutation, a serine to valine mutation, or a serine to threonine mutation.

3. The engineered PAL enzyme of claim **1**, further comprising a second mutation relative to the wild-type PAL enzyme, wherein the second mutation is at a position corresponding to residue 140 of SEQ ID NO: 28.

4. The engineered PAL enzyme of claim **3**, wherein the second mutation is a phenylalanine to histidine mutation.

5. The engineered PAL enzyme of claim **1**, wherein the wild-type PAL enzyme comprises a sequence selected from SEQ ID NO: 28-143 or a sequence having at least 90% identity to one of SEQ ID NO: 28-143.

6. The engineered PAL enzyme of claim **5**, wherein the wild-type PAL enzyme comprises SEQ ID NO: 28 (JaPAL) or SEQ ID NO: 144 (AtPAL1).

7. The engineered PAL enzyme of claim **6**, wherein the engineered PAL enzyme comprises SEQ ID NO: 145 ($\text{JaPAL}^{F140H\_S112I}$), SEQ ID NO: 146 ($\text{AtPAL1}^{F144H\_S116I}$), a sequence having at least 90% identity to SEQ ID NO: 145, or a sequence having at least 90% identity to SEQ ID NO: 146.

8. The engineered PAL enzyme of claim **1**, wherein the engineered PAL enzyme further comprises at least one additional mutation relative to the wild-type enzyme at a position corresponding to residue 102, 121, 138, 267, 444, 448, or 500 of SEQ ID NO: 28.

9. A polynucleotide encoding the engineered PAL enzyme of claim **1**.

10. A construct comprising a promoter operably linked to the polynucleotide of claim **9**.

11. A vector comprising the polynucleotide of claim **9**.

12. A cell comprising the polynucleotide of claim **9**.

13. A seed comprising the polynucleotide of claim **9**.

14. A plant comprising the engineered PAL enzyme of claim **1**.

15. The plant of claim **14**, wherein the plant:

a) produces a greater quantity of lignin as compared to a control plant;

b) produces a greater quantity of phenylpropanoid-derived compounds as compared to a control plant; and/or

c) assimilates a greater quantity of carbon dioxide (CO_2) as compared to a control plant.

16. The plant of claim **14**, wherein the plant is a non-grass land plant.

17. The plant of claim **14**, further comprising:

a) an engineered 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase enzyme that comprises one or more mutation relative to a wild-type enzyme at a position corresponding to residue 109, 114, 159, 240, 244, 245, 247, 248, 319, 322, or 348 of SEQ ID NO: 152;

b) an engineered arogenate dehydrogenase enzyme comprising a non-acidic amino acid residue at a position corresponding to residue 220 of SEQ ID NO: 153; or

c) an engineered prephenate dehydrogenase enzyme comprising an aspartic acid (D) or glutamic acid (E) at a position corresponding to residue 220 of SEQ ID NO: 154.

18. A method of making the plant of claim **14**, the method comprising: introducing a polynucleotide encoding the engineered PAL enzyme into plants and selecting a plant that expresses the engineered PAL enzyme.

19. A method of making the plant of claim **14**, the method comprising: editing a gene encoding a wild-type PAL enzyme in the plant to have a mutation at a position corresponding to residue 112 of SEQ ID NO: 28.

20. The method of claim **19**, wherein the method further comprises: editing the gene to have a mutation at a position corresponding to residue 140 of SEQ ID NO: 28.

21. A method for producing phenylpropanoid-derived products, the method comprising:

a) growing a plant genetically engineered to express the engineered PAL enzyme of claim **1**; and

b) purifying phenylpropanoid-derived products produced by the plant.

22. A method for sequestering CO_2, the method comprising growing a plant genetically engineered to express the engineered PAL enzyme of claim **1**.

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