

Supplementary Materials: Genome-Wide Identification, Evolutionary Analysis and Stress Responses of GRAS Gene Family in Castor Bean

Wei Xu, Zexi Chen, Naem Ahmed, Bing Han, Qinghua Cui and Aizhong Liu

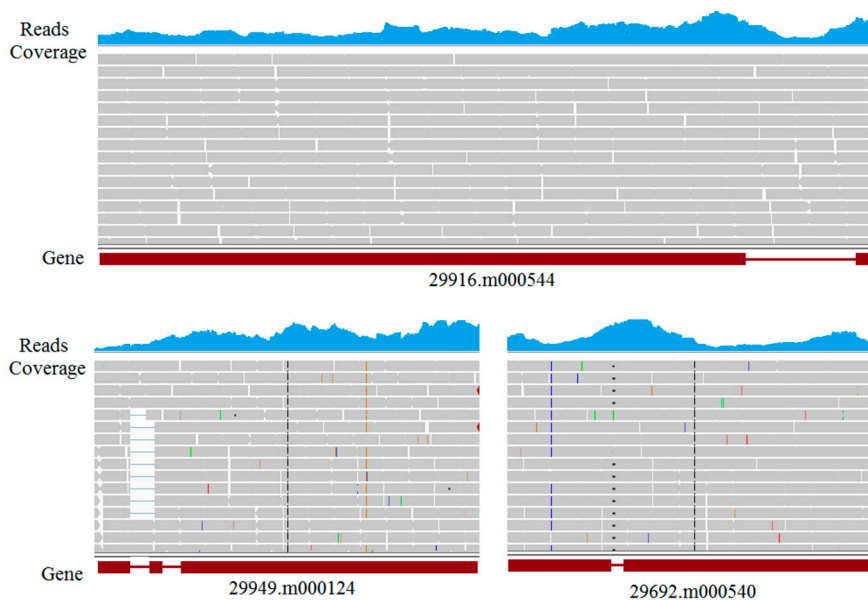


Figure S1. Visualization of the reads coverage on genic regions of three predicted GRAS genes.

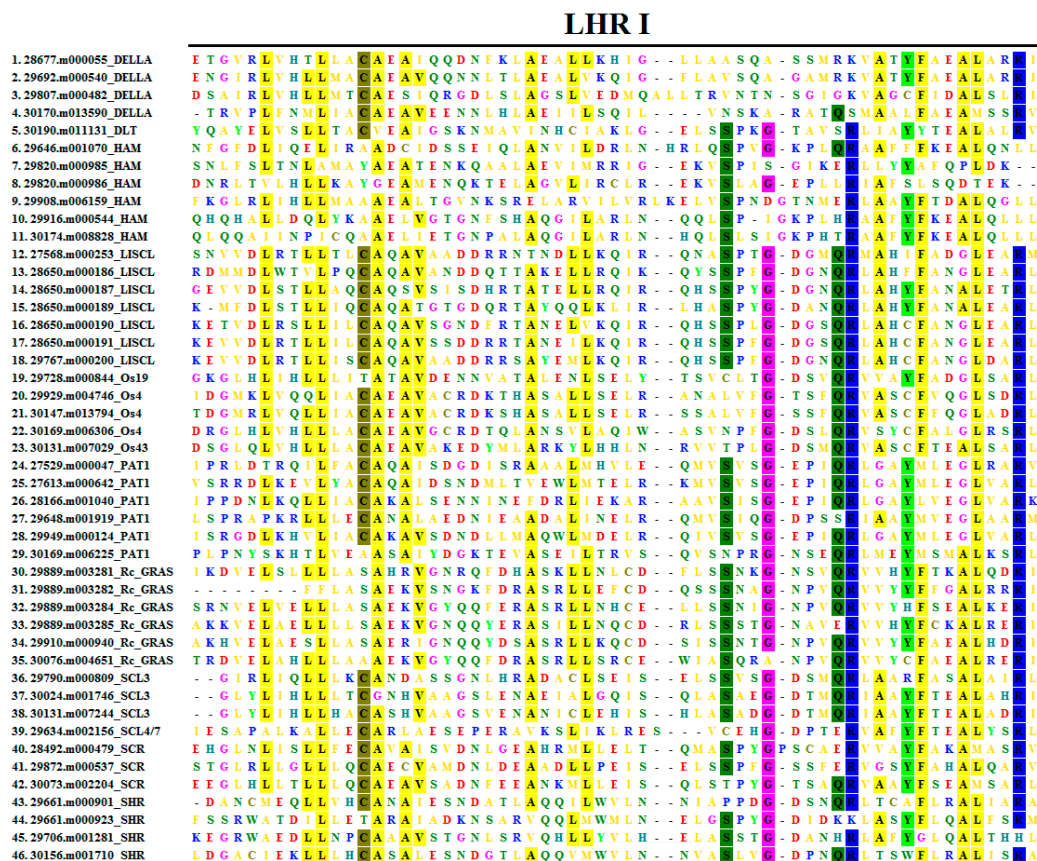


Figure S2. Cont.

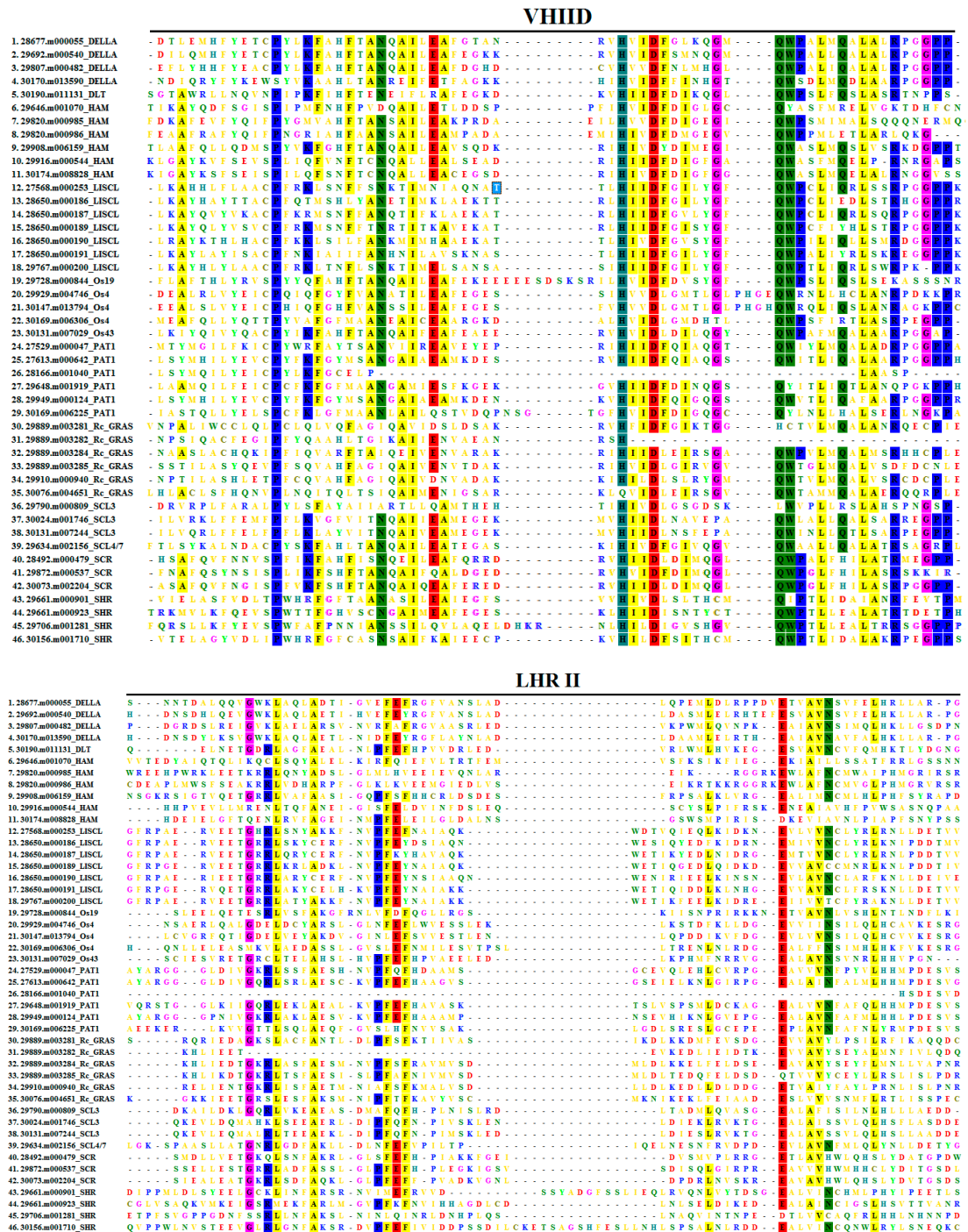


Figure S2. Cont.

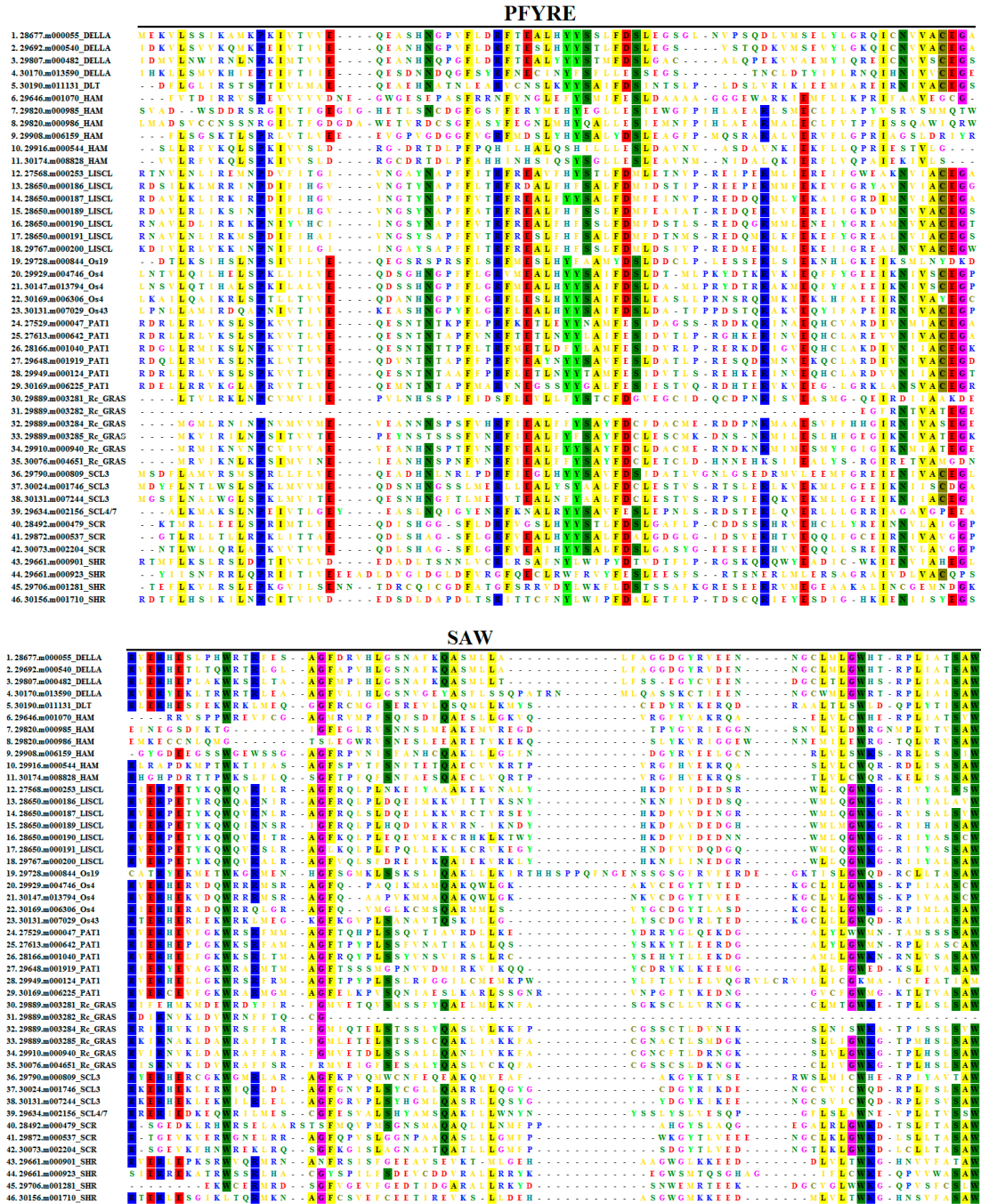


Figure S2. Multiple sequences alignment of amino acid of the conserved domains including LHR I, VHIIID, LHR II, PFIYE and SAM in castor bean.

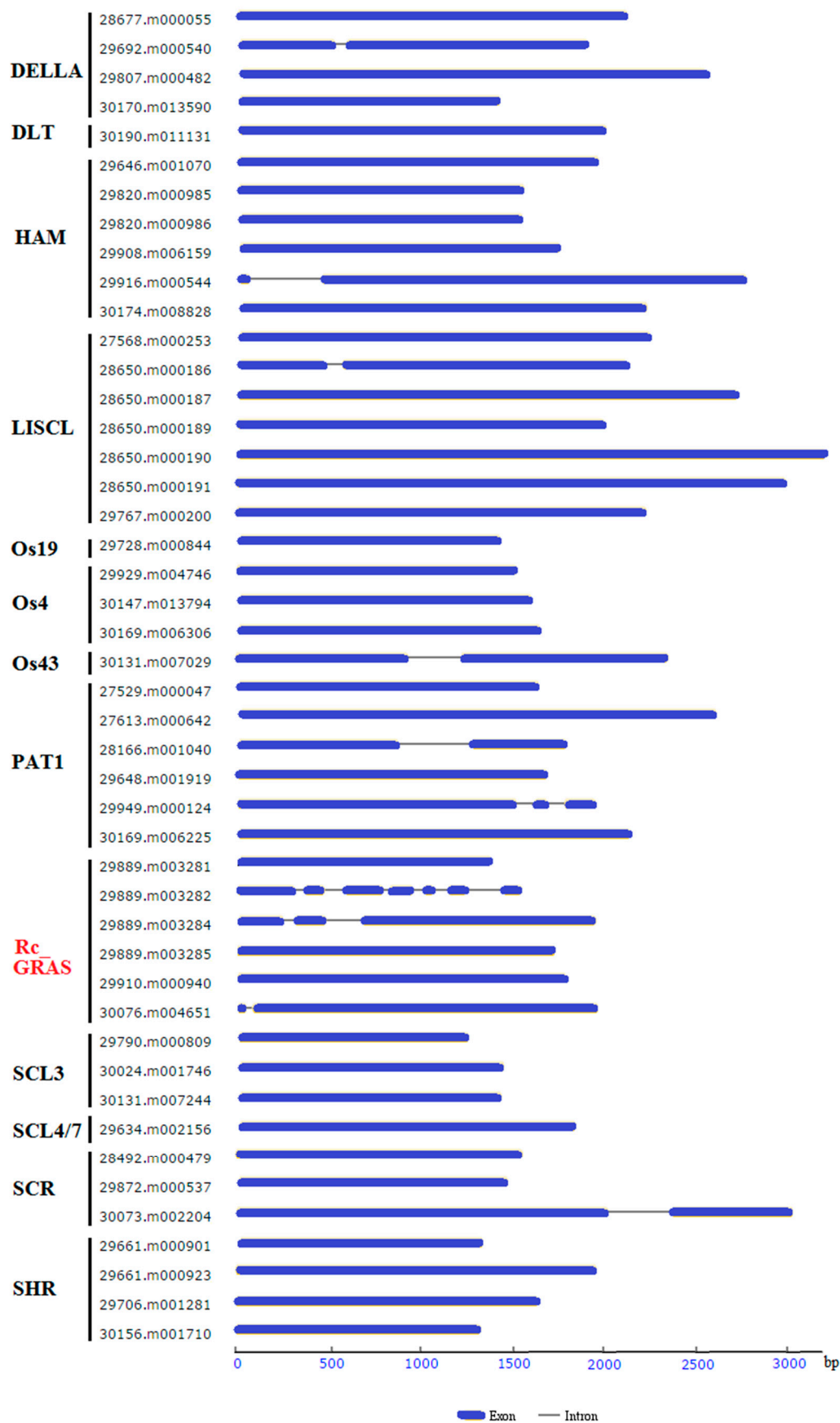


Figure S3. Gene structures of GRAS members in castor bean.

