



Figure S1. Motif organizations of FexLEA proteins

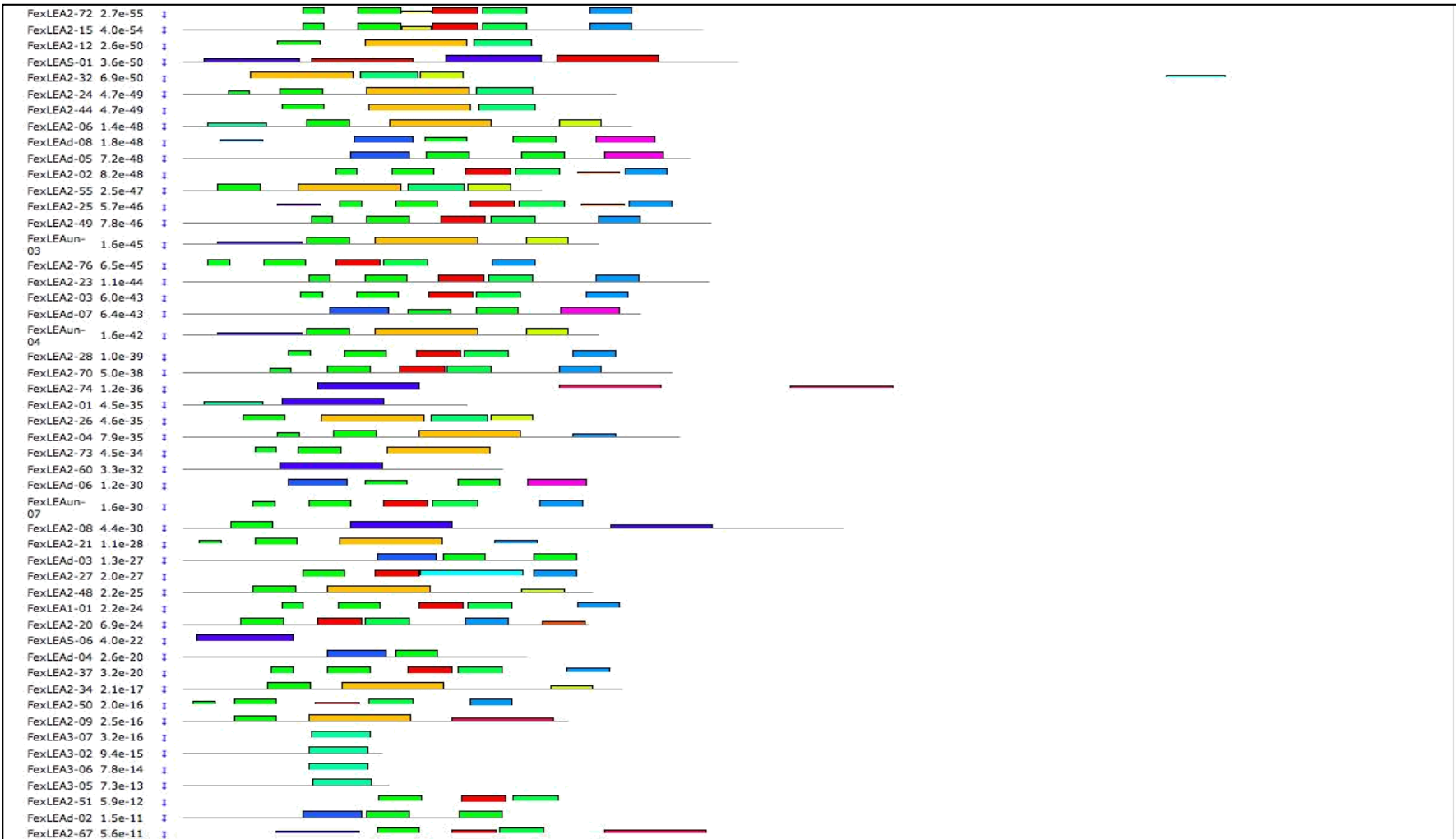


Figure S1. (continued)

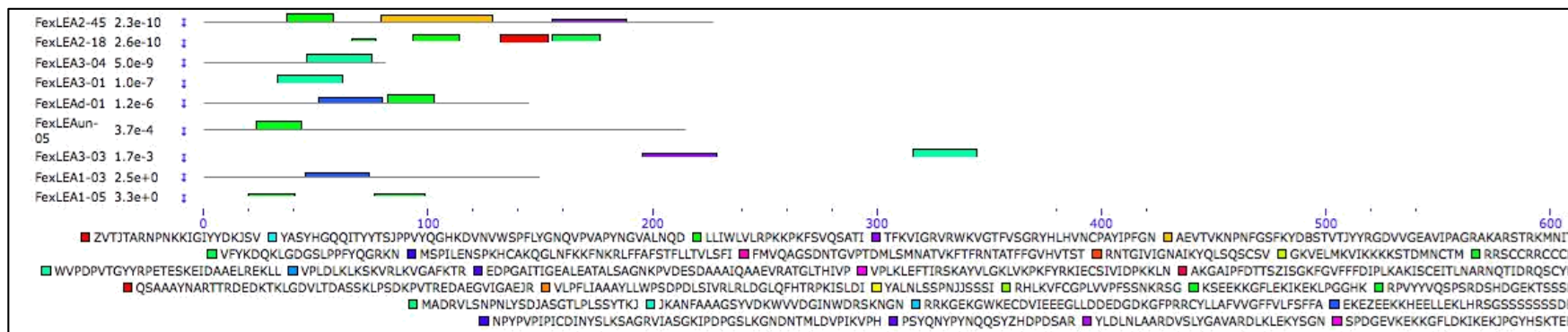


Figure S1. (continued)

Table S1. A list of FexLEA proteins

ID	Ash Tree Genomes Identifier	Physical position on cucumber genome			Protein length (aa)	pI	Molecular weight (Da)	Instability index	Stable or unstable
		Contig	Start position (bp)	End Position (bp)					
FexLEA1-01	FRAEX38873 v2 000000570.1	1	152297	154795	247	9.79	27808.69	35.09	stable
FexLEA1-02	FRAEX38873 v2 000144560.1	273	338087	338975	161	9.33	16755.19	9.53	stable
FexLEA1-03	FRAEX38873 v2 000321830.1	674	8484	9605	150	9.19	15780.38	39.49	stable
FexLEA1-04	FRAEX38873 v2 000070910.1	1751	3909	5472	164	9.62	17449.39	26.07	stable
FexLEA1-05	FRAEX38873 v2 000127010.1	2472	89938	90745	137	7.11	14765.46	27.28	stable
FexLEA1-06	FRAEX38873 v2 000110540.1	22507	1496	2290	124	9.3	13672.4	38.2	stable
FexLEA2-01	FRAEX38873 v2 000000660.1	1	385059	387435	138		14912.13	7.35	stable
FexLEA2-02	FRAEX38873 v2 000231120.1	43	36986	38107	268		29809.89	50.29	unstable
FexLEA2-03	FRAEX38873 v2 000312860.1	64	80639	81950	260		28373.4	31.98	stable
FexLEA2-04	FRAEX38873 v2 000315600.1	65	191305	194598	241		25692.71	38.43	stable
FexLEA2-05	FRAEX38873 v2 000367250.1	85	133766	135236	310		34279.12	55.85	unstable
FexLEA2-06	FRAEX38873 v2 000109800.1	224	50627	51545	218		24614.52	38.06	stable

Table S1. (continued)

ID	Ash Tree Genomes Identifier	Physical position on cucumber genome			Protein length (aa)	pI	Molecular weight (Da)	Instability index	Stable or unstable
		Contig	Start position (bp)	End Position (bp)					
FexLEA2-07	FRAEX38873 v2 000115700.1	232	45000	47235	260		28895.86	41.37	unstable
FexLEA2-08	FRAEX38873 v2 000119960.1	238	142593	146950	320		35775.77	24.35	stable
FexLEA2-09	FRAEX38873 v2 000150200.1	281	143009	144049	187		20548.74	45.5	unstable
FexLEA2-10	FRAEX38873 v2 000210370.1	386	219437	220345	210		23706.6	38.62	stable
FexLEA2-11	FRAEX38873 v2 000210380.1	386	224061	230005	250		28149.94	36.85	stable
FexLEA2-12	FRAEX38873 v2 000223550.1	413	223908	224665	209		23046.78	35.31	stable
FexLEA2-13	FRAEX38873 v2 000234330.1	439	110622	111705	209		23694.55	39.05	stable
FexLEA2-14	FRAEX38873 v2 000234340.1	439	136352	137131	259		28787.7	40.77	unstable
FexLEA2-15	FRAEX38873 v2 000235720.1	442	154985	156129	252		28594.45	41.84	unstable
FexLEA2-16	FRAEX38873 v2 000243000.1	459	112202	113987	306		33551.51	46.54	unstable
FexLEA2-17	FRAEX38873 v2 000243900.1	461	91187	92115	210		23776.74	44.26	unstable
FexLEA2-18	FRAEX38873 v2 000286320.1	566	71120	72605	262		28916.28	38.19	stable
FexLEA2-19	FRAEX38873 v2 000309590.1	630	7676	8500	230		25506.49	38.63	stable
FexLEA2-20	FRAEX38873 v2 000330840.1	705	158076	159051	197		22479.9	22.53	stable
FexLEA2-21	FRAEX38873 v2 000349120.1	778	17095	23074	186		20398.83	36.32	stable
FexLEA2-22	FRAEX38873 v2 000376360.1	886	81465	82515	209		23580.31	41.83	unstable
FexLEA2-23	FRAEX38873 v2 000019040.1	1151	60911	61975	255		28528.6	34.58	stable
FexLEA2-24	FRAEX38873 v2 000024290.1	1209	97204	98490	210	10.01	23541.72	43.55	unstable
FexLEA2-25	FRAEX38873 v2 000038560.1	1360	66507	69445	274	9.56	30347.24	48.73	unstable
FexLEA2-26	FRAEX38873 v2 000045440.1	1437	48209	49055	189	8.88	20674.07	13.42	stable
FexLEA2-27	FRAEX38873 v2 000045480.1	1437	104656	105885	223	9.82	25358.24	36.1	stable
FexLEA2-28	FRAEX38873 v2 000052410.1	1519	34646	35680	254	10.14	27787.51	42.29	unstable
FexLEA2-29	FRAEX38873 v2 000061130.1	1631	47104	48326	209	9.44	23374.95	41.18	unstable
FexLEA2-30	FRAEX38873 v2 000069070.1	1729	13750	14818	208	9.84	23457.43	48.23	unstable
FexLEA2-31	FRAEX38873 v2 000078160.1	1839	1612	3035	256	9.22	28843.8	40.79	unstable
FexLEA2-32	FRAEX38873 v2 000082780.2	1892	29649	42335	611	6.01	68378.62	33.25	stable

Table S1. (continued)

ID	Ash Tree Genomes Identifier	Physical position on cucumber genome			Protein length (aa)	pI	Molecular weight (Da)	Instability index	Stable or unstable
		Contig	Start position (bp)	End Position (bp)					
FexLEA2-33	FRAEX38873 v2_000085440.1	1922	40087	41445	387	10.05	43255.32	28.72	stable
FexLEA2-34	FRAEX38873 v2_000090490.1	1996	108967	110165	213	8.99	23093.5	26.55	stable
FexLEA2-35	FRAEX38873 v2_000111290.1	2262	13425	14521	209	9.95	23442.24	36.85	stable
FexLEA2-36	FRAEX38873 v2_000112340.1	2277	63857	64685	207	9.12	23374.12	41.61	unstable
FexLEA2-37	FRAEX38873 v2_000114740.1	2308	146239	147095	238	9.1	26205.41	37.72	stable
FexLEA2-38	FRAEX38873 v2_000125350.1	2455	18538	19714	222	10.24	24501.94	46.09	unstable
FexLEA2-39	FRAEX38873 v2_000131310.1	2532	7076	9394	341	9.12	38068.57	47.92	unstable
FexLEA2-40	FRAEX38873 v2_000138150.1	2623	61905	63119	193	9.87	21830.6	27.22	stable
FexLEA2-41	FRAEX38873 v2_000146360.1	2759	63972	65920	323	9.82	35541.52	50.37	unstable
FexLEA2-42	FRAEX38873 v2_000149100.1	2795	110384	119485	545	9.33	60839.84	44.66	unstable
FexLEA2-43	FRAEX38873 v2_000154030.1	2868	17660	19987	366	9.61	40470.87	61.85	unstable
FexLEA2-44	FRAEX38873 v2_000159850.1	2951	33940	35245	211	9.63	23520.64	34.19	stable
FexLEA2-45	FRAEX38873 v2_000166330.1	3065	40415	41405	227	9.68	25319.9	36.93	stable
FexLEA2-46	FRAEX38873 v2_000167080.1	3082	25891	33539	258	8.5	29458.93	57.26	unstable
FexLEA2-47	FRAEX38873 v2_000168520.1	3112	40687	44155	287	9.36	32235.6	65.44	unstable
FexLEA2-48	FRAEX38873 v2_000176740.1	3240	45523	46567	199	9.58	21709.25	31.77	stable
FexLEA2-49	FRAEX38873 v2_000201720.1	3690	25688	26765	256	9.76	28638.7	38.03	stable
FexLEA2-50	FRAEX38873 v2_000212720.1	3904	58066	59546	203	9.21	22643.92	25.5	stable
FexLEA2-51	FRAEX38873 v2_000215390.1	3965	39722	40560	261	9.05	28924.3	39.28	stable
FexLEA2-52	FRAEX38873 v2_000231670.1	4307	28777	29792	200	9.6	22718.46	46.24	unstable
FexLEA2-53	FRAEX38873 v2_000247730.1	4705	1278	2275	214	10.17	23933.72	25.98	stable
FexLEA2-54	FRAEX38873 v2_000247740.1	4705	5331	6455	189	10.34	20952.77	43.26	unstable
FexLEA2-55	FRAEX38873 v2_000248310.1	4725	48622	50001	174	9.6	19823.09	26.28	stable
FexLEA2-56	FRAEX38873 v2_000256590.1	4932	2586	3665	200	9.9	22579.32	31.32	stable
FexLEA2-57	FRAEX38873 v2_000258770.1	4988	73596	75026	209	9.43	23422.24	42.6	unstable
FexLEA2-58	FRAEX38873 v2_000278650.1	5487	26636	27805	222	9.35	24820.15	39.54	stable
FexLEA2-59	FRAEX38873 v2_000309870.1	6304	12668	13590	222	9.44	24873.33	26.17	stable
FexLEA2-60	FRAEX38873 v2_000311570.1	6350	30974	32753	155	4.64	17033.78	18.71	stable
FexLEA2-61	FRAEX38873 v2_000356650.1	8085	74408	75342	222	9.68	24586.32	44.72	unstable

