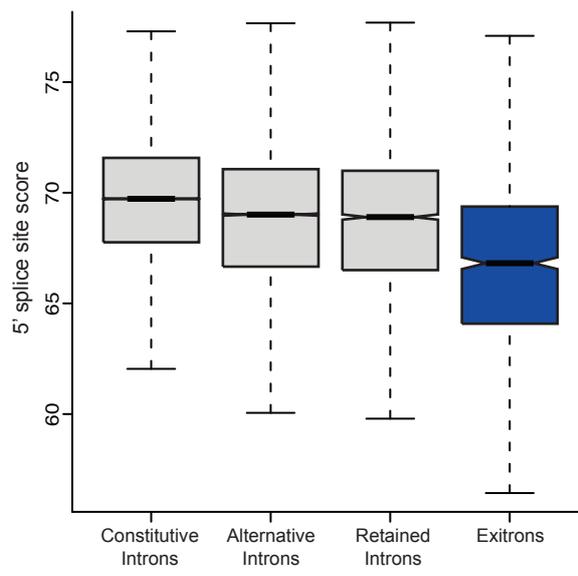
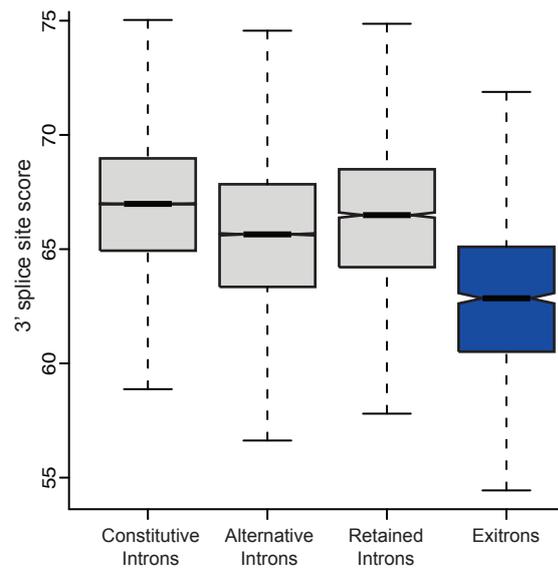
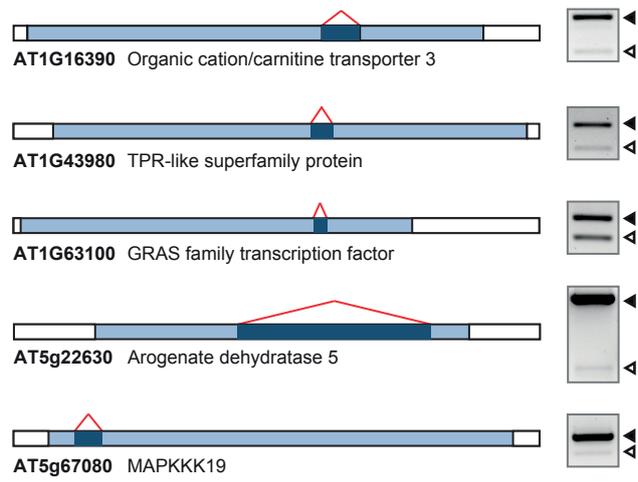
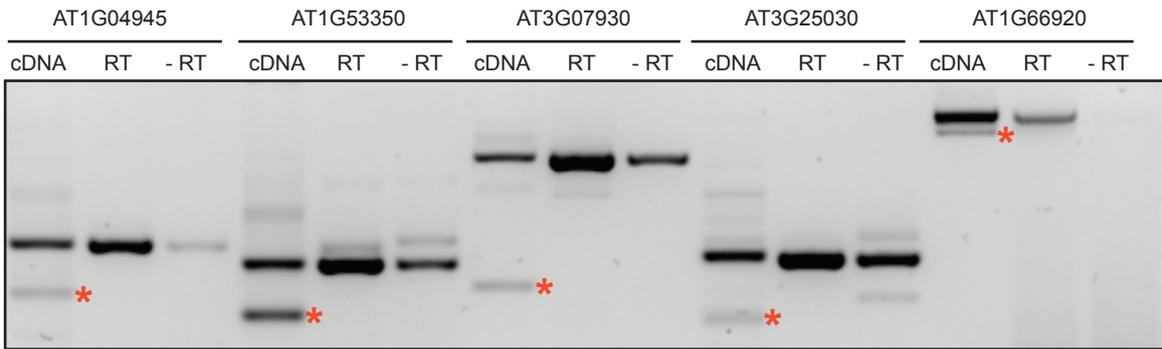


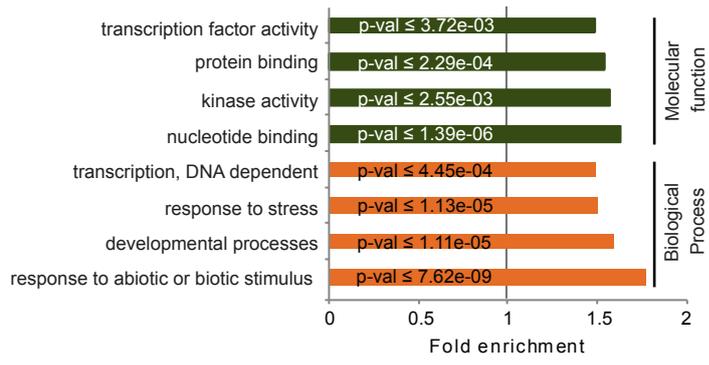
A**B****Supplemental Figure 1.**



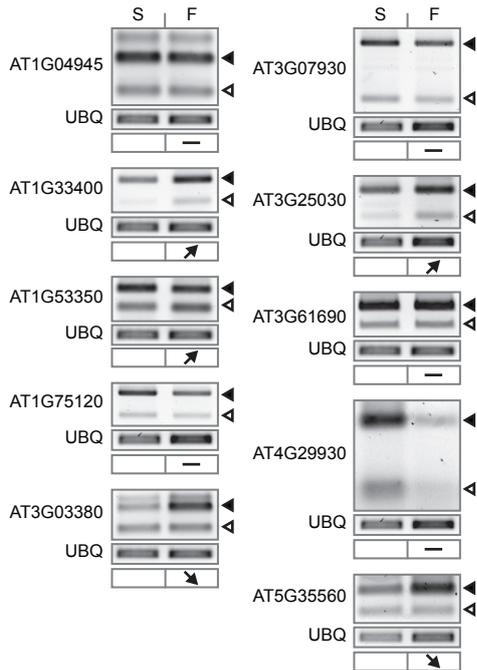
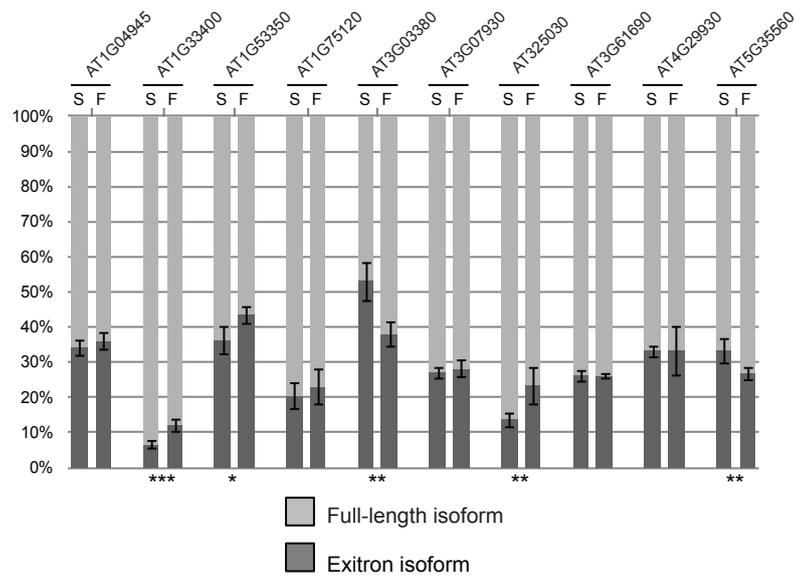
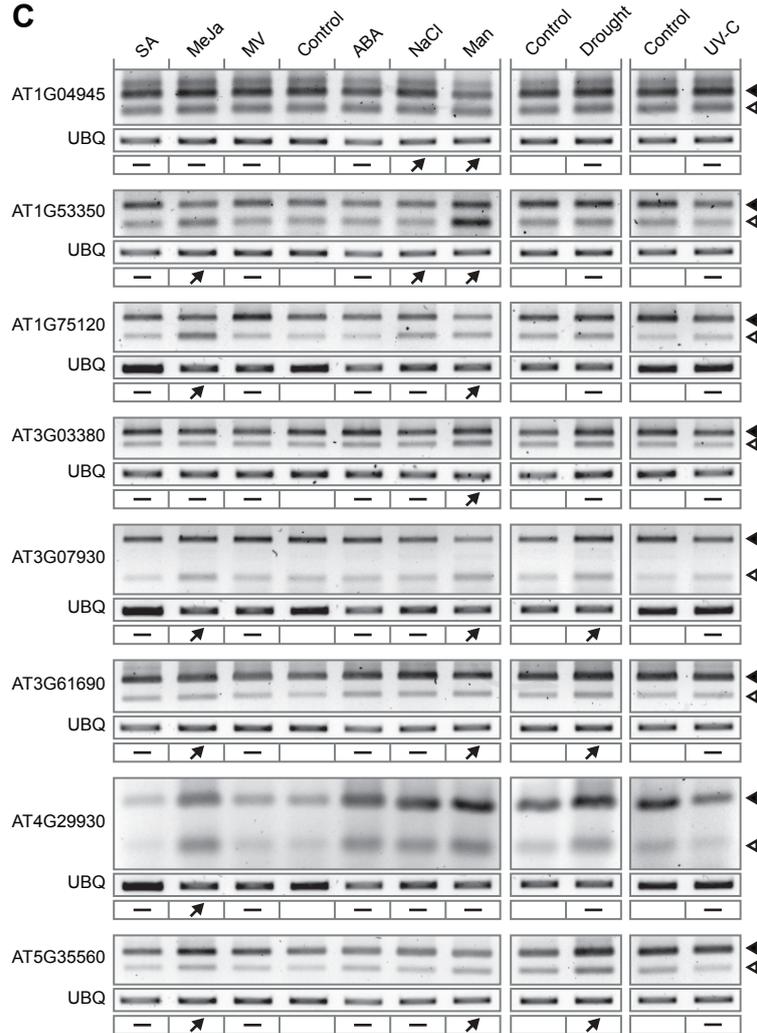
Supplemental Figure 2.