Table S1. The information of 48 GRAS transcription factors identified in castor bean genome.

Gene Model	Scaffold	Gene Start	Gene End	Orientation	Domain Number	E-Value (Pfam)	CDS Length	Protein Length	Molecular Weight/Da	Theoretical pI	Reads Coverage (>10)	Homologs in <i>Arabidopsis</i>
27529.m000047	27529	20956	22584	+	1	1.00E-123	1629	542	61122.84	5.72	yes	AT4G17230.1
27568.m000253	27568	19777	22002	+	1	1.00E-120	2226	741	83116.30	5.37	yes	AT1G07530.1
27613.m000642	27613	218157	220737	-	1	2.70E-137	1617	538	60047.72	5.50	yes	AT1G50600.1
28166.m001040	28166	23949	25728	-	2	6.40E-17	1380	459	51523.05	6.25	yes	AT5G48150.1
28492.m000479	28492	123817	125376	-	1	7.10E-104	1560	519	58016.83	5.92	no	AT3G54220.1
28650.m000186	28650	27256	29354	-	1	2.30E-108	1992	663	75257.66	5.92	no	AT1G07530.1
28650.m000187	28650	31218	33926	-	1	2.80E-118	2067	688	78173.80	6.32	yes	AT1G07530.1
28650.m000189	28650	41918	43906	-	1	1.80E-112	1989	662	75340.73	6.16	no	AT1G07530.1
28650.m000190	28650	48435	51623	-	1	1.60E-113	2448	815	90986.60	5.17	yes	AT1G07530.1
28650.m000191	28650	57247	60227	-	1	6.90E-110	2295	764	85580.05	5.28	yes	AT1G07530.1
28677.m000055	28677	3350	5464	+	1	3.40E-36	1704	567	62550.40	5.14	yes	AT3G03450.1
28966.m000535	28966	125327	126678	-	1	4.10E-15	483	160	17305.22	5.88	no	AT1G55580.1
29634.m002156	29634	607639	609465	+	1	7.20E-109	1827	608	66887.21	4.96	yes	AT5G66770.1
29646.m001070	29646	113881	115836	-	1	4.80E-87	1620	539	60899.08	6.03	yes	AT4G36710.1
29648.m001919	29648	47547	49226	-	1	5.10E-136	1680	559	62597.52	4.89	yes	AT1G21450.1
29661.m000901	29661	20973	22295	-	1	1.60E-89	1323	440	49288.28	5.58	yes	AT3G49950.1
29661.m000923	29661	255682	257645	+	1	7.40E-104	1539	512	58194.98	5.87	yes	AT4G37650.1
29692.m000540*	29692	243910	245798	+	1	2.80E-37	1830	609	67287.91	5.73	yes	AT1G14920.1
29706.m001281	29706	78273	79919	-	1	4.20E-78	1647	548	60960.68	5.85	yes	AT3G13840.1
29728.m000844	29728	310370	311785	-	1	4.20E-89	1416	471	53630.99	6.17	no	AT3G54220.1
29767.m000200	29767	26535	28757	+	1	2.80E-112	2223	740	83933.94	8.40	yes	AT2G37650.1
29790.m000809	29790	48786	50036	-	1	4.30E-99	1251	416	46776.87	6.40	yes	AT1G50420.1
29807.m000482	29807	100421	102935	-	1	5.90E-32	1611	536	58616.68	5.27	yes	AT2G01570.1
29820.m000985	29820	38524	40077	-	1	2.90E-41	1554	517	59681.48	4.82	no	AT4G08250.1
29820.m000986	29820	44796	46325	+	1	8.90E-38	1530	509	57484.06	4.83	no	AT5G66770.1
29872.m000537	29872	117231	118693	-	1	8.40E-114	1329	442	48239.49	5.45	yes	AT5G41920.1
29889.m003281	29889	213307	214671	-	1	2.00E-72	1365	454	51417.81	8.39	no	AT3G03450.1
29889.m003282	29889	216102	217643	-	1	2.30E-10	1008	335	38304.95	5.10	no	AT3G03450.1
29889.m003284	29889	221800	223738	+	1	5.20E-87	1689	562	64012.76	5.50	no	AT1G66350.1
29889.m003285	29889	225519	227249	+	1	1.10E-82	1731	576	64817.84	5.34	no	AT5G17490.1
29908.m006159	29908	273013	274753	+	1	2.30E-99	1476	491	54282.82	5.64	yes	AT4G08250.1
29910.m000940	29910	353874	355658	-	1	3.40E-92	1785	594	67317.41	5.09	no	AT1G66350.1
29916.m000544*	29916	241112	243860	-	1	5.40E-94	2364	787	86369.68	6.32	yes	AT4G00150.1
29929.m004746	29929	1419600	1421123	+	1	2.00E-106	1524	507	56534.09	6.86	no	AT1G50420.1
29949.m000124*	29949	53044	54985	-	1	4.30E-123	1749	582	65343.70	6.30	yes	AT5G48150.1
29957.m001404	29957	285159	285539	-	1	4.60E-09	267	88	10096.76	10.21	no	AT2G01570.1
30024.m001746	30024	1148008	1149444	-	1	8.80E-138	1356	451	50679.56	6.38	yes	AT1G50420.1

Table S1. Cont.

Gene Model	Scaffold	Gene Start	Gene End	Orientation	Domain Number	E-Value (Pfam)	CDS Length	Protein Length	Molecular Weight/Da	Theoretical pI	Reads Coverage (>10)	Homologs in Arabidopsis
30073.m002204	30073	100179	103200	+	1	1.40E-124	2532	843	90820.90	6.11	yes	AT3G54220.1
30076.m004651	30076	1394867	1396826	+	1	1.00E-81	1929	642	73135.35	6.36	no	AT3G03450.1
30131.m007029	30131	1098698	1101046	-	1	2.10E-133	2061	686	75615.20	5.70	no	AT3G54220.1
30131.m007244	30131	2435990	2437414	-	1	2.30E-135	1425	474	53756.93	5.93	yes	AT1G50420.1
30147.m013794	30147	2621522	2623102	+	1	6.50E-111	1581	526	58433.45	5.78	no	AT1G66350.1
30156.m001710	30156	550167	551501	-	1	2.60E-86	1335	444	49717.52	5.13	no	AT3G49950.1
30169.m006225	30169	2156081	2158208	-	1	5.70E-111	1848	615	67440.71	6.16	yes	AT5G52510.1
30169.m006306	30169	395846	397483	+	1	1.30E-109	1638	545	61000.11	4.99	no	AT1G50420.1
30170.m013590	30170	584630	586045	-	1	2.80E-92	1416	471	53788.61	5.68	no	AT2G01570.1
30174.m008828	30174	547369	549570	-	1	2.20E-95	2202	733	80414.81	5.73	yes	AT4G00150.1
30190.m011131	30190	2053590	2055578	-	1	1.20E-127	1989	662	73717.04	5.70	yes	AT1G63100.1

Table S2. Summary of conserved motifs identified from the GRAS proteins in castor bean.

Motif 1						
2.	27568.m000253_LISCL	475	4.85e-31	IMNIAQNATT	LHIIDFGILYGFQWPCLIQRLSSRPGGPP	KLRITGIDFP
1.	28677.m000055_DELLA	301	4.85e-31	ILEAFGTANR	VHVIDFGLKQGMQWPALMQALALRPGGPP	AFRLTGIGPP
25.	27613.m000642_PAT1	276	2.20e-29	IAEAMKDESR	VHIIDFQIAQGSQWITLIQALAARPGGPP	HVRLTGIDDS
2.	29692.m000540_DELLA	341	2.20e-29	ILEAFEGKKR	VHVIDFSMNQGMQWPALLQALALRPGGPP	AFRLTGIGPP
28.	29949.m000124_PAT1	285	4.44e-29	IAEAMKDENEK	VHIIDFQIQGSQWVTLIQAFARPGGPP	RIRITGIDDS
14.	28650.m000187_LISCL	421	6.28e-29	IFKLAEKATR	LHIIDFGVLYGFQWPCLIQRLSQRPGGPP	KLRITGIELP
42.	30073.m002204_SCR	563	2.04e-28	IQEAFEREDR	VHIIDLDMQGLQWPGLFHILASRPGGPP	YVRLTGLGTS
3.	29807.m000482_DELLA	255	3.34e-28	ILEAFDGHDC	VHVVDNFLMHGLQWPALIQALALRPGGPP	LLRLTGIGPP
15.	28650.m000189_LISCL	396	6.36e-28	ITKAVEKATR	LHIIDFGISYGFQWPCFIYHLSTRPGGPP	KVRITGIDYP
24.	27529.m000047_PAT1	280	8.73e-28	IREAVEYEPR	IHIIDFQIAQGTQWIYLMQALADRPGGPP	AIRITGVDDP
23.	30131.m007029_Os43	434	2.22e-27	IFEAFEAEER	VHVIDLDILQGYQWPAFMQALAARPGGAP	FLRITGVGSC
13.	28650.m000186_LISCL	396	2.22e-27	IMKLAEKTR	LHIIDFGILYGFQWPCLIEDLSTRHGGPP	RLHITGIEFP

Table S2. Cont.

17.	28650.m000191_LISCL	499	4.07e-27	ILAVSKNAST	LHIIDFGILYGFQWPALIYRLSKREGGPP	KLRITGIELP
40.	28492.m000479_SCR	262	6.37e-27	ILEAFQRRDR	VHIIDLDIMQGLQWPALFHILATRMEGPP	HIRMTGMGTS
46.	30156.m001710_SHR	155	2.36e-26	IFKAIIECPK	VHILDFSITHCMQWPTLIDALAKRPEGPP	SLRITVPFTR
18.	29767.m000200_LISCL	476	3.61e-26	IMELSANSAS	IHIIDFGILYGFQWPTLIQRLSWRPKPPK	VRITGIDFPQ
5.	30190.m011131_DLT	391	3.22e-25	FLRAFEGKDK	VHIIDFDIKQGLQWPSLFQSLASRTNPPS	HVRITGIGES
4.	30170.m013590_DELLA	192	6.21e-25	IFETFAGKKH	IHVIDFFINHGTTQWSDLMQDLAARPGGPP	TIRISGIGFP
27.	29648.m001919_PAT1	296	1.04e-24	MIESFKGEGK	VHIIDFDINQGSQYITLIQTLANQPGKPP	HLRLTGIDDP
39.	29634.m002156_SCL4/7	344	1.34e-24	ILEATEGASK	IHIVDFGIVQGVQWAALLQALATRSAGRP	LSIRISGIPA
16.	28650.m000190_LISCL	549	1.73e-24	IMHAAEKATT	LHIVDFGVSYGFQWPILIQLLSMRDGGPP	KLRITGIELP
9.	29908.m006159_HAM	220	6.79e-24	ILEAVSQDKR	IHIVDYDIMEGIQWASLMQSLVSRKDGPP	TPHLRITALS
11.	30174.m008828_HAM	481	8.66e-24	LLEACEGSDR	IHIVDFDIGFGGQWASLMQELALRNGGVS	SLKITAFVSP
41.	29872.m000537_SCR	188	2.24e-22	IFQALDGEDR	VHVIDFDIMQGLQWPGLFHILASRSKIR	SMRITGFGSS
45.	29706.m001281_SHR	276	4.35e-22	LAQELDHKRN	LHILDIGVSHGVQWPTLLEALTRRSGGPP	PLVRITVITA
22.	30169.m006306_Os4	280	4.85e-22	ICEAARGKDA	LHVIDLGMMDHTLQWPSFIRTLASRPEGPP	KVRITGLIND
29.	30169.m006225_PAT1	352	6.84e-21	TVDQPNSGTG	FHVIDFDIGQGCQYLNLLHALSERLNGKP	ATVKITAVAD
32.	29889.m003284_Rc_GRAS	303	7.57e-21	IVENVARAKR	IHIIDLEIRSGAQWPVLMQALMSRHHCPL	ELLKISAIGT
34.	29910.m000940_Rc_GRAS	325	1.39e-20	IVDNVADAKK	IHILDLSLRGMQWTVLMQALVSRDCDPL	EHLKITAIGT
37.	30024.m001746_SCL3	136	2.08e-20	IIEAMEGEKM	VHIIDLNAVEPAQWLALLQALSARREGPP	HLRITGIHQQ
38.	30131.m007244_SCL3	156	2.30e-20	IVEAMEGEKM	VHIIDLNSFEPAQWINLLQTLARPEGPP	HLRITGIHEQ
10.	29916.m000544_HAM	535	6.14e-20	LLEALSEADR	IHIIDFDIGFGAQWASFMQELPRNRGAPS	LKITAFASPS
44.	29661.m000923_SHR	235	8.21e-20	IMEAFEGESK	LHIIDISNTYCTQWPTLLEALATRTDETP	HLRLTTIVAS
19.	29728.m000844_Os19	198	3.11e-19	EEESDSKSRI	LHVIDFDVSYGFQWPSLIQSLSEKASSN	RISLRITGLG
30.	29889.m003281_Rc_GRAS	180	1.36e-18	VIDSLDSAKR	VHFIDFGIKTGGHCTVLMQALANRQECPI	ELLKISGVGV
8.	29820.m000986_HAM	235	1.78e-18	LEAMPADAEM	IHIVDFDMGEGVQWPPMLETLARLQKGVV	LTAIKWEQEN
7.	29820.m000985_HAM	238	2.54e-18	LEAKPRDAEI	LHVVDVDIGEGIQWPSMIMALSQQNERM	QQHGYNQRHL
43.	29661.m000901_SHR	146	2.78e-18	ILEAIEGFSV	VHIVDLSLTHCMQIPTLIDAIANRFEVTP	MIKLTVAGCT
33.	29889.m003285_Rc_GRAS	318	4.73e-18	IVENVTDAKR	IHVIDLGIRVGVQWTGLMQALVSDFCNL	ELLKITAVGT
35.	30076.m004651_Rc_GRAS	370	8.71e-18	IMENIGSARK	LQVIDLEIRSGVQWTAMMQALAERQQRPL	EHLKVITALGL
6.	29646.m001070_HAM	279	1.51e-16	LETLDDSPPF	IHVIDFDIGLGCQYASFMRELVGKTDHFC	NKLTSPVLR
21.	30147.m013794_Os4	271	1.19e-15	FEGESFVHV	DLGMTLGLPHGHQWRQLIQSLANRAGKPP	CRLRITAVGL
36.	29790.m000809_SCL3	144	5.48e-15	LLQAMTHEHT	IHIVDLGSGDSKLWVPLLRSLAHSPPNGSP	HLKFTCLNTD
20.	29929.m004746_Os4	251	8.57e-15	FEGESSIHVV	DLGMTLGLPHGEQWRNLLHCLANRPDKKP	RCLRITGVGN

Table S2. Cont.