Table S1. (continued)

ID	Ash Tree Genomes Identifier	Physical position on cucumber genome			Protein length (aa)	pI	Molecular weight (Da)	Instability index	Stable or unstable
		Contig	Start position (bp)	End Position (bp)					
FexLEA2-62	FRAEX38873 v2 000372730.1	8711	16291	20055	220	8.99	24835.95	48.44	unstable
FexLEA2-63	FRAEX38873 v2 000374400.1	8783	1166	2020	204	9.53	22940.77	40.75	unstable
FexLEA2-64	FRAEX38873 v2 000377810.1	8900	5186	6236	208	9.87	23528.57	39.87	stable
FexLEA2-65	FRAEX38873 v2 000380170.1	8992	883	2331	209	9.43	23422.24	42.6	unstable
FexLEA2-66	FRAEX38873 v2 000393260.1	9629	27058	30804	228	9.03	25608.58	49.87	unstable
FexLEA2-67	FRAEX38873 v2 000007120.1	10375	45090	46855	255	9.98	29035.06	49.27	unstable
FexLEA2-68	FRAEX38873 v2 000097730.1	20758	1	1203	169	10.01	18611.84	34.68	stable
FexLEA2-69	FRAEX38873 v2 000119290.1	23698	4362	5545	209	9.43	23422.24	42.6	unstable
FexLEA2-70	FRAEX38873 v2 000123690.1	24322	6317	7574	237	8.98	26900.92	47.63	unstable
FexLEA2-71	FRAEX38873 v2 000218050.1	40151	91	959	200	9.82	22637.36	33.52	stable
FexLEA2-72	FRAEX38873 v2 000233850.1	43773	370	1430	252	9.96	28442.3	40.09	unstable
FexLEA2-73	FRAEX38873 v2 000254730.1	48939	52	597	150	10.43	16507.4	45.84	unstable
FexLEA2-74	FRAEX38873 v2 000265880.1	51807	289	5685	358	8.21	39293.47	44.21	unstable
FexLEA2-75	FRAEX38873 v2 000325820.1	68764	8576	14200	222	7.71	25184.06	53.27	unstable
FexLEA2-76	FRAEX38873 v2 000344320.1	76090	1087	2145	215	10.22	23846.36	40.11	unstable
FexLEA3-01	FRAEX38873 v2 000262360.1	509	94248	94688	68	9.4	7852.04	26.25	stable
FexLEA3-02	FRAEX38873 v2 000363130.1	833	53181	54125	97	10.33	10503.86	58.95	unstable
FexLEA3-03	FRAEX38873 v2 000036310.1	1338	138456	148172	363	8.96	39859.25	32.94	stable
FexLEA3-04	FRAEX38873 v2 000046300.1	1444	9396	10146	81	9.75	9206.67	29.74	stable
FexLEA3-05	FRAEX38873 v2 000163950.1	3016	47296	48293	100	9.91	10485.99	33.87	stable
FexLEA3-06	FRAEX38873 v2 000266280.1	5194	64943	65708	97	10.13	10527.93	46.87	unstable
FexLEA3-07	FRAEX38873 v2 000303320.1	6077	3466	4204	98	9.66	10445.81	30.01	stable
FexLEA4-01	FRAEX38873 v2 000322230.1	675	107301	110305	778	5.03	85827.02	24.31	stable
FexLEA4-02	FRAEX38873 v2 000330100.1	703	162236	164217	482	5.18	53287.3	40.79	unstable
FexLEA4-03	FRAEX38873 v2 000201040.1	3681	1005	2446	374	5.61	40333.35	31.41	stable
FexLEA5-01	FRAEX38873 v2 000034230.1	132	92986	93500	110	5.57	11955.01	43.89	unstable
FexLEA5-02	FRAEX38873 v2 000136760.1	260	77827	80795	176	5.51	19443.58	39.86	stable
FexLEA6-01	FRAEX38873 v2 000124640.1	24434	1916	2295	86	4.94	9047.77	39.07	stable
FexLEA6-02	FRAEX38873 v2 000315100.1	64814	613	925	85	5.59	9824.94	93.52	unstable

Table S1. (continued)

ID	Ash Tree Genomes Identifier	Physical position on cucumber genome			Protein length (aa)	pI	Molecular weight (Da)	Instability index	Stable or unstable
		Contig	Start position (bp)	End Position (bp)					
FexLEAd-01	FRAEX38873 v2 000034350.1	1320	49811	58487	145	9.25	15184.47	40.54	unstable
FexLEAd-02	FRAEX38873 v2 000046700.1	1449	30922	32100	155	4.84	16209.47	30.79	stable
FexLEAd-03	FRAEX38873 v2 000099080.1	2096	45365	46264	191	6.48	20227.11	26.47	stable
FexLEAd-04	FRAEX38873 v2 000122430.1	2413	47422	48435	167	6.3	17966.52	47.93	unstable
FexLEAd-05	FRAEX38873 v2 000136420.1	2595	130219	131525	246	5.22	27746.98	73.85	unstable
FexLEAd-06	FRAEX38873 v2 000168510.1	3112	38189	39151	196	5.48	22281.49	42.98	unstable
FexLEAd-07	FRAEX38873 v2 000248340.1	4726	41716	42874	222	5.54	24830.92	53.4	unstable
FexLEAd-08	FRAEX38873 v2 000377890.1	8902	21720	23186	242	5.06	27305.5	64.79	unstable
FexLEAS-01	FRAEX38873 v2 000128580.1	25	120251	122165	269	4.85	27409.36	37.35	stable
FexLEAS-02	FRAEX38873 v2 000335680.1	725	3416	5008	149	4.87	15545.48	29.72	stable
FexLEAS-03	FRAEX38873 v2 000051830.1	1511	115646	116881	224	4.76	23155.76	31.12	stable
FexLEAS-04	FRAEX38873 v2 000138300.1	2624	26706	28401	239	5.8	24868.76	53.27	unstable
FexLEAS-05	FRAEX38873 v2 000320650.1	6696	6207	7915	236	5.18	24545.2	56.43	unstable
FexLEAS-06	FRAEX38873 v2 000333470.1	7161	34480	35285	78	5.64	7856.82	22.76	stable
FexLEAun-01	FRAEX38873 v2 000288310.1	571	17626	18705	251	10.21	29215.97	34.48	stable
FexLEAun-02	FRAEX38873 v2 000023740.1	1203	41877	43785	470	7.67	52278.1	25.98	stable
FexLEAun-03	FRAEX38873 v2 000081790.1	1884	110136	111280	202	9.97	22272.93	36.57	stable
FexLEAun-04	FRAEX38873 v2 000167410.2	3090	19997	22589	202	10.16	22423.08	37.46	stable
FexLEAun-05	FRAEX38873 v2 000187420.1	3433	8866	12376	215	4.66	23862.8	27.92	stable
FexLEAun-06	FRAEX38873 v2 000248670.1	4732	9446	10579	163	6.35	17454.94	29.35	stable
FexLEAun-07	FRAEX38873 v2 000289770.1	5753	2278	3000	228	9	25975.23	42.86	unstable
FexLEAun-08	FRAEX38873 v2 000322170.2	6749	139876	142505	399	5.49	43138.38	26.21	stable

Table S2. Blast2Go analysis of FexLEA proteins

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA1-01	NDR1/HIN1-like protein 6	247	2.90E-115	65.74			membrane
FexLEA1-02	11 kDa late embryogenesis abundant protein-like	161	1.25E-29	89.81	embryo development ending in seed dormancy		
FexLEA1-03	18 kDa seed maturation protein- like	150	8.18E-53	75.55	embryo development ending in seed dormancy		
FexLEA1-04	18 kDa seed maturation protein- like	164	1.63E-62	75.39	embryo development ending in seed dormancy		
FexLEA1-05	late embryogenesis abundant protein 6- like	137	1.96E-30	81.74	embryo development ending in seed dormancy		
FexLEA1-06	18 kDa seed maturation protein- like	124	1.37E-29	73.66	embryo development ending in seed dormancy		
FexLEA2-01	desiccation protectant protein Lea14 homolog	138	1.52E-67	82.25	cellular response to desiccation; cellular response to salt		cytosol
FexLEA2-02	NDR1/HIN1-like protein 13	268	1.11E-112	76.44			membrane

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA2-03	protein YLS9	260	1.31E-96	79.37			plasma membrane; plasmodesma; internal component of membrane
FexLEA2-04	NDR1/HIN1-like protein 13	241	2.55E-109	90.44	translational initiation	translation initiation factor activity	plasma membrane; integral component of membrane
FexLEA2-05	TRNA-specific 2- thiouridylase	310	5.95E-176	86.27			integral component of membrane
FexLEA2-06	late embryogenesis abundant protein At1g64065-like	218	1.86E-119	76.91			integral component of membrane
FexLEA2-07	protein YLS9-like	260	5.08E-129	73.19			integral component of membrane
FexLEA2-08	desiccation-related protein At2g46140	320	0	94.47	response to desiccation; response to cytokinin; response to cadmium ion		Golgi apparatus; cytosol; plasma membrane; plasmodesma;
FexLEA2-09	putative Late embryogenesis abundant protein, LEA-14	187	8.16E-100	87.2	response to desiccation		integral component of membrane
FexLEA2-10	protein YLS9-like	210	8.11E-105	86.04			integral component of membrane
FexLEA2-11	protein YLS9-like	250	3.76E-127	72.22			integral component of membrane

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA2-12	Ras guanine nucleotide exchange factor G like	209	2.77E-72	76.95			integral component of membrane
FexLEA2-13	NDR1/HIN1-like protein 1	209	2.73E-119	87.23			integral component of membrane
FexLEA2-14	protein YLS9-like	259	1.85E-123	72.44			integral component of membrane
FexLEA2-15	NDR1/HIN1-like protein 6	252	6.62E-114	84.47			integral component of membrane
FexLEA2-16	Late embryogenesis abundant protein, LEA-14	306	6.27E-161	73.09			integral component of membrane
FexLEA2-17	NDR1/HIN1-like protein 1	210	2.01E-108	83.69			integral component of membrane
FexLEA2-18	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	262	1.79E-139	58.58			membrane
FexLEA2-19	NDR1/HIN1-like protein 12	230	5.00E-131	79.08			plasmodesma; integral component of membrane; anchored component of plasma membrane

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA2-20	protein NDR1-like	197	2.14E-90	60.15			membrane; integral component of membrane
FexLEA2-21	NDR1/HIN1-like protein 13	186	1.79E-96	89.21	translational initiation	translation initiation factor activity	plasma membrane; integral component of membrane
FexLEA2-22	NDR1/HIN1-like protein 1	209	5.00E-125	87.28			integral component of membrane
FexLEA2-23	---NA---	255					
FexLEA2-24	Ras guanine nucleotide exchange factor G like	210	1.70E-106	82.9			integral component of membrane
FexLEA2-25	NDR1/HIN1-like protein 13	274	1.01E-114	76.75			integral component of membrane
FexLEA2-26	CUB and sushi domain-containing protein	189	1.07E-57	73.6			membrane
FexLEA2-27	NDR1/HIN1-like protein 26	223	1.26E-137	80.32			integral component of membrane
FexLEA2-28	protein YLS9	254	1.56E-84	75.18			integral component of membrane
FexLEA2-29	NDR1/HIN1-like protein 1	209	2.53E-121	85.1			integral component of membrane

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA2-30	NDR1/HIN1-like protein 1	208	1.74E-109	91.21			integral component of membrane
FexLEA2-31	protein YLS9-like	256	1.04E-132	70.59			membrane
FexLEA2-32	tubulin beta-8 chain	611	0	99.43	microtubule cytoskeleton organization; mitotic cell cycle; response to salt stress	GTPase activity; structural constituent of cytoskeleton; GTP binding	Golgi apparatus; microtubule; membrane
FexLEA2-33	NDR1/HIN1-like protein 26	209	1.20E-121	82.08			integral component of membrane
FexLEA2-34	Late embryogenesis abundant protein, LEA-14	213	2.23E-100	77.58			integral component of membrane
FexLEA2-35	NDR1/HIN1-like protein 26	209	8.01E-126	84.94			integral component of membrane
FexLEA2-36	protein YLS9-like	207	1.03E-115	84.48			plasmodesma; integral component of membrane; anchored component of plasma membrane
FexLEA2-37	Late embryogenesis abundant protein	238	4.58E-114	65.34			membrane
FexLEA2-38	Late embryogenesis abundant protein	222	5.03E-128	81.84	response to desiccation		plasma membrane; integral component of membrane

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA2-39	Late embryogenesis abundant protein	341	0	71.66			membrane
FexLEA2-40	Late embryogenesis abundant protein, LEA-14 protein	193	1.39E-86	74.08			integral component of membrane
FexLEA2-41	uncharacterized protein LOC111368163	323	4.19E-175	83.93			integral component of membrane
FexLEA2-42	NDR1/HIN1-like protein 1	545	2.05E-136	85.77			integral component of membrane
FexLEA2-43	NDR1/HIN1-Like protein	309	4.32E-177	89.63	RNA biosynthetic process	DNA-directed 5'-3' RNA polymerase activity	integral component of membrane
FexLEA2-44	Ras guanine nucleotide exchange factor G like	211	6.34E-109	77.48			integral component of membrane
FexLEA2-45	Late embryogenesis abundant hydroxyproline-rich glycoprotein family, putative	227	5.28E-131	68.84			membrane
FexLEA2-46	uncharacterized protein LOC111369031	258	2.50E-112	73.73			membrane