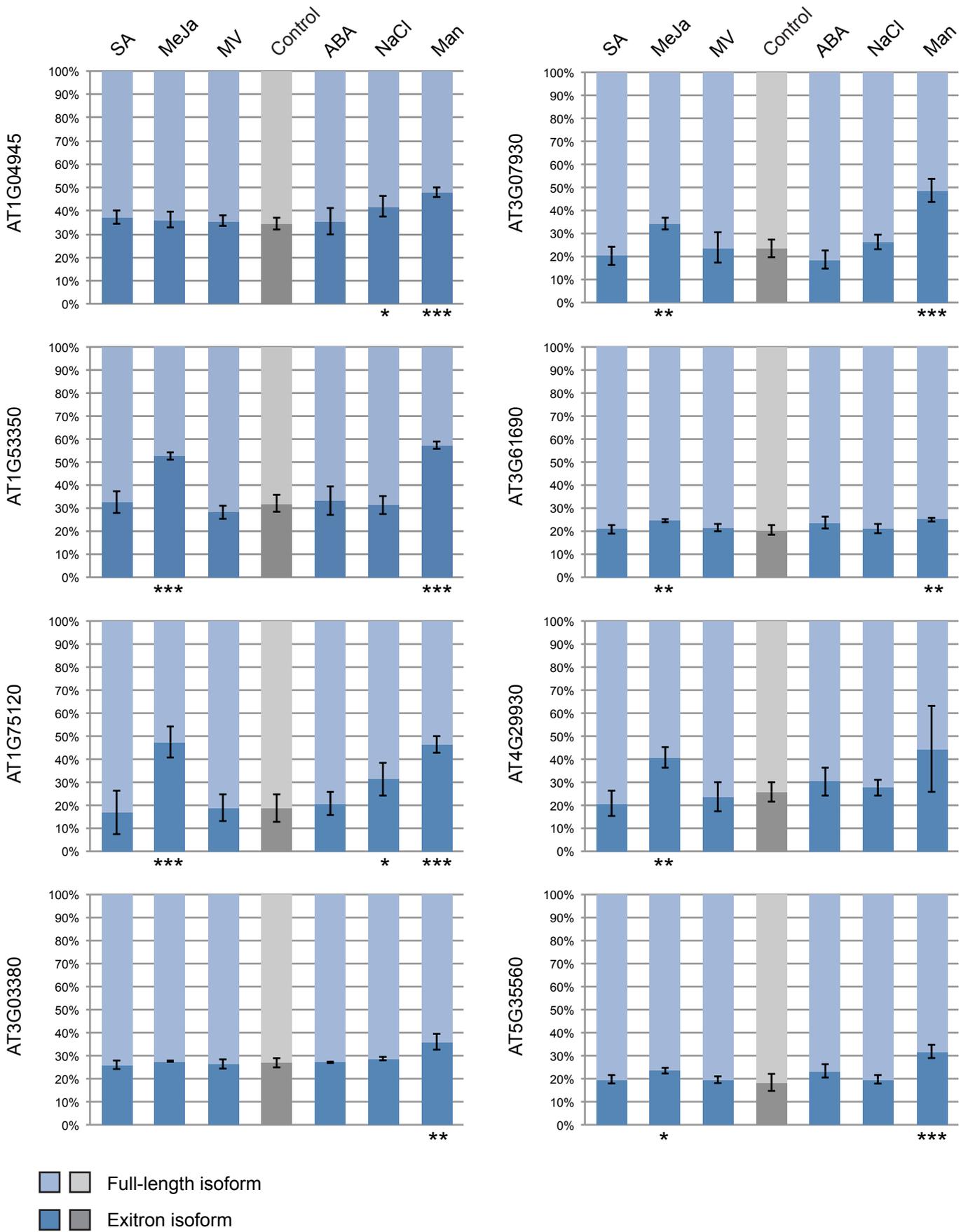


Supplemental Figure 3.

