

## Supplemental Data

**Supplemental Figure S1.** Schematic view of a plant F-box kelch protein.

**Supplemental Figure S2.** Alignment of F-box associated domains and individual kelch repeats from *A. thaliana* proteins.

**Supplemental Figure S3.** Rooted NJ trees including FBKs and FBAs of *V. vinifera*, *P. trichocarpa*, *O. sativa*, *S. bicolor* and *S. moellendorffii*.

**Supplemental Figure S4.** NJ tree generated using full-length FBK protein sequences of *A. thaliana*, *P. trichocarpa*, *V. vinifera*, *O. sativa*, *S. bicolor*, *S. moellendorffii* and *P. patens*.

**Supplemental Figure S5.** Representative phylogenetic trees.

**Supplemental Figure S6.** Protein sequence alignment of 43 representative FBKs.

**Supplemental Figure S7.** NJ tree of *A. thaliana* and *A. lyrata* FBKs.

**Supplemental Figure S8.** Density plot of the permutation test.

**Supplemental Figure S9.** Relative transcript level of closely related FBKs.

**Supplemental Table S1.** Identifiers of F-box kelch proteins in *A. thaliana*, *P. trichocarpa*, *V. vinifera*, *O. sativa*, *S. bicolor*, *S. moellendorffii* and *P. patens*.

**Supplemental Table S2.** Number of F-box kelch proteins in non-plant model species.

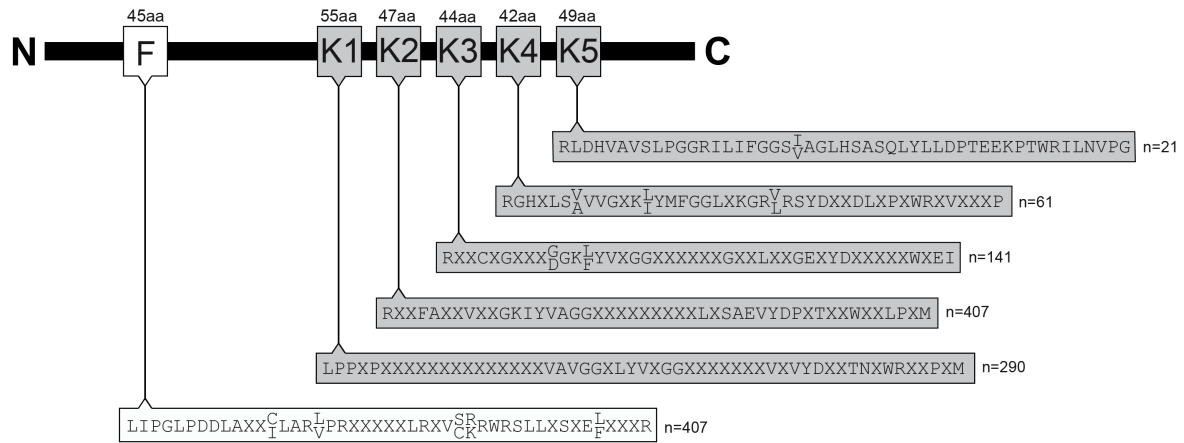
**Supplemental Table S3.** Identifiers of F-box proteins with F-box associated domains in *A. thaliana*, *P. trichocarpa*, *V. vinifera*, *O. sativa*, *S. bicolor*, *S. moellendorffii* and *P. patens*.

**Supplemental Table S4.** Comparison of three tree topologies obtained with NJ, ML and Bayesian Algorithms.

**Supplemental Table S5.** Absolute numbers of unstable, stable, ancient and superstable FBKs in plant genomes.

**Supplemental Table S6.** Sequences of q-RT PCR primers.

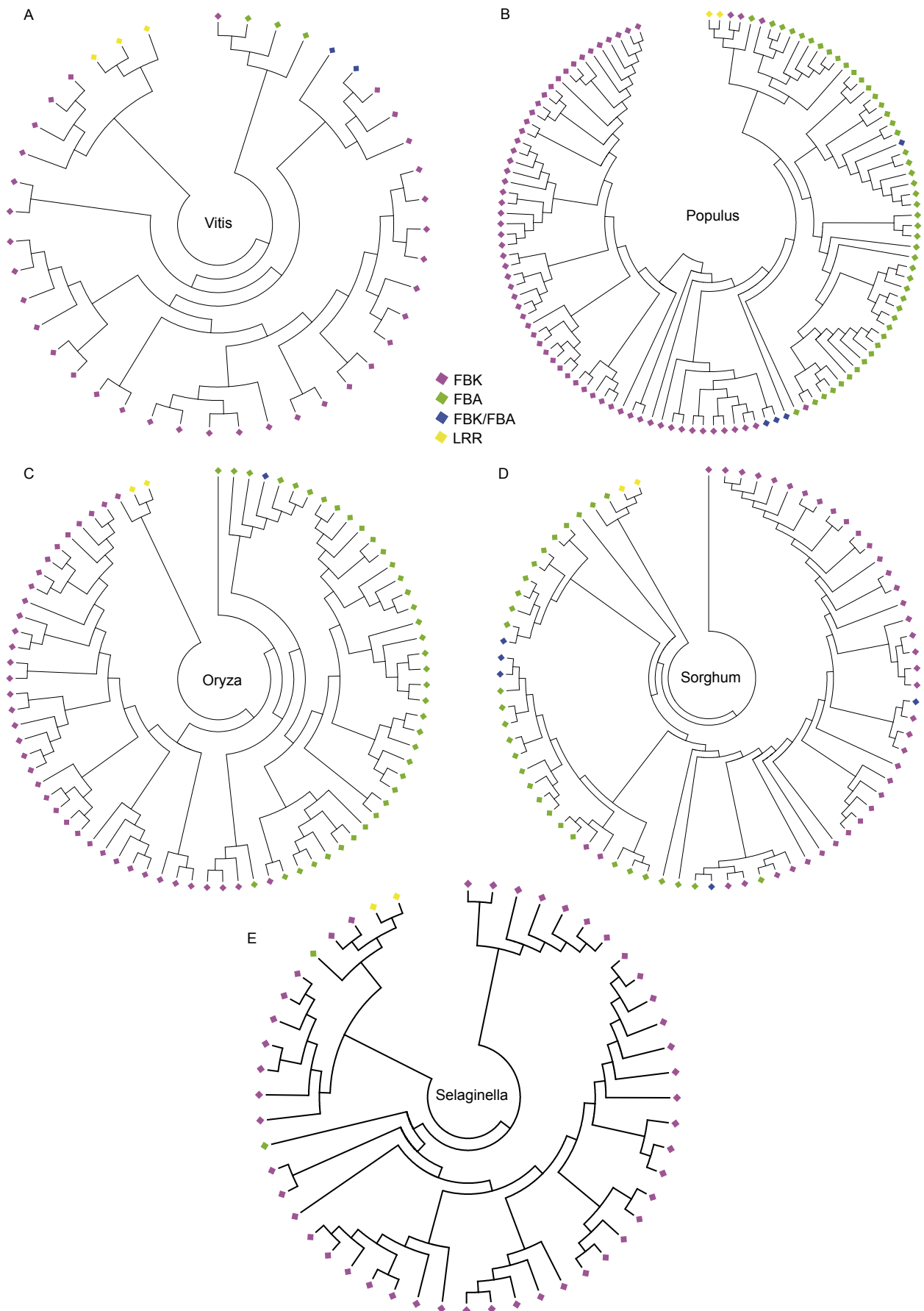
**Supplemental Dataset S1.** Tissue-specific expression data of *A. thaliana* FBKs extracted from ATGenExpress\_Plus – extended tissue series.