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA2-47	uncharacterized protein LOC105173008	287	5.51E-136	73.59			integral component of membrane
FexLEA2-48	Late embryogenesis abundant protein	199	3.99E-139	88.9			integral component of membrane
FexLEA2-49	---NA---	256					
FexLEA2-50	protein NDR1-like	203	2.30E-100	79.57			plasma membrane; integral component of membrane
FexLEA2-51	NDR1/HIN1-like protein 13	261	1.53E-164	63.54			membrane; integral component of membrane
FexLEA2-52	Late embryogenesis abundant protein, LEA-14 protein	200	2.31E-113	76.9			plasmodesma; integral component of membrane; anchored component of plasma membrane
FexLEA2-53	late embryogenesis abundant protein At1g64065-like	214	1.42E-123	76.35			membrane
FexLEA2-54	late embryogenesis abundant protein At1g64065-like	189	5.48E-38	75.16			membrane

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA2-55	late embryogenesis abundant protein At1g64065-like	174	5.32E-59	73.35			membrane
FexLEA2-56	Late embryogenesis abundant protein, LEA-14 protein	200	8.01E-98	76.19			integral component of membrane
FexLEA2-57	NDR1/HIN1-like protein 26	209	6.73E-113	82.21			integral component of membrane
FexLEA2-58	Late embryogenesis abundant protein, LEA-14	222	2.93E-108	76.14			membrane
FexLEA2-59	Late embryogenesis abundant protein	222	1.46E-99	73.35			membrane
FexLEA2-60	desiccation protectant protein Lea14 homolog	155	3.13E-97	84.95	response to desiccation		cytosol; integral component of membrane
FexLEA2-61	NDR1/HIN1-like protein 12	222	6.15E-122	79.05			plasmodesma; integral component of membrane; anchored component of plasma membrane
FexLEA2-62	Late embryogenesis abundant protein, LEA-14 protein	220	7.73E-126	79.13			integral component of membrane

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA2-63	NDR1/HIN1-like protein 1	204	1.85E-95	76.32			membrane
FexLEA2-64	NDR1/HIN1-like protein 1	208	4.16E-123	87.81			integral component of membrane
FexLEA2-65	NDR1/HIN1-like protein 26	209	6.73E-113	82.21			integral component of membrane
FexLEA2-66	putative Late embryogenesis abundant protein, LEA-14	228	6.08E-144	77.96			integral component of membrane
FexLEA2-67	NDR1/HIN1-like protein 2	255	2.60E-142	81.97			integral component of membrane
FexLEA2-68	Late embryogenesis abundant protein, LEA-14 protein	169	1.33E-108	87.5			integral component of membrane
FexLEA2-69	NDR1/HIN1-like protein 26	209	6.73E-113	82.21			integral component of membrane
FexLEA2-70	NDR1/HIN1-like protein 3	237	1.99E-125	81.45			integral component of membrane
FexLEA2-71	Late embryogenesis abundant protein, LEA-14 protein	200	9.99E-99	76.77			integral component of membrane

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA2-72	NDR1/HIN1-like protein 6	252	1.32E-136	84.7			integral component of membrane
FexLEA2-73	Immunoglobulin-like fold containing protein	150	4.86E-83	81.23	response to desiccation		integral component of membrane
FexLEA2-74	RING-H2 finger protein ATL67-like	358	5.44E-107	85.5	response to desiccation		integral component of membrane
FexLEA2-75	Late embryogenesis abundant protein, LEA-14 protein	222	2.92E-147	73.78			membrane
FexLEA2-76	protein YLS9	215	4.73E-85	81			integral component of membrane
FexLEA3-01	protein SENESCENCE-ASSOCIATED GENE 21, mitochondrial-like	68	4.90E-27	65.26			
FexLEA3-02	protein SENESCENCE-ASSOCIATED GENE 21, mitochondrial-like	97	1.57E-43	79.07			mitochondrion

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA3-03	replication factor C subunit 1	363	6.10E-101	68.3	DNA metabolic process; cellular response to DNA damage stimulus	nucleotide binding; DNA binding	intracellular organelle
FexLEA3-04	protein SENESCENCE- ASSOCIATED GENE 21, mitochondrial-like	81	1.35E-31	71.64			
FexLEA3-05	protein SENESCENCE- ASSOCIATED GENE 21, mitochondrial-like	100	2.93E-30	75.31			
FexLEA3-06	protein SENESCENCE- ASSOCIATED GENE 21, mitochondrial-like	97	1.33E-45	74.98			mitochondrion
FexLEA3-07	protein SENESCENCE- ASSOCIATED GENE 21, mitochondrial-like	98	1.48E-40	74.69			

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEA4-01	embryonic protein DC-8-like	778	1.97E-97	57.9			extracellular region; cell wall; cytoplasm
FexLEA4-02	embryonic protein DC-8	482	7.40E-66	62.62			
FexLEA4-03	late embryogenesis abundant protein D- 29	314	5.59E-90	58.61			membrane; integral component of membrane
FexLEA5-01	protein SLE1	110	2.49E-65	96.01			
FexLEA5-02	em-like protein GEA6	176	9.20E-50	92.21	response to abscisic acid; acquisition of desiccation tolerance in seed; protein stabilization		cytosol
FexLEA6-01	Late embryogenesis abundant protein	86	1.07E-47	82.15			
FexLEA6-02	Late embryogenesis abundant protein	85	2.41E-13	74.35	methylation	methyltransferase activity; transferase activity	
FexLEAd-01	---NA---	145			response to water		
FexLEAd-02	dehydrin DHN1-like	155	5.59E-42	66.06	response to water		

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEAd-03	embryogenic cell protein 40	191	4.30E-32	95.3	response to water deprivation; cold acclimation; response to abscisic acid		cytosol
FexLEAd-04	late embryogenesis abundant protein	167	1.40E-10	91.19	response to water deprivation; cold acclimation; response to abscisic acid		cytosol
FexLEAd-05	phosphoprotein ECPP44-like	246	2.37E-61	73.91	response to water		
FexLEAd-06	phosphoprotein ECPP44-like	196	2.57E-65	63.71	response to water		membrane; integral component of membrane
FexLEAd-07	dehydrin	222	2.69E-34	75.81	response to water		
FexLEAd-08	phosphoprotein ECPP44-like	242	2.41E-18	74.36	response to water		
FexLEAS-01	late embryogenesis abundant protein D- 34-like	269	3.18E-147	81.91			
FexLEAS-02	late embryogenesis abundant protein D- 34-like	149	2.05E-42	77.82			

Table S2. (continued)

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEAS-03	late embryogenesis abundant protein D- 34-like	224	1.72E-72	70.45			
FexLEAS-04	late embryogenesis abundant protein D- 34-like	239	1.02E-132	72.72			
FexLEAS-05	late embryogenesis abundant protein D- 34	236	5.43E-133	74.85			
FexLEAS-06	late embryogenesis abundant protein D- 34-like	78	6.74E-12	76.25			
FexLEAun-1	late embryogenesis abundant protein At1g64065-like	251	4.68E-94	69.61	phosphorylation	kinase activitiy	membrane; integral component of membrane
FexLEAun-2	DUF4149 domain- containing protein	470	0	54.73			membrane; integral component of membrane
FexLEAun-3	late embryogenesis abundant protein At1g64065-like	202	2.50E-112	73.21			integral component of membrane
FexLEAun-4	late embryogenesis abundant protein At1g64065-like	202	1.19E-110	73.01			integral component of membrane

Table S2. (continued)-

Sequence Name	Description	Length	e-Value	Similarity (%)	GO:Biological Process	GO:Molecular Function	GO:Cellular Component
FexLEAun-5	desiccation-related protein At2g46140	215	5.68E-34	77.1	response to desiccation		membrane; cytoplasmic part
FexLEAun-6	late embryogenesis abundant protein Dc3-like	163	1.98E-63	72.58			
FexLEAun-7	NDR1/HIN1-like protein 6	228	2.04E-118	75.77	integral component of membrane		
FexLEAun-8	embryonic protein DC-8-like	399	0	59.53			

Table S3. The Ka/Ks ratios and estimated divergence times for orthologus LEA proteins

<i>Ash Tree-Poplar</i>							
GeneIDs	Chromosome	GeneIDs	Chromosome	Ks	Ka	Ka/Ks	Mya
FexLEA2-01	contig 1	Potri.014G090800.1	Chr.14	2.6173	0.3571	0.136438	20.133077
FexLEA2-04	contig 65	Potri.T165600.1	scaffold 862	3.3842	0.1899	0.056114	26.032308
FexLEA2-04	contig 65	Potri.001G208000.1	Chr.01	2.3557	0.2041	0.086641	18.120769
FexLEA2-05	contig 85	Potri.007G045000.1	Chr.07	2.3231	0.1978	0.085145	17.87
FexLEA2-05	contig 85	Potri.002G124600.2	Chr.02	10.2934	0.2488	0.024171	79.18
FexLEA2-05	contig 85	Potri.002G124600.1	Chr.02	10.2785	0.2488	0.024206	79.065385
FexLEA2-05	contig 85	Potri.014G026800.1	Chr.14	26.8894	0.2426	0.0090	206.84154
FexLEA2-08	contig 238	Potri.007G146300.1	Chr.07	1.9806	0.0903	0.045592	15.235385
FexLEA2-08	contig 238	Potri.007G146300.2	Chr.07	2.0813	0.0860	0.04132	16.01
FexLEA2-08	contig 238	Potri.007G146300.3	Chr.07	2.0813	0.0860	0.04132	16.01
FexLEA2-09	contig 281	Potri.001G218400.1	Chr.01	2.8211	0.2498	0.088547	21.700769
FexLEA2-10	contig 386	Potri.016G071500.1	Chr.16	1.6146	0.2931	0.181531	12.42
FexLEA2-13	contig 439	Potri.016G071500.1	Chr.16	1.3605	0.2570	0.188901	10.465385
FexLEA2-15	contig 442	Potri.015G148200.1	Chr.15	2.0001	0.2288	0.114394	15.385385
FexLEA2-15	contig 442	Potri.012G145500.1	Chr.12	2.1143	0.2170	0.102634	16.263846
FexLEA2-16	contig 459	Potri.002G124600.2	Chr.02	2.4251	0.1781	0.07344	18.654615
FexLEA2-16	contig 459	Potri.002G124600.1	Chr.02	2.4251	0.1781	0.07344	18.654615
FexLEA2-19	contig 630	Potri.002G180000.1	Chr.02	1.3416	0.2860	0.213178	10.32
FexLEA2-19	contig 630	Potri.T181400.1	scaffold 2703	1.4243	0.2578	0.1810	10.956154
FexLEA2-19	contig 630	Potri.014G106100.2	Chr.14	1.5013	0.3550	0.236462	11.548462
FexLEA2-19	contig 630	Potri.014G106100.1	Chr.14	1.5013	0.3550	0.236462	11.548462
FexLEA2-21	contig 778	Potri.001G208000.1	Chr.01	2.8251	0.2413	0.085413	21.731538
FexLEA2-21	contig 778	Potri.T165600.1	scaffold 862	3.0324	0.2302	0.075913	23.326154
FexLEA2-22	contig 886	Potri.016G071500.1	Chr.16	2.7618	0.3271	0.118437	21.244615
FexLEA2-23	contig 1151	Potri.017G154000.1	Chr.17	1.9512	0.2942	0.150779	15.009231
FexLEA2-23	contig 1151	Potri.004G067100.1	Chr.04	2.2458	0.3132	0.13946	17.275385
FexLEA2-29	contig 1631	Potri.016G071500.1	Chr.16	2.7582	0.3192	0.115728	21.216923
FexLEA2-30	contig 1729	Potri.016G071500.1	Chr.16	54.8581	0.3059	0.005576	421.98538
FexLEA2-30	contig 1729	Potri.006G204200.1	Chr.06	9.8548	0.3321	0.033699	75.806154
FexLEA2-32	contig 1892	Potri.009G040200.1	Chr.09	3.7554	0.0279	0.007429	28.887692
FexLEA2-32	contig 1892	Potri.003G125400.1	Chr.03	1.7551	0.0209	0.011908	13.500769
FexLEA2-32	contig 1892	Potri.001G106100.1	Chr.01	1.9252	0.0233	0.012103	14.809231
FexLEA2-32	contig 1892	Potri.001G246900.1	Chr.01	2.6934	0.0311	0.011547	20.718462

Table S3. (continued)