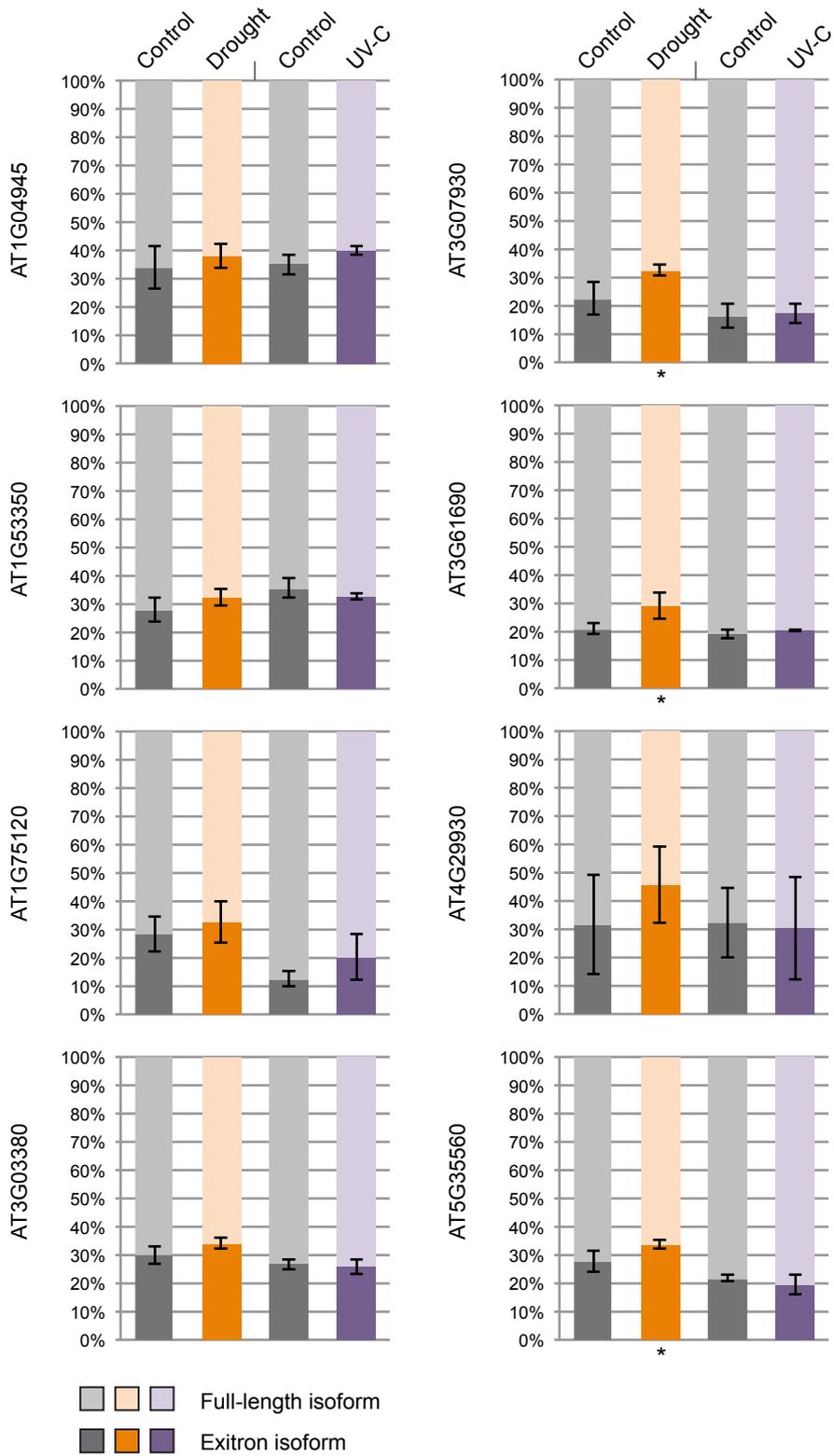


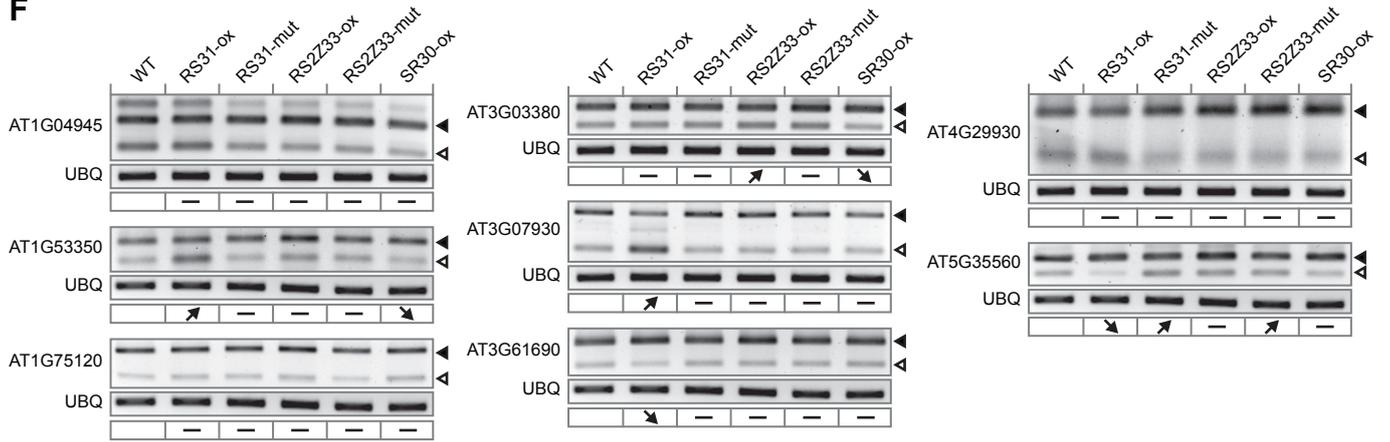
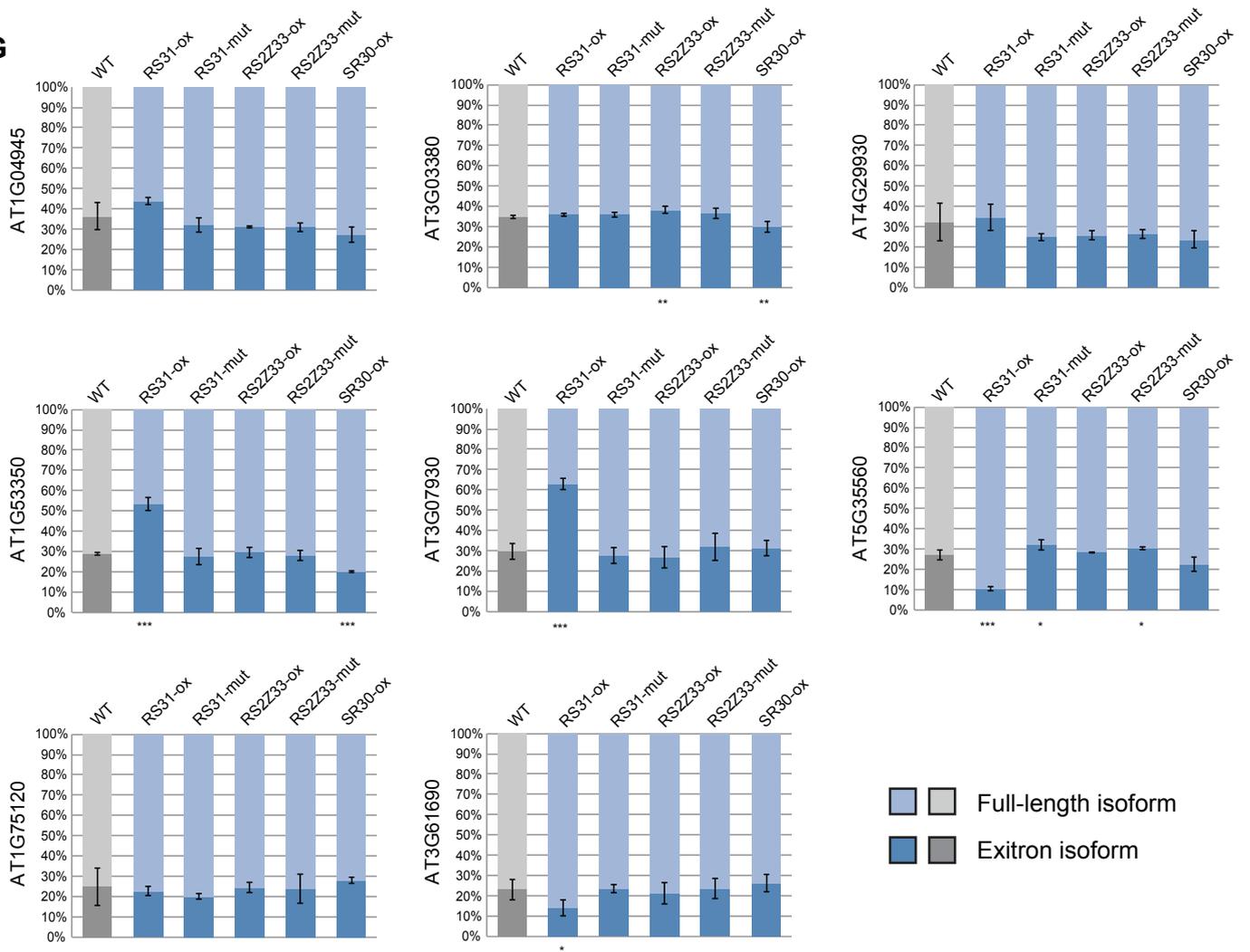
Supplemental Figure 5.

A**B****C**

D

F

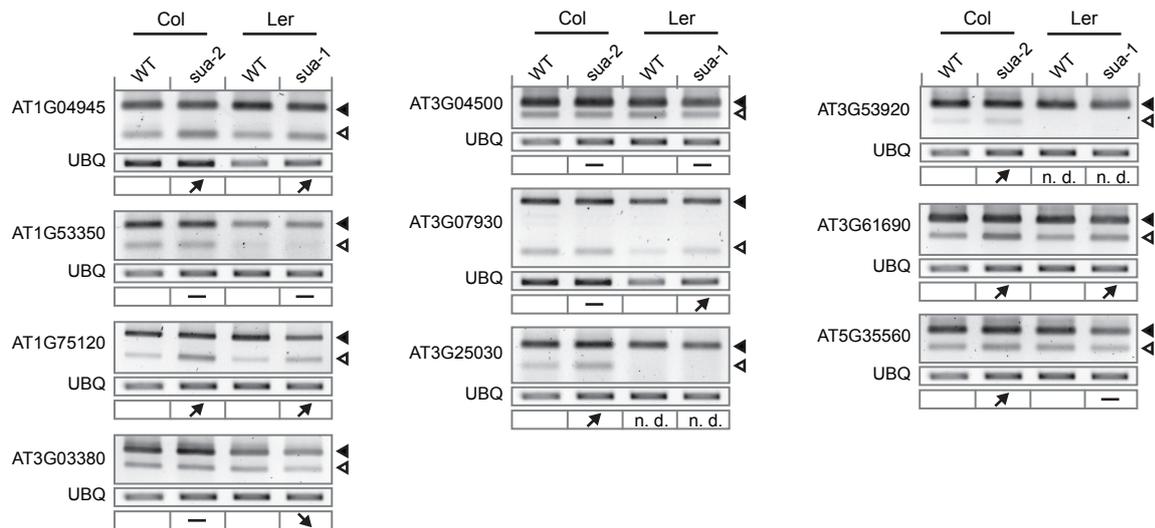


F**G**

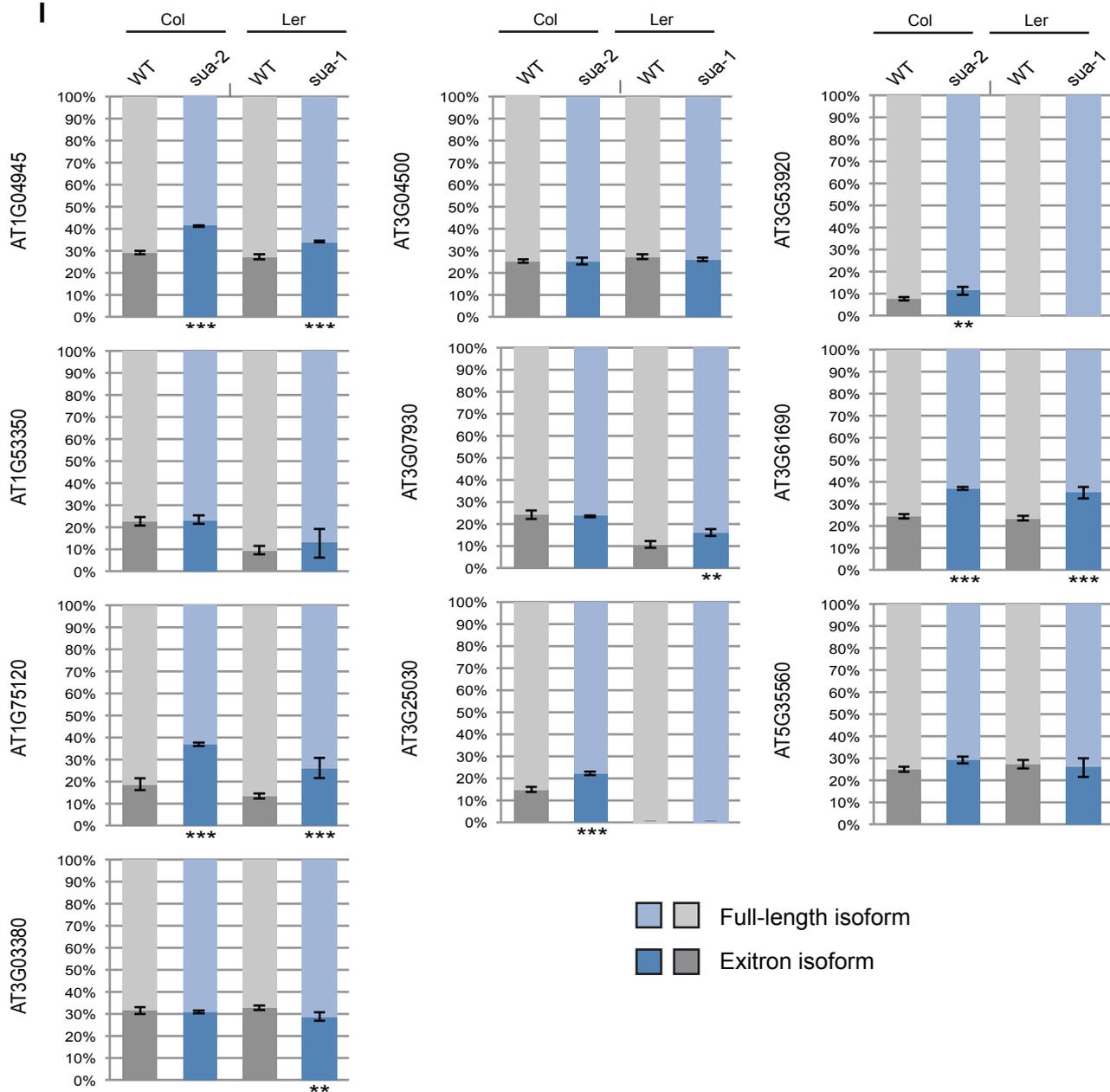
Full-length isoform

 Exitron isoform

H



I



Supplemental Figure 6.

```

Ath_FL 347 TCTATGCTTACGGTTTCGAAAAGCCTTCTGCTATTCAGCAAAGAGGAATGTACCCCTTTT
Ath_EI 347 TCTATGCTTACGGTTTCGAAAAGCCTTCTGCTATTCAGCAAAGAGGAATGTACCCCTTTT
Bna_EI_1 283 TCTATGCCATATGGTTTGGAAAAGCCTTCTGCTATTCAGCAAAGAGGAATCGTCCCTTCT
Bna_EI_2 283 TCTATGCCATATGGTTTGGAAAAGCCTTCTGCTATTCAGCAAAGAGGAATCGTCCCTTCT
Bna_FL 271 TCTATGCCATATGGTTTGGAAAAGCCTTCTGCTATTCAGCAAAGAGGAATCGTCCCTTCT
Rra_EI 270 TCTATGCCATATGGTTTGGAAAAGCCTTCTGCTATTCAGCAAAGAGGAATCGTCCCTTTT
Hsa_FL 276 TCTATGCCATATGGTTTGAAGGCCCTCTGCCATCCAGCAACGAGCCATTCTACCTTGTGTA
Hsa_EI 1 -----AAGGCCCTCTGCCATCCAGCAACGAGCCATTCTACCTTGTGTA