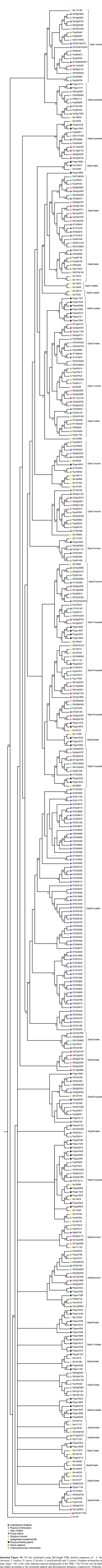
**Supplemental Figure S1.** Schematic view of a plant FBK protein. Consensus sequences of the F-box domain and kelch repeats are depicted below. In general, amino acids that share at least 30% homology between all sequences of an alignment are given in the one letter amino acid code, whereas amino acids with less than 30% homology are depicted as an “X”. Exceptionally, in the case of the kelch 5 repeat amino acids with less than 50% homology are depicted as an “X”. Gaps occurring in the alignment were deleted if more than 50% of the aligned sequences contained a gap at the same position. The positions of each domain within the alignment were determined using Pfam (Sonnhammer et al., 1997). n = number of sequences that underly the respective consensus sequence.

kelch repeats	AT1G61540 (K3)	-----HDIGYRCFVSLG-----LDG-KIYMFGESEFVYVNFEE-----DRWKICIGDYNLYH-----AV-----
	AT2G18910 (K3)	-----HPRSWHSSCTLD-----GT-KLIVSGCCADSGAL-----LSDTFLLDLSMDIFA-----WRETFVPPW
	AT3G08810 (K2)	-----LSSISASVR-----DG---NQGGHGYSDSR-----KNSFVFAYNSKEGR-----WDHLVGL-
	AT5G39560 (K2)	-----RSDPVAVLID-----QR-IYVLGGREMDDESDDWF-----EVFD-IKTQWRALPS-----F
	AT2G29770 (K1)	IKSLPPLNHGSAVVTIG-----YH-MYVLGGHNQPTSN-----VSIID-LRFHTSCSLPR-----M-----
	AT4G39240 (K1)	--LVPP-SFPSIFCWG-----MSIVAIDSE-IYVLGGCIELVSTG-----FVVECPSHTCRLLPS-----M-----
	AT1G51550 (K5)	-----RVGHSATLVL-----GGR-ILYVGGEDSYRHRKDD-----FWVLDVKTIPSSGLKPGGLSLNGSSVWKKLDRIS
	AT2G18910 (K5)	-----RLDHVAISLP-----GGR-ILYVGGSVAGLDS-----ASQLYLLDPNEEKPA-----WRILNVQG
	AT1G27420 (K4)	-YSYTVVR-NKVY-FMD-----RNMPGR-LGV-----FD-----PEE-NS-----WSSVFPVP
	AT5G57360 (K4)	-----SRLGHTLSVYG-----GRKILMFGGLAKSGPLKFR-----SSDVFTMDLSEEEPC-----WRCVTGSG
	AT1G32430	--SYFIDDKRLVICSCD-----ETGRAWIYVVGNNKLVSKTQLD-----SVVDPWPLHCTVFPSP-----LVLVLP
	AT1G62270	--SFLVDEENKVIVC-----CDEE-EDDINDTVYVIGENEFWRKE-----DIVQRSYRPRMFSYVPS-----LVQI
	AT2G27520	--RIFIEEDKVVIVV-----DCDDRWKENMIYIVGKNGFKKLSYEK-----DRSNLWRLPFFFSYVPS-----LVGLY
	AT3G16880	--IFFIDEKKVIVVFD-----KDKEMRNRITAYIVIGENGFYFRKVD-----LGD-SESEF-PVRC SYVPS-----SVETK
	AT3G17280	--SFLLEDEKKVAVCSDAV-CSDTDEDEDRIYIVGEGVDFVYDEV-----STETSHNWPFLVSYVPS-----LVHIE
AT3G17530	--SFLLEENKVAVC-----SDVDTKDGLRSRIYIVGKDFYKEVFKD-----TRGSDNNWPLLQYVPS-----LVSTIQ	
AT3G17540	--SFLLEENKVAVC-----CDRHIDDEKTRIVYVGVDFYKEVYKER-----TKGAHFNWPLLISYVPS-----LVHIIQ	
AT3G20710	--NFFIDEKKVAVVFEKDSWSWYMNPNYNKAVIACENGFYFKSVNLL-----KSPNTLQLG-HLVCS-----Y	
AT4G05080	--NFFIDEKKVAVVIDKVESEDCKRSNSHIN-SYIIGDDGYLKKMNSLG-----NTARSYTAIMLSSCYVSS-----LVQID	
AT4G33290	--GFFIDEKKK-VALG-----FDEEF-GRKTFNIIIGEDGYFREFDRITFNIEEAGERAGVNCGSYVCSYVPS-----LVRIK	
	1.....10.....20.....30.....40.....50.....60.....70.....80.....90..	

**Supplemental Figure S2.** Alignment of F-box associated domains and individual kelch repeats (K1-K5) from randomly chosen *A. thaliana* proteins obtained with ClustalX.