GeneIDs	Chromosome	GeneIDs	Chromosome	Ks	Ka	Ka/Ks	Mya
FexLEA2-32	contig 1892	Potri.001G272800.2	Chr.01	3.8855	0.0321	0.008261	29.888462
FexLEA2-32	contig 1892	Potri.001G272800.1	Chr.01	3.8849	0.0321	0.008263	29.883846
FexLEA2-32	contig 1892	Potri.016G033200.1	Chr.16	4.0388	0.0328	0.008121	31.067692
FexLEA2-32	contig 1892	Potri.009G067200.1	Chr.09	4.6301	0.0309	0.006674	35.616154
FexLEA2-32	contig 1892	Potri.006G035400.2	Chr.06	3.2924	0.0339	0.010296	25.326154
FexLEA2-32	contig 1892	Potri.006G035400.3	Chr.06	3.2925	0.0339	0.010296	25.326923
FexLEA2-32	contig 1892	Potri.006G035400.1	Chr.06	3.2925	0.0339	0.010296	25.326923
FexLEA2-32	contig 1892	Potri.009G067100.1	Chr.09	4.8827	0.0297	0.006083	37.559231
FexLEA2-32	contig 1892	Potri.001G464400.1	Chr.01	3.4022	0.0331	0.009729	26.170769
FexLEA2-32	contig 1892	Potri.011G162500.1	Chr.11	4.3411	0.0317	0.007302	33.393077
FexLEA2-32	contig 1892	Potri.006G095000.2	Chr.06	4.4513	0.0341	0.007661	34.240769
FexLEA2-32	contig 1892	Potri.015G038800.1	Chr.15	2.5508	0.0406	0.015917	19.621538
FexLEA2-32	contig 1892	Potri.016G107300.1	Chr.16	5.5602	0.0400	0.007194	42.770769
FexLEA2-32	contig 1892	Potri.016G109300.1	Chr.16	5.3481	0.0382	0.007143	41.139231
FexLEA2-32	contig 1892	Potri.001G272700.1	Chr.01	4.9018	0.0324	0.00661	37.706154
FexLEA2-32	contig 1892	Potri.001G272700.2	Chr.01	4.9044	0.0324	0.006606	37.726154
FexLEA2-32	contig 1892	Potri.012G047600.1	Chr.12	2.3561	0.0390	0.016553	18.123846
FexLEA2-32	contig 1892	Potri.005G239900.1	Chr.05	5.0038	0.0426	0.008514	38.490769
FexLEA2-32	contig 1892	Potri.006G095000.1	Chr.06	4.4986	0.0351	0.007802	34.604615
FexLEA2-32	contig 1892	Potri.003G126800.1	Chr.03	5.2394	0.0472	0.0090	40.303077
FexLEA2-32	contig 1892	Potri.002G021800.1	Chr.02	26.4139	0.0454	0.001719	203.18385
FexLEA2-32	contig 1892	Potri.001G104600.1	Chr.01	6.7789	0.0509	0.007509	52.145385
FexLEA2-32	contig 1892	Potri.009G067200.2	Chr.09	8.1289	0.0763	0.009386	62.53
FexLEA2-32	contig 1892	Potri.006G095000.3	Chr.06	4.9057	0.0424	0.008643	37.736154
FexLEA2-33	contig 1922	Potri.015G002400.1	Chr.15	1.5782	0.2551	0.16164	12.14
FexLEA2-33	contig 1922	Potri.015G002400.2	Chr.15	1.5782	0.2551	0.16164	12.14
FexLEA2-33	contig 1922	Potri.012G006000.1	Chr.12	1.6551	0.2560	0.154673	12.731538
FexLEA2-35	contig 2262	Potri.012G006000.1	Chr.12	1.8083	0.2176	0.120334	13.91
FexLEA2-35	contig 2262	Potri.015G002400.1	Chr.15	1.6159	0.2394	0.148153	12.43
FexLEA2-35	contig 2262	Potri.015G002400.2	Chr.15	1.6159	0.2394	0.148153	12.43
FexLEA2-36	contig 2277	Potri.016G071500.1	Chr.16	1.8901	0.2886	0.15269	14.539231
FexLEA2-41	contig 2759	Potri.014G026800.1	Chr.14	11.7383	0.1456	0.012404	90.294615
FexLEA2-41	contig 2759	Potri.002G124600.2	Chr.02	2.6315	0.1438	0.054646	20.242308

Table S3. (continued)

GeneIDs	Chromosome	GeneIDs	Chromosome	Ks	Ka	Ka/Ks	Mya
FexLEA2-41	contig 2759	Potri.002G124600.1	Chr.02	2.6314	0.1438	0.054648	20.241538
FexLEA2-41	contig 2759	Potri.007G045000.1	Chr.07	16.1875	0.2129	0.013152	124.51923
FexLEA2-43	contig 2868	Potri.001G183600.1	Chr.01	1.3243	0.1493	0.112739	10.186923
FexLEA2-43	contig 2868	Potri.003G052900.1	Chr.03	1.2816	0.1659	0.129448	9.8584615
FexLEA2-43	contig 2868	Potri.001G183600.2	Chr.01	1.3135	0.1472	0.112067	10.103846
FexLEA2-48	contig 3240	Potri.003G141200.1	Chr.03	2.3740	0.1713	0.072157	18.261538
FexLEA2-48	contig 3240	Potri.001G090400.1	Chr.01	2.2059	0.1889	0.085634	16.968462
FexLEA2-49	contig 3690	Potri.017G154000.1	Chr.17	1.8474	0.3012	0.1630	14.210769
FexLEA2-49	contig 3690	Potri.004G067100.1	Chr.04	1.7001	0.2968	0.174578	13.077692
FexLEA2-57	contig 4988	Potri.012G006000.1	Chr.12	1.6376	0.2228	0.136053	12.596923
FexLEA2-57	contig 4988	Potri.015G002400.1	Chr.15	1.6224	0.2223	0.1370	12.48
FexLEA2-57	contig 4988	Potri.015G002400.2	Chr.15	1.6225	0.2223	0.1370	12.480769
FexLEA2-60	contig 6350	Potri.014G090800.1	Chr.14	4.2663	0.2651	0.0621	32.817692
FexLEA2-60	contig 6350	Potri.002G165000.1	Chr.02	4.7464	0.2687	0.0566	36.510769
FexLEA2-61	contig 8085	Potri.002G180000.1	Chr.02	1.3524	0.2929	0.2166	10.403077
FexLEA2-61	contig 8085	Potri.T181400.1	scaffold_2703	1.3735	0.2743	0.1997	10.565385
FexLEA2-64	contig 8900	Potri.016G071500.1	Chr.16	12.3863	0.3393	0.0274	95.279231
FexLEA2-65	contig 8992	Potri.012G006000.1	Chr.12	1.6376	0.2228	0.1361	12.596923
FexLEA2-65	contig 8992	Potri.015G002400.1	Chr.15	1.6224	0.2223	0.1370	12.48
FexLEA2-65	contig 8992	Potri.015G002400.2	Chr.15	1.6225	0.2223	0.1370	12.480769
FexLEA2-68	contig 20758	Potri.014G026800.1	Chr.14	3.7503	0.1975	0.0527	28.848462
FexLEA2-68	contig 20758	Potri.002G124600.2	Chr.02	2.7415	0.1916	0.0699	21.088462
FexLEA2-68	contig 20758	Potri.002G124600.1	Chr.02	2.7416	0.1916	0.0699	21.089231
FexLEA2-68	contig 20758	Potri.007G045000.1	Chr.07	1.8350	0.2215	0.1207	14.115385
FexLEA2-69	contig 23698	Potri.012G006000.1	Chr.12	1.6376	0.2228	0.1361	12.596923
FexLEA2-69	contig 23698	Potri.015G002400.1	Chr.15	1.6224	0.2223	0.1370	12.48
FexLEA2-69	contig 23698	Potri.015G002400.2	Chr.15	1.6224	0.2223	0.1370	12.48
FexLEA2-72	contig 43773	Potri.015G148200.1	Chr.15	1.6389	0.2266	0.1383	12.606923
FexLEA2-72	contig 43773	Potri.012G145500.1	Chr.12	1.7305	0.2251	0.1301	13.311538
FexLEA2-74	contig 51807	Potri.002G165200.1	Chr.02	3.8445	0.3026	0.0787	29.573077
FexLEA2-74	contig 51807	Potri.014G091000.1	Chr.14	2.4127	0.3619	0.1500	18.559231
FexLEAS-04	contig 2624	Potri.005G048000.1	Chr.05	7.3016	0.3495	0.0479	56.166154
FexLEAS-05	contig 6696	Potri.005G048000.1	Chr.05	8.8134	0.3538	0.0401	67.795385
MEAN				4.4220	0.1826	0.0802	34.015128

Table S3. (continued)

<i>Ash Tree-Ocalyptus</i>							
GeneIDs	Chromosome	GeneIDs	Chromosome	Ks	Ka	Ka/Ks	Mya
FexLEA2-01	contig 1	Eucgr.D02327.1	Chr.04	4.7043	0.3269	0.0695	36.186923
FexLEA2-04	contig 65	Eucgr.I02708.1	Chr.09	3.8328	0.1993	0.0520	29.483077
FexLEA2-05	contig 85	Eucgr.H01684.1	Chr.08	3.6088	0.2206	0.0611	27.76
FexLEA2-05	contig 85	Eucgr.F00213.1	Chr.06	8.1289	0.2590	0.0319	62.53
FexLEA2-08	contig 238	Eucgr.H00245.2	Chr.08	2.5229	0.1183	0.0469	19.406923
FexLEA2-08	contig 238	Eucgr.H00245.1	Chr.08	2.5229	0.1183	0.0469	19.406923
FexLEA2-08	contig 238	Eucgr.H00245.3	Chr.08	2.2378	0.0861	0.0385	17.213846
FexLEA2-09	contig 281	Eucgr.J00502.1	Chr.10	51.2709	0.2033	0.0040	394.39154
FexLEA2-10	contig 386	Eucgr.J00542.1	Chr.10	2.3659	0.3246	0.1372	18.199231
FexLEA2-13	contig 439	Eucgr.A02596.1	Chr.01	18.4793	0.3386	0.0183	142.14846
FexLEA2-21	contig 778	Eucgr.I02708.1	Chr.09	57.1199	0.2524	0.0044	439.38385
FexLEA2-30	contig 1729	Eucgr.A02596.1	Chr.01	52.3497	0.2702	0.0052	402.69
FexLEA2-30	contig 1729	Eucgr.A02596.2	Chr.01	59.5242	0.2590	0.0044	457.87846
FexLEA2-32	contig 1892	Eucgr.B02285.1	Chr.02	3.4723	0.0235	0.0068	26.71
FexLEA2-32	contig 1892	Eucgr.K00264.1	Chr.11	3.8662	0.0218	0.0056	29.74
FexLEA2-32	contig 1892	Eucgr.K01666.1	Chr.11	3.4139	0.0397	0.0116	26.260769
FexLEA2-32	contig 1892	Eucgr.D01612.1	Chr.05	4.2630	0.0352	0.0083	32.792308
FexLEA2-32	contig 1892	Eucgr.F01663.1	Chr.06	5.0275	0.0319	0.0063	38.673077
FexLEA2-32	contig 1892	Eucgr.D01847.1	Chr.04	5.8988	0.0655	0.0111	45.375385
FexLEA2-35	contig 2262	Eucgr.L03718.1	scaffold 4799	2.6646	0.2759	0.1035	20.496923
FexLEA2-35	contig 2262	Eucgr.K00036.1	Chr.11	2.6632	0.2724	0.1023	20.486154
FexLEA2-38	contig 2455	Eucgr.E00095.1	Chr.05	55.5537	0.2457	0.0044	427.33615
FexLEA2-41	contig 2759	Eucgr.F00213.1	Chr.06	12.2348	0.1903	0.0156	94.113846
FexLEA2-43	contig 2868	Eucgr.F03033.1	Chr.06	1.8827	0.1410	0.0749	14.482308
FexLEA2-48	contig 3240	Eucgr.D01751.1	Chr.04	56.3430	0.1519	0.0027	433.40769
FexLEA2-60	contig 6350	Eucgr.D02327.1	Chr.04	4.4772	0.2479	0.0554	34.44
FexLEA2-68	contig 20758	Eucgr.H02051.1	Chr.08	3.8812	0.2699	0.0695	29.855385
FexLEA2-68	contig 20758	Eucgr.H01684.1	Chr.08	3.5356	0.2710	0.0766	27.196923
FexLEA2-68	contig 20758	Eucgr.F00213.1	Chr.06	4.0897	0.2347	0.0574	31.459231
FexLEA2-72	contig 43773	Eucgr.F02922.1	Chr.06	14.2635	0.2562	0.0180	109.71923
FexLEA2-73	contig 48939	Eucgr.E00095.1	Chr.05	54.7527	0.2212	0.0040	421.17462
FexLEAS-01	contig 25	Eucgr.H03461.1	Chr.08	7.4639	0.2237	0.0300	57.414615
FexLEAS-01	contig 25	Eucgr.L02495.1	scaffold 959	35.4026	0.3183	0.0090	272.32769

Table S3. (continued)

GeneIDs	Chromosome	GeneIDs	Chromosome	Ks	Ka	Ka/Ks	Mya
FexLEAS-01	contig 25	Eucgr.B01083.1	Chr.02	43.0338	0.3166	0.0074	331.02923
FexLEAS-04	contig 2624	Eucgr.B01734.1	Chr.02	3.2474	0.3131	0.0964	24.98
FexLEAun-07	contig 5753	Eucgr.K00959.1	Chr.11	2.8639	0.3000	0.1048	22.03
MEAN				16.7490	0.2068	0.0389	128.8384
<i>Ash Tree-Sweet Orange</i>							
FexLEA2-01	contig 1	orange1.1g031863m	scaffold00046	2.7512	0.3215	0.1169	21.163077
FexLEA2-04	contig 65	orange1.1g023930m	scaffold00148	3.9966	0.2041	0.0511	30.743077
FexLEA2-05	contig 85	orange1.1g047795m	scaffold00006	1.9592	0.2630	0.1342	15.070769
FexLEA2-05	contig 85	orange1.1g020687m	scaffold00002	2.3312	0.2543	0.1091	17.932308
FexLEA2-08	contig 238	orange1.1g018706m	scaffold00230	1.5731	0.0822	0.0523	12.100769
FexLEA2-09	contig 281	orange1.1g030102m	scaffold00082	3.0747	0.1866	0.0607	23.651538
FexLEA2-10	contig 386	orange1.1g028399m	scaffold00018	4.0578	0.2986	0.0736	31.213846
FexLEA2-13	contig 439	orange1.1g028208m	scaffold00079	1.8496	0.2519	0.1362	14.227692
FexLEA2-13	contig 439	orange1.1g028399m	scaffold00018	4.0060	0.2644	0.0660	30.815385
FexLEA2-15	contig 442	orange1.1g045040m	scaffold00036	2.9837	0.2522	0.0845	22.951538
FexLEA2-19	contig 630	orange1.1g038323m	scaffold00001	7.1186	0.3466	0.0487	54.758462
FexLEA2-21	contig 778	orange1.1g023930m	scaffold00148	53.2815	0.2272	0.0043	409.85769
FexLEA2-23	contig 1151	orange1.1g047356m	scaffold00105	2.6902	0.2774	0.1031	20.693846
FexLEA2-30	contig 1729	orange1.1g028399m	scaffold00018	4.4396	0.2942	0.0663	34.150769
FexLEA2-32	contig 1892	orange1.1g013291m	scaffold00062	2.7946	0.0272	0.0097	21.496923
FexLEA2-32	contig 1892	orange1.1g013165m	scaffold00026	2.1628	0.0242	0.0112	16.636923
FexLEA2-32	contig 1892	orange1.1g013335m	scaffold00083	5.0150	0.0317	0.0063	38.576923
FexLEA2-32	contig 1892	orange1.1g013391m	scaffold00010	3.3200	0.0304	0.0092	25.538462
FexLEA2-32	contig 1892	orange1.1g013154m	scaffold00138	4.7586	0.0364	0.0076	36.604615
FexLEA2-32	contig 1892	orange1.1g013161m	scaffold00138	4.7624	0.0364	0.0076	36.633846
FexLEA2-32	contig 1892	orange1.1g013439m	scaffold00009	3.2874	0.0513	0.0156	25.287692
FexLEA2-32	contig 1892	orange1.1g036688m	scaffold00002	3.9765	0.0423	0.0106	30.588462
FexLEA2-32	contig 1892	orange1.1g047757m	scaffold00039	12.0952	0.0807	0.0067	93.04
FexLEA2-32	contig 1892	orange1.1g038476m	scaffold00039	46.5455	0.1598	0.0034	358.04231
FexLEA2-36	contig 2277	orange1.1g028399m	scaffold00018	41.6920	0.3139	0.0075	320.70769
FexLEA2-41	contig 2759	orange1.1g020687m	scaffold00002	12.6572	0.1515	0.0120	97.363077
FexLEA2-43	contig 2868	orange1.1g022177m	scaffold00256	2.6292	0.2270	0.0863	20.224615
FexLEAS-01	contig 25	Eucgr.L02495.1	scaffold 959	35.4026	0.3183	0.0090	272.32769