```

```

Ath_EIF4A I Y A Y G F E K P S A I Q Q R G I V P F
Hsa_EIF4A1 I Y A Y G F E K P S A I Q Q R A I L P C
Q-motif

```

```

Ath_FL 407 GCAAGGGTCTTGATGTGATCCAGCAGGCAAGTCTGGTACTGGAAAACCGCCACTTTCT
Ath_EI 407 GCAAGGGTCTTGATGTGATCCAGCAG-----
Bna_EI_1 343 GCAAGGGTCTTGATGTGATCCAGCAG-----
Bna_EI_2 343 GCAAGGGTCTTGATGTGATCCAGCAG-----
Bna_FL 331 GCAAGGGTCTTGATGTGATCCAGCAGGCTCAGTCTGGTACTGGAAAACCGCCACTTTCT
Rra_EI 330 GCAAGGGTCTTGATGTGATCCAGCAG-----
Hsa_FL 336 TCAAGGGTATATGATGTGATGCTCAAAGCCATCTGGGACTGGAAAACCGCCACATTG
Hsa_EI 41 TCAAGGGTATATGATGTGATGCTCAA-----

```

```

Ath_EIF4A C K G L D V I Q Q A Q S G T G K T A T F
Hsa_EIF4A1 I K G Y D V I A Q A Q S G T G K T A T F
Motif I (Walker A)

```

```

Ath_FL 467 GCTCTGGTCTTTGCAGCAGCTTGACTATGCCCTCTCCAGTGCCAGGCTCTCGTTTGG
Ath_EI 435 -----GCTCTCGTTTGG
Bna_EI_1 373 -----GCTCTCGTCTTGG
Bna_EI_2 373 -----GCTCTCGTCTTGG
Bna_FL 391 GCTCTGGTCTTTGCAGCAGCTTGACTTCTCCCTCTCCAGTGCCAGGCTCTCGTCTGG
Rra_EI 360 -----GCTCTCGTCTTGG
Hsa_FL 396 CCATATCGTCTTGCAGCAGATTGAAATTACATCTAAAGCCACCCAGGCTTGGTCTTAG
Hsa_EI 70 -----GCCTTGGTCTTAG

```

```

Ath_EIF4A C S G V L Q Q L D Y A L L Q C Q A L V L
Hsa_EIF4A1 A I S I L Q Q I E L D L K A T Q A L V L

```

```

Ath_FL 527 CTCCCACCAGAGAGCTTGCTCAGCAGATCGAGAAGGTCATGCGTGGCCTTGGTACTACC
Ath_EI 446 CTCCCACCAGAGAGCTTGCTCAGCAGATCGAGAAGGTCATGCGTGGCCTTGGTACTACC
Bna_EI_1 382 CTCCCACCAGAGAGCTTGCTCAGCAGATCGAGAAGGTCATGCGTGGTCTCGGAGACTACC
Bna_EI_2 382 CTCCCACCAGAGAGCTTGCTCAGCAGATCGAGAAGGTCATGCGTGGTCTCGGAGACTACC
Bna_FL 451 CTCCCACCAGAGAGCTTGCTCAGCAGATCGAGAAGGTCATGCGTGGTCTCGGAGACTACC
Rra_EI 369 CTCCCACCAGAGAGCTTGCTCAGCAGATCGAGAAGGTCATGCGTGGTCTCGGAGACTACC
Hsa_FL 456 CACCCACTCGAGATTGGCTCAGCAGATCGAGAAGGTCATGCGTGGTCTCGGAGACTACA
Hsa_EI 80 CACCCACTCGAGATTGGCTCAGCAGATCGAGAAGGTCATGCGTGGTCTCGGAGACTACA

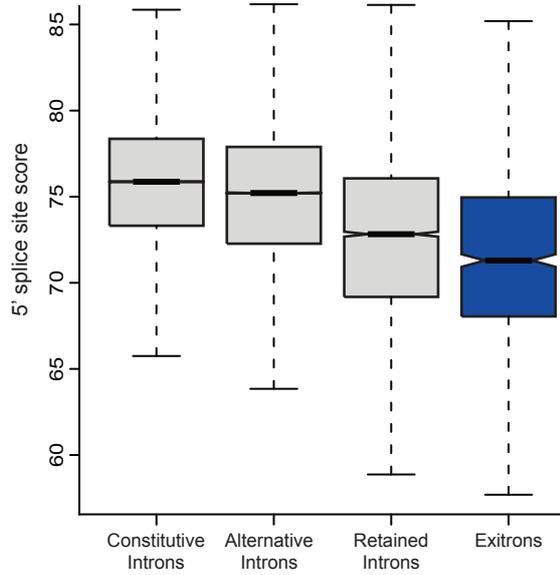
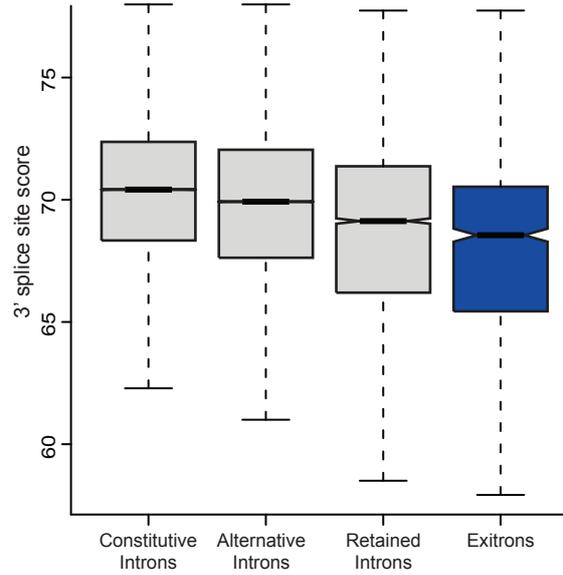
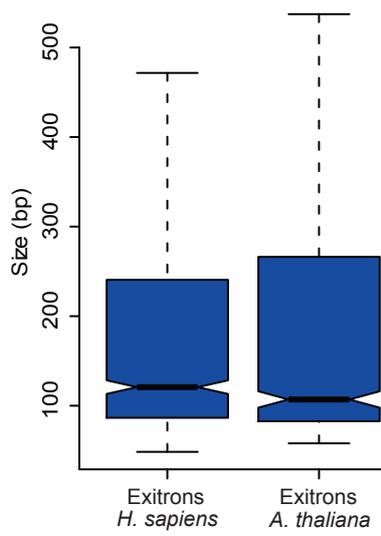
```

```

Ath_EIF4A A P T R E L A Q Q I E K V M R A L G D Y
Hsa_EIF4A1 A P T R E L A Q Q I Q K V V M A L G D Y
Motif Ia

```

Supplemental Figure 7.

A**B****C****Supplemental Figure 8.**

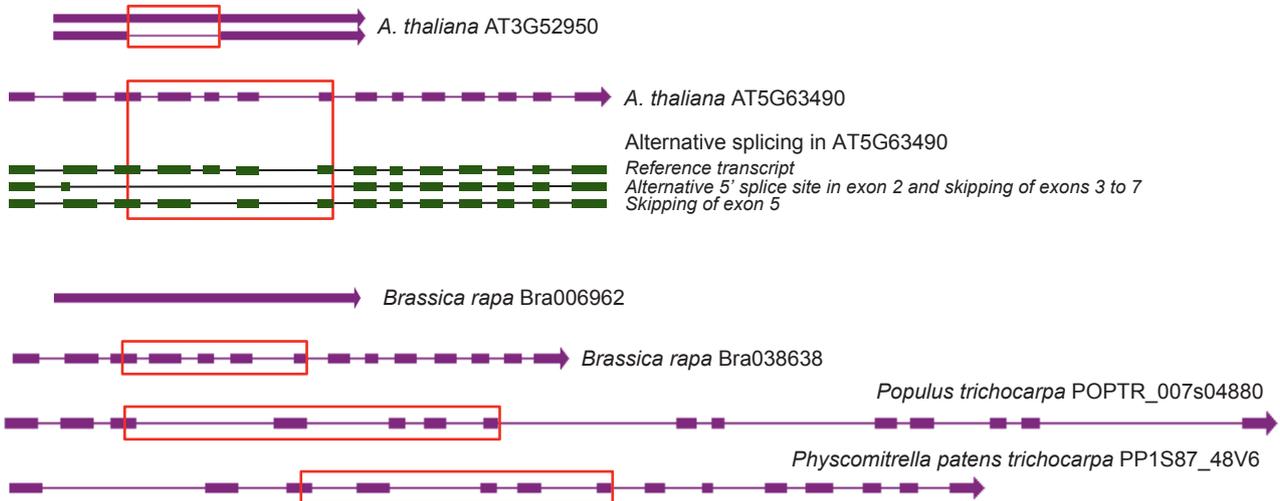
PTMs encoded by exons and other types of exons			
Phosphorylation sites			
	Exons	Constitutive Exons	Alternative Exons
%	29.03	16.7	23.06
P-value	-	7.84e-12	0.002097
Ubiquitylation sites			
	Exons	Constitutive Exons	Alternative Exons
%	14.34	5.17	8.15
P-value	-	0.000001	0.001965

Supplemental Figure 9.