Motif 2						
28.	29949.m000124_PAT1	466	1.49e-34	RINVEQHCLA	RDVVNIIACEGTERVERHELLGKWRSRFRMAGFTP	YPLSSLRFGG
12.	27568.m000253_LISCL	656	3.35e-34	RMLIEREIFG	WEAKNVIACEGAERIERPETYKQWQVRILRAGFRQ	LPLNKEIYAA
25.	27613.m000642_PAT1	457	6.32e-34	RINVEQHCLA	REVVNIVACEGAERIERHEPLGKWKS RFAMAGFTP	YPLSSFVNAT
18.	29767.m000200_LISCL	656	6.32e-34	RMLIEKEIIG	REALNVVACEGWERVERPETYKQWQVRALRAGFVQ	LSFDREIVKQ
26.	28166.m001040_PAT1	378	2.51e-33	RIGVEQHCLA	KDIVNIIACEGKERVERHELFGKWKSR LTMAGFRQ	YPLSSYVNSV
2.	29692.m000540_DELLA	516	2.92e-33	DKVMSEVYLG	KQICNVVACEGADRVERHETLTQWRTRLGLAGFAP	VHLG SNAFKQ
27.	29648.m001919_PAT1	477	2.93e-32	RMNVEKQCLA	RDIVNIVACEGDERIEREYVAGKWRARMTMAGFTS	SSMGP NVVDM
13.	28650.m000186_LISCL	577	1.31e-31	RMMFEKEVFG	RYAVNVIACEGGERVERPETYRQWQARNIRAGFRQ	LPLDQEIMKK
17.	28650.m000191_LISCL	680	3.30e-31	RLKFEKEFYG	REALNVIACEGSERVERPETYKQWQVRS LRAGLKQ	LPLEPQLLKK
20.	29929.m004746_Os4	424	4.28e-31	RVKIEQFFYG	EEIKNIVSCEGP ARVERHERVDQWRRRMSRAGFQP	AQIKMAMQAK
21.	30147.m013794_Os4	444	1.53e-30	RAKMEQFYFA	EEIKNIVSCEGP ARVERHEKVDQWRRRMSRAGFQA	APVKMMAQAK
36.	29790.m000809_SCL3	334	2.22e-30	DRMVLEEMFG	REIENIVACEGLERYERHERCGK WGMRLARAGFKP	VQMWCFEQE
15.	28650.m000189_LISCL	577	4.11e-30	RLVFERELIG	KDVMNVVACEGSE RFERPETYKQWQIRNSRIGFRQ	LPLHQDIVKR
1.	28677.m000055_DELLA	479	9.56e-30	DLVMSELYLG	RQICNVVACEGAHRVERHESLPHWRTRFESAGFDR	VHLG SNAFKQ
3.	29807.m000482_DELLA	432	1.72e-28	EKVVAEMYIQ	REICNVVSC EGSARLERHEPLAKWKSRLTAAGFMP	LHLG SNAFKQ
38.	30131.m007244_SCL3	387	2.15e-28	RQKVEKMLLG	EEIKNIIACEGIERKERHEKLEK WILRLELAGFGR	VPLSYHGMLQ
5.	30190.m011131_DLT	563	1.11e-27	VRIKIEEMFA	REIRNIVACEGSDRLERHESFEKWRK LMEQGGFRC	MGISEREVLQ
29.	30169.m006225_PAT1	531	4.88e-27	ERVKVEEGLG	RKLAN SVACEGRDRVERCEVFGKWRARMGMAGFEL	KPVSQ NIAES
23.	30131.m007029_Os43	603	1.37e-26	RAKVEQYIFA	PEIRNIVACEGPERTERHERLEKWRK LMEGKGFKG	VPLSANA VTQ
37.	30024.m001746_SCL3	366	1.86e-26	RLKVEKMLFG	EEIKNIISCDGAERKERHEKLERW IQRLDLAGFGN	VPLSYCGLLQ
22.	30169.m006306_Os4	458	2.52e-26	RMKIEKLHFA	EEIRNIVAYEGCDRIERHERADQWRRQLGRAGFQV	MGLKCMSQAR
4.	30170.m013590_DELLA	362	3.95e-25	NCLDTYIFLR	NQIHNI VVCEGEYRVERYEKLTRWRTRLEAAGFVL	IHLG SNVGEY
43.	29661.m000901_SHR	357	1.67e-21	QRQWYEADIC	WKIENVIAHEGLQRVERLEPKSRWVQRM RNANFRS	ISFGEEAVSE
34.	29910.m000940_Rc_GRAS	499	2.83e-20	RMIMESMYFG	IGIKNMIATEGEERVIRNVKLD AWRAFFARFGMVE	TDLSSSALLQ
32.	29889.m003284_Rc_GRAS	477	4.54e-20	RMAAESVFFH	HGIRNIVASEGEERRIRHV KIDVWRSFFARFGMIQ	TELSTSSLYQ
33.	29889.m003285_Rc_GRAS	491	8.47e-20	RMILES LHFHG	EGIKNIVATEGKERKIRNAKLD AWRAFFTRFGMLE	TELSTSSL CQ
46.	30156.m001710_SHR	357	1.69e-19	QRIEYESDIG	HKIENIISYEGSQRTERLESGIKLTQRMKNAGFCS	VEFCEETIRE
44.	29661.m000923_SHR	429	4.22e-19	ERLMLERSAG	RAIVDLVACQPSESIERREKATR WSSRLHACGYSP	ILFSDEVCDD

Table S2. Cont.

Motif 3



21.	30147.m013794_Os4	396	4.50e-30	LSPKILALVE	QDSSHNGPFFLGRFMEALHYYS AIFDSDL	AMLPRYDTRR
22.	30169.m006306_Os4	409	6.89e-29	LSPDLLTVVE	QDANHNGPFFLGRFLESLHYYS AIFDLSLE	ASLLPRNSRQ
2.	29692.m000540_DELLA	471	1.51e-28	MKPEIVTIVE	QEANHNGPVFLDRFTESLHYYS TLFDLSLE	GSVSTQDKVM
1.	28677.m000055_DELLA	431	1.51e-28	MKPKIVTVVE	QEASHNGPVFLDRFTEALHYYS SLFDLSLE	GSGLNVP SQD
34.	29910.m000940_Rc_GRAS	451	2.68e-28	VNPCVIVVAE	VEANHNSPTFVNRVFEALFYYS AYFDCLD	ACMERNDKNR
20.	29929.m004746_Os4	376	1.41e-27	LSPKLLILVE	QDSGHNGPFFLGRVMEALHYYS AIFDSDL	TMLPKYDTKR
14.	28650.m000187_LISCL	554	2.85e-27	IRPDIFIHGV	INGTYNAPFFVTRFREALFYYS ALFDMFE	INVPREDDQR
3.	29807.m000482_DELLA	387	1.32e-26	LNPKIMTVVE	QEANHNPQGFDRFTEALYYYY STMFDSLG	ACALQPEKVV
35.	30076.m004651_Rc_GRAS	497	2.55e-26	LKPSIMVINE	IEANHNSPNFVNRFIEALFFYS AYFDCLE	TCLDHNNEHK
23.	30131.m007029_Os43	555	4.86e-26	QAPNIVTIVE	KEASHNGPYFLGRFLEALHYYS AIFDSDL	ATFPPDSTQR
16.	28650.m000190_LISCL	683	2.09e-24	IKPNIYVHCI	INGSYNAPFFVTRFREALHFSS LFDMDFD	STLSREDQGR
13.	28650.m000186_LISCL	529	2.40e-24	INPDIFIHGV	VNGTYNAPFFLTRFRDALHFH SALSALFDMID	STIPREEPER
25.	27613.m000642_PAT1	409	6.38e-24	LSPKVVTLVE	QESNTNTAPFVNRFTETLNYY LAIFESID	VTLPRGHKER
32.	29889.m003284_Rc_GRAS	429	7.32e-24	INPNVMVME	VEANNNSPSFVHRFIEALFFYS AYFDCFD	ACMERDDPNR
27.	29648.m001919_PAT1	429	7.32e-24	LNPKLVTVVE	QDVNTNTAPFFPRFVEAYNYYS AVFESLD	ATLPRESQDR
15.	28650.m000189_LISCL	529	1.44e-23	INPVIFLHGV	VNGSYNAPFFATRFREALHFH SSSLFDMFE	AIATREDQER
12.	27568.m000253_LISCL	608	1.44e-23	MNPDVFITGI	VNGAYNAPFFITRFREAVFH YSTLFDMLE	TNVPREIPER
28.	29949.m000124_PAT1	418	9.01e-23	LSPKVVTLVE	QESNTNTAAFFPRFLETLNYY T AMFESID	VTLSREHKER
24.	27529.m000047_PAT1	413	9.01e-23	LSPKVVTLIE	QESNTNTKPFLLPRFKETLEY YNAMFESID	AGSSRDDKQR
17.	28650.m000191_LISCL	632	9.01e-23	MSPDIFIHAI	VNGSYSAPFFVTRFRFRESLF HFSALSALFDMFD	TNMSREDQMR
26.	28166.m001040_PAT1	330	1.92e-22	LNPKVVTLVE	QESNTNTTPFLTRFMETLDFY LAMFESID	VRLPRERKDR
18.	29767.m000200_LISCL	608	6.54e-22	INPNIFILGI	INGAYSAPFFITRFREALHFH SSSLFDMLE	SIVPREDMER
33.	29889.m003285_Rc_GRAS	444	7.55e-21	LNPSITVVTE	PEYNSTSSSFVNRFIEALFYFS AYFDCLE	SCMKDNSNRM
42.	30073.m002204_SCR	683	1.18e-20	RLAPKVVTVV	EQDLSHAGSFLGRFVEAIHYYS ALSALFDSL G	ASYGEESEER
41.	29872.m000537_SCR	309	1.18e-20	LLRPKLITTA	EQDLSHAGSFLGRFVEALHYYS ALSALFDAL G	DGLGIDSVER
38.	30131.m007244_SCL3	339	2.05e-20	LSPKLMVITE	QESNHNGFTLMERVTEALNFY AALFDCLE	STVSRPSIER
36.	29790.m000809_SCL3	285	2.05e-20	MSPRLLFLVE	QEADHNLNRLPDRFIEGLHYYS AVFDSID	ATLVGNLGSE

Table S2. Cont.

37.	30024.m001746_SCL3	318	7.14e-19	LSPKLMVVME	QDSNHNGSSLMERLLEALYSYAALFDCLE	STVSRSTLER
40.	28492.m000479_SCR	382	1.17e-18	ELSPRIMTLV	EQDISHGGSFLDRFVGLHYYSTLFDSLGL	AFLPCDDSSR
19.	29728.m000844_Os19	322	1.17e-18	LNPSIVILVE	QEGSRSPRSFLSRFMESLHYFAAMYDSL	DCLPLESSER
39.	29634.m002156_SCL4/7	475	1.43e-18	LNPEIVTLGE	YEASLNQIGYENRFKNALRYYS AVFESLE	PNLSRDSTER
29.	30169.m006225_PAT1	484	7.25e-18	LAPRVVTLVE	QEMNTNTAPFMARVNEGSSYYGALFESIE	STVQRDHTE
5.	30190.m011131_DLT	516	1.83e-17	TSPTIVLMAE	QEA EHNATNLEARVCNSLKYYS AIFDSIN	TSLPLDSLVR
9.	29908.m006159_HAM	355	2.88e-17	SPRLVTLVEE	EVGPGVDGGFVGRFMDSLYHYSALYDSLE	AGFPMQSRAR
4.	30170.m013590_DELLA	320	3.07e-15	IEPEIFTIIE	QESDNNQDQGSYRFNECINYSFLESSE	GSTNCLDTYI
6.	29646.m001070_HAM	414	1.04e-12	PEVVVVVDNE	GWGESEPA SFRNFVNGLEFYSMIFESLD	AAAAGGGGEWA
30.	29889.m003281_Rc_GRAS	307	1.19e-12	LNPCVMVHIE	PVLNHSSPIFIDSFLEVLLFYSTCFD GVE	GCIDQCDPNR
44.	29661.m000923_SHR	382	4.24e-12	IITIVEEEAD	LDVGIDGLDFVRGFQECLELRWFRVYFESLE	ESFSRTSNER
46.	30156.m001710_SHR	310	1.19e-11	LNPCITVIVD	EDSDL DAPDLTSRITTCFNYLWIPF DALE	TFLPTDSCQR
8.	29820.m000986_HAM	381	1.19e-11	GILTFGDGDA	WETVRDCSGFASYFEGNLMHYQALLESIE	MNFPIHLAEA
11.	30174.m008828_HAM	607	1.97e-11	LSPKIVVSLD	RGCDRTDLPFAHHINHSIQSYSGLLESLE	AVNMNIDALQ
43.	29661.m000901_SHR	310	6.37e-11	LDPTIVVLVD	EDADLTSNNLVCR LRS AFNYLWIPYDTVD	TFLPRGSKQR
7.	29820.m000985_HAM	389	1.97e-10	GIVTFGEGIG	HETLSNCDGFGSFFERYMEHYEGLLESIE	WGFPIHLAEA

Motif 4



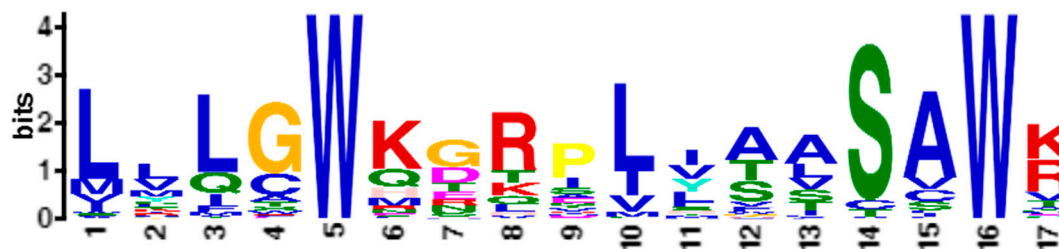
2.	29692.m000540_DELLA	311	7.94e-34	IDHSLSDILQ	MHFYETCPYLKFAHFTANQAILEAFEGKK	RVHVIDFSMN
3.	29807.m000482_DELLA	225	3.83e-31	ASAYENEFY	HHFYEACPYLKFAHFTANQAILEAFDGH	CVHVVDNLM
1.	28677.m000055_DELLA	271	4.98e-30	LDPSYSDTLE	MHFYETCPYLKFAHFTANQAILEAFGTAN	RVHVIDFGLK
23.	30131.m007029_Os43	404	1.81e-26	SNSMEILKIY	QIVYQACPYIKFAHFTANQAIFEAFEAEE	RVHVIDLDIL
39.	29634.m002156_SCL4/7	314	2.64e-25	SSEEDFTLSY	KALNDACPYSKFAHLTANQAILEATEGAS	KIHIVDFGIV
28.	29949.m000124_PAT1	255	1.10e-24	PASADLLSYM	HILYEVCPYFKFGYMSANGAIAEAMKDEN	KVHIIDFQIG
19.	29728.m000844_Os19	159	1.50e-24	PTSEEEFLAF	THLYRVSPYYQFAHFTANQAILEAFEKEE	EEESDSKSRI
25.	27613.m000642_PAT1	246	2.04e-24	PASAELLSYM	HILYEVCPYFKFGYMSANGAIAEAMKDES	RVHIIDFQIA
42.	30073.m002204_SCR	533	9.18e-24	THTQKMASAF	QVFNGISPFVKFSHTANQAIQEAFERED	RVHIIDL DIM
9.	29908.m006159_HAM	190	3.39e-23	HHQADTLAAF	QLLDMSPYVKFGHFTANQAILEAVSQDK	RIHIVDYDIM

Table S2. Cont.