Table S3. (continued)

GeneIDs	Chromosome	GeneIDs	Chromosome	Ks	Ka	Ka/Ks	Mya
FexLEA2-47	contig 3112	orange1.1g021795m	scaffold00023	2.5093	0.2034	0.0811	19.302308
FexLEA2-48	contig 3240	orange1.1g048760m	scaffold00009	2.9092	0.2139	0.0735	22.378462
FexLEA2-60	contig 6350	orange1.1g031863m	scaffold00046	4.5675	0.2498	0.0547	35.134615
FexLEA2-60	contig 6350	orange1.1g045101m	scaffold00001	4.9847	0.2828	0.0567	38.343846
FexLEA2-64	contig 8900	orange1.1g028399m	scaffold00018	3.9995	0.3156	0.0789	30.765385
FexLEA2-68	contig 20758	orange1.1g020687m	scaffold00002	1.9474	0.2054	0.1055	14.98
FexLEA2-68	contig 20758	orange1.1g047795m	scaffold00006	1.5713	0.2626	0.1671	12.086923
FexLEA2-72	contig 43773	orange1.1g045040m	scaffold00036	2.3406	0.2520	0.1077	18.004615
FexLEA2-74	contig 51807	orange1.1g029203m	scaffold00001	4.3460	0.2853	0.0656	33.430769
FexLEA5-01	contig 132	orange1.1g040090m	scaffold00098	6.1472	0.0725	0.0118	47.286154
FexLEAS-01	contig 25	orange1.1g038380m	scaffold00011	3.9284	0.2379	0.0606	30.218462
FexLEAS-04	contig 2624	orange1.1g046001m	scaffold00144	43.7685	0.2785	0.0064	336.68077
FexLEAS-05	contig 6696	orange1.1g046001m	scaffold00144	14.8137	0.2871	0.0194	113.95154
MEAN				8.3289	0.1948	0.0556	64.0688
<i>Ash Tree-Duplication</i>							
FexLEA1-01	contig 1	FexLEA2-37	contig 2308	0.2077	0.1272	0.6124	1.5976923
FexLEA1-03	contig 674	FexLEA1-04	contig 1751	0.8960	0.1381	0.1541	6.8923077
FexLEA2-01	contig 1	FexLEA2-60	contig 6350	1.5926	0.2357	0.1480	12.250769
FexLEA2-02	contig 43	FexLEA2-25	contig 1360	1.2007	0.2435	0.2028	9.2361538
FexLEA2-03	contig 64	FexLEA2-28	contig 1519	1.1454	0.1712	0.1495	8.8107692
FexLEA2-03	contig 64	FexLEA2-76	contig 76090	0.8329	0.1332	0.1599	6.4069231
FexLEA2-04	contig 65	FexLEA2-21	contig 778	0.3864	0.1069	0.2767	2.9723077
FexLEA2-05	contig 85	FexLEA2-41	contig 2759	1.9049	0.2516	0.1321	14.653077
FexLEA2-07	contig 232	FexLEA2-14	contig 439	0.2452	0.0646	0.2635	1.8861538
FexLEA2-07	contig 232	FexLEA2-11	contig 386	0.9658	0.1736	0.1797	7.4292308
FexLEA2-07	contig 232	FexLEA2-31	contig 1839	0.9181	0.1919	0.2090	7.0623077
FexLEA2-10	contig 386	FexLEA2-36	contig 2277	0.3022	0.0900	0.2978	2.3246154
FexLEA2-10	contig 386	FexLEA2-13	contig 439	0.8898	0.1556	0.1749	6.8446154
FexLEA2-10	contig 386	FexLEA2-63	contig 8783	0.3914	0.1578	0.4032	3.0107692
FexLEA2-11	contig 386	FexLEA2-31	contig 1839	0.3124	0.0648	0.2074	2.4030769
FexLEA2-11	contig 386	FexLEA2-14	contig 439	0.8999	0.1598	0.1776	6.9223077
FexLEA2-12	contig 413	FexLEA2-24	contig 1209	1.1267	0.2427	0.2154	8.6669231
FexLEA2-13	contig 439	FexLEA2-36	contig 2277	1.0283	0.2085	0.2028	7.91

Table S3. (continued)

GeneIDs	Chromosome	GeneIDs	Chromosome	Ks	Ka	Ka/Ks	Mya
FexLEA2-13	contig 439	FexLEA2-63	contig 8783	0.8800	0.2789	0.3169	6.7692308
FexLEA2-13	contig 439	FexLEA2-30	contig 1729	11.2714	0.3601	0.0319	86.703077
FexLEA2-14	contig 439	FexLEA2-31	contig 1839	0.8644	0.1776	0.2055	6.6492308
FexLEA2-15	contig 442	FexLEA2-72	contig 43773	0.1983	0.0362	0.1826	1.5253846
FexLEA2-16	contig 459	FexLEA2-41	contig 2759	0.3568	0.0540	0.1513	2.7446154
FexLEA2-16	contig 459	FexLEA2-68	contig 20758	0.0000	0.0000	0.0000	0
FexLEA2-17	contig 461	FexLEA2-42	contig 2795	0.3105	0.1037	0.3340	2.3884615
FexLEA2-17	contig 461	FexLEA2-30	contig 1729	1.6282	0.1859	0.1142	12.524615
FexLEA2-17	contig 461	FexLEA2-64	contig 8900	1.3519	0.2034	0.1505	10.399231
FexLEA2-17	contig 461	FexLEA2-29	contig 1631	1.2100	0.2333	0.1928	9.3076923
FexLEA2-17	contig 461	FexLEA2-22	contig 886	1.1989	0.2075	0.1731	9.2223077
FexLEA2-19	contig 630	FexLEA2-61	contig 8085	0.2743	0.0932	0.3398	2.11
FexLEA2-22	contig 886	FexLEA2-29	contig 1631	0.3337	0.0647	0.1939	2.5669231
FexLEA2-22	contig 886	FexLEA2-30	contig 1729	1.4081	0.1464	0.1040	10.831538
FexLEA2-22	contig 886	FexLEA2-64	contig 8900	1.2445	0.1488	0.1196	9.5730769
FexLEA2-22	contig 886	FexLEA2-42	contig 2795	1.0378	0.1872	0.1804	7.9830769
FexLEA2-23	contig 1151	FexLEA2-49	contig 3690	0.2588	0.0670	0.2589	1.9907692
FexLEA2-24	contig 1209	FexLEA2-44	contig 2951	0.2946	0.1228	0.4168	2.2661538
FexLEA2-28	contig 1519	FexLEA2-76	contig 76090	0.4282	0.0910	0.2125	3.2938462
FexLEA2-29	contig1631	FexLEA2-30	contig 1729	1.6303	0.1729	0.1061	12.540769
FexLEA2-29	contig 1631	FexLEA2-64	contig 8900	1.5579	0.1692	0.1086	11.983846
FexLEA2-29	contig 1631	FexLEA2-42	contig 2795	1.1515	0.2085	0.1811	8.8576923
FexLEA2-30	contig 1729	FexLEA2-64	contig 8900	0.3512	0.0976	0.2779	2.7015385
FexLEA2-30	contig 1729	FexLEA2-36	contig 2277	2.5236	0.3570	0.1415	19.412308
FexLEA2-33	contig 1922	FexLEA2-69	contig 23698	0.2709	0.0746	0.2754	2.0838462
FexLEA2-33	contig 1922	FexLEA2-65	contig 8992	0.2709	0.0746	0.2754	2.0838462
FexLEA2-33	contig 1922	FexLEA2-57	contig 4988	0.2709	0.0746	0.2754	2.0838462
FexLEA2-33	contig 1922	FexLEA2-35	contig 2262	0.7886	0.2086	0.2645	6.0661538
FexLEA2-35	contig 2262	FexLEA2-69	contig 23698	0.7094	0.1811	0.2553	5.4569231
FexLEA2-35	contig 2262	FexLEA2-65	contig 8992	0.7094	0.1811	0.2553	5.4569231
FexLEA2-35	contig 2262	FexLEA2-57	contig 4988	0.7094	0.1811	0.2553	5.4569231
FexLEA2-36	contig 2277	FexLEA2-63	contig 8783	0.1692	0.1808	1.0686	1.3015385
FexLEA2-38	contig 2455	FexLEA2-73	contig 48939	0.0092	0.0030	0.3261	0.0707692

Table S3. (continued)

GeneIDs	Chromosome	GeneIDs	Chromosome	Ks	Ka	Ka/Ks	Mya
FexLEA2-40	contig 2623	FexLEA2-71	contig 40151	1.0194	0.2202	0.2160	7.8415385
FexLEA2-40	contig 2623	FexLEA2-56	contig 4932	1.0148	0.2236	0.2203	7.8061538
FexLEA2-40	contig 2623	FexLEA2-52	contig 4307	0.8479	0.2340	0.2760	6.5223077
FexLEA2-41	contig 2759	FexLEA2-68	contig 20758	0.2899	0.0353	0.1218	2.23
FexLEA2-42	contig 2795	FexLEA2-64	contig 8900	1.3147	0.1781	0.1355	10.113077
FexLEA2-46	contig 3082	FexLEA2-75	contig 68764	0.3068	0.1181	0.3849	2.36
FexLEA2-46	contig 3082	FexLEA2-66	contig 9629	1.1200	0.2913	0.2601	8.6153846
FexLEA2-46	contig 3082	FexLEA2-62	contig 8711	0.8925	0.3716	0.4164	6.8653846
FexLEA2-52	contig 4307	FexLEA2-71	contig 40151	0.2374	0.0794	0.3345	1.8261538
FexLEA2-52	contig 4307	FexLEA2-56	contig 4932	0.2374	0.0820	0.3454	1.8261538
FexLEA2-53	contig 4705	FexLEAun-01	contig 571	0.4219	0.1404	0.3328	3.2453846
FexLEA2-56	contig 4932	FexLEA2-71	contig 40151	0.0000	0.0021	0.0000	0
FexLEA2-57	contig 4988	FexLEA2-69	contig 23698	0.0000	0.0000	0.0000	0
FexLEA2-57	contig 4988	FexLEA2-65	contig 8992	0.0000	0.0000	0.0000	0
FexLEA2-58	contig 5487	FexLEA2-59	contig 6304	0.2740	0.1359	0.4960	2.1076923
FexLEA2-62	contig 8711	FexLEA2-66	contig 9629	0.4212	0.1519	0.3606	3.24
FexLEA2-62	contig 8711	FexLEA2-75	contig 68764	1.0936	0.3308	0.3025	8.4123077
FexLEA2-65	contig 8992	FexLEA2-69	contig 23698	0.0000	0.0000	0.0000	0
FexLEA2-66	contig 9629	FexLEA2-75	contig 68764	1.1030	0.2527	0.2291	8.4846154
FexLEAd-05	contig 2595	FexLEAd-08	contig 8902	0.2895	0.0809	0.2794	2.2269231
FexLEAs-04	contig 2624	FexLEAs-05	contig 6696	0.1957	0.0609	0.3112	1.5053846
FexLEAun-03	contig 1884	FexLEAun-04	contig 3090	0.2300	0.0557	0.2422	1.7692308
MEAN				0.8525	0.1492	0.2353	6.5573