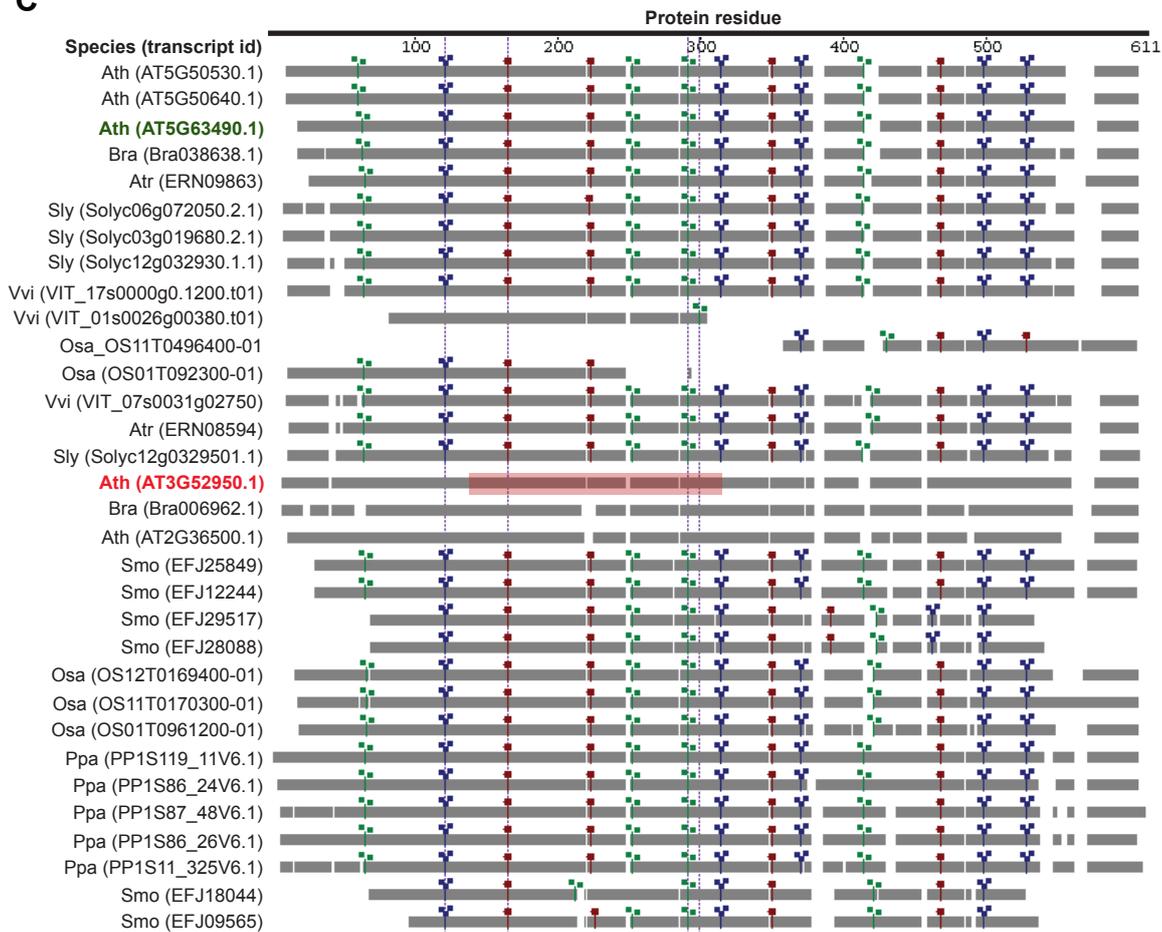
A
 THIC phosphomethylpyrimidine synthase AT2G29630



B
 CBS/octicosapeptide/Phox/Bemp1 domain-containing protein AT3G52950



C



Supplemental Figure 11.

A

Cre 1 -----MLPALRVGAQQA---AGAAASLLFTRGYAD-LSSLKKTMLYDFHVAHGGK
Vca 1 MSSTRLLTLPLQLRAGALRASEHASATGSLLFTRGFAD-DANLKKTVLYDFHVAHGGK
Smo_1 1 -----MRKLVAEKLRLVSNAGQIRRFAS---AAPLASESPPLKKTLYDFHVENGA
Smo_2 1 -----MRKLVAEKLRLVSNAGQIRRFAS---AAPLASESPPLKKTLYDFHVENGA
Bra_2 1 -----MRGSSLWQLQOSTTRRLAQSDKKPLSP--RRHFAS-GADLKKTALYDFHVAHGGK
Bra_1 1 -----MRGSSLWQLQOSTTRRLAQSDKKALS---RRCFSS-DADLKKTALYDFHVAHGGK
Ath_FL 1 -----MRGSSLWQLQOSTTRRLAQSDKKVVS---RRYFAS-EADLKKTALYDFHVAHGGK
Ath_EI 1 -----MRGSSLWQLQOSTTRRLAQSDKKVVS---RRYFAS-EADLKKTALYDFHVAHGGK
Aly 1 -----MRGSSLWQLQOSTTRRLAQSDKKGVS---RRYFAS-EADLKKTALYDFHVAHGGK
Ptr_2 1 -----MRGSSLWQLQOSTTRRLAQVDKKVVG---RRYFAS-EAELKKTLYDFHVAHGGK
Ptr_1 1 -----MRGSSLWQLQLSTTRRLAQADKKAVG---RRYFAS-EAELKKTLYDFHVAHGGK
Vvi 1 -----MRGSSLWQLQOSTTRRLAQADKKAVA---RRCFAS-EAELKKTLYDFHVAHGGK
Osa 1 -----MRG---LLACATARRAGATSTARRHLAGAAEA-EAELKKTALYDFHVAHGGK
Ppa_1 1 -----MKRAVSQLEGTVRRTLAQSSNALRETSRRCYADDAANLKKTMLYDFHVENGGK
Ppa_2 1 -----MKRAVSQLEGTVRRTLAQSSNALRETSRRCYADDAANLKKTMLYDFHVENGGK
Hsa_FL 1 -----MQRVSVVVARLQFRLQAFPP-ALCRPLSCAQEVLRRTPLYDFHVAHGGK
Hsa_ES 1 -----MQRVSVVVARLQFRLQAFPP-ALCRPLSCAQEVLRRTPLYDFHVAHGGK

Cre 48 MVDFAGWAMPVIOYKDSIMDSTHFCRQNASLFDVSHMCGFLKQKDAIQFLEGLVVGDIAG
Vca 60 MVPPFAGWSMPLVYKDIILNSTNCRQNGSLFDVSHMCGFLKQKDAIQFLEGLVVGDIAG
Smo_1 53 MVPPFAGWSMPLVYKDIILNSTNCRQNGSLFDVSHMCGFLKQKDAIQFLEGLVVGDIAG
Smo_2 53 MVPPFAGWSMPLVYKDIILNSTNCRQNGSLFDVSHMCGFLKQKDAIQFLEGLVVGDIAG
Bra_2 53 MVPPFAGWSMPLVYKDSIIDSTNCRVNGSLFDVAHMCGLSLKQKDCVPFLETLLVVDVAG
Bra_1 52 MVPPFAGWSMPLVYKDSIIDSTNCRVNGSLFDVAHMCGLSLKQKDCVPFLETLLVVDVAG
Ath_FL 52 MVPPFAGWSMPLVYKDSIIDSTNCRVNGSLFDVAHMCGLSLKQKDCVPFLETLLVVDVAG
Ath_EI 52 MVPPFAGWSMPLVYKDSIIDSTNCRVNGSLFDVAHMCGLSLKQKDCVPFLETLLVVDVAG
Aly 52 MVPPFAGWSMPLVYKDSIIDSTNCRQNGSLFDVAHMCGLSLKQKDCVPFLETLLVVDVAG
Ptr_2 52 MVPPFAGWSMPLVYKDSIIDSTNCRQNGSLFDVSHMCGFLKQKDCVPFLETLLVVDVAA
Ptr_1 52 MVPPFAGWSMPLVYKDSIIDSTNCRQNGSLFDVSHMCGFLKQKDCVPFLETLLVVDVAA
Vvi 52 MVPPFAGWSMPLVYKDSIIDSTNCRVNGSLFDVSHMCGFLKQKDCVPFLETLLVVDVAG
Osa 52 MVPPFAGWSMPLVYKDSIIDSTNCRVNGSLFDVSHMCGFLKQKDCVPFLETLLVVDVAA
Ppa_1 55 MVPPFAGWSMPLVYKDSIIDSTNCRVNGSLFDVSHMCGFLKQKDCVPFLETLLVVDVAG
Ppa_2 53 MVPPFAGWSMPLVYKDSIIDSTNCRVNGSLFDVSHMCGFLKQKDCVPFLETLLVVDVAG
Hsa_FL 49 MVAFAGWSLVPVQYRDSHTDSHHTRQHCSLFDVSHMLQKILGSDRWKLMESLVVGDIAE
Hsa_ES 49 MVAFAGWSLVPVQYRDSHTDSHHTRQHCSLFDVSHMLQKILGSDRWKLMESLVVGDIAE

Cre 108 LKDGCGSLVFTNEGGGIDDDVITKVNQGHLYTVVFNAGCRDKDLAHLKHLAAAKSKGL
Vca 120 LKDGCGSLVFTNEGGGIDDDVITKVNQGHLYTVVFNAGCRDKDLAHLKHLAAAKSKGL
Smo_1 113 LSDGCGSLVFTNEGGGIDDDVITKVKDGHLYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Smo_2 113 LSDGCGSLVFTNEGGGIDDDVITKVKDGHLYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Bra_2 113 LAPGCGSLVFTNEGGGIDDDSVITKVTDEHTYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Bra_1 112 LAPGCGSLVFTNEGGGIDDDSVITKVTDEHTYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Ath_FL 112 LAPGCGSLVFTNEGGGIDDDSVITKVTDEHTYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Ath_EI 94 -----VTDEHTYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Aly 112 LAPGCGSLVFTNEGGGIDDDSVITKVTDEHTYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Ptr_2 112 LAPGCGSLVFTNEGGGIDDDSVITKVTDEHTYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Ptr_1 112 LAPGCGSLVFTNEGGGIDDDSVITKVTDDHMYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Vvi 112 LAPGCGSLVFTNEGGGIDDDSVITKVKDGHLYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Osa 112 LKDGCGSLVFTNEGGGIDDDSVITKVTDDHMYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Ppa_1 115 LANGCGSLVFTNEGGGIDDDVITKVTDDHMYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Ppa_2 73 LAPGCGSLVFTNEGGGIDDDVITKVTDDHMYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Hsa_FL 109 LRPNGCGSLVFTNEGGGIDDDVITKVTDDHMYLVVFNAGCRDKDLAHLKHLAAAKSKGL
Hsa_ES 109 LRPNGCGSLVFTNEGGGIDDDVITKVTDDHMYLVVFNAGCRDKDLAHLKHLAAAKSKGL

Cre 168 DVAMTVHDSRSLALQGPAAAEVWAGLVAPGVDLKAMYFSDFKPIDLGGIP-CWVTRTCY
Vca 180 DVAMTVHDSRSLALQGPAAAKVWAGLVAPGVDLKAMYFSDFKPIFDVAGIP-CWVTRTCY
Smo_1 173 DVSSVHDSRSLALQGPAAASTLQHLVKE--DLSKLYFGNERLISVNGAE-CFITRTGY
Smo_2 173 DVSSVHDSRSLALQGPAAASTLQHLVKE--DLSKLYFGNERLISVNGAE-CFITRTGY
Bra_2 173 DVSWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNEFQILDINGST-CFITRTGY
Bra_1 172 DVSWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNEFQILDINGST-CFITRTGY
Ath_FL 172 DVSWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNEFQILDINGST-CFITRTGY
Ath_EI 128 DVSWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNEFQILDINGST-CFITRTGY
Aly 172 DVSWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNEFQILDINGST-CFITRTGY
Ptr_2 172 DVSWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNERITDINGAY-CFITRTGY
Ptr_1 172 DVSWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNERITDINGAR-CFITRTGY
Vvi 172 DVSWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNEFQILDINGAT-CFITRTGY
Osa 172 DVKWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNERITDINGAY-CFITRTGY
Ppa_1 175 SVGWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNERITDINGSE-CFITRTGY
Ppa_2 133 SVGWHHDSRSLALQGPAAAPVLOHLTKR--DLSKLYFGNERITDINGSE-CFITRTGY
Hsa_FL 169 DVGLEWLDN-ALLALQGPAAAPVLOHLTKR--DLSKLYFGNERITDINGSE-CFITRTGY
Hsa_ES 125 DVGLEWLDN-ALLALQGPAAAPVLOHLTKR--DLSKLYFGNERITDINGSE-CFITRTGY