20.	29929.m004746_Os4	217	6.99e-21	SFTA EKDEAL	RLVYEICPQIQFGYFVANATILEAFEGES	SIHVVDLGMT
41.	29872.m000537_SCR	158	7.92e-21	TQSQKIFNAF	QSYNSISPLIKFSHFTANQAIQALDGED	RVHVIDFDIM
21.	30147.m013794_Os4	237	1.15e-20	IASDKKEEAL	SLVYEICPHIQFGHFVANSSILEAFEGES	FVHVVDLGMT
27.	29648.m001919_PAT1	266	2.39e-20	PPSSDRLAAM	QILFEICPCFKFGFMAANGAMIESFKGEK	GVHIIDFDIN
38.	30131.m007244_SCL3	126	5.51e-20	YLVSEEILVQ	RLFFELFPFLKLAYVITNQAIVEAMEGEK	MVHIIDLNSF
40.	28492.m000479_SCR	232	8.83e-20	INHKTVHSAF	QVFNNVSPFIKFAHFISNQEILEAFQRRD	RVHIIDLDIM
37.	30024.m001746_SCL3	106	9.92e-20	TLVSEEILVR	KLFFEMFPFLKVG VITNQAIIEAMEGEK	MVHIIDLNAV
11.	30174.m008828_HAM	451	3.92e-19	CNLILKIGAY	KSFSEISPILQFSNFTCNQALLEACEGSD	RIHIVDFDIG
44.	29661.m000923_SHR	205	7.66e-19	CSFESTRKMV	LKFQEVSPWTTFGHVSCNGAIMEAFEGES	KLHIIDISNT
22.	30169.m006306_Os4	250	1.33e-18	ITREEKMEAF	QLLYQTTTPYVAFGFMAANEAICEAARGKD	ALHVIDLGMD
7.	29820.m000985_HAM	207	7.33e-18	ESFKNFDKAF	EVFYQIFPYGMVAHFTANSAILEAKPRDA	EILHVVD FDI
10.	29916.m000544_HAM	505	8.13e-18	FDVIFKLGAY	KVFSEVSPLIQFVNFTCNQALLEALSEAD	RIHIIDFDIG
14.	28650.m000187_LISCL	391	1.11e-17	TPVSDILKAY	QVYVKACPFKRMSNFFANQTIFKLAEKAT	RLHIIDFGVL
15.	28650.m000189_LISCL	366	3.08e-17	TNTADILKAY	QLYVSVCPFRKMSNFFTNRITITKAVEKAT	RLHIIDFGIS
8.	29820.m000986_HAM	204	6.82e-17	ESSNNFEAAF	RAFYQIFPNGRIAHFAANSAILEAMPADA	EMIHIVDFDM
24.	27529.m000047_PAT1	250	1.80e-16	PVSSDLMTYM	GILFKICPYWRFAYTSANVIIREAVEYEP	RIHIIDFQIA
16.	28650.m000190_LISCL	519	5.61e-16	RTAADILRAY	KTHLHACPFKLSILFANKMIMHAAEKAT	TLHIVDFGVS
29.	30169.m006225_PAT1	318	7.41e-16	LFAKEHIAST	QLLYELSPCFKLGMAANLAILQSTVDQP	NSGTGFHVID
43.	29661.m000901_SHR	116	1.07e-15	DAHKFSVIEL	ASFVDLTPWHRFGFTAANASILEAIEGFS	VVHIVDLSLT
4.	30170.m013590_DELLA	162	2.65e-15	FDYSYLNDIQ	RYFYKEWSYVKA AHLTANREIFETFAGKK	HIHVIDFFIN
12.	27568.m000253_LISCL	445	5.37e-15	TTAADVLKAH	HLFLAACPFKLSNFFSNKTIMNIAQNAT	TLHIIDFGIL
5.	30190.m011131_DLT	361	5.37e-15	RVDDDSGTAW	RLLNQVNPIPKFIHFTENEIFLRAFEGKD	KVHIIDFDIK
33.	29889.m003285_Rc_GRAS	288	8.30e-15	EAIMAPSSTI	LASYQEV PFSQVAHFAGIQAIVENVTDAK	RIHVIDLGIR
31.	29889.m003282_Rc_GRAS	220	2.13e-14	SLVIIPNSI	QACFEGIPFYQAAHLTGIKAIENVAEAN	RSHLLKITAV
32.	29889.m003284_Rc_GRAS	273	3.51e-14	PVDPNHNAAS	LACHQKIPFIQVARFTAIQEIVENVARAK	RIHIIDLEIR
45.	29706.m001281_SHR	242	3.82e-14	IDPKFFQ RSL	LKFYEVSPWFAPNNIANS SILQVLAQEL	DHKRNLHILD
13.	28650.m000186_LISCL	366	8.00e-14	TSAAGMLKAY	HAYTTACPFQTM SHLYANETIMKLAEKTT	RLHIIDFGIL
18.	29767.m000200_LISCL	446	9.41e-14	TSAANVLKAY	HLYLAACPFKRLTNFLSNKTIMELSANSA	SIHIIDFGIL
17.	28650.m000191_LISCL	469	1.79e-13	LSAADMLKAY	LAYISACPFNKIAIIFANHNILAVSKNAS	TLHIIDFGIL
46.	30156.m001710_SHR	125	2.65e-13	QRRQMSVTEL	AGYVDLIPWHRFGFCASNSAIFKAIEECP	KVHILDFSIT
34.	29910.m000940_Rc_GRAS	295	2.87e-13	EAMMTPNPTI	LASHLET PFCQVAHFAGIQAIVDNVADAK	KIHILDLSLR
6.	29646.m001070_HAM	248	1.06e-12	SEVVQTIKAY	QDFSGISPIPMFNHFPVDQAILETLDDSP	PFIHVIDFDI
35.	30076.m004651_Rc_GRAS	340	4.06e-11	PDGTSLHLAC	LSFHQNVPLNQITQLTSIQAIMENIGSAR	KLQVIDLEIR

Table S2. Cont.

Motif 5



2.	29692.m000540_DELLA	583	5.23e-18	GYRVDENNGC	LMLGWHTRPLIATSAWR	LASKQVVLAQ
18.	29767.m000200_LISCL	722	1.79e-17	NFLINEDGRW	LLQGWKGRIIYALSAWK	PM
34.	29910.m000940_Rc_GRAS	566	3.86e-17	CFTLDRNGKS	LVLGWKGTPHLSLAWK	FISHEKKGVN
21.	30147.m013794_Os4	509	1.90e-16	GYTVVEEKGC	LVLGWKSKPIVAASCWK	C
1.	28677.m000055_DELLA	546	1.90e-16	GYRVEENNGC	LMLGWHTRPLIATSAWQ	LSDSK
25.	27613.m000642_PAT1	522	2.24e-16	KYTLERDGA	LYLGWMNRPLIASCRAW	
6.	29646.m001070_HAM	522	3.12e-16	GFYVAKRQAE	LVLCWHERPLIATSVWK	C
22.	30169.m006306_Os4	522	3.66e-16	GYTLASDKGC	LLLGWKGRPIMLASAWK	AHNPVSS
17.	28650.m000191_LISCL	746	6.88e-16	DFVVDQDQGW	MLQGWKGRIIYASSAWV	PA
20.	29929.m004746_Os4	489	9.35e-16	GYTVTEDEKGC	LILGWKSKPIIAASCWK	CC
23.	30131.m007029_Os43	669	1.09e-15	GYRLTEDEKGC	LLLGWQDRAILAASAWR	C
15.	28650.m000189_LISCL	642	1.96e-15	DFAVDEDEGHV	MLMGWKGRIIHAISAWK	PIEE
10.	29916.m000544_HAM	770	1.96e-15	GFHVEKRQAS	LVLCWQRRDLISASAWR	C
16.	28650.m000190_LISCL	797	2.27e-15	DFVIDEDNNW	MLQGWKGRIIYASSCWV	PA
33.	29889.m003285_Rc_GRAS	558	3.01e-15	ACTLSMDGKS	LLIGWKGTPMHLSLAWK	FI
4.	30170.m013590_DELLA	435	3.01e-15	KCTIEENNGC	WMLGWRTRPLIAISAWR	ADNRILISDE
3.	29807.m000482_DELLA	498	3.01e-15	GYCVEENDGC	LTLGWHSRPLIAASAWQ	AVPDIGSPLG
11.	30174.m008828_HAM	716	5.24e-15	GFHVEKRQST	LVLCWQRKELISASAWR	C
42.	30073.m002204_SCR	796	6.87e-15	GYTLVEDNGT	LKLGWKDLCLLTASAWR	PFHATATAAA
41.	29872.m000537_SCR	423	7.86e-15	YTLVEEENGC	LKLGWKDLSLLTASAWK	PSD
37.	30024.m001746_SCL3	432	1.02e-14	GYRIKDENGK	VVICWQDRPLFSLSAWR	CKK
35.	30076.m004651_Rc_GRAS	611	1.33e-14	SCSLDKNGKC	LIVGWKGTPHLSLAWK	FCGDRLGRRF
26.	28166.m001040_PAT1	443	1.33e-14	HYTLLEKDGA	MLLGWKNRNLVSASAWY	
19.	29728.m000844_Os19	453	1.33e-14	RVFERDEGKT	ISLGWQDRCLLTASAWR	CV

Table S2. Cont.

36.	29790.m000809_SCL3	399	1.71e-14	GYKTVSERWS	LMICWHERPIYAVTAWT	C
44.	29661.m000923_SHR	495	2.21e-14	WSMTQSGHAG	IFLCWKEQPVVWASAWK	P
40.	28492.m000479_SCR	498	3.20e-14	GYSLAQGEA	LRLGWKDTSLFTASAWT	SLASR
13.	28650.m000186_LISCL	643	4.60e-14	NFIVDEDSQW	MLQGWKGRIIYALAVWK	PVHD
38.	30131.m007244_SCL3	453	5.18e-14	GYKIKEENG	SVICWQDRPLFSVSAWR	FRRYD
14.	28650.m000187_LISCL	668	6.56e-14	DFVVDENGRW	MLQGWKGRVISALSVWK	PVQD
12.	27568.m000253_LISCL	722	1.04e-13	DFVIDEDSRW	LLQGWKGRIVYALSSWE	PDH
27.	29648.m001919_PAT1	543	2.54e-13	RYKLKEEMGA	LLFGWEDKSLIVASAWR	
30.	29889.m003281_Rc_GRAS	421	4.83e-13	SCLLVRNGKC	LMTGWKETPLLSLAWN	FQQEHSKNC
29.	30169.m006225_PAT1	599	1.63e-12	GFTVKEDNGG	VCFGWMGKTLTVASAWR	
24.	27529.m000047_PAT1	526	3.85e-12	RYGLQEKDGA	LYLWWMNTAMSSSSAWR	
43.	29661.m000901_SHR	422	6.69e-12	GWGLKKEEDD	LVLTWKGHNVVVFATAWM	PT
5.	30190.m011131_DLT	631	7.32e-12	RVKERQDRAA	LTLSWLDQPLYTISAWA	PVDVVGSSSS
9.	29908.m006159_HAM	467	8.01e-12	YRVEELGCNR	LVLWKSRRLLSASIWT	SPSSDCDL
39.	29634.m002156_SCL4/7	592	2.09e-11	YSLVESQPGF	LSLAWNEVPLLVSSWR	
46.	30156.m001710_SHR	422	2.70e-11	GWGMKKEEDM	LVLTWKGHNSVFASAWL	PSCLED
8.	29820.m000986_HAM	492	3.76e-11	VRIGGEWNE	MILEWRGTQLVRVSAWR	N
45.	29706.m001281_SHR	524	7.18e-11	EMRTEEKDGC	VGLWVKGQPVSFCSLWR	LDMKGNDS
32.	29889.m003284_Rc_GRAS	544	9.11e-11	SCTLDVNEKS	LNISWKATPISLSVWK	FI

Motif 6



15.	28650.m000189_LISCL	322	8.57e-22	KLIRLHASPY	GDANQRLAHYFANALEARLAG	SGKLMPTLFI
14.	28650.m000187_LISCL	347	8.89e-20	RQIRQHSSPY	GDGNQRLAHYFANALETLAG	TGTPAYSPLL
17.	28650.m000191_LISCL	425	5.87e-19	KQIRQHSSPF	GDGSQRLAHCFANGLEARLAG	TGAQIYTALS
16.	28650.m000190_LISCL	472	5.87e-19	KQIRQHSSPL	GDGSQRLAHCFANGLEARLAG	SVTGMQSFYT
13.	28650.m000186_LISCL	322	6.91e-19	RQIKQYSSPF	GDGNQRLAHFFANGLEARLAG	TGTPGYAPAV
37.	30024.m001746_SCL3	61	8.13e-19	GQISQLASAE	GDTMQRIAAYFTEALAHRIIK	AWPGVHRALN
23.	30131.m007029_Os43	355	9.54e-19	HHLNRVVTPL	GDSMQRVASCFTEALSARLAA	TLTTQPSNTA
18.	29767.m000200_LISCL	402	2.44e-18	KQIRQHSSPF	GDGNQRLAHCFANGLDARLAG	TGSQIYKGLV

Table S2. Cont.