Table S4. miRNAs identified by psRNATarget

Arabidopsis thaliana					
miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR5629	FexLEA1-01	5	-1	UUAGGGUAGUUAACGGAAGUUA	CUCUUUCUGUUAGUCAUCUUGA
ath-miR829-5p	FexLEA1-01	5	-1	ACUUUGAAGCUUUGAUUUGAA	ACAAUGUCAAAACUUUGAAGU
ath-miR396a-5p	FexLEA1-05	3,5	-1	UUCCACAGCUUUCUUGAACUG	CAUGUCAACAAAGCUGUGGAA
ath-miR396b-5p	FexLEA1-05	3,5	-1	UUCCACAGCUUUCUUGAACUU	CAUGUCAACAAAGCUGUGGAA
ath-miR773a	FexLEA1-05	5	-1	UUUGCUUCCAGCUUUUGUCUC	AAGGCCAAGGCUG-AAGCAAA
ath-miR838	FexLEA1-05	5	-1	UUUUCUUCUACUUCUUGCACA	GAAGCAA-AAGAGGAAGAAAA
ath-miR5658	FexLEA1-06	5	-1	AUGAUGAUGAUGAUGAUGAAA	ACCCAUGGGCAUCAUCAUCAG
ath-miR867	FexLEA1-06	4,5	-1	UUGAACAUAGGUUUAUUAGGAA	CUCAUAAUAAAC-AUGUUUAA
ath-miR171b-5p	FexLEA2-01	4,5	-1	AGAUAAUAGUGCGGUUCAAUC	GUUGGAACUUCGUUGAUUCU
ath-miR171c-5p	FexLEA2-01	5	-1	AGAUAAUUGGUGCGGUUCAAUC	GUUGGAACUUCGUUGAUUCU
ath-miR172b-5p	FexLEA2-01	5	-1	GCAGACCAUUAAGAUCAC	GUGGAUCUUAAGGAUGUUGG
ath-miR172d-5p	FexLEA2-01	3,5	-1	GCAACAUCUUAAGAUCAG	UGUGGAUCUUAAGGAUGUUGG
ath-miR172e-5p	FexLEA2-01	5	-1	GCAGACCAUUAAGAUCAC	GUGGAUCUUAAGGAUGUUGG
ath-miR2112-3p	FexLEA2-01	5	-1	CUUUAUAUCCGCAUUUGCGCA	AUCACAGAUGUGGAUCUUAAG
ath-miR2112-5p	FexLEA2-01	5	-1	CGCAAUUGCGGAUAUCAUGU	GCGUUUCUGUCCCAUUUGCG
ath-miR5022	FexLEA2-01	4	-1	GUCAUGGGGUUAUGAUCGAAUG	ACUUCGUUGAUUCUCAUGGC
ath-miR5643a	FexLEA2-01	5	-1	AGGCUUUUAAGAUCUGGUUGC	GACACCGGAUCCUGGGAGCUU
ath-miR5643b	FexLEA2-01	5	-1	AGGCUUUUAAGAUCUGGUUGC	GACACCGGAUCCUGGGAGCUU
ath-miR161.2	FexLEA2-02	4,5	-1	UCAAUGCAUUGAAAGUGACUA	ACGUCAUUGUUGAUGCAUUA
ath-miR397b	FexLEA2-02	4,5	-1	UCAUUGAGUGCAUCGUUGAUG	CAUUGUUGAUGCAUUAAGA
ath-miR5663-5p	FexLEA2-02	5	-1	AGCUAAGGAUUUGCAUUCUCA	CCAGAGAGCAAUCUCCGCU
ath-miR849	FexLEA2-02	4,5	-1	UACUAAACAUUGGUGUAGUA	UUCUACAACGACGUUAAGUUA
ath-miR4243	FexLEA2-03	4	-1	UUGAAAUUGUAGAUAUCGUAC	CUUUGAAAUCUGUAAUAUCA
ath-miR779.2	FexLEA2-03	5	-1	UGAUUGGAAAUUUCGUUGACU	CUCCAACCAAAUUCGGAUGG

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR5020a	FexLEA2-04	5	-1	UGGAAGAAGGUGAGACUUGCA	UACAAG-CUCAUCCUCUUCCU
ath-miR5021	FexLEA2-04	5	-1	UGAGAAGAAGAAGAAGAAAA	CCUUUUUCUUCU-CUUCUCG
ath-miR5024-3p	FexLEA2-04	4,5	-1	CCGUAUCUUGGCCUUGUCAUU	AAUGACCGGGUCGAGUUGC GG
ath-miR8165	FexLEA2-05	4,5	-1	AAUGGAGGCAAGUGUGAAGGA	UGCUAUUUGCUUGCCUUUAUU
ath-miR824-3p	FexLEA2-05	5	-1	CCUUCUCAUCGAUGGUCUAGA	UUGAUGCCAUGAAGAGGAGG
ath-miR5645c	FexLEA2-06	5	-1	AACCUAUUUAACGACAUGACU	GGUCGUGUCGAUGAAGAGGUG
ath-miR5998a	FexLEA2-06	4,5	-1	ACAGUUUGUGUUUUGUUUUGU	GGAAAAUAAGACAGAAGCAGU
ath-miR5998b	FexLEA2-06	4,5	-1	ACAGUUUGUGUUUUGUUUUGU	GGAAAAUAAGACAGAAGCAGU
ath-miR865-3p	FexLEA2-07	4	-1	UUUUUCCUCAAUUUAUCCAA	AGGGUUAAGUUUGAGGCGAAG
ath-miR414	FexLEA2-08	4,5	-1	UCAUCUUCAUCAUCAUCGUCA	CAACGAUGACGAUGAGGAUUG
ath-miR779.2	FexLEA2-08	5	-1	UGAUUGGAAAUUUCGUUGACU	GAGCAAUGAAGUUACCCAUCA
ath-miR832-5p	FexLEA2-08	4,5	-1	UGCUGGGAUCGGGAAUCGAAA	GCUUGAUUCCUGAUGCCGGGA
ath-miR838	FexLEA2-08	5	-1	UUUUCUUCUACUUCUUGCACA	GUCUUAAGAAGAAGAAGGAAG
ath-miR863-5p	FexLEA2-08	5	-1	UUAUGUCUUGUUGAUCUCAAU	GAUGAUUCAAGAACACAUAU
ath-miR865-3p	FexLEA2-08	5	-1	UUUUUCCUCAAUUUAUCCAA	GGUGAGAAAAUUGAGGAAACA
ath-miR169g-3p	FexLEA2-09	4	-1	UCCGGCAAGUUGACCUUGGCU	CUUCAAGCUCAACUCCCCGGU
ath-miR1886.1	FexLEA2-09	5	-1	UGAGAGAAGUGAGAUGAAAU	CCCUUGACCUCACUCCCUCA
ath-miR169g-3p	FexLEA2-10	5	-1	UCCGGCAAGUUGACCUUGGCU	AACCAGGAUCAAUGGUCGGA
ath-miR5632-5p	FexLEA2-10	4,5	-1	UUGAUUCUCUUAUCCAACUGU	UAAGGUGGGUGGAAGAAUCAG
ath-miR5658	FexLEA2-10	3,5	-1	AUGAUGAUGAUGAUGAUGAAA	AUUCAUCGUCCUCUUCAUCAU
ath-miR5648-3p	FexLEA2-11	5	-1	AUCUGAAGAAAAUAGCGGCAU	AAGCCGUGAUUUUUUACAAAU
ath-miR169f-3p	FexLEA2-12	5	-1	GCAAGUUGACCUUGGCUCUGC	ACAUAGCCAGGGUCAAGUGU
ath-miR169g-3p	FexLEA2-13	5	-1	UCCGGCAAGUUGACCUUGGCU	AAUCAAGAUCAGCUAGCAGGA
ath-miR833b	FexLEA2-13	5	-1	UGUUUGUUGACAUCGGUCUAG	CAGGAACGGUGUUGAUCAACA
ath-miR8176	FexLEA2-14	5	-1	GGCCGGUGGUCGCGAGAGGGA	CCCCUCCUCCAACCACCGGCU

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR822-3p	FexLEA2-15	4,5	-1	UGUGCAA AUGCUUUCUACAGG	GCUGUAGAAAGUGCUUGUGCU
ath-miR8181	FexLEA2-16	3,5	-1	UGGGGGUGGGGGGGUGACAG	GGGUCCCCUCCUCACUCCCA
ath-miR837-3p	FexLEA2-16	4,5	-1	AAACGAACAAAAA-CUGAUGG	UUGUCGGAUUUUUUGUGCGUUU
ath-miR5658	FexLEA2-17	3,5	-1	AUGAUGAUGAUGAUGAUGAAA	GAUUAUCAUCUUCUUCUUCU
ath-miR5020b	FexLEA2-18	5	-1	AUGGCAUGAAAGAAGGUGAGA	GGACACCCUCCUUC AUGCAAU
ath-miR8167a	FexLEA2-18	5	-1	AGAUGUGGAGAUCGUGGGGAUG	ACCUCCCAC-AUUUCCACAUC
ath-miR8167b	FexLEA2-18	5	-1	AGAUGUGGAGAUCGUGGGGAUG	ACCUCCCAC-AUUUCCACAUC
ath-miR8167c	FexLEA2-18	5	-1	AGAUGUGGAGAUCGUGGGGAUG	ACCUCCCAC-AUUUCCACAUC
ath-miR8167d	FexLEA2-18	5	-1	AGAUGUGGAGAUCGUGGGGAUG	ACCUCCCAC-AUUUCCACAUC
ath-miR8167e	FexLEA2-18	5	-1	AGAUGUGGAGAUCGUGGGGAUG	ACCUCCCAC-AUUUCCACAUC
ath-miR8167f	FexLEA2-18	5	-1	AGAUGUGGAGAUCGUGGGGAUG	ACCUCCCAC-AUUUCCACAUC
ath-miR854a	FexLEA2-18	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	UUCUUCUCUUC AUCCUCCUC
ath-miR854b	FexLEA2-18	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	UUCUUCUCUUC AUCCUCCUC
ath-miR854c	FexLEA2-18	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	UUCUUCUCUUC AUCCUCCUC
ath-miR854d	FexLEA2-18	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	UUCUUCUCUUC AUCCUCCUC
ath-miR854e	FexLEA2-18	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	UUCUUCUCUUC AUCCUCCUC
ath-miR4240	FexLEA2-19	3,5	-1	UGACUAGACCCGUAACAUUAC	UCAAAGUUGUGAGUCUAGUCA
ath-miR5648-3p	FexLEA2-20	5	-1	AUCUGAAGAAA AUAGCGGCAU	CUACCACUGGUUUUUCAGGU
ath-miR5024-3p	FexLEA2-21	3,5	-1	CCGUAUCUUGGCCUUGUCAUU	AAUGACAGGUGCGAGUUGCGG
ath-miR863-5p	FexLEA2-21	5	-1	UUAUGUCUUGUUGAUCUCAAU	AACGAAGUGAACAAGAUAUAG
ath-miR4221	FexLEA2-23	5	-1	UUUUCUCUGUUGAAUUCUUGC	CAAAGAAUUC AUCCGGGGGAGG
ath-miR5656	FexLEA2-23	5	-1	ACUGAAGUAGAGAUUGGGUUU	ACACUCAAUUUCGACUUGAGC
ath-miR779.1	FexLEA2-23	4	-1	UUCUGCUAUGUUGCUGCUCAU	AGGAGCAGCAACAGACUGGAA
ath-miR401	FexLEA2-24	5	-1	CGAAACUGGUGUCGACCGACA	UCACCGUCGACACCAGCGUCG
ath-miR403-5p	FexLEA2-24	4,5	-1	UGUUUUGUGCUUGAAUCUAAAU	AGUGGGAUUC AAGUACAAAAAC

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR5663-5p	FexLEA2-25	4,5	-1	AGCUAAGGAUUUGCAUUCUCA	CCAGAGAGCAAAUCCUACGCU
ath-miR834	FexLEA2-25	3,5	-1	UGGUAGCAGUAGCGGUGGUAA	CUGCCGCCGUUGCUGCUACUU
ath-miR414	FexLEA2-26	5	-1	UCAUCUUCAUCAUCAUCGUCA	CAACGGUGGUGAUGAUCGUGG
ath-miR4243	FexLEA2-26	5	-1	UUGAAAUUGUAGAUUUCGUAC	ACACCAAUUCUAUCACUUUAA
ath-miR5641	FexLEA2-27	4	-1	UGGAAGAAGAUGAUAGAAUUA	GCAUUGAAUUAUCUCCUCCA
ath-miR5654-5p	FexLEA2-27	5	-1	AUAAAUCCCAACAUCUCCA	ACCAGAAUGUUGGGUUUUAU
ath-miR390a-5p	FexLEA2-28	5	-1	AAGCUCAGGAGGGAUAGCGCC	ACCGCCCUUCCUUCUCAGUUU
ath-miR390b-5p	FexLEA2-28	5	-1	AAGCUCAGGAGGGAUAGCGCC	ACCGCCCUUCCUUCUCAGUUU
ath-miR4243	FexLEA2-28	4,5	-1	UUGAAAUUGUAGAUUUCGUAC	CUUUGAGAACUGUAAUUUCAA
ath-miR5650	FexLEA2-28	5	-1	UUGUUUUGGAUCUUAGAUAACA	UUGAUCCAAGAUUCAAGAUA
ath-miR8171	FexLEA2-28	5	-1	AUAGGUGGGCCAGUGGUAGGA	AGCUGCUGCUGCUCUAUCUGU
ath-miR870-5p	FexLEA2-28	5	-1	AAGAACAUCAAAUUAGAAUGU	GAACUGUAAUUUCAAGUUCUU
ath-miR447a-3p	FexLEA2-29	5	-1	UUGGGGACGAGAUGUUUUGUUG	GGCCUCAACGUCUCGUCCCCUA
ath-miR447b	FexLEA2-29	5	-1	UUGGGGACGAGAUGUUUUGUUG	GGCCUCAACGUCUCGUCCCCUA
ath-miR5659	FexLEA2-29	5	-1	CGAUGAAGGUCUUUGGAACGGUA	CCGAAAUACAGGGAUUUUCAUCG
ath-miR841a-3p	FexLEA2-29	5	-1	AUUUCUAGUGGGUCGUUUUA	CGAAUAU-ACCAUCGGAAAU
ath-miR5658	FexLEA2-30	4,5	-1	AUGAUGAUGAUGAUGAUGAAA	CUUCAUCAUUCUCCUUGUCAU
ath-miR854a	FexLEA2-30	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	AUUCUCCUUGUCAUCCUCAUC
ath-miR854b	FexLEA2-30	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	AUUCUCCUUGUCAUCCUCAUC
ath-miR854c	FexLEA2-30	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	AUUCUCCUUGUCAUCCUCAUC
ath-miR854d	FexLEA2-30	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	AUUCUCCUUGUCAUCCUCAUC
ath-miR854e	FexLEA2-30	4,5	-1	GAUGAGGAUAGGGAGGAGGAG	AUUCUCCUUGUCAUCCUCAUC
ath-miR161.2	FexLEA2-32	4	-1	UCAAUGCAUUGAAAGUGACUA	AGGUCAGGUUCAUGCAAUGG
ath-miR397b	FexLEA2-32	4,5	-1	UCAUUGAGUGCAUCGUUGAUG	UGACAAUGAGGCACUCUAUGA
ath-miR4243	FexLEA2-32	4,5	-1	UUGAAAUUGUAGAUUUCGUAC	AUAUGAAUUCUGGGAUUUAA