Cre 227 TGEDGFEISVPSNHAVALAEKLTAN--KRVRAAGLGRDLSRLEAGLCLYGNLDNEDLTP
Vca 238 TGEDGFEISVPSNHAVALAEKLTAS--ERVRAAGLGRDLSRLEAGLCLYGNLDNEDLTP
Smo_1 230 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Smo_2 230 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Bra_2 230 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Bra_1 229 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Ath_FL 229 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Ath_EI 185 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Aly 229 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Ptr_2 229 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Ptr_1 229 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Vvi 229 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Osa 229 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Ppa_1 232 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP
Ppa_2 190 TGEDGFEISVPSNHAVALAEKLTAKALLEKSEGKIRLTGLGARDSLRLEAGLCLYGNLDNEDLTP

Hsa_FL 226 TGEDGVEI SVPVAGAVHLATATLTKN--PEVVKLAGLAARDSLRLEAGLCLYGNDIDEHTTP
Hsa_ES 182 TGEDGVEI SVPVAGAVHLATATLTKN--PEVVKLAGLAARDSLRLEAGLCLYGNDIDEHTTP

Cre 285 VEAGLAWTIGKRRREKFDLGGDIKKQLAEGV KRRVGFVSTGAPARQHSVISTPDGKV
Vca 296 VEAGLAWTIGKRRREGFDLGGDVIKKQLAEGV KRRVGFVSSGAPARQHSVISTPDGQV
Smo_1 290 VEAGLAWTIGKRRRAEGGFLGADVILKQLKEGVSRRVGMISGAPARAHCPINYNASDEV
Smo_2 290 VEAGLAWTIGKRRRAEGGFLGADVILKQLKEGVSRRVGMISGAPARAHCPINYNASDEV
Bra_2 290 VEAGLTWALGKRRRAEGGFLGADVILKQLEDEPTIRRVFFSSGPPARSHSEVHDESGNK
Bra_1 289 VEAGLTWALGKRRRAEGGFLGADVILKQLQDGP TIRRVFFSSGPPARSHSEVHDESGNK
Ath_FL 289 VEAGLTWALGKRRRAEGGFLGADVILQQLKDGPTIRRVFFSSGPPARSHSEVHDESGNK
Ath_EI 245 VEAGLTWALGKRRRAEGGFLGADVILQQLKDGPTIRRVFFSSGPPARSHSEVHDESGNK
Aly 289 VEAGLTWALGKRRRAEGGFLGADVILQQLKDGPTIRRVFFSSGPPARSHSEVHDESGNK
Ptr_2 289 VEAGLSWALGKRRRAEGGFLGAEVILKQLAEGPKILLVGFTSTGPPERSHSEIQDEKGTN
Ptr_1 289 VEAGLNWALGKRRRAEGGFLGAEVILKQLAEGPKVRLVGFSSGPPERSHSEIQDEKGTN
Vvi 289 VEAGLTWALGKRRRAEGGFLGAEVILKQLEGGPSVRRVGFSSGPPARSHSEIQDDKGN
Osa 289 VEAGLSWALGKRRRAEGGFLGADVILKQLQEGPKIRRVGLLSGPPERSHSEIVSNSGEN
Ppa_1 292 VEAGLAWTIGKRRRAEGNFLGAEPILRQIKDGVSRRVGFISTGAPARAHSEILDLEGKN
Ppa_2 250 VEAGLAWTIGKRRRAEGNFLGAEPILRQIKDGVSRRVGFISTGAPARAHSEILDLEGKN
Hsa_FL 284 VEGSLSWTLGKRRRAAMDFGAKVIVPOLKGRVQRRRVGLMCEGAPMRAHSPILNMEGTK
Hsa_ES 240 VEGSLSWTLGKRRRAAMDFGAKVIVPOLKGRVQRRRVGLMCEGAPMRAHSPILNMEGTK

Cre 345 VGEITSGAFSPCLKKNIAMGYVDKDFAKAGTAKLVVVRGKVNDAVVTKMPFVPTPKYYKRP
Vca 356 VGEITSGAFSPCLKKNIAMGYVEKDFSKPGTQLKVEVRGKQNEAVVTKMPFLPTPKYYKRP
Smo_1 350 IGEVTSGGFSPCLKKNIAMGYVSTGNHKEGTPISAVRDKKNAQVITKMPFVPAKYHKKP
Smo_2 350 IGEVTSGGFSPCLKKNIAMGYVSTGNHKEGTPISAVRDKKNAQVITKMPFVPAKYHKKP
Bra_2 350 IGEITSGGFSPNLKKNIAMGYVKSQGHKGTGKWKLLVVRGKPYEGNITKMPFVATKYYKPT
Bra_1 349 IGEITSGGFSPNLKKNIAMGYVKSQGHKGTGKWKLLVVRGKPYEGNITKMPFVATKYYKPS
Ath_FL 349 IGEITSGGFSPNLKKNIAMGYVKSQGHKGTGKWKLLVVRGKPYEGSITKMPFVATKYYKPT
Ath_EI 305 IGEITSGGFSPNLKKNIAMGYVKSQGHKGTGKWKLLVVRGKPYEGSITKMPFVATKYYKPT
Aly 349 IGEITSGGFSPNLKKNIAMGYVKSQGHKGTGKWKLLVVRGKPYEGSITKMPFVATKYYKPT
Ptr_2 349 IGEITSGGFSPCLKKNIAMGYVKSQGHKAGTKAKILVRGKAYDCAVTKMPFVPTKYYKPS
Ptr_1 349 IGEITSGGFSPCLKKNIAMGYVKSQGHKAGTKAKILVRGKAYDCVVTKKPFVPTKYYKPS
Vvi 349 IGEITSGGFSPCLKKNIAMGYVKSQGHKAGTKAKILVRGKPYDCVVTKMPFVPTKYYKPS
Osa 349 IGEVTSGGFSPCLKKNIAMGYVKSGLHKAETEFKVVVRGKSYDAVVTKMPFVPTKYYKPS
Ppa_1 352 IGEITSGGFSPCLKKNIAMGYVATGHHKNTQKVVVRSKSYDAVVTKMPFVPSKYYKPP
Ppa_2 310 IGEITSGGFSPCLKKNIAMGYVATGHHKNTKVKLAVRSKTYDATVTKMPFVPSKYYKPP
Hsa_FL 344 ICTVTSGCPSPLKKNIAMGYVPCEYSRPGTMLLVVVRKQQMAVVS KMFPVPTNYITLK
Hsa_ES 300 ICTVTSGCPSPLKKNIAMGYVPCEYSRPGTMLLVVVRKQQMAVVS KMFPVPTNYITLK

Cre 405 EPAKK-
Vca 416 EAAKK-
Smo_1 410 -----
Smo_2 410 -----
Bra_2 410 -----
Bra_1 409 -----
Ath_FL 409 -----
Ath_EI 365 -----
Aly 409 -----
Ptr_2 409 -----
Ptr_1 409 -----
Vvi 409 -----
Osa 409 -----
Ppa_1 412 Q-----
Ppa_2 370 QEAAKS
Hsa_FL 404 -----
Hsa_ES 360 -----

B

SpliceAid2

Smo_1 220 CTC AAT T G T C G C C A G A A T G G T A G C C T T T T C G A C G T G T C T C A T A T G T G T G G C C T C A C C C T C
 Smo_2 220 CTC AAT T G T C G C C A G A A T G G T A G C C T T T T C G A C G T G T C T C A T A T G T G T G G C C T C A C C C T C
 Ath_FL 217 G T T A A C T G C A G G G A A A T G G G A G T T G T T T G A T G T T G C A C A T A T G T G T G G T T T G A C C C T T
 Ath_EI 217 G T T A A C T G C A G G G A A A T G G G A G T T G T T T G A T G T T G C A C A T A T G T G T G G T T T G A C C C T T
 Aly 217 G T T A A C T G C A G G C A A A T G G G A G T T G T T T G A T G T T G C A C A T A T G T G T G G T T T G A C C C T T
 Bra_1 217 G T T A A C T G C A G A G T C A A T G G C A G T T T T T T G A T G T T G T C A C A T G T G T G G T T T T A G C C T C
 Bra_2 220 G T T A A C T G C A G G T C A A C G G G A G T T G T T T G A T G T T G C G C A C A T G T G T G C T T G A C C C T C
 Ptr_2 217 G T G A A T T G T A G A C A G A A C G G T A G C C T T T T T G A T G T C T C A C A T A T G T G T G G G T T G A C C C T C
 Ptr_1 217 G T G A A T T G T A G A C A G A A T G G T A G C C T T T T T G A T G T C T C A C A T A T G T G T G G G T T T A G C C T G
 Vvi 217 G T G A A T T G T C G G G A G A A T G G T A G C C T C T T T G A T G T C T C C C A T A T G T G T G G G C T A A G C C C T C
 Osa 217 C T C A A C T G C C G C C A A C G C A G C C T C T T C G A C G T C T C C C A C A T G T G C G G C C T C A G C C T C
 Ppa_1 226 A T C A A T T G C C G G A C T A A C G G C A G T T G T T C G A T G T G C G C A T A T G T G T G G G C T G A G C T T G
 Ppa_2 100 A C G A A T T G C C G C T C C A A T G C C A G T T G T T T G A T G T C T C G C A C A T G T G T G G G T T G A C C C T C
 Cre 205 A C G A C T G C C G T C A G A A C C C T C G T G T T C G A C G T G T C G C A C A T G T G T G G T T T C T C G C T G
 Vca 241 A T T T T T T G C C G A A A G A A T G C A T C T C T T T T T G A C G T G T C C C A C A T G T G T G G C T C A C G C T C