38.	30131.m007244_SCL3	80	3.30e-18	EHISHLASAD	GDTMQRIAAYFTEALADRILK	KGWPCLHRAL
28.	29949.m000124_PAT1	211	1.55e-16	DELRQIVSVS	GEPIQRLGAYMLEGLVARLAS	SGSSIIKSLR
25.	27613.m000642_PAT1	202	1.55e-16	TELKRMVSVS	GEPIQRLGAYMLEGLVARLAS	SGSSIYRALR
12.	27568.m000253_LISCL	401	1.75e-16	KQIRQNASPT	GDMQRMAMHIFADGLEARMAG	SGTQIYKAFM
34.	29910.m000940_Rc_GRAS	245	1.99e-16	KQCDSISSNT	GNPVQRVVYFAEALHDRIDI	ETGKTKSKEL
39.	29634.m002156_SCL4/7	272	3.25e-16	IKLRESVCEH	GDPTERVAFYFTEALYSRLCL	QAEKSLAMFE
19.	29728.m000844_Os19	116	5.92e-16	SELYTSVCLT	GDSVQRVVAYFADGLSARLLT	RKSPFYEMIM
2.	29692.m000540_DELLA	274	6.66e-16	KQIGFLAVSQ	AGAMRKVATYFAEALARRIYR	LYPQSPIDHS
30.	29889.m003281_Rc_GRAS	98	8.43e-16	NLCDFLSSNK	GNSVQRVVHYFTKALQDRISQ	ESETVSSKRS
1.	28677.m000055_DELLA	234	1.19e-15	KHIGLLAASQ	ASSMRKVATYFAEALARRIYK	IYPQESLDPS
42.	30073.m002204_SCR	488	1.68e-15	LEISQLSTPY	G TSAQRVAAYFSEAMSARLIN	SCLGIYATLP
35.	30076.m004651_Rc_GRAS	293	2.36e-15	SRCEWIASQR	ANPVQRVVYCFEALRERIDK	ATGRFIPKER
24.	27529.m000047_PAT1	206	6.31e-15	HVLEQMVSVS	GEPIQRLGAYMLEGLRARVEL	SGSKIYRALK
27.	29648.m001919_PAT1	222	1.07e-14	NELRQMVSQI	GDPSSRIAAYMVEGLAARMAA	SGKYLYKALK
33.	29889.m003285_Rc_GRAS	242	1.32e-14	NQCDSLSSST	GNAVERVVHYFCKALRERIDR	ETGKSLGKQH
32.	29889.m003284_Rc_GRAS	227	1.32e-14	NHCELLSSNI	GNPVQRVVYHFSEALKERIDR	ETGRFPSIEY
31.	29889.m003282_Rc_GRAS	181	2.00e-14	EFCDQSSSNA	GNPVQRVVYFFGALRRRIDQ	ELGKITSRSL
36.	29790.m000809_SCL3	69	2.45e-14	SEISELSSVS	GDSMQRLAARFASALAIRLVK	RWPGLYKALN
20.	29929.m004746_Os4	169	3.32e-14	SELRANALVF	GTSFQRVASCVFQGLSDRLTL	LQPLGAVGVL
6.	29646.m001070_HAM	206	5.45e-14	RLNHRLQSPV	GKPLQRAAFFKKEALQNLLAG	SPRTPHTPTS
41.	29872.m000537_SCR	111	1.08e-13	PEISELSSPF	GSSFERVGSYFAHALQARVVS	SCLGTYSPLT
21.	30147.m013794_Os4	188	1.57e-13	SELRSSALVF	GSSFQRVASCFFQGLADRLSL	VQPLGTVSLV
9.	29908.m006159_HAM	139	1.73e-13	RLKELVSPND	GTNMERLAAYFTDALQGLLEG	HGTSTKHLIH
26.	28166.m001040_PAT1	233	2.29e-13	EKARAASVIS	GEPIQRLGAYLVEGLVARKES	SGNNIYHALR
22.	30169.m006306_Os4	200	8.94e-13	AQIWASVNP	GDSLQRVSYCFALGLRSRLSL	LQNATSNGTF
5.	30190.m011131_DLT	315	9.77e-13	AKLGELSSPK	GTAVSRLIAYYTEALALRVTR	LWPHIFHIST
43.	29661.m000901_SHR	66	1.16e-12	WVLNNIAPPD	GDSNQRLTCAFLRALIARAAS	SGTCKLLAAM
46.	30156.m001710_SHR	80	1.27e-12	WVLNNVASLV	GDPNQRLT SWFLRALISRASK	VCPTAMNFDG
10.	29916.m000544_HAM	459	1.51e-12	ARLNQQLSPI	GKPLHRAAFYFKEALQLLLLM	NNNPVTSLPP
11.	30174.m008828_HAM	409	2.32e-12	RLNHQLSLSI	GKPHTRAAAFYFKEALQLLHLM	NNTANPSSLS
45.	29706.m001281_SHR	197	4.96e-12	YVLHELASST	GDANHRLAFYGLQALTHHLSS	SRTSASIGSV
44.	29661.m000923_SHR	158	1.54e-11	WMLNELGSPY	GDIDKKLASYFLQALFSRMTD	SGERCYRTLA
40.	28492.m000479_SCR	192	2.68e-11	ELTQMSPY	PSCAERVVAYFAKAMASRVIN	SWLGICSPLI
29.	30169.m006225_PAT1	278	4.26e-11	TRVSQVSNPR	GNSEQRLMEYMSMALKSRLNS	ADNPPVAEL
4.	30170.m013590_DELLA	126	6.72e-11	ILSQILVNSK	ARATQSMALFAEAMSSRVYR	LYPQYFDYSY
3.	29807.m000482_DELLA	184	1.16e-9	MQALLTRVNT	NSGIGKVAGCFIDALSLRIFS	PVNGVGVAVG

Table S2. Cont.

				Motif 7																		
18.	29767.m000200_LISCL	519	5.05e-29	GIDFPQPGFR	PAERVEETGRRLATYAKKFNVPFEYNAIA	KKWETIKFEE																
12.	27568.m000253_LISCL	519	4.48e-28	GIDFPHPGFR	PAERVEETGHRLSNYAKKFNVPFEFNAIA	QKWDTVQIEQ																
16.	28650.m000190_LISCL	593	8.41e-27	GIELPQQGFR	PAERIEETGRRLARYCERFNVPFEYNSIA	AQNWENIRIE																
15.	28650.m000189_LISCL	440	1.33e-26	GIDYPQPGFR	PGERVEETGRRLKRLADKLNVPFEYNAIA	QKWETIQGED																
17.	28650.m000191_LISCL	543	4.97e-26	GIELPQSGFR	PGERVQETGRRLAKYCELHKVPFEYNAIA	KKWETIQIDD																
14.	28650.m000187_LISCL	465	2.62e-25	GIELPQPGFR	PAERVEETGRRLQRYCERFNVPFKYHAVA	QKWETIKYED																
13.	28650.m000186_LISCL	440	2.20e-24	GIEFPQPGFR	PAERVEETGRRLSKYCERFNVPFEYDSIA	QNWESIYED																
5.	30190.m011131_DLT	429	1.03e-21	SHVRITGIGE	SKQELNETGDRLAGFAEALNLPFEFHPVV	DRLEDVRLWM																
27.	29648.m001919_PAT1	340	1.02e-20	GIDDPESVQR	STGGLKIIGQRLEKLAELKVPFEFHAVA	SKTSLVSPSM																
23.	30131.m007029_Os43	472	1.54e-20	PFLRITGVGS	CIESVRETGRCLTELAHSLHVPFEFHPVA	EELEDLKPHM																
42.	30073.m002204_SCR	601	2.30e-20	PYVRLTGLGT	SIEALEATGKRLSDFAQKLGLPFEFFPVA	DKVGNLDPDR																
32.	29889.m003284_Rc_GRAS	343	3.43e-20	LLKISAIGTT	SKHLIEDTGKRLASFAESMNVFDFRAVM	VSDMLDLKKE																
41.	29872.m000537_SCR	226	6.60e-20	RSMRITGFGS	SSELLESTGRRLADFASSLGLPFEFHPL	GKIGSVSDIS																
28.	29949.m000124_PAT1	329	4.85e-19	GIDDSTSAYA	RGGGPNIVGKRLAKLAESVKVPFEFHAAA	MPNSEVHIKN																
24.	27529.m000047_PAT1	324	4.85e-19	GVDDPQSAYA	RGGGLDIVGKRLSSFAESHNVPFQFHDA	MSGCEVQLEH																
2.	29692.m000540_DELLA	383	6.17e-19	LTGIGPPSHD	NSDHLQEVGWKLAQLAETIHVEFEYRGFV	ANSLADLDAS																
25.	27613.m000642_PAT1	320	1.25e-18	GIDDSTSAYA	RGGGLDIVGQRLSRLAESCKVPFEFHAA	VSGSEIELKN																
40.	28492.m000479_SCR	300	1.58e-18	PHIRMTGMGT	SMDLLVETGKQLSNFAKRLGLSFEFHPIA	KKFGEIDVSM																
1.	28677.m000055_DELLA	343	2.23e-18	LTGIGPPQSN	NTDALQQVGVKLAQLADTIGVEFEFRGFV	ANSLADLQPE																
38.	30131.m007244_SCL3	194	1.05e-16	PHLRITGIHE	QKEVLEQMALRLTEAEKLDIPFQFNPI	SKLEDLDIES																
4.	30170.m013590_DELLA	234	1.56e-16	ISGIGFPNHD	NSDYLSVGVKLAQLAETLNIDFEYRGFL	AYNLADLDA																
33.	29889.m003285_Rc_GRAS	358	1.90e-16	LLKITAVGTT	SKHLIKDTGKRLTSFAESISLPFAFNIVM	VSDMLDLTED																
35.	30076.m004651_Rc_GRAS	411	2.31e-16	LKV TALGLTG	KGKKIEETGRSLESFAKSMNIPFTFKAVY	VSCMKNIKEK																
37.	30024.m001746_SCL3	174	4.53e-16	PHLRITGIHQ	QKEVLDQMAHKLSEEAERLDIPFQFNPIV	SKLENLDIEK																
9.	29908.m006159_HAM	267	4.53e-16	LSRGGNSGKR	SIGTVQETGRRLVAFASIGQPFSEHHC	LDSEDFRPS																
39.	29634.m002156_SCL4/7	389	7.26e-16	GIPAPVLGKS	PAASLLATGNRLGDFAKLLDLNFEFVPI	TPIQELNESN																
46.	30156.m001710_SHR	200	2.00e-15	PFTRPQVPPW	LNVSTEEVGLRLGNFAKSRDVPFEFIVID	DPSSDILCKE																

Table S2. Cont.

34.	29910.m000940_Rc_GRAS	365	2.19e-15	HLKITAIGTT	SRELIENTGKRLISFAETMNIASFVKMAL	VSDLLDLKED
44.	29661.m000923_SHR	291	3.13e-15	GGGGNCGLVS	AQKVMKEIGSRMEKFARLMGVPFKFNVIH	HAGDLCDLNL
3.	29807.m000482_DELLA	297	8.94e-15	LTGIGPPSPD	GRDSLREIGVKLAELARSVNVRFARGVA	ASRLEDVKPW
20.	29929.m004746_Os4	290	1.37e-14	RCLRITGVGN	SAERLQALGDELDCYARSLGLNFELWVE	SSLEKCLKSTD
30.	29889.m003281_Rc_GRAS	221	4.38e-14	LKISGVGVKA	SRQRIEDAGKSLACFANTLDLPFSFKTII	VASIKDLKKD
29.	30169.m006225_PAT1	395	2.13e-13	ITAVADNSAE	EKERLKVVGTTLSQLAEQFVSLHFNVVS	AKLGDLSRES
43.	29661.m000901_SHR	191	1.83e-12	AGCTEDIPPM	LDLSYEELGCKLINFARSNVIMEFRVVD	SSYADGFSSL
21.	30147.m013794_Os4	310	2.12e-12	CRLRITAVGL	CVGRFQTIGDELVEYAKDVGINLEFSVVE	STLENLQPDD
7.	29820.m000985_HAM	293	3.72e-12	ITAIKWREEH	PWRKLEETKRRLQNYADSLGLMLHVEEIE	VQNLAREIKR
36.	29790.m000809_SCL3	182	4.91e-12	PHLKFTCLNT	DKAILDKLGQRLVKEAEASDMAFQFHPLN	ISLRDLTADM
22.	30169.m006306_Os4	321	3.63e-11	RITGLINDHQ	NLLELEASMKVLAEDASSLGVSLFNMIL	ESVTPSLLTR
11.	30174.m008828_HAM	522	9.99e-11	KITAFVSPSH	DEIELGFTQENLRVFAGEINMPFELEILG	LDALNSGSWS
6.	29646.m001070_HAM	325	9.99e-11	LRITAVVTED	YAIQTQLIKQCLSQYALELKIRFQIEFVL	TRTFEMVSFK
10.	29916.m000544_HAM	576	2.21e-10	ITAFASPSTH	HPVEVLLMRENLTQFANEIGISFELDVIN	FDSLEQSCYS

Motif 8



17.	28650.m000191_LISCL	384	3.82e-34	GGKARAKRQG	NKKEVVDLRTLILCAQAVSSDDRRTANEILKQIRQHSSPF	GDGSQRLAHC
18.	29767.m000200_LISCL	361	2.09e-31	GGKGRGKKHN	GKKEVVDLRTLILISCAQAVAADDRRSAYEMLKQIRQHSSPF	GDGNQRLAHC
16.	28650.m000190_LISCL	431	1.12e-30	GGKTRSKKQS	KKKETVDLRSLILCAQAVSGNDFRTANELVKQIRQHSSPL	GDGSQRLAHC
2.	29692.m000540_DELLA	233	9.91e-28	PTTRPVVLD	SQENGIRLVHLLMACAEAVQQNNLTAEALVKQIGFLAVSQ	AGAMRKVATY
12.	27568.m000253_LISCL	360	1.40e-27	SGKGRGKKQK	GKSNVVDLRTLTLCAQAVAADDRRNTNDLLKQIRQNASPT	GDGMQRMARI
42.	30073.m002204_SCR	447	1.04e-26	EKKEEQRQOK	RDEEGLHLLTLLQCAEAVSADNFEEANKMLLEISQLSTPY	GTSAQRVAAY
1.	28677.m000055_DELLA	193	8.27e-26	EPNRPMLVID	SQETGVRLVHTLLACAEAIQQDNFKLAEALLKHIGLLAASQ	ASSMRKVATY
28.	29949.m000124_PAT1	170	1.31e-25	PEMDIWRQMM	EAISRGDLKHVLIACAKAVSDNDLLMAQWLMDELRLQIVSVS	GEPIQRLGAY
15.	28650.m000189_LISCL	281	3.87e-24	PNNTRMRRHA	KDKKMFDLSTLLIQCAQATGTGDQRTAYQQLKLRILHASPY	GDANQRLAHY
14.	28650.m000187_LISCL	306	4.46e-24	GRTARGRRQG	NKGEVVDLSTLLAQAQSVSISDHRTATELLRQIRQHSSPY	GDGNQRLAHY
13.	28650.m000186_LISCL	281	2.34e-23	RTARTKKRGS	NKRDMMDLWTVLPQCAQAVANDDQTTAKELLRQIKQYSSPF	GDGNQRLAHF
22.	30169.m006306_Os4	159	1.69e-22	MVPSMEEVSY	GVDRGLHLVHLLACAEAVGCRDTQLANSVLAQIIVASVNF	GDSLQRVSYC
20.	29929.m004746_Os4	128	1.69e-22	MISKKNEIKE	EDIDGMKLVQQLIACAEAVACRDKTHASALLSELRANALVF	GTSFQRVASC

Table S2. Cont.