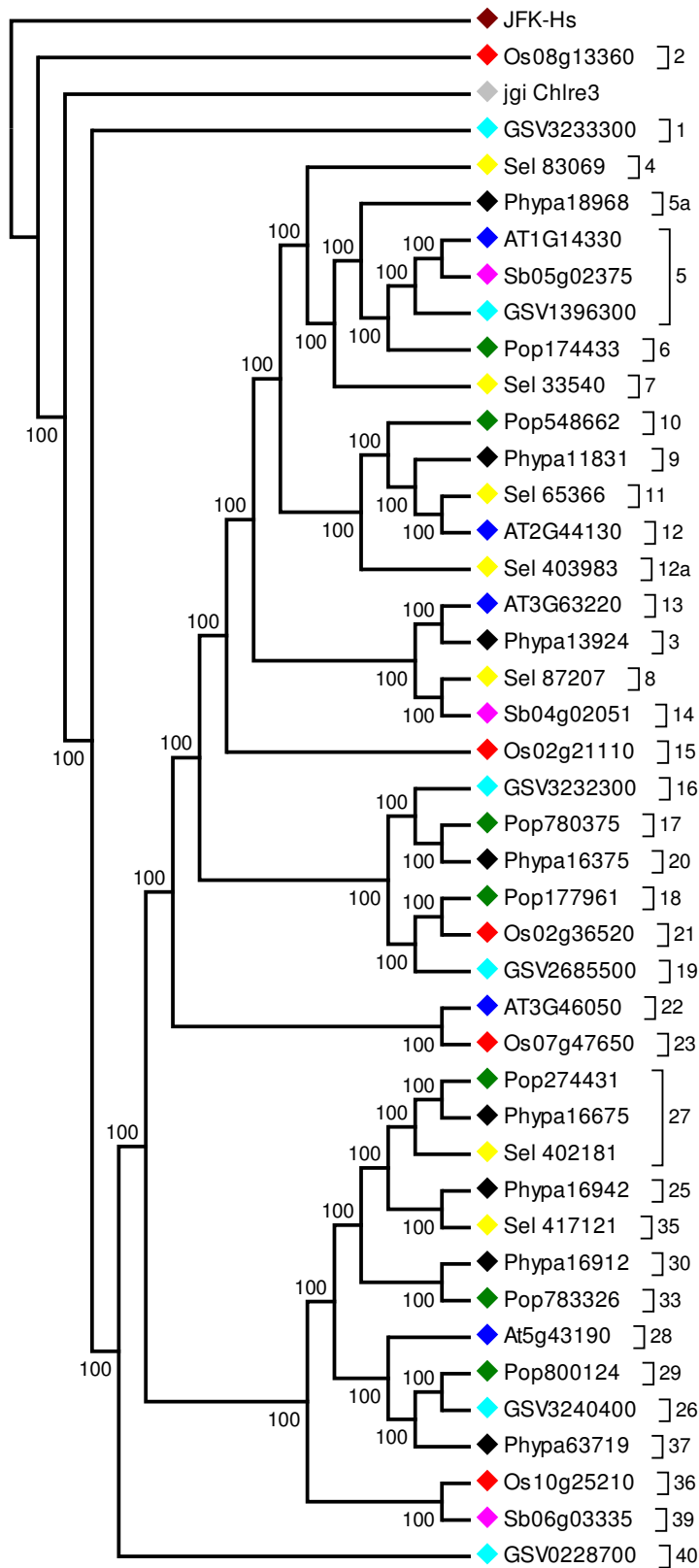


**Supplemental Figure S3.** FBKs and FBAs are closely related to each other. Rooted NJ trees including FBKs and FBAs of **A:** *V. vinifera*, **B:** *P. trichocarpa*, **C:** *O. sativa*, **D:** *S. bicolor* and **E:** *S. moellendorffii*. Alignment of full-length protein sequences and construction of the NJ trees was performed in MEGA, using a bootstrap value of 1000. Trees were rooted with leucine-rich repeat containing F-box proteins (LRRs) of the respective species identified by BlastP search with AtTIR1. FBK/FBA proteins are characterized by overlapping positions of the F-box associated domain and individual kelch repeats.

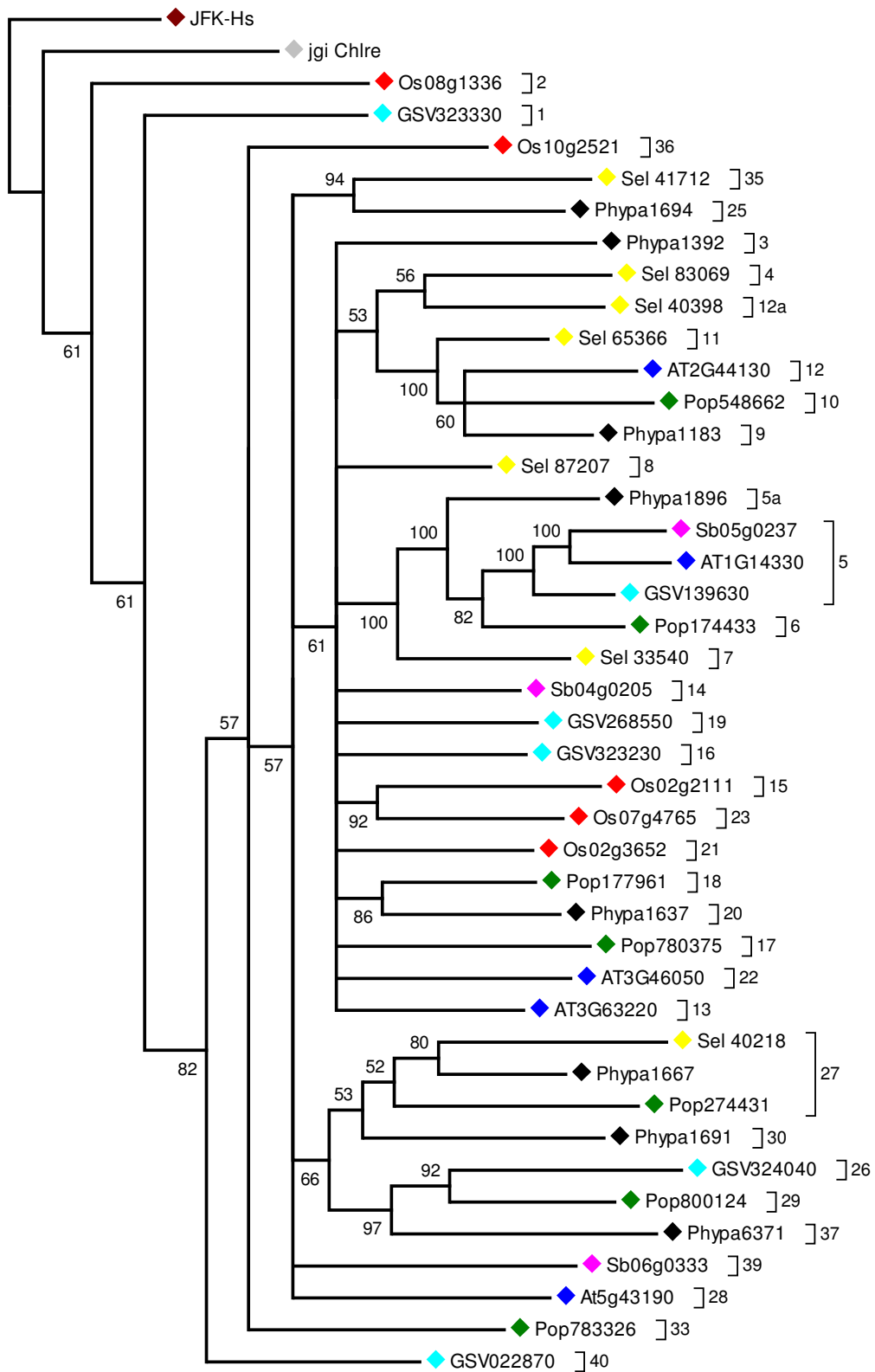


**Supplemental Figure S4.** NJ tree generated using full-length FBK protein sequences of *A. thaliana*, *P. trichocarpa*, *V. vinifera*, *O. sativa*, *S. bicolor*, *S. moellendorffii* and *P. patens*. Numbers at branches indicate bootstrap values >50. Color code indicates species background of the FBKs. The NJ tree was divided in 40 ortholog clades according to the bootstrap support and phylogenetic distances, respectively. Ortholog clades were categorized in: (i) unstable: lineage-specific clades, (ii) stable: clades including orthologs in at least two species, (iii) ancient: clades including orthologs in at least one lower land plant, one monocot and one eudicot species, (iv) superstable: clades with orthologs in all analyzed land plant species.