Protein

V N C R E N G S L F D V A H M C G L S L

Smo_1 280 A A G G C A A G G A C G C G A T T C C T T T C T C G A G A C G C T G G T C T T G G G T G A T A T C G C G G T C T G
 Smo_2 280 A A G G C A A G G A C G C G A T T C C T T T C T C G A G A C G C T G G T C T T G G G T G A T A T C G C G G T C T G
 Ath_FL 277 A A G G T A A A G A T T G T G T T C C T T T T C T T G A G A C A C T T G T G T T G C T G A T G T G G C T G T T T G
 Ath_EI 277 A A G G T A A A G A T T G T G T T C C T T T T C T T G A G A C A C T T G T G T T G C T G A T G T G G C T G T T T G
 Aly 277 A A G G T A A A G A T T G T G T T C C T T T T C T T G A G A C A C T T G T G T T G C T G A T G T G G C T G T T T G
 Bra_1 277 A A G G C A A A G A C T G T G T T C C T T T C T C G A G A C G C T C G T G T T G C T G A C T G G C T G T T T G
 Bra_2 280 A A G G C A A A G A C T G T G T T C C C T T T C T C G A G A C G C T A G T G T T G C T G A C T G G C T G T T T G
 Ptr_2 277 A A G G C A A A G A C T G T A T T C C T T T C T A G A G A A G C T T G T T A T T G C T G A T G T T G C C G C G C T T
 Ptr_1 277 A A G G A A A A G A C T G T G T T C C T T T C T A G A G A A A C T T G T T A T T G C T G A T G T T G C T G C G C T T
 Vvi 277 A A G G A A A A G A C T G C A T T C C T T T T C T G A A A A G C T T G T C A T T G C T G A T G T T G C T G G G C T T
 Osa 277 C A G G C C C C A G G C C A T C C C C T T C C T C G A C T C C C T C G T C C C C G A C G T C G C G G C G C T C
 Ppa_1 286 A A A G G C C C A G A T G C C A T T G A T T T C T T G A G A C G C T T G T T C T C G C C G A C A T C A A A G C C T C
 Ppa_2 160 A A G G C C C T G A T G C C A T C G A C T T C C T T G A G A C G C T C G T C T T G C C G A C A T T A A G G C C T C
 Cre 265 A A G G C A A A G A C G C C A T C C A G T T C C T T G A G G G G C T G G T G T T G G T G A C A T C G C C G C C T C
 Vca 301 A A G G C A A A G A C G C G A T C A A G T T C C T T G A G G G C C T T G T G T G G G C A C A T C G C T G G C T C

Protein

K G K D C V P F L E T L V V A D V A G L

Smo_1 340 T C A G A C G G C T C G T C T A G T C T C G C G T T C A C C A A C G A G A A G G G A G G G A C C A T C G A C G A C
 Smo_2 340 T C A G A C G G C T C G T C T A C T C T C T C G C G T T C A C C A A C G A G A A G G G A G G A C C A T C G A C G A C
 Ath_FL 337 G C T C T G G A A C T G G G A G C T A A A C T G T T T A C A A A C G A G A A G G A G G T C C C A T T G A T G A C
 Ath_EI 281 G C T C T G G A A C T G G G A G C T A A A C T G T T T A C A A A C G A G A A G G A G G T C C C A T T G A T G A C
 Aly 337 G C T C T G G A A C T G G G A G C T A A A C T G T T T A C A A A C G A G A A G G A G G T C C C A T T G A T G A C
 Bra_1 337 G C T C T G G A C C G G G A G C T T G A C C T G T T C A C G A A C G A G A A G G G A G G T C C T A T T G A T G A C
 Bra_2 340 G C T C T G G A A C T G G G A G C T T G A C T G T T T A C G A A T G A G A A G G G T G G T C C T A T T G A T G A C
 Ptr_2 337 G C A C C T G G A A C T G G G A C T C T A A C T G T T T A C T A A T G A G A A A G G A G G A C A A T T G A T G A T
 Ptr_1 337 G C A C C T G G A A C T G G G A C T C T A A C T C T T T A C T A A T G A G A A A G G A G G A C A A T T G A T G A T
 Vvi 337 G C C C C T G G A A C T G G G A C T T A A C C C T C T T A C A A A T G A G A A A G G A G G G C C A A T T G A T G A T
 Osa 337 A A G A A G G C A C C G G A C G T C A C C C T T C A C A A G A C C C G G G C G C C C A T C G A C G A C
 Ppa_1 346 G C C A A T T G T A C C G C A C G C T C C C T C T T A C G A A C G A G A A T G G T G G A G T G A T C G A T G A C
 Ppa_2 220 G C A C C T G G C A C T G G C A C G C T C C C T G T T A C G A A C G A G A A T G G A G G C C T T A T T G A C G A C
 Cre 325 A A G G A C G G C A C C G C T C C C T T G A G C C C T T C A C C A A C G A A A G G G T G G C A T C A T T G A C G A C
 Vca 361 A A G G A T G G C A C C G C T C G C T C T C G T G T T C A C C A A C G A G C A G G G C G G C A T C A T C G A C G A C

Protein

A P C T C S L I V F T N E K C G A I D D

SpliceAid2

Smo_1 400 A C C G T G A T A A C C A A G T G A A G G A T G G T C A C T C T A C C T G G T G T A A A T G C G G G T T G C C G A
 Smo_2 400 A C T G T G A T A A C C A A G T G A A A G A T G G T C A C T C T A C C T G G T G T A A A T G C G G G T T G C C G A
 Ath_FL 397 T C G S T G A T T A C C A A G T G A C A G A T G A A C A T A T C T A T T T G G T G T C A A T G C T G G C T G T A G G
 Ath_EI 281 T G A C A G A T G A A C A T A T C T A T T T G G T G T C A A T G C T G G C T G T A G G
 Aly 397 T C G S T C A T T A C C A A G T G A C A G A T G A A C A T A T C T A T T T G G T G T C A A T G C T G G T T G T A G G
 Bra_1 397 T C G S T G A T T A C C A A G T G A C G G A T G A G C A T A T C T A T T T G G T G T C A A T G C T G G T T G T A G G
 Bra_2 400 T C G S T G A T T A C T A A A G T G A C T G A T G A G C A T A T C T A C T T G G T G T C A A T G C T G G T T G T A G G
 Ptr_2 397 T C A G T G A T C A C C A A G T T C A G A A T G A T C A G A T G A C A T A G T T G T G A A T G C A G G G T G T A G A
 Ptr_1 397 T C A G T G A T C A C C A A G T G A C G G A T G A T C A G A T G A C A T A G T T G T G A A T G C A G G G T G T A G A
 Vvi 397 T C T G T G A T C A C C A A G T G A A G G A T A C C A G A T C T A C C T G G T T G T G A A T G C G G G T G T A G G
 Osa 397 T C C G T C G T T A C C A A G T C A C C G A C C A G C A C A T C T A C C T C G T C G T C A A C G C C G G G T G C A G G
 Ppa_1 406 A C T G T C A T C A C A A A G T G T C A G A C A T G A C C A T C T A C C T G G T T G T C A A T G C G G G T G C C G G
 Ppa_2 280 A C C G T C A T C A C A A A G T G T C A G A C G A T C A C A T C T A C T T G G T G T C A A T G C G G G T T G T C G T
 Cre 385 A C C G T C A T C A C C A A G T G A A C G C C A G C A C A T C T A C A C G T G T C A A C G C G G G C T G C C G C
 Vca 421 A C C G T C A T C A C C A A G T C A A T G C C A G G A G A T C T A C G T G G T G T C A A T G C G G G C T G C C G C