41.	29872.m000537_SCR	70	2.83e-22	AIKEGEEEE	EDSTGLRLLGLLLQCAECVAMDNLDEAADLLPEISELSSPF	GSSFERVGSY
21.	30147.m013794_Os4	147	2.83e-22	SEEGENHGEG	GNTDGMRLVQLLIACAEAVACRDKSHASALLSELRSSALVF	GSSFQRVASC
23.	30131.m007029_Os43	314	2.33e-21	MVPLPIGPEQ	EQDSGLQLVHLLACAEAVAKEDYMLARKYLHHLNRVVTPL	GDSMQRVASC
24.	27529.m000047_PAT1	165	8.67e-21	QARWDWTRME	EMIPRLDTRQILFACAQAISDGDISRAAALMHVLEQMVSVS	GEPIQRLGAY
25.	27613.m000642_PAT1	161	9.75e-21	SEEEKWKFLM	ETVSRDDLKEVLYACAQAIDSNDMLTVEWLMTELKRMVSVS	GEPIQRLGAY
36.	29790.m000809_SCL3	28	1.55e-20	LSSASPSPYE	TQERGIRLIQLLLKCANDASSGNLHRADACLSEISELSSVS	GDSMQRLAAR
40.	28492.m000479_SCR	150	2.46e-20	GASNGRGLSR	IDEHGLNLISLLFECVAIVSDNLGEAHRMELLELTQMASPY	GPSCAERVVA
38.	30131.m007244_SCL3	39	3.88e-20	SPYPWLRELK	SEERGLYLIHLLHACASHVAAGSVENANICLEHISHLASAD	GDTMQRIAAY
43.	29661.m000901_SHR	25	3.53e-19	GFPTSKALGN	NFGDANCMEQLLVHCANAIESNDATLAQQILWVLNNIAPPD	GDSNQRLTCA
27.	29648.m001919_PAT1	181	3.94e-19	SSSTSSNKEV	SQLSPRAPKRLLECANALAEADNIEAADALINELRQMVSQI	GDPSSRIAAY
35.	30076.m004651_Rc_GRAS	252	5.42e-19	FGYALSGLSE	EETRDVELAHLAAAIAEKVGYQQFDRASRLSRCEWIASQR	ANPVQRVVYC
37.	30024.m001746_SCL3	20	1.02e-18	SPYPWLRELK	SEERGLYLIHLLLTGCGNHVAAGSLENAEIALGQISQLASAE	GDTMQRIAAY
45.	29706.m001281_SHR	156	2.88e-18	KGAANNANS	NNKEGRWAEDLLNPCAAAVSTGNLSRVQHLLYVLHELASST	GDANHRLAFY
32.	29889.m003284_Rc_GRAS	186	4.80e-18	FGLFFSDLSD	DESRNVELVELLLASAEKVGYYQFERASRLLNHCELLSSNI	GNPVQRVVYH
5.	30190.m011131_DLT	274	9.68e-18	TEEAAGANHQ	EYQAYELVSLTACVEAIGSKNMAVINHCIAKLGELSSPK	GTAVSRLIAY
33.	29889.m003285_Rc_GRAS	201	3.14e-17	FDLSFGLSV	DEAKKVELAELLLSAEKVGNQYERASILLNQCDRLSSST	GNAVERVVHY
19.	29728.m000844_Os19	75	2.74e-16	KPDQKKKGVV	EDGKGLHLIHLITATAVDENNVATALENLSELYTSVCLT	GDSVQRVVAY
46.	30156.m001710_SHR	39	6.22e-16	SLSGALRGCL	GSLDGACIEKLLHLCASALESNDGTLAQQVMWVLNNVASLV	GDPNQRLTSW
10.	29916.m000544_HAM	418	1.16e-15	EVGGGHQQQQ	QAQHQHALLDQLYKAAELVGTGNFSHAQGILARLNQQLSPI	GKPLHRAAFY
30.	29889.m003281_Rc_GRAS	57	1.39e-15	FDGSQFGLSG	EEIKDVELSLLLASAHRVGNRQFDHASKLLNLCDLSSNK	GNSVQRVVHY
3.	29807.m000482_DELLA	141	1.65e-15	QNQLRVVTAT	EEDSAIRLVHLLMTCAESIQRGDLSLAGSLVEDMQALLTRV	NTNSGIGKVA
34.	29910.m000940_Rc_GRAS	204	1.81e-15	FDLYFGLSD	EDAKHVELAESLLASAERIGNQYDSASRLKQCDSSSNT	GNPVQRVVYY
44.	29661.m000923_SHR	117	7.80e-15	FSFSPSHDLN	FDSSRWATDILLETARAIADKNSARVQQLMWMLNELGSPY	GIDDKKLASY
26.	28166.m001040_PAT1	192	1.19e-14	YHKGIEETGL	QSIPDNLKQLLIACAKALSENINEFDRLIEKARAAVSIS	GEPIQRLGAY
31.	29889.m003282_Rc_GRAS	140	1.16e-13	AGQGLSTEEI	KRQNMWSSLNFFLASAEKVSNGKFDRASRLLEFCQSSSNA	GNPVQRVVYY
7.	29820.m000985_HAM	132	1.85e-13	QSLIMPKECM	GISNLFSLTNLAMAYAEATENKQAALAEVIMRRIGEKVSPI	SGIKERLLYY
29.	30169.m006225_PAT1	237	3.43e-13	PTSSSSSTSV	TTPLPNYSKHTLVEAASAIYDGKTEVASEILTRVSQVSNPR	GNSEQLRMEY
6.	29646.m001070_HAM	164	3.44e-12	SLDLSHNIGN	WSNFGFDLIQELIRAADCIDSSEIQLANVILDRNLHRLQSP	VGKPLQRAAF
11.	30174.m008828_HAM	367	9.98e-12	KQKIMTDELA	AQQLQQAIIINPICQAAELIETGNPALAQGILARLNHQLSLS	IGKPHTRAAF
4.	30170.m013590_DELLA	264	1.75e-8	IDFEYRGFLA	YNLADLDAAMLELRTHEAIAVNAVVFALHKLLARPGDIHKLL	SMVKHIEPEI

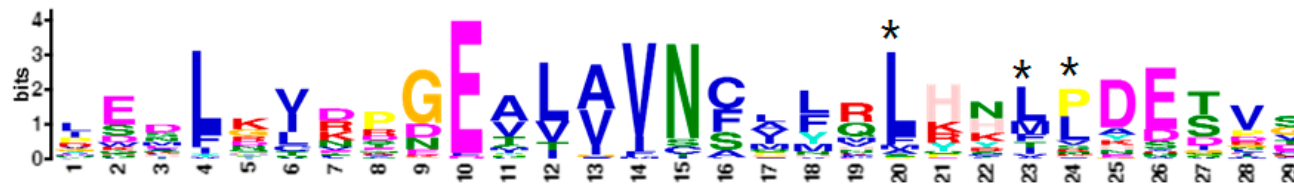
Table S2. Cont.

				Motif 9																	
26.	28166.m001040_PAT1	309	4.58e-21	HSDESVDVSN	PRDGLLRMIKSLNPKVVTLVE	QESNTNTTPF															
28.	29949.m000124_PAT1	397	1.94e-20	LPDESVSTQN	HRDRLRLVKLSLSPKVVTLVE	QESNTNTAAF															
25.	27613.m000642_PAT1	388	1.94e-20	MPDESVGTQN	HRDRLRLVKLSLSPKVVTLVE	QESNTNTAPF															
24.	27529.m000047_PAT1	392	2.05e-18	MPDESVSTWN	HRDRLRLVKLSLSPKVVTLIE	QESNTNTKPF															
27.	29648.m001919_PAT1	408	4.94e-18	MPDESVSTVN	ERDQLLRMVKSLNPKLVTVVE	QDVNTNTAPF															
3.	29807.m000482_DELLA	366	3.50e-17	LLGSDPNRNL	SIDMVLNWRNLPKIMTVVE	QEANHNQPGF															
2.	29692.m000540_DELLA	450	8.14e-16	ELHKLLARPG	AIDKVLVSVKQMKPEIVTIVE	QEANHNGPVF															
29.	30169.m006225_PAT1	463	2.58e-15	MPDESVSTEN	PRDELLRRVKGLAPRVVTLVE	QEMNTNTAPF															
1.	28677.m000055_DELLA	410	8.60e-15	ELHRLLARPG	GMEKVLSSIKAMKPKIVTVVE	QEASHNGPVF															
17.	28650.m000191_LISCL	611	1.91e-14	LLDETVVNS	PRNAVLNLRKMSPDIFIHAI	VNGSYSAPFF															
14.	28650.m000187_LISCL	533	2.98e-14	LPDDTVVANS	ARDAVLKLRKIRPDIFIHGV	INGTYNAPFF															
15.	28650.m000189_LISCL	508	3.70e-14	LPDDTIVLDS	PRDAVLRLIKSNPVIFLHG	VNGSYNAPFF															
18.	29767.m000200_LISCL	587	4.58e-14	LLDETVVDS	PKDIVLRLVKKINPNIFILGI	INGAYSAPFF															
39.	29634.m002156_SCL4/7	454	5.10e-14	LYNLLDETYG	AVETALKMAKSLNPEIVTLGE	YEASLNQIGY															
46.	30156.m001710_SHR	289	2.13e-13	EQKCRAQDSS	LRDTFLHSIKILNPCITVIVD	EDSDLDAPDL															
37.	30024.m001746_SCL3	297	2.13e-13	SSPLSSTASV	KMDYFLNLTWLSLSPKLMVVME	QDSNHNGSSL															
19.	29728.m000844_Os19	301	2.85e-13	SHLNTLNDFL	KIPDTLKSISHLNPSIVILVE	QEGSRSPRSF															
13.	28650.m000186_LISCL	508	5.05e-13	IPDDTMVVNS	MRDSILKLMRRINPDIFIHGV	VNGTYNAPFF															
34.	29910.m000940_Rc_GRAS	430	6.67e-13	LPRNLISLPN	RLDSMMRMKIKNVNPNVIVVAE	VEANHNSPTF															
16.	28650.m000190_LISCL	662	6.67e-13	LLDEIVEVDC	PRNAVLDLIRKIKPNIVVHCI	INGSYNAPFF															
10.	29916.m000544_HAM	641	1.05e-12	PVWSASNQPA	ALPSLLRFVKQLSPKIVVSLD	RGDRDLDLPP															
12.	27568.m000253_LISCL	587	1.26e-12	LLDETVVDES	PRTNVNLNIREMNPVDFITGI	VNGAYNAPFF															
43.	29661.m000901_SHR	289	2.33e-12	ESSSSSSMSS	LRTMFLKSLRSLDPTIVVLVD	EDADLTSNNL															
11.	30174.m008828_HAM	586	2.33e-12	PIAPFSNYP	SLPVVLRVFKQLSPKIVVSLD	RGCDRTDLPP															
23.	30131.m007029_Os43	534	2.54e-12	VNRLHHVPGN	CLPNLLAMIRDQAPNIVTIVE	KEASHNGPYF															
32.	29889.m003284_Rc_GRAS	408	4.22e-12	FLMNLLVAPN	RLESIMGMLRNINPNVMVVME	VEANNNSPSF															

Table S2. Cont.

35.	30076.m004651_Rc_GRAS	476	6.37e-12	FLRTLISPE	CLENLMRVIKNLKPSIMVINE	IEANHNSPNF
22.	30169.m006306_Os4	388	6.92e-12	LHKFVKESRG	SLKAILQAIKRLSPTLLTVVE	QDANHNGPFF
30.	29889.m003281_Rc_GRAS	286	7.50e-12	ILRFIKAQOD	CLQCLLTVLRKLNPCVMVHIE	PVLNHSSPIF
33.	29889.m003285_Rc_GRAS	423	8.13e-12	LLRSLISLPD	RLNSVMKVIRILNPSITVVTE	PEYNSTSSSF
45.	29706.m001281_SHR	394	1.21e-11	LHHLNHNNPD	ERTEFLKVLRSLEPKGVILSE	NNTDRCQICG
21.	30147.m013794_Os4	375	1.31e-11	LHCVVKESRG	ALNSVLQTIHALSPKILALVE	QDSSHNGPFF
38.	30131.m007244_SCL3	318	1.66e-11	LSPLSLAPSP	KMGSFNLALWGLSPKLMVITE	QESNHNGFTL
20.	29929.m004746_Os4	355	2.84e-11	LHCAVKESRG	ALNTVLQILHELSPKLLILVE	QDSGHNGPFF
5.	30190.m011131_DLT	495	2.84e-11	HKTLYDGNNG	ALRDFLGLIRSTSPTIVLMAE	QEAEHNATNL
44.	29661.m000923_SHR	357	3.83e-11	SLHSVTTVAN	RRDYIISNFRRLQPRIITIVE	EEADLDVGDID
36.	29790.m000809_SCL3	264	9.88e-11	NRSTCIKDKC	QMSDFLAMVRSMSPRLLFLVE	QEADHNLNRL
9.	29908.m006159_HAM	333	1.22e-10	LPHFSYRAPD	SVASFSLGSKTLPRLVTLVE	EEVGPVGDGG
6.	29646.m001070_HAM	391	1.61e-10	TFRRLGSSNN	NINSFVTDIRRVSPVVVVVD	NEGWGESEPA

Motif 10



28.	29949.m000124_PAT1	365	1.05e-25	AAAMPNSEVH	IKNLGVEPGEALAVNFAFMLHHLDPDESVS	TQNHRDRLLR
24.	27529.m000047_PAT1	360	2.34e-25	DAAMSGCEVQ	LEHLCVRPGEAVVVNFPYVLHHPDESVS	TWNHRDRLLR
27.	29648.m001919_PAT1	376	4.38e-25	AVASKTSLVS	PSMLDCKAGEALVVNFAFQLHHPDESVS	TVNERDQLLR
25.	27613.m000642_PAT1	356	5.96e-25	AAGVSGSEIE	LKNLGIKIRPGEALAINFALMLHHPDESVD	TQNHRDRLLR
12.	27568.m000253_LISCL	555	1.71e-24	AIAQKWDTVQ	IEQLKIDKNEVLVVNCLYRLRNLLDETIV	VESPRTNVLN
14.	28650.m000187_LISCL	501	1.28e-23	AVAQKWETIK	YEDLNIDRGEMTVVNCLYRLRNLPDDTVV	ANSARDAVLK
17.	28650.m000191_LISCL	579	1.33e-21	AIAKKWETIQ	IDDLKLNHGEEVAVNCLFRSKNLLDETIV	VNSPRNAVLN
13.	28650.m000186_LISCL	476	2.71e-21	SIAQNWESIQ	YEDFKIDRNEMIVVNCLYRLKNIIPDDTMV	VNSMRDSILK
39.	29634.m002156_SCL4/7	425	6.85e-21	PILTPIQELN	ESNFRVDPDEVLA VNFMLQLYNLLDETYG	AVETALKMAK
15.	28650.m000189_LISCL	476	6.93e-20	AIAQKWETIQ	GEDLQIDKDEVVA VCCMNRLKNLPDDTIV	LDSPRDAVLR
16.	28650.m000190_LISCL	630	1.30e-19	IAAQNWENIR	IEELKINSNEVLA VNCARFKNLLDEIVE	VDCPRNAVLD
29.	30169.m006225_PAT1	431	1.97e-19	VVSAKLGDL	RESLGCPEEPLAVNFAFNLYRMPDESVS	TENPRDELLR
5.	30190.m011131_DLT	465	1.95e-18	PVVDRLEDVR	LWMLHVKEGESVA VNCVFQMHKTLVDGNG	GALRDFLGLI

Table S2. Cont.