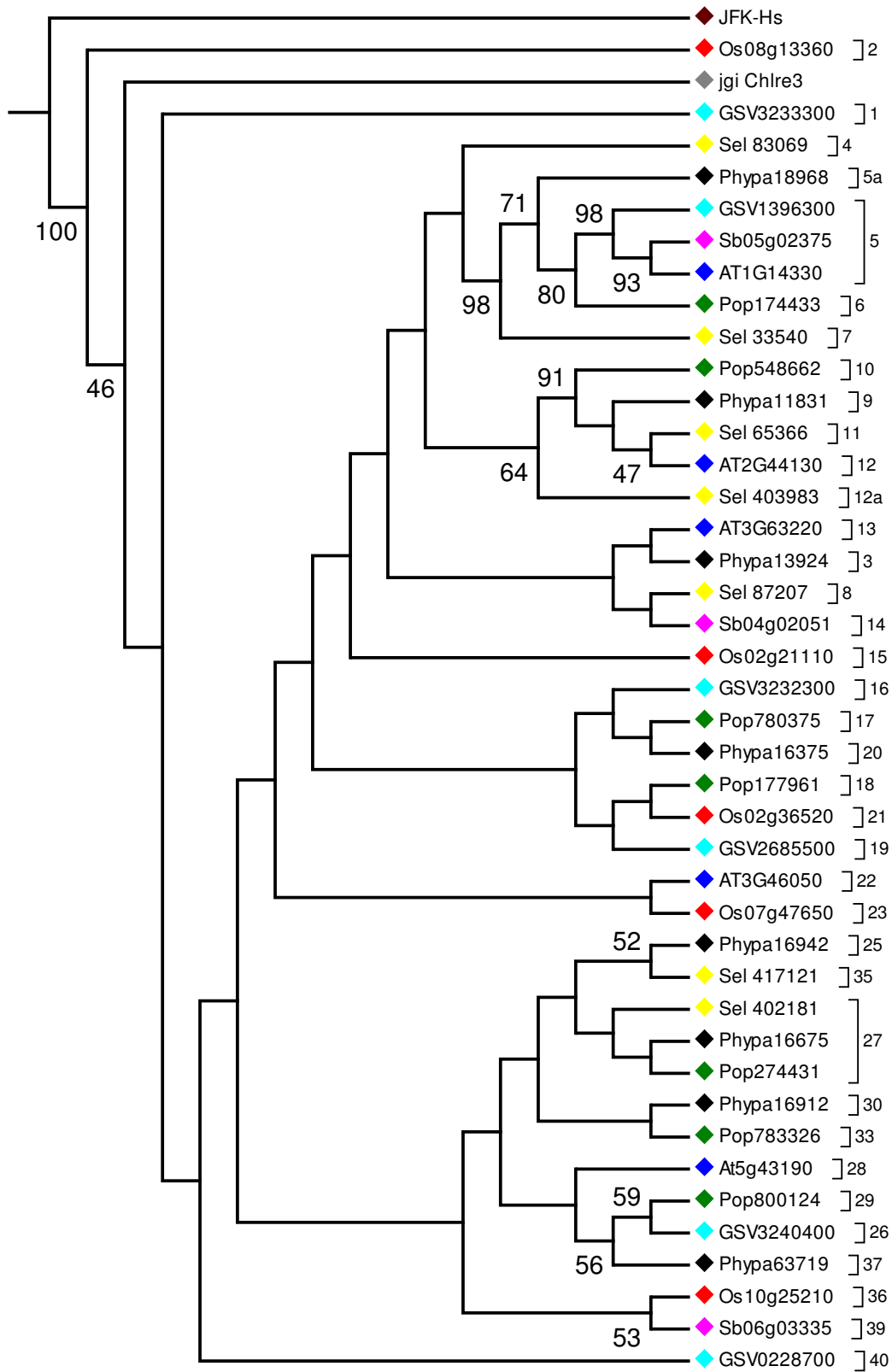
A Maximum Likelihood



B Bayesian



C Neighbor-joining





**Supplemental Figure S5.** Representative phylogenetic trees. **A:** Maximum likelihood (ML), **B:** Bayesian and **C:** Neighbor-Joining (NJ) trees from 43 representative FBK protein sequences. At least one sequence from each of the clades of the NJ tree from Supplementary Figure 4 was randomly sampled. The number of the clade from which the sequence was sampled is displayed after the bracket. Single sequences not belonging to a group of orthologs are labeled as clade #a. The Bayesian and NJ trees display numbers at the nodes that have bootstrap values >45%; the ML tree displays nodes with bootstrap values of 100%. Sequence names are abbreviated as in Supplemental Fig. S6.

F-Box

Kelch-1

Multiple sequence alignment for F-Box domain proteins. Header: jgi\_Ch1re3, Sel\_417121, Sel\_65366, Sel\_87207, Sel\_33540, Sel\_402181, Sel\_403983, Sel\_83069, Sb04g02051, Sb05g02375, Sb06g03335, GSV1396300, GSV2685500, GSV3232300, GSV3233300, GSV3240400, GSV0228700, Os02g21110, Os02g36520, Os07g47650, Os08g13360, Os10g25210, Pop174433, Pop177961, Pop274431, Pop548662, Pop780375, Pop800124, Pop783326, At1g14330, At2g44130, At3g46050, At3g63220, At5g43190, Phyta11831, Phyta13924, Phyta16375, Phyta16675, Phyta16942, Phyta18968, Phyta16912, Phyta63719, JFK-Hs. The alignment shows conserved residues across species, with gaps indicated by dashes.

Kelch-1

Kelch-2

Multiple sequence alignment for Kelch-1 and Kelch-2 domain proteins. Header: jgi\_Ch1re3, Sel\_417121, Sel\_65366, Sel\_87207, Sel\_33540, Sel\_402181, Sel\_403983, Sel\_83069, Sb04g02051, Sb05g02375, Sb06g03335, GSV1396300, GSV2685500, GSV3232300, GSV3233300, GSV3240400, GSV0228700, Os02g21110, Os02g36520, Os07g47650, Os08g13360, Os10g25210, Pop174433, Pop177961, Pop274431, Pop548662, Pop780375, Pop800124, Pop783326, At1g14330, At2g44130, At3g46050, At3g63220, At5g43190, Phyta11831, Phyta13924, Phyta16375, Phyta16675, Phyta16942, Phyta18968, Phyta16912, Phyta63719, JFK-Hs. The alignment shows conserved residues across species, with gaps indicated by dashes.