Protein

S V I T K V T D E H I Y L V V N A G C R

C

```
Ocu_FL 1 ---MRQAVSMVAHLGFRRLRALPSALSRSLSAODVLHRTPLYDFHLAHGGKMFVAFAGWSL
Ocu_ES 1 ---MRQAVSMVAHLGFRRLRALPSALSRSLSAODVLHRTPLYDFHLAHGGKMFVAFAGWSL
Eca_FL 1 ---MQRAVSMVARLGLRLQAFPSLGRPLSCTQDVLRRTPLYDFHLAHGGKMFVAFAGWSL
Eca_ES 1 ---MQRAVSMVARLGLRLQAFPSLGRPLSCTQDVLRRTPLYDFHLAHGGKMFVAFAGWSL
Mmu_FL 1 ---MQRVSVVAHLGFRLLQALPPALCRPLSCAODVLRRTPLYDFHLAHGGKMFVAFAGWSL
Mmu_ES 1 ---MQRVSVVAHLGFRLLQALPPALCRPLSCAODVLRRTPLYDFHLAHGGKMFVAFAGWSL
Hsa_FL 1 ---MQRVSVVVARLGFRLQAFPPALCRPLSCAODVLRRTPLYDFHLAHGGKMFVAFAGWSL
Hsa_ES 1 ---MQRVSVVVARLGFRLQAFPPALCRPLSCAODVLRRTPLYDFHLAHGGKMFVAFAGWSL
Ptr_FL 1 ---MQRVSVVVARLGFRLQAFPPALCHPLSCAODVLRRTPLYDFHLAHGGKMFVAFAGWSL
Ptr_ES 1 ---MQRVSVVVARLGFRLQAFPPALCHPLSCAODVLRRTPLYDFHLAHGGKMFVAFAGWSL
Pab_FL 1 ---MQRVSVVAHLGSRRLQAFSPALCRPFSCAODVLRRTPLYDFHLAHGGKMFVAFAGWSL
Pab_ES 1 ---MQRVSVVAHLGSRRLQAFSPALCRPFSCAODVLRRTPLYDFHLAHGGKMFVAFAGWSL
Ath_FL 1 MRGSLWQLGQSI TRRLAQS DKKVVSRRYFASEADLKKTA L YDFHVAHGKMPFAGWSM
Ath_EI 1 MRGSLWQLGQSI TRRLAQS DKKVVSRRYFASEADLKKTA L YDFHVAHGKMPFAGWSM
```

```
Ocu_FL 58 PVQYQDSHMDLHLHTRQHCSLFDVSHMLQTKIFGSDRVKLMESLVVGDIAELRPNOGTL
Ocu_ES 58 PVQYQDSHMDLHLHTRQHCSLFDVSHMLQTKIFGSDRVKLMESLVVGDIAELRPNOGTL
Eca_FL 58 PVQYRDSHVDSHLHTRQHCSLFDVSHMLQTKIFGSDRVKLMESLVVGDIAELRPNOGTL
Eca_ES 58 PVQYRDSHVDSHLHTRQHCSLFDVSHMLQTKIFGSDRVKLMESLVVGDIAELRPNOGTL
Mmu_FL 58 PVQYRDSHTDSHLHTRQHCSLFDVSHMLQTKIFGSDRVKLMESLVVGDIAELRPNOGTL
Mmu_ES 58 PVQYRDSHTDSHLHTRQHCSLFDVSHMLQTKIFGSDRVKLMESLVVGDIAELRPNOGTL
Hsa_FL 58 PVQYRDSHTDSHLHTRQHCSLFDVSHMLQTKILGSDRVKLMESLVVGDIAELRPNOGTL
Hsa_ES 58 PVQYRDSHTDSHLHTRQHCSLFDVSHMLQTKILGSDRVKLMESLVVGDIAELRPNOGTL
Ptr_FL 58 PVQYRDSHTDSHLHTRQHCSLFDVSHMLQTKILGSDRVKLMESLVVGDIAELRPNOGTL
Ptr_ES 58 PVQYRDSHTDSHLHTRQHCSLFDVSHMLQTKILGSDRVKLMESLVVGDIAELRPNOGTL
Pab_FL 58 PVQYRDSHTDSHLHTRQHCSLFDVSHMLQTKILGSDRVKLMESLVVGDIAELRPNOGTL
Pab_ES 58 PVQYRDSHTDSHLHTRQHCSLFDVSHMLQTKILGSDRVKLMESLVVGDIAELRPNOGTL
Ath_FL 61 PIQYKDSIMDSTVNCRENGSLFDVAHMCGLSLKGRKDCVPELETLVVADVAGLAEPTGSLT
Ath_EI 61 PIQYKDSIMDSTVNCRENGSLFDVAHMCGLSLKGRKDCVPELETLVVADVAGLAEPTGSLT
```

```
Ocu_FL 118 LFTNEAGGIIDDLIVTNTSEGYLYVVSNAGCWDKDLALM QNKVRELQNKGS DVGLEVVVDN
Ocu_ES 114 -----NKKVRELQNKGS DVGLEVVVDN
Eca_FL 118 LFTNEAGGIIDDLIVTNTSEGHLYVVSNAGCWDKDLALM QDKVRELQNI GSDVGLEVVVDN
Eca_ES 114 -----DKVRELQNI GSDVGLEVVVDN
Mmu_FL 118 LFTNEAGGIIDDLIVTNTSEGHLYVVSNAGCWEKDLALM QDKVRELQNGRQDVGLEVLND
Mmu_ES 114 -----DKVRELQNGRQDVGLEVLND
Hsa_FL 118 LFTNEAGGIIDDLIVTNTSEGHLYVVSNAGCWEKDLALM QDKVRELQNGRQDVGLEVLND
Hsa_ES 114 -----DKVRELQNGRQDVGLEVLND
Ptr_FL 118 LFTNEAGGIIDDLIVTNTSEGHLYVVSNAGCWEKDLALM QDKVRELQNGRQDVGLEVLND
Ptr_ES 114 -----DKVRELQNGRQDVGLEVLND
Pab_FL 118 LFTNEAGGIIDDLIVTNTSEGHLYVVSNAGCWEKDLALM QDKVRELQNGRQDVGLEVLND
Pab_ES 114 -----DKVRELQNGRQDVGLEVLND
Ath_FL 121 VFTNEKGGAIIDDSVITKVTDEHIYLVVNAGCRDKDLAHEEHMRAFKSKGCDVSWHITHDE
Ath_EI 94 -----VITDEHIYLVVNAGCRDKDLAHEEHMRAFKSKGCDVSWHITHDE
```

```
Ocu_FL 178 -ALLALQGPTAAQVLQAGVAHDLRKLPFMTSAVMEVFGVAGCRVTRCGYTGEDGMEISVP
Ocu_ES 134 -ALLALQGPTAAQVLQAGVAHDLRKLPFMTSAVMEVFGVAGCRVTRCGYTGEDGMEISVP
Eca_FL 178 -ALLALQGPTAAQVLQAGVADDLKKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Eca_ES 134 -ALLALQGPTAAQVLQAGVADDLKKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Mmu_FL 178 -ALLALQGPTAAQVLQASVADDLKKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Mmu_ES 134 -ALLALQGPTAAQVLQASVADDLKKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Hsa_FL 178 -ALLALQGPTAAQVLQAGVADDLRLKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Hsa_ES 134 -ALLALQGPTAAQVLQAGVADDLRLKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Ptr_FL 178 -ALLALQGPTAAQVLQAGVADDLRLKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Ptr_ES 134 -ALLALQGPTAAQVLQAGVADDLRLKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Pab_FL 178 -ALLALQGPTAAQVLQAGVADDLRLKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Pab_ES 134 -ALLALQGPTAAQVLQAGVADDLRLKLPFMTSAVMEVFGVSGCRVTRCGYTGEDGVEISVP
Ath_FL 181 RSLALQGPAAAPVLQHLTKEDLSKLYFGNFQILDINGSI-CFLTRTGYTGEDGFEISVP
Ath_EI 137 RSLALQGPAAAPVLQHLTKEDLSKLYFGNFQILDINGSI-CFLTRTGYTGEDGFEISVP
```

```
Ocu_FL 237 APGAVRLATAFLLENPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Ocu_ES 193 APGAVRLATAFLLENPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Eca_FL 237 AVGAVRLATAFLLENPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Eca_ES 193 AVGAVRLATAFLLENPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Mmu_FL 237 AAFAVHLATAALLKNPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Mmu_ES 193 AAFAVHLATAALLKNPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Hsa_FL 237 VAGAVHLATAALLKNPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Hsa_ES 193 VAGAVHLATAALLKNPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Ptr_FL 237 VAGAVHLATAALLKNPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Ptr_ES 193 VAGAVHLATAALLKNPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Pab_FL 237 VAGAVHLATAALLKNPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Pab_ES 193 VAGAVHLATAALLKNPE--VKLAGLAARDSLRLEAGLCLYGNIDIDEHTTPVEGSLSWTLGK
Ath_FL 240 DEHAVDLARATILEKSEKGVRLTGLGARDSLRLEAGLCLYGNIDMECHISPVEAGLWVAIGK
Ath_EI 196 DEHAVDLARATILEKSEKGVRLTGLGARDSLRLEAGLCLYGNIDMECHISPVEAGLWVAIGK
Ocu_FL 295 RRRRAAMDFPGAEIFVVPQLKGVQRRRVGLMCEGAPMRAHSPILNVEGTRIGTVTSGCPSP
```

Ocu_ES	251	RRRAAMDFPGA	E	V	I	V	P	Q	L	K	G	K	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	N	V	E	G	T	R	I	G	T	V	T	S	G	C	P	S	P	
Eca_FL	295	RRRAAMDFPGAT	V	I	V	P	Q	L	K	G	K	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	S	T	E	G	T	V	I	G	T	V	T	S	G	C	P	S	P		
Eca_ES	251	RRRAAMDFPGAT	V	I	V	P	Q	L	K	G	K	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	S	T	E	G	T	V	I	G	T	V	T	S	G	C	P	S	P		
Mmu_FL	295	RRRAAMDFPGAK	V	I	V	P	Q	L	K	G	K	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	N	M	E	G	T	K	I	G	T	V	T	S	G	C	P	S	P		
Mmu_ES	251	RRRAAMDFPGAK	V	I	V	P	Q	L	K	G	K	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	N	M	E	G	T	K	I	G	T	V	T	S	G	C	P	S	P		
Hsa_FL	295	RRRAAMDFPGAK	V	I	V	P	Q	L	K	G	R	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	N	M	E	G	T	K	I	G	T	V	T	S	G	C	P	S	P		
Hsa_ES	251	RRRAAMDFPGAK	V	I	V	P	Q	L	K	G	R	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	N	M	E	G	T	K	I	G	T	V	T	S	G	C	P	S	P		
Ptr_FL	295	RRRAAMDFPGAK	V	I	V	P	Q	L	K	G	K	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	N	M	E	G	T	K	I	G	T	V	T	S	G	C	P	S	P		
Ptr_ES	251	RRRAAMDFPGAK	V	I	V	P	Q	L	K	G	K	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	N	M	E	G	T	K	I	G	T	V	T	S	G	C	P	S	P		
Pab_FL	295	RRRAAMDFPGAK	V	I	V	P	Q	L	K	G	K	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	N	M	E	G	T	K	I	G	T	V	T	S	G	C	P	S	P		
Pab_ES	251	RRRAAMDFPGAK	V	I	V	P	Q	L	K	G	K	V	Q	R	R	R	V	G	L	M	C	E	G	A	P	M	R	A	H	S	P	I	L	N	M	E	G	T	K	I	G	T	V	T	S	G	C	P	S	P		
Ath_FL	300	RRRAEGGF	T	G	A	D	V	I	L	Q	L	K	D	G	P	T	I	R	R	V	G	F	F	S	S	G	P	E	A	R	S	H	S	E	V	H	D	E	S	G	N	K	I	G	E	I	T	S	G	F	S	P
Ath_EI	256	RRRAEGGF	T	G	A	D	V	I	L	Q	L	K	D	G	P	T	I	R	R	V	G	F	F	S	S	G	P	E	A	R	S	H	S	E	V	H	D	E	S	G	N	K	I	G	E	I	T	S	G	F	S	P

Ocu_FL	355	CLKKNVAMGYV	P	L	E	Y	S	R	P	G	T	P	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Ocu_ES	311	CLKKNVAMGYV	P	L	E	Y	S	R	P	G	T	P	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Eca_FL	355	CLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	P	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Eca_ES	311	CLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	P	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Mmu_FL	355	SLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	M	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Mmu_ES	311	SLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	M	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Hsa_FL	355	SLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	M	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Hsa_ES	311	SLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	M	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Ptr_FL	355	SLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	M	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Ptr_ES	311	SLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	M	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Pab_FL	355	SLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	M	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Pab_ES	311	SLKKNVAMGYV	P	C	E	Y	S	R	P	G	T	M	L	L	V	E	V	R	R	K	Q	M	A	V	V	S	K	M	P	F	V	P	T	N	Y	T	L	K
Ath_FL	360	NLKKNIAMGYV	K	S	G	H	K	T	G	T	K	V	K	L	V	R	G	K	P	Y	E	G	S	I	T	K	M	P	F	V	A	T	K	Y	K	P	T	
Ath_EI	316	NLKKNIAMGYV	K	S	G	H	K	T	G	T	K	V	K	L	V	R	G	K	P	Y	E	G	S	I	T	K	M	P	F	V	A	T	K	Y	K	P	T	

Supplemental Figure 12.