21.	30147.m013794_Os4	346	4.18e-18	VVESTLENLQ	PDDIKVFDGEVLVVNSILQLHCVVKESRG	ALNSVLQTIH
3.	29807.m000482_DELLA	334	1.16e-17	VAASRLEDVK	PWMLQVNPKEAIVNSIMQLHKLLGSDPN	RNLSIDMVLN
18.	29767.m000200_LISCL	555	1.82e-17	AIAKKWETIK	FEELKIDREEIIVVTCFYRAKNLLDETVV	VDSPKDIVLR
22.	30169.m006306_Os4	359	8.17e-17	LESVTPSLLT	RENLNLRDGEALFFNSIMHLHKFVKESRG	SLKAILQAIK
38.	30131.m007244_SCL3	230	3.73e-16	PIMSKLEDLD	IESLRVKTGEALAVSSVLQLHSLLAADDE	LLKQKSPATK
37.	30024.m001746_SCL3	210	1.47e-15	PIVSKLENLD	IEKLRVKTGEALAISSVLQLHSFLASDDE	LRKRSPVTLK
46.	30156.m001710_SHR	254	3.49e-15	HFESLLNHL	PSALNLRDDEALVINCQNWLRYLSNEQKC	RAQDSSLRDT
9.	29908.m006159_HAM	304	5.53e-15	CRLDSEDFR	PSALKLVRGEALIMNCMLHLPFHSYRAPD	SVASFLSGSK
20.	29929.m004746_Os4	326	1.83e-14	WVESSELEKL	STDFKLLDGEVVIINSILQLHCAVKESRG	ALNTVLQILH
43.	29661.m000901_SHR	236	1.27e-13	FSSLIEQLRV	QNLVYTDSGEALVINCHMLPHYIPEETLS	GIHNTTSSN
36.	29790.m000809_SCL3	218	2.06e-13	PLNISLRDLT	ADMLQVASGEALAFISILNLHLLAEDDR	VDAHFGGNRS
45.	29706.m001281_SHR	365	3.07e-12	LDNHPLQSLN	AQVINTNPEDTLVVCAQFRLHHLNHNNPD	ERTEFLKVL

Motif 11



15.	28650.m000189_LISCL	69	4.51e-33	YNSETSNFSQ	AVLKYISDMLMEEDLEDKPCMLQDCLA	LQAAEKSLYD
14.	28650.m000187_LISCL	77	1.29e-31	SSEGHPN	AVLKYISDMLMEEDLEGKTCMLQDCLA	LQAAEKSLYD
17.	28650.m000191_LISCL	84	1.86e-30	SPSDDNDFSE	TVLNYSQMLMEEDMEQKPCMFHDPLA	LQAAERSLYD
18.	29767.m000200_LISCL	82	1.02e-29	DSPEDCDFSD	TVLRYSQMLMEEDIEDKTCMLQDSDL	LQAAEKSFYD
12.	27568.m000253_LISCL	80	2.35e-28	DLHEDFDFSD	VVLKYISDMLMEEDIEEKTCTMFQESSA	ALQAAEKSLY
16.	28650.m000190_LISCL	111	2.01e-27	SPSDDSDSSD	PVLKYISQMLMEENMEDKPPMYDPLD	LKATEKSLYD
13.	28650.m000186_LISCL	82	1.01e-25	DSPDNDISN	VVLKYISDMLMEEELSKNFMFEDCLA	LQAAEKSFYD

Table S2. Cont.

Motif 12



25.	27613.m000642_PAT1	441	9.53e-15	AIFESIDVTL	PRGHKERINVEQHCL	AREVVNIVAC
28.	29949.m000124_PAT1	450	1.15e-14	AMFESIDVTL	SREHKERINVEQHCL	ARDVVNIAC
27.	29648.m001919_PAT1	461	3.94e-14	AVFESLDATL	PRESQDRMNVEKQCL	ARDIVNIVAC
24.	27529.m000047_PAT1	445	4.96e-12	AMFESIDAGS	SRDDKQRINAEQHCV	ARDIVNMIAC
13.	28650.m000186_LISCL	561	6.38e-12	ALFDMIDSTI	PREEPERMMFEKEVF	GRYAVNVIAC
26.	28166.m001040_PAT1	362	7.22e-12	AMFESIDVRL	PRERKDRIGVEQHCL	AKDIVNIAC
17.	28650.m000191_LISCL	664	9.24e-12	ALFDMFDTNM	SREDQMRLKFEKEYF	GREALNVIAC
22.	30169.m006306_Os4	442	1.18e-11	IFDSLEASLL	PRNSRQRMKIEKLHF	AEEIRNIVAY
18.	29767.m000200_LISCL	640	1.18e-11	SLFDMLDIV	PREDMERMLIEKEII	GREALNVVAC
37.	30024.m001746_SCL3	350	1.68e-11	ALFDCLESTV	SRTSLERLKVEMLF	GEEIKNIISC
12.	27568.m000253_LISCL	640	1.89e-11	TLFDMLETNV	PREIPERMLIEREIF	GWEAKNVIAC
14.	28650.m000187_LISCL	586	3.76e-11	ALFDMFEINV	PREDDQRMLYEKAIF	GRDIMNVIAC
23.	30131.m007029_Os43	587	1.37e-10	AIFDSLDATE	PPDSTQRAKVEQYIF	APEIRNIVAC
39.	29634.m002156_SCL4/7	507	5.49e-10	AVFESLEPNL	SRDSTERLQVERLLL	GRRIAGAVGP
21.	30147.m013794_Os4	428	5.49e-10	AIFDSLDAAML	PRYDTRRAKMEQFYF	AEEIKNIVSC
15.	28650.m000189_LISCL	561	6.63e-10	SLFDMFEAIA	TREDQERLVFERELI	GKDVMNVVAC
16.	28650.m000190_LISCL	715	7.99e-10	SLFDMFDSTL	SREDQGRMMLENEIY	GREAMNVVAC
38.	30131.m007244_SCL3	371	9.61e-10	ALFDCLESTV	SRPSIERQKVEKMLL	GEEIKNIAC
29.	30169.m006225_PAT1	516	1.15e-9	ALFESIESTV	QRDHTERVKVEEGLG	RKLANSVACE
20.	29929.m004746_Os4	408	1.51e-9	AIFDSLDTML	PKYDTRKRVKIEQFFY	GEEIKNIVSC
42.	30073.m002204_SCR	715	1.80e-9	ALFDSLGAZY	GESEERHVVEQQLL	SREIRNVLAV
34.	29910.m000940_Rc_GRAS	483	2.15e-9	AYFDCLDACM	ERNDKNRMIMESMYF	GIGIKNMIAT
41.	29872.m000537_SCR	341	3.92e-9	ALFDALGDGL	GIDSVERHTVEQQLF	GCEIRNIVAV
43.	29661.m000901_SHR	342	1.23e-8	IPYDVTDTFL	PRGSKQRQWYEADIC	WKIENVIAHE

Table S2. Cont.

32.	29889.m003284_Rc_GRAS	461	1.55e-8	AYFDCFDACM	ERDDPNRMAAESVFF	HHGIRNIVAS
44.	29661.m000923_SHR	414	2.85e-8	VYFESLEESF	SRTSNERLMLERSAG	RAIVDLVACQ
19.	29728.m000844_Os19	354	3.07e-8	AMYDSLDDCL	PLESSERLSIEKNHL	GKEIKSMLNY
5.	30190.m011131_DLT	548	3.07e-8	AIFDSINTSL	PLDSLVRIKIEEMFA	REIRNIVACE
46.	30156.m001710_SHR	342	3.56e-8	IPFDALETFL	PTDSCQRIEYESDIG	HKIENIISYE
40.	28492.m000479_SCR	414	3.83e-8	TLFDSLGAFL	PCDDSSRHRVEHCLL	YREINNVLAI
45.	29706.m001281_SHR	450	4.43e-8	FLDSTSSAFK	GRESEERRVMEGEAA	KALINCGEMN
9.	29908.m006159_HAM	387	2.48e-7	ALYDSLEAGF	PMQSRARALVERVFL	GPRIAGSLDR
33.	29889.m003285_Rc_GRAS	475	4.43e-7	SAYFDCLESC	MKDNSNRMILESLHF	GEGIKNIVAT

Motif 13



2.	29692.m000540_DELLA	551	1.22e-19	TRLGLAGFAP	VHLGSNAFKQASMLLALFAGG	DGYRVDENNG
1.	28677.m000055_DELLA	514	1.22e-19	TRFESAGFDR	VHLGSNAFKQASMLLALFAGG	DGYRVEENNG
39.	29634.m002156_SCL4/7	559	4.62e-16	ILMESC GFES	VALSHYAMSQAKILLWYNYS	SLYSLVESQP
23.	30131.m007029_Os43	638	1.61e-15	KLMGKGFKG	VPLSANAVTQSKILLGLYSCD	GYRLTEDKGC
42.	30073.m002204_SCR	765	5.29e-15	EKLRSQGFKG	ISLAGNAATQATLLLGMFSPD	GYTLVEDNGT
41.	29872.m000537_SCR	391	6.52e-15	NELRRAGFQP	VSLGGNPAAQASLLLGMFPWK	GYTLVEEENG
3.	29807.m000482_DELLA	467	1.09e-14	SRLTAAGFMP	LHLGSNAFKQASMLLTLFSSE	GYCVEENDGC
37.	30024.m001746_SCL3	401	4.79e-14	QRDLAGFGN	VPLSYCGLLQARRLLQGYGCD	GYRIKDENG
38.	30131.m007244_SCL3	422	5.27e-14	LRLELAGFGR	VPLSYHGMQLQASRLLQSYGYD	GYKIKEENG
32.	29889.m003284_Rc_GRAS	512	5.27e-14	SFFARFGMIQ	TELSTSSLYQASLVLKKFPCG	SSCTLDVNEK
9.	29908.m006159_HAM	436	3.29e-13	EWSSGAGFRP	VNISFANHCAKLLLGLFNDG	YRVEELGCNR
33.	29889.m003285_Rc_GRAS	526	4.68e-13	AFFTRFGMLE	TELSTSSLCQAKLIKKFACG	NACTLSMDGK
34.	29910.m000940_Rc_GRAS	534	1.01e-12	AFFARFGMVE	TDLSSALLQANLIVKKFACG	NCFTLDRNGK
35.	30076.m004651_Rc_GRAS	579	1.67e-12	AFFSRFRMVE	IGFSESALYQASLVCKQFACG	SSCSLDKNGK
30.	29889.m003281_Rc_GRAS	389	2.51e-12	DYFIRFGMVE	TQVSMSSFYQAEMLKNFASG	KSCLLVRNGK
40.	28492.m000479_SCR	466	2.72e-12	LAARSTFMQ	VPMSGNSMAQAQLILNMFPPA	HGYSLAQGEG
5.	30190.m011131_DLT	598	1.04e-11	KLMEQGGFRC	MGISEREVLQSQMLLKMYSC	DYRVKERQDR
19.	29728.m000844_Os19	407	1.34e-10	GRMENHGFSG	MKLSSKSLIQAKLLLKIRTHH	SPPQFNGENS
43.	29661.m000901_SHR	392	3.43e-8	QRMRNANFRS	ISFGEEAVSEVKTMLGEHAAG	WGLKKEEDDL

Table S2. Cont.

Motif 14



5.	30190.m011131_DLT	420	1.12e-10	SLASRTNPPS	HVRITGIG	ESKQELNETG
38.	30131.m007244_SCL3	185	3.65e-10	TLSARPEGPP	HLRITGIH	EQKEVLEQMA
37.	30024.m001746_SCL3	165	3.65e-10	ALSARREGPP	HLRITGIH	QQKEVLDQMA
12.	27568.m000253_LISCL	504	9.99e-10	RLSSRPGGPP	KLRITGID	FPHPGFRPAE
17.	28650.m000191_LISCL	528	1.47e-9	RLSKREGGPP	KLRITGIE	LPQSGFRPGE
16.	28650.m000190_LISCL	578	1.47e-9	L LSMRDGGPP	KLRITGIE	LPQQGFRPAE
14.	28650.m000187_LISCL	450	1.47e-9	RLSQRPGGPP	KLRITGIE	LPQPGFRPAE
15.	28650.m000189_LISCL	425	2.60e-9	HLSTRPGGPP	KVRITGID	YPQPGFRPGE
27.	29648.m001919_PAT1	325	6.99e-9	TLANQPGKPP	HLRLTGID	DPESVQRSTG
28.	29949.m000124_PAT1	314	7.58e-9	AFAARPGGPP	RIRITGID	DSTSAYARGG
34.	29910.m000940_Rc_GRAS	355	1.00e-8	LVSRCDCPLE	HLKITAIG	TTSRELIENT
25.	27613.m000642_PAT1	305	1.53e-8	ALAARPGGPP	HVRLTGID	DSTSAYARGG
20.	29929.m004746_Os4	281	3.09e-8	LANRPDKKPR	CLRITGVG	NSAERLQALG
3.	29807.m000482_DELLA	284	4.33e-8	ALALRPGGPP	LLRLTGIG	PPSPDGRDSL
23.	30131.m007029_Os43	463	4.92e-8	ALAARPGGAP	FLRITGVG	SCIESVRETG
21.	30147.m013794_Os4	301	6.74e-8	LANRAGKPPC	RLRITAVG	LCVGRFQTIG
19.	29728.m000844_Os19	229	6.74e-8	SEKASSNRI	SLRITGLG	RSLEELQETE
24.	27529.m000047_PAT1	309	1.83e-7	ALADRPGGPP	AIRITGVD	DPQSAYARGG
2.	29692.m000540_DELLA	370	2.04e-7	ALALRPGGPP	AFRLTGIG	PPSHDNSDHL
1.	28677.m000055_DELLA	330	2.04e-7	ALALRPGGPP	AFRLTGIG	PPQSNNTDAL
4.	30170.m013590_DELLA	221	2.44e-7	DLAARPGGPP	TIRISGIG	FPNHDNSDYL
13.	28650.m000186_LISCL	425	2.92e-7	DLSTRHGGPP	RLHITGIE	FPQPGFRPAE
44.	29661.m000923_SHR	264	5.36e-7	ALATRTDETP	HLRLTTIV	ASKTNGGGGG
33.	29889.m003285_Rc_GRAS	348	6.32e-7	LVSDFDCNLE	LLKITAVG	TTSKHLIKDT

Table S2. Cont.