Kelch-3

Kelch-4

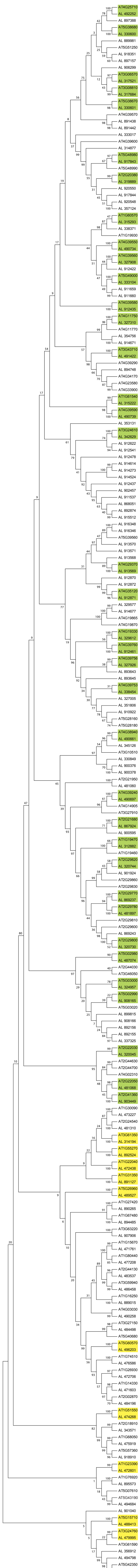
Multiple sequence alignment for Kelch-3 and Kelch-4. The alignment shows conserved regions across various species, with gaps indicated by dashes. The sequence starts with 'jgi\_Ch1r3' and ends with 'JFK-Hs'. The alignment is approximately 300 amino acids long.

Kelch-4

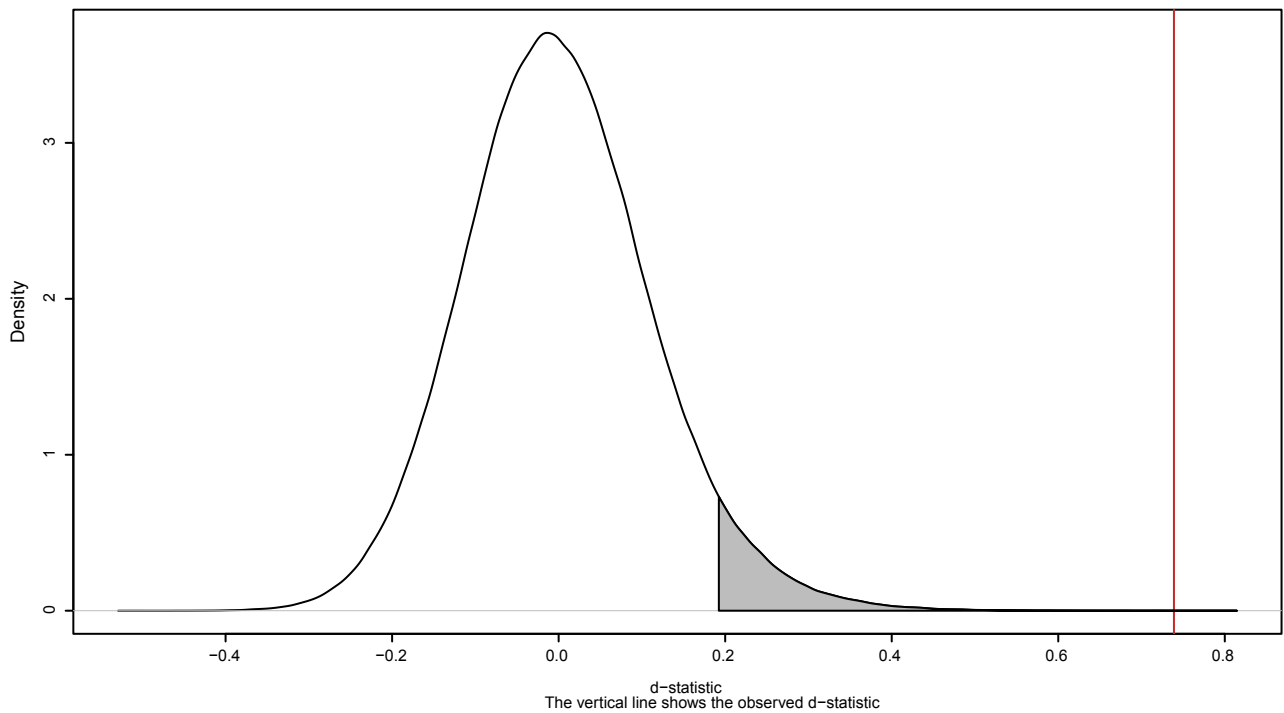
Kelch-5

Multiple sequence alignment for Kelch-4 and Kelch-5. The alignment shows conserved regions across various species, with gaps indicated by dashes. The sequence starts with 'jgi\_Ch1r3' and ends with 'JFK-Hs'. The alignment is approximately 300 amino acids long.

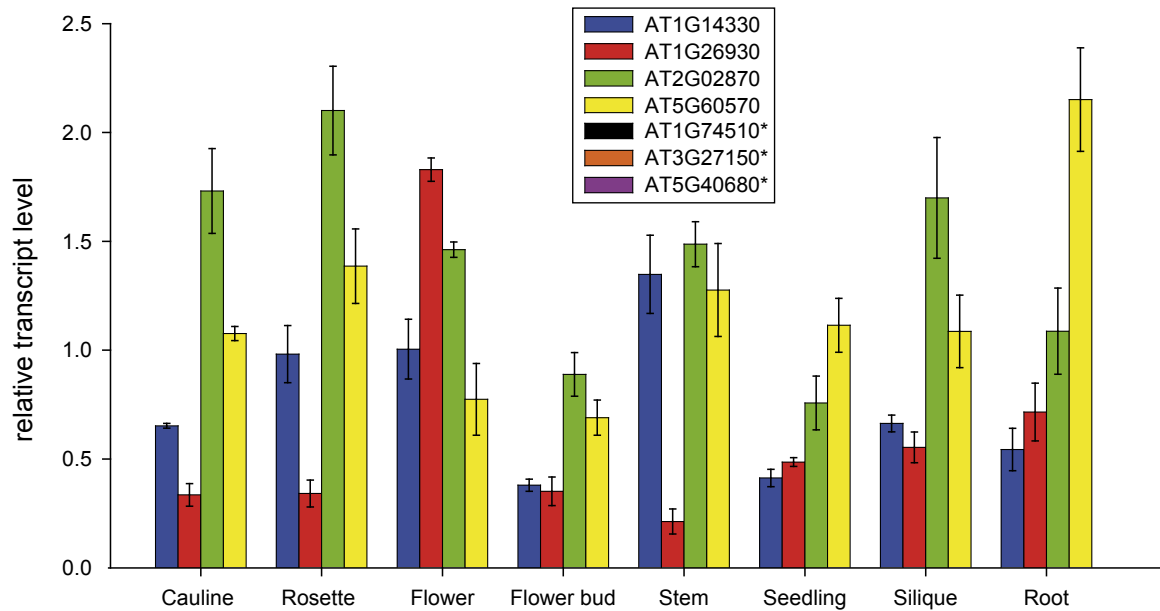
**Supplemental Figure S6.** Protein sequence alignment created with hmalign of 43 representatives of the FBKs, where at least one sequence was sampled from each of the clades of the gene tree in Supplemental Fig. S4. Positions of F-box domain and kelch repeats are indicated with black bars on top of the alignment, except for kelch repeat 4 and 5, which are enclosed in a box inside the alignment. Sequence names are abbreviated for visualization purposes. Abbreviations are: Chlre= *Chlamydomonas reinhardtii* jgi#; Phypa= *Physcomitrella patens*#=jgi number; Selmo= *Selaginella moellendorffii*#=jgi number; Os# = *Oryza sativa* LOC\_OS#, where # stands for locus number given at MSU (TIGR); Sb#= *Sorghum bicolor* (jgi); Pop\_#= *Populus trichocarpa*#=jgi number; GSV # = Genoscope number first 7 digits; ATI code (TAIR) is used for *Arabidopsis thaliana*; JFK-Hs = *Homo sapiens* FBX42 (AAH43410.1).