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR5998a	FexLEA2-32	4,5	-1	ACAGUUUGUGUUUUGUUUUGU	CCAAAACAAAACACAGACAAC
ath-miR5998b	FexLEA2-32	4,5	-1	ACAGUUUGUGUUUUGUUUUGU	CCAAAACAAAACACAGACAAC
ath-miR833a-5p	FexLEA2-32	5	-1	UGUUUGUUGUACUCGGUCUAGU	CUUGAACCGGGUACCAUGGACA
ath-miR5640	FexLEA2-33	5	-1	UGAGAGAAGGAAUAGAUUCA	CAAAGCCGAAUUUUUCUCUCA
ath-miR776	FexLEA2-33	5	-1	UCUAAGUCUUCUAUUGAUGUU	AACUUCGAUGGAAGGUUGGGA
ath-miR781a	FexLEA2-33	5	-1	UUAGAGUUUUCUGGAUACUUA	AAGGUAUUCGGAAACUUCGA
ath-miR781b	FexLEA2-33	5	-1	UUAGAGUUUUCUGGAUACUUA	AAGGUAUUCGGAAACUUCGA
ath-miR830-3p	FexLEA2-33	5	-1	UAACUAUUUUGAGAAGAAGUG	AUUUUUCUCUCAAGAGGUUG
ath-miR839-5p	FexLEA2-33	5	-1	UACCAACCUUCAUCGUUCCC	AACUUCGAUGGAAGGUUGGGA
ath-miR5644	FexLEA2-34	4,5	-1	GUGGGUUGCGGAUAACGGUA	GACCGUUAUACGAAAUCCAA
ath-miR858a	FexLEA2-34	4	-1	UUUCGUUGUCUGUUCGACCUU	AUGGUCGGGGAGACAAUGGAG
ath-miR858b	FexLEA2-34	4,5	-1	UUCGUUGUCUGUUCGACCUUG	GAUGGUCGGGGAGACAAUGGA
ath-miR1886.1	FexLEA2-35	4,5	-1	UGAGAGAAGUGAGAUGAAAUUC	CUAUUCGUCUCACU-CUCUCA
ath-miR8166	FexLEA2-35	4,5	-1	AGAGAGUGUAGAA-AGUUUCUCA	CAAGAAACUCUUCUAUGCUUUCU
ath-miR169g-3p	FexLEA2-36	5	-1	UCCGGCAAGUUGACCUUGGCU	AACCAGGAUCAAAUGGUCGGA
ath-miR5658	FexLEA2-36	5	-1	AUGAUGAUGAUGAUGAUGAAA	AUUCAUCGUCCUCCUCAUCGC
ath-miR774b-5p	FexLEA2-36	4,5	-1	UGAGAUGAAGAU AUGGGUGAU	GCCAUUCAAAUCCUCAUUUCA
ath-miR8167a	FexLEA2-36	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UCGCCUCUUGAUCGCCAUAUCC
ath-miR8167b	FexLEA2-36	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UCGCCUCUUGAUCGCCAUAUCC
ath-miR8167c	FexLEA2-36	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UCGCCUCUUGAUCGCCAUAUCC
ath-miR8167d	FexLEA2-36	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UCGCCUCUUGAUCGCCAUAUCC
ath-miR8167e	FexLEA2-36	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UCGCCUCUUGAUCGCCAUAUCC
ath-miR8167f	FexLEA2-36	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UCGCCUCUUGAUCGCCAUAUCC
ath-miR403-5p	FexLEA2-37	5	-1	UGUUUUGUGCUUGAAUCUAAUU	AAAUGGAUUCAAGAACAAGAAU
ath-miR5020c	FexLEA2-37	5	-1	UGGCAUGGAAGAAGGUGAGAC	CUGGUGCCUUUUUCUAUGCCU

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR5660	FexLEA2-37	4	-1	CAGGUGGUUAGUGCAAUGGAA	CACCACUGCAAAAACCACCUG
ath-miR834	FexLEA2-37	5	-1	UGGUAGCAGUAGCGGUGGUAA	UGAUCAUUGCUGCUGGUGCCU
ath-miR156d-3p	FexLEA2-38	4,5	-1	GCUCACUCUCUUUUUGUCAU	AUGGCAGAAAGAGAGCAAGU
ath-miR419	FexLEA2-39	5	-1	UUAUGAAUGCUGAGGAUGUUG	UAAAUUCUUUGGCAUUCAUGU
ath-miR420	FexLEA2-39	4	-1	UAAACUAAUCACGGAAAUGCA	GUUUUUUCCGUGAUUUGUUUG
ath-miR865-3p	FexLEA2-39	5	-1	UUUUUCCUCAAUUUAUCCAA	UCGAGUCAGCUUGAGGGAAAA
ath-miR868-3p	FexLEA2-39	5	-1	CUUCUUAAGUGCUGAUAAUGC	UCAUUAGCAGCAUUGGAUAAG
ath-miR2111a-5p	FexLEA2-40	5	-1	UAAUCUGCAUCCUGAGGUUUA	AGUUUCUUGUGAUGCAGAUUA
ath-miR2111b-5p	FexLEA2-40	5	-1	UAAUCUGCAUCCUGAGGUUUA	AGUUUCUUGUGAUGCAGAUUA
ath-miR399c-5p	FexLEA2-40	5	-1	GGGCAUCUUUCUAUUGGCAGG	CUUGAAAAUGGAGAGAGGCUC
ath-miR859	FexLEA2-40	5	-1	UCUCUCUGUUGUGAAGUCAAA	AAAGACUUGAAAAUGGAGAGA
ath-miR164a	FexLEA2-41	5	-1	UGGAGAAGCAGGGCACGUGCA	AGCUUGGCCCCUUCUUCUCCA
ath-miR164b-5p	FexLEA2-41	5	-1	UGGAGAAGCAGGGCACGUGCA	AGCUUGGCCCCUUCUUCUCCA
ath-miR164c-5p	FexLEA2-41	5	-1	UGGAGAAGCAGGGCACGUGCG	AGCUUGGCCCCUUCUUCUCCA
ath-miR5656	FexLEA2-41	5	-1	ACUGAAGUAGAGAUUGGGUUU	GUUCUCGUUCUUUGCUUUGGU
ath-miR8181	FexLEA2-41	4	-1	UGGGGGUGGGGGGUGACAG	GGGUCCCCUCCUCAUUCCCA
ath-miR3933	FexLEA2-42	5	-1	AGAAGCAAAAUGACGACUCGG	GAGCGUAGUCAUUUUUCUCCU
ath-miR402	FexLEA2-42	5	-1	UUCGAGGCCUAUUAACCUCUG	UACAAGUCUAAUACGCUUUGGA
ath-miR8172	FexLEA2-42	4,5	-1	AUGGAUCAUCUAGAUGGAGAU	AUCUCCAUC-AGAUGAUCAAU
ath-miR829-5p	FexLEA2-42	4,5	-1	ACUUUG-AAGCUUUGAUUUGAA	AUCAAACGAAGCUUUCAAAGU
ath-miR156a-5p	FexLEA2-43	5	-1	UGACAGAAGAGAGUGAGCAC	CUUUUUACUGUCUUCUGUUU
ath-miR156b-5p	FexLEA2-43	5	-1	UGACAGAAGAGAGUGAGCAC	CUUUUUACUGUCUUCUGUUU
ath-miR156c-5p	FexLEA2-43	5	-1	UGACAGAAGAGAGUGAGCAC	CUUUUUACUGUCUUCUGUUU
ath-miR156d-5p	FexLEA2-43	5	-1	UGACAGAAGAGAGUGAGCAC	CUUUUUACUGUCUUCUGUUU

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR156e	FexLEA2-43	5	-1	UGACAGAAGAGAGUGAGCAC	CUUUUUACUGUCUUCUGUUU
ath-miR156f-5p	FexLEA2-43	5	-1	UGACAGAAGAGAGUGAGCAC	CUUUUUACUGUCUUCUGUUU
ath-miR156g	FexLEA2-43	5	-1	CGACAGAAGAGAGUGAGCAC	CUUUUUACUGUCUUCUGUUU
ath-miR157d	FexLEA2-43	5	-1	UGACAGAAGAUAGAGAGCAC	CUUUUUACUGUCUUCUGUUU
ath-miR837-3p	FexLEA2-43	5	-1	AAACGAACAAAAACUGAUGG	UUGUGGGUUUAUUGUUCUUUU
ath-miR842	FexLEA2-43	4,5	-1	UCAUGGUCAGAUCCGUCAUCC	CUAUGAUGAAUUUGAUGAUGA
ath-miR403-5p	FexLEA2-44	5	-1	UGUUUUGUGCUUGAAUCUAAUU	AGUUGGUUUCGAGUACAAAAAC
ath-miR4243	FexLEA2-44	5	-1	UUGAAAUUGUAGAUUUCGUAC	UGGUGAUUAUCUGUGGUUUUAG
ath-miR2933a	FexLEA2-45	4	-1	GAAAUCGGAGAGGAAAUUCGCC	CAUCUGUUUCUUCUCUGAUUUU
ath-miR2933b	FexLEA2-45	4	-1	GAAAUCGGAGAGGAAAUUCGCC	CAUCUGUUUCUUCUCUGAUUUU
ath-miR415	FexLEA2-45	5	-1	AACAGAGCAGAAACAGAACAU	UUCAUCUGUUUCUUCUCUGAU
ath-miR417	FexLEA2-45	5	-1	GAAGGUAGUGAAUUUGUUCGA	CAAAACAAAUUCAAUUUUUC
ath-miR447a-3p	FexLEA2-45	4,5	-1	UUGGGGACGAGAUGUUUUGUUG	AUUCUAAAUAUUACGUUCCAA
ath-miR447b	FexLEA2-45	4,5	-1	UUGGGGACGAGAUGUUUUGUUG	AUUCUAAAUAUUACGUUCCAA
ath-miR5021	FexLEA2-45	4	-1	UGAGAAGAAGAAGAAGAAAA	GUUUCAUCUGUUUCUUCUCU
ath-miR5654-3p	FexLEA2-45	4	-1	UGGAAGAUGCUUUGGGAUUUAUU	UCUGAAUCCAAUGCAUUCUCCA
ath-miR773b-5p	FexLEA2-45	5	-1	GGCAAUAACUUGAGCAAACA	GGUCAGGUUAAGUUAUGGCC
ath-miR835-3p	FexLEA2-45	5	-1	UGGAGAAGAUACGCAAGAAAG	GUUUCAUCUGUUUCUUCUCUG
ath-miR173-3p	FexLEA2-46	5	-1	UGAUUCUCUGUGUAAGCGAAA	GAUCGGGUACAGAGGGGAUCG
ath-miR418	FexLEA2-46	3	-1	UAAUGUGAUGAUGAACUGACC	UCUCAAUACGUCAUCGCAUUA
ath-miR8181	FexLEA2-46	5	-1	UGGGGGUGGGGGGGUGACAG	UUGUGCCUCCUCCACCGCCG
ath-miR823	FexLEA2-46	5	-1	UGGGUGGUGAUCAUAUAAGAU	GUCUUAUGUGAACGCCACGCU
ath-miR841a-3p	FexLEA2-46	5	-1	AUUUCUAGUGGGUCGUUUCA	UGACUAUGAUUCAUUAGAUGU
ath-miR8167a	FexLEA2-47	5	-1	AGAUGUGGAGAUCGUGGGGAUG	CGCCACCGCGGUCUCCACGGCG
ath-miR8167b	FexLEA2-47	5	-1	AGAUGUGGAGAUCGUGGGGAUG	CGCCACCGCGGUCUCCACGGCG

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR8167c	FexLEA2-47	5	-1	AGAUGUGGAGAUCGUGGGGAUG	CGCCACCGCGGUCUCCACGGCG
ath-miR8167d	FexLEA2-47	5	-1	AGAUGUGGAGAUCGUGGGGAUG	CGCCACCGCGGUCUCCACGGCG
ath-miR8167e	FexLEA2-47	5	-1	AGAUGUGGAGAUCGUGGGGAUG	CGCCACCGCGGUCUCCACGGCG
ath-miR8167f	FexLEA2-47	5	-1	AGAUGUGGAGAUCGUGGGGAUG	CGCCACCGCGGUCUCCACGGCG
ath-miR8181	FexLEA2-47	4,5	-1	UGGGGGUGGGGGGGUGACAG	AUGUCACUUCUACACCCCUU
ath-miR826a	FexLEA2-47	4,5	-1	UAGUCCGUUUUGGAUACGUG	AAUGCAUGCAAAAUCGGAUUC
ath-miR857	FexLEA2-47	5	-1	UUUUGUAUGUUGAAGGUGUAU	GAAAAUUUUUAAUGUACAAGC
ath-miR866-5p	FexLEA2-47	4,5	-1	UCAAGGAACGGAUUUUGUUA	UUGACAAGAUCUGGUUCUUGU
ath-miR408-3p	FexLEA2-48	5	-1	AUGCACUGCCUCUCCCCUGGC	CUCCGGCAAGACGCAGUACAU
ath-miR5657	FexLEA2-48	5	-1	UGGACAAGGUUAGAUUUGGUG	GCACAAAUUUAGCCUCGUGCA
ath-miR8181	FexLEA2-48	5	-1	UGGGGGUGGGGGGGUGACAG	CCGUCACCUUCACAUUCUCA
ath-miR5656	FexLEA2-49	5	-1	ACUGAAGUAGAGAUUGGGUUU	ACACUCAAUUUCGACUUGAGC
ath-miR779.1	FexLEA2-49	4	-1	UUCUGCUAUGUUGCUGCUCAU	AGGAGCAGCAACAGACUGGAA
ath-miR4228-5p	FexLEA2-50	4	-1	AUAGCCUUGAACGCCGUCGUU	GGUGGCGGCUUUUGAGGCUGU
ath-miR5020a	FexLEA2-50	3	-1	UGGAAGAAGGUGAGACUUGCA	CAUAAAUUUCACCUUUUUCUA
ath-miR5647	FexLEA2-50	5	-1	UCAAGUUUGAUGACGAUUGCA	UUUCUUUAUCAUCAAGCUUGA
ath-miR826a	FexLEA2-50	4,5	-1	UAGUCCGUUUUGGAUACGUG	AUUGUAUCUAAAGUUGGUCUG
ath-miR837-3p	FexLEA2-50	5	-1	AAACGAACAAAAACUGAUGG	ACAGCAGUUUUUGGUUCCUUC
ath-miR1886.2	FexLEA2-51	4,5	-1	UGAGAUGAAAUCUUUGAUUGG	AAAGACCAAGAUUUUAUCACA
ath-miR5654-3p	FexLEA2-51	5	-1	UGGAAGAUGC UUUGGAUUUAUU	CAAGAAUGCCAAACCAAUUUCUA
ath-miR5658	FexLEA2-52	4,5	-1	AUGAUGAUGAUGAUGAUGAAA	UCUCACCCUCGUCGUCGUUGU
ath-miR773b-3p	FexLEA2-53	5	-1	UUUGAUUCCAGCUUUUGUCUC	AAUGCAGAGUUUGGAAUCAAG
ath-miR826b	FexLEA2-54	4,5	-1	UGGUUUUGGACACGUGAAAAU	AAGUUCAUCUGUUCAAAGUCA
ath-miR826b	FexLEA2-54	5	-1	UGGUUUUGGACACGUGAAAAU	AUUUUUACGCGUAAAAACCC
ath-miR5641	FexLEA2-56	5	-1	UGGAAGAAGAUGAUAGAAUUA	CAGUCCAUUUUCUUCUCAA