6.	29646.m001070_HAM	314	6.90e-7	DHFCNKLTSP	VLRTAVV	TEDYAIQTQL
9.	29908.m006159_HAM	251	7.43e-7	VSRKDGPTTP	HLRITALS	RGGNSGKRSI
41.	29872.m000537_SCR	217	8.06e-7	ILASRSKKIR	SMRITGFG	SSSELLESTG
40.	28492.m000479_SCR	291	8.06e-7	ILATRMEGPP	HIRMTGMG	TSMDLLVETG
22.	30169.m006306_Os4	309	8.74e-7	TLASRPEGPP	KVRITGLI	NDHQNLLELE
39.	29634.m002156_SCL4/7	374	1.03e-6	LATRSAGRPL	SIRISGIP	APVLGKSPAA
7.	29820.m000985_HAM	280	1.10e-6	GYNQRHLQOI	TLKITAIK	WREEHPWRKL
31.	29889.m003282_Rc_GRAS	252	1.50e-6	ENVAEANRSH	LLKITAVE	TTSKHLIEET
42.	30073.m002204_SCR	592	1.74e-6	ILASRPGGPP	YVRTLGLG	TSIEALEATG
45.	29706.m001281_SHR	306	1.86e-6	LTRRSGGPPP	LVRITVIT	ATVESDQNTE
35.	30076.m004651_Rc_GRAS	400	2.01e-6	LAERQQRPLE	HLKVITALG	LTGKGGKIEE
30.	29889.m003281_Rc_GRAS	210	2.49e-6	LANRQECPIE	LLKISGVG	VKASRQRIED
29.	30169.m006225_PAT1	382	3.78e-6	LSERLNGKPA	TVKITAVA	DNSAEKERL
11.	30174.m008828_HAM	510	5.30e-6	ELALRNGGVS	SLKITAFV	SPSHDEIELG
46.	30156.m001710_SHR	184	3.18e-5	ALAKRPEGPP	SLRITVPF	TRPQVPPWLN
8.	29820.m000986_HAM	481	4.24e-5	ETVKEKQSLY	KVRIGGEW	NNEMILEWRG
32.	29889.m003284_Rc_GRAS	150	1.38e-4	GSSRGLSTEE	VIRIAGAR	FIQSCWQAVD

Motif 15



2.	29692.m000540_DELLA	54	5.80e-46	IWEDEEAKGD	GGMDELLAVLGYKVRSSDMAEVAQKLEQLEEVMGNVQED	GLCQLASETV
1.	28677.m000055_DELLA	37	5.73e-44	EEEEQQQDQD	GGMDELLAVLGYKVRSSDMAEVAQKLEQLEMVMGIAQED	GISHLSDTVH
3.	29807.m000482_DELLA	27	1.37e-27	SSSSITNKP	PEIDNLLAGAGYKVRSSDLRHVAQRLELETAMLNSPSS	HLSVLASDTV

Table S2. Cont.

Motif 16



28.	29949.m000124_PAT1	234	1.06e-19	GLVARLASSG	SSIYKSLRCKEPASADLLSYM	HILYEVCYPF
18.	29767.m000200_LISCL	425	1.34e-18	GLDARLAGTG	SQIYKGLVSKRTSAANVLKAY	HLILAACPFR
25.	27613.m000642_PAT1	225	1.96e-18	GLVARLASSG	SSIYRALRCKEPASAEELLSYM	HILYEVCYPF
12.	27568.m000253_LISCL	424	4.09e-18	GLEARMAGSG	TQIYKAFMSRPTTAADVKAH	HLFLAACPFR
17.	28650.m000191_LISCL	448	4.59e-17	GLEARLAGTG	AQIYTALSSEKLSAADMLKAY	LAYISACPFN
27.	29648.m001919_PAT1	245	3.41e-16	GLAARMAASG	KYLYKALKCKEPPSSDRLAAM	QILFEICPCF
26.	28166.m001040_PAT1	256	5.11e-16	GLVARKESSG	NNIYHALRCREPESKDLLSYM	QILYEICPYL
24.	27529.m000047_PAT1	229	3.21e-15	GLRARVELSG	SKIYRALKCEAPVSSDLMTYM	GILFKICPYW
16.	28650.m000190_LISCL	498	3.62e-14	ARLAGSVTGM	QSFYTSLASRRRRTAADILRAY	KTHLHACPFK
14.	28650.m000187_LISCL	370	3.37e-13	ALETRLAGTG	TPAYSPLSSKTPVSDILKAY	QVYVKACPFK
13.	28650.m000186_LISCL	345	2.49e-12	GLEARLAGTG	TPGYAPAVNSTTSAAGMLKAY	HAYTTACPFQ

Motif 17



16.	28650.m000190_LISCL	278	2.77e-38	GDGIMGSSPS	EMVQNMFSDTDSVLQFKRGLEEASKFLPRASQLVIDLE	SNSFANGQKE
17.	28650.m000191_LISCL	230	1.95e-31	HDVMGSFESK	IVVPNFFSERELALQFQRGVEEANRFLPKENQLVIDLE	TNASIPEMKE
12.	27568.m000253_LISCL	211	4.65e-28	AADGLVDSPL	STISEIFSDSESIHQFKKGFEASKFLPNGSLFIDLES	TGLFLKDLRE
18.	29767.m000200_LISCL	206	9.34e-27	DGLVHSPNST	FPVPHWNNESQSIHQFIKGVVEASKFLPNGDDLFRNIE	VNRFLEKPK

Table S2. Cont.

Motif 18



15.	28650.m000189_LISCL	97	3.50e-20	PCMLQDCLAL	QAAEKSLYDVLGEKYP	PICDQSPSSI
13.	28650.m000186_LISCL	110	8.30e-20	NFMFEDCLAL	QAAEKSFYDVLGQKYP	ASLDQSPFLD
18.	29767.m000200_LISCL	110	1.06e-19	TCMLQDSL DL	QAAEKSFYEV LGKKYP	PSPEPKR VSI
17.	28650.m000191_LISCL	112	2.48e-19	PCMFHDPLAL	QAAERSLYDVLGEKYP	SSPNQSSSFG
14.	28650.m000187_LISCL	105	1.44e-18	TCMLQDCLAL	QAAEKSLYDVLGQEYP	HLSHCPQIV
12.	27568.m000253_LISCL	109	2.73e-18	CMFQESSAAL	QAAEKSLYELIGEKYP	PSINYDSA AH
16.	28650.m000190_LISCL	139	2.98e-15	PPMYDPLDL	KATEKSLYDVLGEQDP	SSLESPQYI

Motif 19



	Name	Start	P-Value	Sites		
2.	29692.m000540_DELLA	97	6.38e-30	GNVQEDGLCQ	LASETVHYNPSDLSTWLESMLSELNPN	PNFDPSQQPD
1.	28677.m000055_DELLA	79	1.18e-29	MGIAQEDGIS	HLSDTVHYNPSDLSGWVQSMLSELNPN	LDTIQNQDS
3.	29807.m000482_DELLA	70	1.20e-23	LNSPSSHLSV	LASDTVLYNPSDLSSWVDSLLETFNQS	QPLPSLPPDL

Table S2. Cont.

Motif 20



16.	28650.m000190_LISCL	784	3.86e-15	EKCRHKLKTW	YHKDFVIDEDN	NWMLQGWKGR
12.	27568.m000253_LISCL	709	1.43e-14	AAAKEKVNAL	YHKDFVIDEDS	RWLLQGWKGR
14.	28650.m000187_LISCL	655	6.70e-14	KKVRCTVRSE	YHKDFVVDENG	RWMLQGWKGR
15.	28650.m000189_LISCL	629	1.72e-13	VKRVRNIKND	YHKDFAVDEDG	HWMLMGWKGR
17.	28650.m000191_LISCL	733	1.54e-12	KKLKCRVKEG	YHNDFVVDQDG	QWMLQGWKGR
13.	28650.m000186_LISCL	630	4.07e-11	KKVITTVKSN	YKNFIVDEDS	QWMLQGWKGR
18.	29767.m000200_LISCL	709	4.78e-11	KQAIEKVRKL	YHKNFLINEDG	RWLLQGWKGR

Table S3. Information of all primers used in this study.

Gene Name	Forward (from 5' to 3')	Reverse (from 5' to 3')
28677.m000055	TCAAAAGCTTGAACAGCTTGAA	ACCAGGAATGGCTCTAAGATCA
29692.m000540	GGTTGGAAATTGGCTCAGTTAG	CGTTCTTGCTCAACGATAGTA
29807.m000482	CATTTGTTGATGACATGTGCTG	GGACACGCCTCATAAAAGTGAT
30170.m013590	TTTCGGATTTAGCCAAGTCAAT	AAATATTGGGGGTAGAGCCTGT
30190.m011131	CAGGCTCCTTCTCTCTGACAT	TCCACAACATTCTCACTTGGTC
29646.m001070	GAGGATTCCACTCCTACGCTAA	CTGCTCGGATAAGCTCTTGAAT
29820.m000985	TGGCTCTTCTCAACAACAAAA	AGGCTAGCCATTCTTTTCTTCC
29820.m000986	CGGTCTCAAATTAAGGTGGAG	CATCCCCATCTCCAAAAGTAAG
29908.m006159	ACTTGCAACTCAAACCCAAACT	TTGCAAGGCGTCAGTAAAATAA
29916.m000544	AAGAAAGGATGAATGGGCTACA	ATCTACAATCCCTAACCCAGCA
30174.m008828	CCTTGAATTCTGGTTCTTGGTC	GCTTCCAGTGATTCAAGTAGGC
27568.m000253	TAGCACAGAAGTGGGACACAGT	AGTAGTGGAAAACAGCCTCTCG
28650.m000186	ATTAGCACATTTCTTCGCCAAT	AGGCCATTGAAAACCATAAAGA
28650.m000187	ACAATGCACCATTCTTTGTCAC	TGATCTAGTGAGAGCTGCCTGA
28650.m000189	ATCTGCAGCCTTTTAGATCGAG	AGAAGAAGGGGATTGATCACAA
28650.m000190	ATCAAATGGTGGAAAGACTCGT	TAAAAGCTTTGCATTCCAGTGA
28650.m000191	AGGTGGTTGTGAAGGAAGAGAA	TGTAGTGCCTTGTTTGATCCAC
29767.m000200	TCGTAACATTGAGGTCAACAGG	TTACCCTCCCCAGCACTATAAA
29728.m000844	TGGCAATCGTTGATACAGATTC	AGCTGTGGCTACATTGTTCTCA
29929.m004746	ATCGAAGCTATGGAAGAAGCAG	AAGTAGCGTAAGCCGATCAGAC
30147.m013794	CGAGCTCTAAGTTTCGCAGAAT	TCTCCATGATTTTCACCTTCT
30169.m006306	AATCCTCCAAGCAATCAAGAGA	GCCTCTCAATCCTATCACAACC
30131.m007029	AGCTGGATGGAGATGTTGAAGT	TGGACTCTGTCCTTCCCTTTA
27529.m000047	GAGCAAATGGTGTGAGTCTCTG	AATCCTAGGCTCGTATTCCACA
27613.m000642	AGGATGGATCCAATCAAATCAC	AGAACTTCTGAAGATGCCAAC
28166.m001040	TCCACCAGACAATCTAAAGCAA	TCTGCATGTACGAAAGCAAATC
29648.m001919	GTGAATTTTGCTTCCAACCTCC	TTTCAACATTCATCCTGTCTG
29949.m000124	GCATTTCGTATTACAGGCATTGA	TGGTTCTGAGTGCTGACACTTT
30169.m006225	TGTTTGCCAAAGAACATATTGC	TATTATCCGCAACAGCTGTGAT
29889.m003281	TTTTGAGCACATGAAGATGGAC	TCTTGGTGCAATCTTCTTTGA
29889.m003282	CAAGCTGCTGAAATTCAAAATG	ACTGATCACAAAACCTCGAGCAA
29889.m003284	TTCCTGCAATCCAAGAAATTG	TGACTGCCCTAAAAGAGAAAGG
29889.m003285	TGACTGCAATCTGGAGCTTTTA	AGAATTTAGCCTATCGGGCAGT
29910.m000940	TTTGCTGAAGCTCTCCATGATA	GTCCATTGCATTCCATATCTGA
30076.m004651	TATGTTCTGAATATGGCGCTTG	GTTGAGCAGCTCCAAAGAAGAT
29790.m000809	TGGGAAGTGAAGATAGGATGGT	CATGCCAACAAATCATCAAACCT
30024.m001746	ACTTGTGGAAATCATGTTGCTG	TCAAGAATGGAAACATCTCGAA
30131.m007244	GCCTTGAGCATATCTCTCACCT	ATTGCTTCTACAATGGCCTGAT
29634.m002156	GTGAACATGGAGATCCAACCTGA	AACGATCCCAAAATCCACTATG
28492.m000479	TGTTTCACATCCTGGCTACAAG	CCTGTTGCATCGTACAGTGAAT
29872.m000537	GAGACTCCTCGGTCTTTTGCTA	GGAAAGCGTTGAAGATTTTCTG
30073.m002204	AGCTACTTTGCTTCTTGGGATG	TCAACAAAATGGTATTGGCAAG
29661.m000901	CCACAAACTCATCAAATCCGTA	TCATACCATTGTCTTTGCTTGC
29661.m000923	TGTGGATGCTTAATGAACTTGG	TCAAATGCTTCCATTATTGCAC
29706.m001281	ATGAGGTTAGTCCTTGGTTTGC	ACTGAAAATGGGGTCTCAGTGT
30156.m001710	TCTTGGTAGTCTTGATGGAGCA	ACTCATTGCTCCTTTGGATA