**Supplemental Figure S7.** NJ tree generated using partial FBK protein sequences (joined F-box and kelch domain) of *A. thaliana* and *A. lyrata*. Numbers at branches indicate bootstrap values (1000 replicates). AL numbers represent *A. lyrata* protein IDs according to Joint Genome Institute (genome.jgi-psf.org/Arly1). Boxed sequences designate proteins used for Ka/Ks ratios in Figure 5: yellow = superstable, green = unstable.



**Supplemental Figure S8.** Density plot of the test statistic  $d$  generated from the permutation test (one million repeats).  $D$ -statistic is defined as difference of the average means between the similarity of all kelch repeats within a protein and the similarity of kelch repeats between different proteins. Genetic distances among different kelch repeats were estimated using protdist from the PHYLIP suite (Felsenstein, 1989). The red line shows the  $d$ -statistic value for the observed arrangement of kelch repeats. The gray shaded area corresponds to the critical region ( $\alpha=0.05$ ), with a critical value of  $d$  as 0.1923.



**Supplemental Figure S9.** Relative transcript level of a subset of closely related FBKs. Plant organs were harvested from 6-week-old *A. thaliana* Col-0 plants cultivated under long day conditions at 20°C. Seedlings were cultivated for 7 days on ATS medium under long day conditions at 20°C. Three biological replicates were measured, each in two technical replicates. Error bars represent SE. Transcript level of genes labeled with asterisks were under the detection limit in the analyzed plant organs.

**Supplemental Table S1.** Identifiers of F-box kelch proteins in *A. thaliana*, *P. trichocarpa*, *V. vinifera*, *O. sativa*, *S. bicolor*, *S. moellendorffii* and *P. patens*.

Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT1G14330	Pop 174433	GSV00121001	Os01g33490	Sb01g013220	Selm 115581	jgi Phypa1_1 101961
AT1G15670	Pop 177961	GSV02287001	Os01g47050	Sb01g013240	Selm 121243	jgi Phypa1_1 104453
AT1G16250	Pop 230616	GSV02498001	Os01g50840	Sb01g022240	Selm 14013	jgi Phypa1_1 108027
AT1G19460	Pop 244788	GSV02750001	Os01g69940	Sb01g022460	Selm 174189	jgi Phypa1_1 114815
AT1G19470	Pop 265449	GSV02843001	Os02g02350	Sb01g045700	Selm 23216	jgi Phypa1_1 118316
AT1G19930	Pop 267446	GSV02903001	Os02g05700	Sb01g046015	Selm 272238	jgi Phypa1_1 126823
AT1G22040	Pop 274431	GSV07630001	Os02g10850	Sb02g001990	Selm 33540	jgi Phypa1_1 131411
AT1G23390	Pop 283960	GSV13963001	Os02g11790	Sb02g002025	Selm 33948	jgi Phypa1_1 137266
AT1G26930	Pop 287991	GSV15284001	Os02g15950	Sb02g003160	Selm 402181	jgi Phypa1_1 139248
AT1G27420	Pop 298158	GSV16869001	Os02g21110	Sb02g005040	Selm 403983	jgi Phypa1_1 141114
AT1G30090	Pop 420602	GSV17315001	Os02g30210	Sb02g005880	Selm 404324	jgi Phypa1_1 153643
AT1G31350	Pop 547623	GSV19396001	Os02g35530	Sb02g025486	Selm 404826	jgi Phypa1_1 156376
AT1G51550	Pop 547631	GSV24520001	Os02g36520	Sb02g032340	Selm 405137	jgi Phypa1_1 158495
AT1G55270	Pop 548662	GSV24761001	Os02g51350	Sb02g042690	Selm 405262	jgi Phypa1_1 159848
AT1G60570	Pop 548664	GSV25445001	Os03g07160	Sb03g030090	Selm 406718	jgi Phypa1_1 159974
AT1G61540	Pop 549362	GSV26849001	Os03g07530	Sb03g041500	Selm 407049	jgi Phypa1_1 159978
AT1G67480	Pop 551335	GSV26855001	Os03g30160	Sb03g041730	Selm 409427	jgi Phypa1_1 160103
AT1G68050	Pop 552235	GSV26967001	Os04g31120	Sb04g001090	Selm 411128	jgi Phypa1_1 160232
AT1G74510	Pop 553842	GSV28309001	Os04g52830	Sb04g003660	Selm 411144	jgi Phypa1_1 161137
AT1G76920	Pop 555218	GSV29589001	Os04g57290	Sb04g007310	Selm 412518	jgi Phypa1_1 162266
AT1G80440	Pop 558147	GSV30594001	Os06g39370	Sb04g009700	Selm 417121	jgi Phypa1_1 162989
AT2G02870	Pop 559358	GSV31346001	Os06g44500	Sb04g009920	Selm 421271	jgi Phypa1_1 163528
AT2G18915	Pop 559574	GSV31580001	Os06g47890	Sb04g020510	Selm 421284	jgi Phypa1_1 163752
AT2G20380	Pop 561211	GSV32323001	Os06g49750	Sb04g023200	Selm 422132	jgi Phypa1_1 164205
AT2G21680	Pop 561242	GSV32333001	Os07g02910	Sb04g023750	Selm 422192	jgi Phypa1_1 164284
AT2G21950	Pop 563452	GSV32404001	Os07g03100	Sb04g027910	Selm 424145	jgi Phypa1_1 166753
AT2G22030	Pop 564672	GSV33280001	Os07g05880	Sb05g002260	Selm 426714	jgi Phypa1_1 166966
AT2G22050	Pop 565042	GSV33282001	Os07g47650	Sb05g006950	Selm 429669	jgi Phypa1_1 167883
AT2G24540	Pop 566051	GSV33571001	Os08g13360	Sb05g006960	Selm 429850	jgi Phypa1_1 168336
AT2G29600	Pop 572245	GSV34447001	Os09g38300	Sb05g021030	Selm 431561	jgi Phypa1_1 169046



Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT2G29770	Pop 572337	GSV34454001	Os10g04890	Sb05g023750	Selm 438121	jgi Phypa1_1 169120
AT2G29780	Pop 583883	GSV34587001	Os10g21930	Sb06g012290	Selm 441635	jgi Phypa1_1 169426
AT2G29800	Pop 589736	GSV34781001	Os10g24900	Sb06g025030	Selm 448225	jgi Phypa1_1 169940
AT2G29810	Pop 592319	GSV37006001	Os10g25210	Sb06g028820	Selm 55890	jgi Phypa1_1 171546
AT2G29820	Pop 597156	GSV37841001	Os10g26990	Sb06g032150	Selm 65366	jgi Phypa1_1 172502
AT2G29830	Pop 649911	GSV38104001	Os11g04330	Sb06g033350	Selm 75526	jgi Phypa1_1 172546
AT2G29860	Pop 651336		Os11g14140	Sb06g033750	Selm 766041	jgi Phypa1_1 172882
AT2G41360	Pop 658140		Os11g34460	Sb07g002320	Selm 78419	jgi Phypa1_1 180856
AT2G44030	Pop 708739		Os12g04130	Sb07g006910	Selm 79476	jgi Phypa1_1 181624
AT2G44130	Pop 754910			Sb10g023140	Selm 83069	jgi Phypa1_1 188742
AT2G44630	Pop 756767			Sb10g026080	Selm 85806	jgi Phypa1_1 188796
AT2G44700	Pop 758312			Sb10g026580	Selm 87207	jgi Phypa1_1 189687
AT3G06570	Pop 758319			Sb10g028340	Selm 88328	jgi Phypa1_1 201289
AT3G08810	Pop 762216			Sb10g029710	Selm 92558	jgi Phypa1_1 202273
AT3G10510	Pop 763659				Selm 92689	jgi Phypa1_1 229126
AT3G24610	Pop 764261				Selm 92722	jgi Phypa1_1 229344
AT3G24760	Pop 768560					jgi Phypa1_1 231395
AT3G27150	Pop 771222					jgi Phypa1_1 233086
AT3G27910	Pop 780347					jgi Phypa1_1 233535
AT3G43710	Pop 780375					jgi Phypa1_1 233728
AT3G46050	Pop 783326					jgi Phypa1_1 233823
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AT4G03030	Pop 807217					jgi Phypa1_1 44026
AT4G11750	Pop 809263					jgi Phypa1_1 44304
AT4G11770	Pop 811754					jgi Phypa1_1 45289
AT4G14905	Pop 822050					jgi Phypa1_1 45319
AT4G19330	Pop 825819					jgi Phypa1_1 5127
AT4G19865	Pop 830083					jgi Phypa1_1 63719

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Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
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AT4G25710	PtX002172					jgi Phypa1_1 70860
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AT4G34170	Pt129000020					jgi Phypa1_1 96028
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AT4G39550						
AT4G39560						
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AT4G39580						
AT4G39590						
AT4G39600						
AT4G39753						
AT4G39756						
AT4G39760						
AT5G02980						
AT5G02990						
AT5G03000						
AT5G03020						
AT5G07610						
AT5G15710						
AT5G26960						
AT5G28160						
AT5G28180						
AT5G38670						
AT5G38680						
AT5G39560						
AT5G40680						

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Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT5G42350						
AT5G42360						
AT5G43190						
AT5G48980						
AT5G48990						
AT5G49000						
AT5G51250						
AT5G57360						
AT5G60570						

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**Supplemental Table S2.** Number of F-box kelch proteins in non-plant model species

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Species	Number of FBKs	Number of kelch repeats (Pfam)	Protein ID
Bacteria	-	-	-
<i>Saccharomyces cerevisiae</i>	-	-	-
<i>Chlamydomonas reinhardtii</i>	1	3	EDP09183 <sup>a</sup>
<i>Caenorhabditis elegans</i>	1	3	Q9N3K6 <sup>b</sup>
<i>Drosophila melanogaster</i>	1	3	Q9W281 <sup>b</sup>
<i>Mus Musculus</i>	1	3	Q6PDJ6 <sup>b</sup>
<i>Homo sapiens</i>	1	3	Q6P3S6 <sup>b</sup>

<sup>a</sup>GenBank ID; <sup>b</sup>Swiss Prot ID

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**Supplemental Table S3:** Identifiers of F-box proteins with F-box associated domains in *A. thaliana*, *P. trichocarpa*, *V. vinifera*, *O. sativa*, *S. bicolor*, *S. moellendorffii* and *P. patens*.

Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT1G09650	Pop 241644	GSV02287001*	Os02g10600	Sb01g003460	Selm 428410	jgi Phypa1_1 163116
AT1G10890	Pop 246916	GSV26022001	Os02g33840	Sb01g013220*	Selm 413145	jgi Phypa1_1 164205*
AT1G11620	Pop 547750	GSV26967001*	Os02g35560	Sb01g013240*	Selm 33948*	jgi Phypa1_1 234287
AT1G11810	Pop 548688	GSV33571001	Os03g25640	Sb01g018980		jgi Phypa1_1 234728
AT1G12170	Pop 548689	GSV33582001	Os03g46690	Sb01g031390		jgi Phypa1_1 65071
AT1G12190	Pop 549801		Os04g11450	Sb01g034970		jgi Phypa1_1 90500*
AT1G12870	Pop 560159		Os04g11660	Sb01g037880		jgi Phypa1_1 91913
AT1G13200	Pop 563457		Os04g11790	Sb02g001040		
AT1G24793	Pop 565298		Os04g50200	Sb02g002025*		
AT1G24880	Pop 568920		Os05g02570	Sb02g005870		
AT1G25141	Pop 569113		Os05g08010	Sb02g005880*		
AT1G30780	Pop 569545		Os05g08350	Sb02g005890		
AT1G30790	Pop 569549		Os05g08440	Sb02g008113		
AT1G30920	Pop 570279		Os05g08460	Sb02g023440		
AT1G30925	Pop 571268		Os06g07380	Sb02g027685		
AT1G30930	Pop 571296		Os06g07390	Sb03g044080		
AT1G30935	Pop 574752		Os06g07460	Sb04g000800		
AT1G31000	Pop 575938		Os07g08570	Sb04g003010		
AT1G31080	Pop 579428		Os07g09710	Sb04g006790		
AT1G31090	Pop 581757		Os07g09814	Sb04g009700*		
AT1G32140	Pop 581764		Os07g09870	Sb04g025085		
AT1G32420	Pop 585979		Os07g13870	Sb04g026045		
AT1G32430	Pop 587549		Os07g13890	Sb05g020470		
AT1G32660	Pop 590131		Os07g16420	Sb05g025730		
AT1G33010	Pop 590133		Os07g16800	Sb05g025750		
AT1G33020	Pop 590935		Os07g35050	Sb06g027040		
AT1G33530	Pop 592321		Os07g35060	Sb08g003880		
AT1G46840	Pop 597059		Os08g10340	Sb08g015610		
AT1G46984	Pop 666139		Os08g36960	Sb08g021860		
AT1G47340	Pop 241644		Os09g20650	Sb08g021900		

Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT1G47390	Pop 752836		Os09g27570	Sb09g027720		
AT1G47730	Pop 753649		Os09g30180	Sb09g030410		
AT1G47765	Pop 754910*		Os09g34200	Sb10g010900		
AT1G47790	Pop 756767*		Os10g04850	Sb10g024600		
AT1G47800	Pop 761635		Os10g25210*			
AT1G47810	Pop 761790		Os10g25660			
AT1G48060	Pop 763809		Os12g03440			
AT1G50870	Pop 764347		Os12g06740			
AT1G50880	Pop 764712		Os06g0170866			
AT1G51290	Pop 765277					
AT1G51320	Pop 766270					
AT1G52490	Pop 770387					
AT1G53370	Pop 771222*					
AT1G53550	Pop 775680					
AT1G53790	Pop 783326					
AT1G54550	Pop 786330					
AT1G55070	Pop 787092					
AT1G58090	Pop 799299					
AT1G59680	Pop 801694					
AT1G60370	Pop 805278					
AT1G61060	Pop 807217*					
AT1G62270	Pop 808297					
AT1G65990						
AT1G66490						
AT1G67130						
AT1G67450						
AT1G67455						
AT1G70380						
AT1G70390						
AT1G70960						

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Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT1G70970						
AT1G71320						
AT1G76830						
AT1G77650						
AT2G02890						
AT2G04920						
AT2G07140						
AT2G13130						
AT2G14710						
AT2G15640						
AT2G16220						
AT2G16450						
AT2G16810						
AT2G17310						
AT2G17830						
AT2G18780						
AT2G19630						
AT2G21930						
AT2G23160						
AT2G27520						
AT2G31470						
AT2G33655						
AT2G34280						
AT2G38590						
AT2G40910						
AT2G40920						
AT2G40925						
AT2G43260						
AT2G43440						
AT3G04660						

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Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT3G06240						
AT3G07870						
AT3G08750						
AT3G10240						
AT3G10430						
AT3G10790						
AT3G13680						
AT3G13820						
AT3G13830						
AT3G16210						
AT3G16555						
AT3G16580						
AT3G16590						
AT3G16740						
AT3G16820						
AT3G16880						
AT3G17265						
AT3G17280						
AT3G17320						
AT3G17480						
AT3G17490						
AT3G17500						
AT3G17530						
AT3G17540						
AT3G17560						
AT3G17570						
AT3G17620						
AT3G17710						
AT3G18320						
AT3G18330						

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Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT3G18340						
AT3G18910						
AT3G18980						
AT3G19410						
AT3G19470						
AT3G19560						
AT3G19880						
AT3G19890						
AT3G20030						
AT3G20690						
AT3G20710						
AT3G21120						
AT3G21130						
AT3G21170						
AT3G21410						
AT3G22350						
AT3G22421						
AT3G22650						
AT3G22700						
AT3G22710						
AT3G22720						
AT3G22730						
AT3G22870						
AT3G22940						
AT3G23260						
AT3G23420						
AT3G23880						
AT3G23960						
AT3G24580						
AT3G25460						

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Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT3G44120						
AT3G44130						
AT3G47020						
AT3G47030						
AT3G47150						
AT3G49450						
AT3G49510						
AT3G49520						
AT3G49980						
AT3G52320						
AT3G57580						
AT3G57590						
AT3G59610						
AT3G61340						
AT4G04690						
AT4G05080						
AT4G09190						
AT4G09790						
AT4G09870						
AT4G10740						
AT4G11590						
AT4G12560						
AT4G17200						
AT4G17780						
AT4G19930						
AT4G19940						
AT4G21240						
AT4G29970						
AT4G33160						
AT4G33290						

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Arabidopsis	Populus	Vitis	Oryza	Sorghum	Selaginella	Physcomitrella
AT4G38870						
AT5G07610*						
AT5G10340						
AT5G15660						
AT5G15670						
AT5G18160						
AT5G36200						
AT5G36730/ AT5G36820						
AT5G37040						
AT5G38810						
AT5G41490						
AT5G41500						
AT5G41510						
AT5G42430						
AT5G42460						
AT5G47300						
AT5G50220						
AT5G51000						
AT5G52610						
AT5G52620						
AT5G60560						
AT5G62060						
AT5G62510						
AT5G62660						
AT5G65850						

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\* F-box proteins with F-box associated domain and kelch repeats.

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**Supplemental Table S4:** Comparison of three tree topologies obtained with three different algorithms (NJ=Neighbor-Joining, Bayesian and ML=Maximum Likelihood) using Shimodaira-Hasegawa (Shimodaira and Hasegawa, 1999) and one-sided Kishino-Hasegawa (1sKH, Kishino and Hasegawa, 1989) tests, implemented in Treepuzzle (Schmidt and von Haeseler, 2007). In addition, a Chi-square test was performed to compare the likelihoods (l) of the three trees to the best tree (in this case the ML tree). The ML and NJ trees have the same likelihood.

Tree	l	$\Delta l$	S.E.	p1-skh	p-SH	2 $\Delta l$	Chi-square	p-value
NJ	-30957.15	0	0.0024	1	0.737	0	0	0
Bayesian	-31069.27	112.12	22.7059	0	0	224.24	0.406	0.03
ML	-30957.15	0	best tree	1	1	0	0	0

**Schmidt HA, von Haeseler A (2007)** Maximum-likelihood analysis using TREE-PUZZLE. Curr Prot Bioinformatics **Chapter 6:** Unit 6.6

**Supplemental Table S5.** Number of unstable, stable, ancient and superstable FBKs in *A. thaliana*, *V. vinifera*, *P. trichocarpa*, *O. sativa*, *S. bicolor*, *S.moellendorffii* and *P. patens*.

Species	Number of unstable FBKs	Number of stable FBKs	Number of ancient FBKs	Number of superstable FBKs	Total number of FBKs
<i>Arabidopsis thaliana</i>	66	14	12	11	103
<i>Vitis vinifera</i>	0	15	9	12	36
<i>Populus trichocarpa</i>	0	21	30	17	68
<i>Oryza sativa</i>	0	11	15	13	39
<i>Sorghum bicolor</i>	0	18	16	10	44
<i>Selaginella moellendorffii</i>	5	16	11	14	46
<i>Physcomitrella patens</i>	19	20	5	27	71

**Supplemental Table S6.** Sequences of q-RT PCR primers

Primer	Sequence
AT1G14330_F	5' ACTGAGATACCGGAAATGTGCGC 3'
AT1G14330_R	5' TCAGCATGATCAGCAGCATACA 3'
AT1G26930_F	5' AGAGATTGCGGTTTTAGCGG 3'
AT1G26930_R	5' CATCCATAAACACACCGGAACA 3'
AT1G74510_F	5' AGCTTTATGCTGCGAATTACGC 3'
AT1G74510_R	5' CACTAACTGATCCCCACAAGCC 3'
AT2G02870_F	5' TGATCACGCCGATATGGAAGT 3'
AT2G02870_R	5' AGCAAGTCCCATCCGTTTAC 3'
AT3G27150_F	5' CGTGTTGGACGATGTTTGACA 3'
AT3G27150_R	5' CGCAAAGCGATTCTTTATCTCC 3'
AT5G40680_F	5' CGTATTGTGGTGTGGCGATA 3'
AT5G40680_R	5' CTTGATTCCTCCAGCGAAAA 3'
AT5G60570_F	5' ATGGTGGACTCGTCAAACGGT 3'
AT5G60570_R	5' CAAGAATTCACCACAATGCCCT 3'