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR162a-3p	FexLEA2-57	5	-1	UCGAUAAACCUCUGCAUCCAG	UGGGAUGUAUAGGUUUAAGU
ath-miR162b-3p	FexLEA2-57	5	-1	UCGAUAAACCUCUGCAUCCAG	UGGGAUGUAUAGGUUUAAGU
ath-miR1886.3	FexLEA2-57	5	-1	AAUUAAGAUUUCUUCUACU	UUUAAUGUGAACUGUUUAGUU
ath-miR5653	FexLEA2-57	4,5	-1	UGGGUUGAGUUGAGUUGAGUUGGC	UUGAAAUCAA-UCAACUCAACCUC
ath-miR830-3p	FexLEA2-57	5	-1	UAACUAUUUUGAGAAGAAGUG	AGUUUUCUCUCAAGAGGUUG
ath-miR5014a-5p	FexLEA2-58	4,5	-1	ACACUUAGUUUUGUACAACAU	CAGCUAUACAAAAUAAGUGG
ath-miR5658	FexLEA2-58	4,5	-1	AUGAUGAUGAUGAUGAUGAAA	GGUCAAGAUUAUCAACAUUAU
ath-miR5014a-5p	FexLEA2-59	4,5	-1	ACACUUAGUUUUGUACAACAU	UAGCUAUACAAAAUAAGUGG
ath-miR165a-5p	FexLEA2-60	3,5	-1	GGAAUGUUGUCUGGAUCGAGG	GAUUGCUUCGGGCAAUAUCC
ath-miR166e-5p	FexLEA2-60	4,5	-1	GGAAUGUUGUCUGGCACGAGG	GAUUGCUUCGGGCAAUAUCC
ath-miR2112-3p	FexLEA2-60	5	-1	CUUUUAUACCGCAUUGCGCA	UGC-UAGAUGUGGAAUAAAG
ath-miR403-3p	FexLEA2-60	4,5	-1	UUAGAUUCACGCACAAACUCG	AUAGUGUGUUGGUGAGUCUAA
ath-miR406	FexLEA2-60	5	-1	UAGAAUGCUAUUGUAAUCCAG	GGGAAUGACAAUACCAUGCUA
ath-miR830-3p	FexLEA2-60	5	-1	UAACUAUUUUGAGAAGAAGUG	UCCUCUUUCUCAAAGGGUGA
ath-miR401	FexLEA2-61	5	-1	CGAAACUGGUGUCGACCGACA	GGUGGGGCGGUACCGGUGUCG
ath-miR418	FexLEA2-61	5	-1	UAAUGUGAUGAUGAACUGACC	UGCACGAUCAUCGUCAUAUUA
ath-miR5017-5p	FexLEA2-62	4,5	-1	AUUUGUUACUAAUUGGAAUG	CUUCCCAGAUUAGUGGGAGAU
ath-miR776	FexLEA2-62	4	-1	UCUAAGUCUUCUAUUGAUGUU	CAGAUUAGUGGGAGAUUUGGA
ath-miR776	FexLEA2-62	5	-1	UCUAAGUCUUCUAUUGAUGUU	UCUGUUGCUGGAAGACUUGGC
ath-miR857	FexLEA2-62	5	-1	UUUUGUAUGUUGAAGGUGUAU	CCUCACCAUCAAGGUACGGAA
ath-miR839-5p	FexLEA2-63	5	-1	UACCAACCUUCAUCGUUCCC	AAGUACGAUGGAGAGUUGGAA
ath-miR5658	FexLEA2-64	4	-1	AUGAUGAUGAUGAUGAUGAAA	CUUCAUCAUUCUCUUUAUCAU
ath-miR773b-3p	FexLEA2-64	4	-1	UUUGAUUCCAGCUUUGUCUC	GUGAUAGGAGCUGCAAUUAAG
ath-miR774b-5p	FexLEA2-64	3,5	-1	UGAGAUGAAGAUUGGGUGAU	UUCUCCCUUAUCUUAUCUUC

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR854a	FexLEA2-64	4	-1	GAUGAGGAU-AGGGAGGAGGAG	UGCCUUCUCCCUUAUCUUCAUC
ath-miR854b	FexLEA2-64	4	-1	GAUGAGGAU-AGGGAGGAGGAG	UGCCUUCUCCCUUAUCUUCAUC
ath-miR854c	FexLEA2-64	4	-1	GAUGAGGAU-AGGGAGGAGGAG	UGCCUUCUCCCUUAUCUUCAUC
ath-miR854d	FexLEA2-64	4	-1	GAUGAGGAU-AGGGAGGAGGAG	UGCCUUCUCCCUUAUCUUCAUC
ath-miR854e	FexLEA2-64	4	-1	GAUGAGGAU-AGGGAGGAGGAG	UGCCUUCUCCCUUAUCUUCAUC
ath-miR162a-3p	FexLEA2-65	5	-1	UCGAUAAACCUCUGCAUCCAG	UGGGAUGUAUAGGUUUAUGU
ath-miR162b-3p	FexLEA2-65	5	-1	UCGAUAAACCUCUGCAUCCAG	UGGGAUGUAUAGGUUUAUGU
ath-miR1886.3	FexLEA2-65	5	-1	AAUUAAGAUUUCUUCUACU	UUUAAUGUGAACUGUUUAGUU
ath-miR5653	FexLEA2-65	4,5	-1	UGGGUUGAGUUGAGUUGAGUUGGC	UUGAAAUCAA-UCAACUCAACCUC
ath-miR830-3p	FexLEA2-65	5	-1	UACUAUUUUGAGAAGAAGUG	AGUUUUCUCUCAAGAGGUUG
ath-miR2936	FexLEA2-66	4	-1	CUUGAGAGAGAGAACACAGACG	GCUCGGUGUUUCUUUUUCGAA
ath-miR854a	FexLEA2-67	5	-1	GAUGAGGAUAGGGAGGAGGAG	AGCCUCUCCUGAUCUUCUUU
ath-miR854b	FexLEA2-67	5	-1	GAUGAGGAUAGGGAGGAGGAG	AGCCUCUCCUGAUCUUCUUU
ath-miR854c	FexLEA2-67	5	-1	GAUGAGGAUAGGGAGGAGGAG	AGCCUCUCCUGAUCUUCUUU
ath-miR854d	FexLEA2-67	5	-1	GAUGAGGAUAGGGAGGAGGAG	AGCCUCUCCUGAUCUUCUUU
ath-miR854e	FexLEA2-67	5	-1	GAUGAGGAUAGGGAGGAGGAG	AGCCUCUCCUGAUCUUCUUU
ath-miR162a-3p	FexLEA2-69	5	-1	UCGAUAAACCUCUGCAUCCAG	UGGGAUGUAUAGGUUUAUGU
ath-miR162b-3p	FexLEA2-69	5	-1	UCGAUAAACCUCUGCAUCCAG	UGGGAUGUAUAGGUUUAUGU
ath-miR1886.3	FexLEA2-69	5	-1	AAUUAAGAUUUCUUCUACU	UUUAAUGUGAACUGUUUAGUU
ath-miR5653	FexLEA2-69	4,5	-1	UGGGUUGAGUUGAGUUGAGUUGGC	UUGAAAUCAA-UCAACUCAACCUC
ath-miR830-3p	FexLEA2-69	5	-1	UACUAUUUUGAGAAGAAGUG	AGUUUUCUCUCAAGAGGUUG
ath-miR775	FexLEA2-70	5	-1	UUCGAUGUCUAGCAGUGCCA	UGGCA-UGUUUGAUUUGAA
ath-miR5641	FexLEA2-71	5	-1	UGGAAGAAGAUAGAAUUA	CAGUCCAUUUUCUUCUCAA
ath-miR5653	FexLEA2-72	4	-1	UGGGUUGAGUUGAGUUGAGUUGGC	AUGAGAAUACUCAAUUCAUCUA
ath-miR822-3p	FexLEA2-72	5	-1	UGUGCAAAUGCUUUCUACAGG	GCUGUAGAAAGUGCUUGUGUU

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR156d-3p	FexLEA2-73	4,5	-1	GCUCACUCUCUUUUUGUCAU	AUGGCAGAAAGAGAGCAAGU
ath-miR5023	FexLEA2-74	5	-1	AUUGGUAGUGGAUAAGGGGGC	CCACCCUUAACCACCACCAAA
ath-miR870-3p	FexLEA2-74	4,5	-1	UAAUUUGGUGUUUCUUCGAUC	UCUCCAAGAAAAACGGAAUUA
ath-miR163	FexLEA2-75	5	-1	UUGAAGAGGACUUGGAACUUCGAU	UGGGAAGUUCGGAGUUUUCUUCUU
ath-miR418	FexLEA2-75	3,5	-1	UAAUGUGAUGAUGAACUGACC	UCUCAAUACGUCAUCGUAUUA
ath-miR5647	FexLEA2-75	5	-1	UCAAGUUUGAUGACGAUUGCA	CUCCAUCGACAUCAAACUCGA
ath-miR8167a	FexLEA2-75	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UGGCCCUCCGAUCCCUACCUCU
ath-miR8167b	FexLEA2-75	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UGGCCCUCCGAUCCCUACCUCU
ath-miR8167c	FexLEA2-75	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UGGCCCUCCGAUCCCUACCUCU
ath-miR8167d	FexLEA2-75	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UGGCCCUCCGAUCCCUACCUCU
ath-miR8167e	FexLEA2-75	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UGGCCCUCCGAUCCCUACCUCU
ath-miR8167f	FexLEA2-75	5	-1	AGAUGUGGAGAUCGUGGGGAUG	UGGCCCUCCGAUCCCUACCUCU
ath-miR841a-3p	FexLEA2-75	5	-1	AUUUCUAGUGGGUCGUAUUA	UGAUUAUGAUUCAUUAGCAGU
ath-miR848	FexLEA2-75	5	-1	UGACAUGGGACUGCCUA--AGCUA	GAGCUCGUGGGAAGUCCUAUGUCA
ath-miR854a	FexLEA2-75	5	-1	GAUGAGGAUAGGGAGGAGGAG	GCCGUUCUCCGUUCCUCAUC
ath-miR854b	FexLEA2-75	5	-1	GAUGAGGAUAGGGAGGAGGAG	GCCGUUCUCCGUUCCUCAUC
ath-miR854c	FexLEA2-75	5	-1	GAUGAGGAUAGGGAGGAGGAG	GCCGUUCUCCGUUCCUCAUC
ath-miR854d	FexLEA2-75	5	-1	GAUGAGGAUAGGGAGGAGGAG	GCCGUUCUCCGUUCCUCAUC
ath-miR854e	FexLEA2-75	5	-1	GAUGAGGAUAGGGAGGAGGAG	GCCGUUCUCCGUUCCUCAUC
ath-miR2934-3p	FexLEA2-76	4	-1	CAUCCAAGGUGUUUGUAGAAA	CGACUGCAAAUACUAUGGAUG
ath-miR5015	FexLEA2-76	5	-1	UUGGUGUUAUGUGUAGUCUUC	UCUCACUGCACGUAACCCUAA
ath-miR5650	FexLEA2-76	5	-1	UUGUUUUGGAUCUUAAGAUACA	UUGAUCCAAGAUUCAAGAUA
ath-miR8171	FexLEA2-76	4,5	-1	AUAGGUGGGCCAGUGGUAGGA	AGCUGCUGCUGCUCCAUCUGU
ath-miR8181	FexLEA2-76	5	-1	UGGGGGUGGGGGGGUGACAG	GUUUCGACCCUCCACCUCUC
ath-miR834	FexLEA2-76	4,5	-1	UGGUAGCAGUAGCGGUGGUAA	CCACCGCCGUAGCUGCUGCUG

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR870-3p	FexLEA2-76	5	-1	UAAUUUGGUGUUUCUUCGAUC	AAACGAAGAAGCUCAGAAUUA
ath-miR396a-5p	FexLEA3-01	5	-1	UUCCACAGCUUUCUUGAACUG	UUGAUAAAAGAAAGCGGUUGAA
ath-miR396b-5p	FexLEA3-01	5	-1	UUCCACAGCUUUCUUGAACUU	UUGAUAAAAGAAAGCGGUUGAA
ath-miR164c-3p	FexLEA3-03	5	-1	CACGUGUUCUACUACUC-CAAC	UUUGUGAUUAGUGGAACACUUG
ath-miR166e-5p	FexLEA3-03	5	-1	GGAAUGUUGUCUGGCACGAGG	AUGGGUGAUAGAUGAUAUUCC
ath-miR414	FexLEA3-03	3	-1	UCAUCUUCAUCAUCAUCGUCA	UGAUGAAAGUGAUGAAGAUGA
ath-miR414	FexLEA3-03	3,5	-1	UCAUCUUCAUCAUCAUCGUCA	UGACGACGAUGAUGAAGAUUU
ath-miR5632-5p	FexLEA3-03	5	-1	UUGAUUCUCUUAUCCAACUGU	UGGGGUGGGUAAGGGAGUUGC
ath-miR832-5p	FexLEA3-03	4,5	-1	UGCUGGGAUCGGGAAUCGAAA	GCUGGAUUCUGAUCCACGCA
ath-miR169a-3p	FexLEA3-05	5	-1	GGCAAGUUGUCCUUGGCUAC	GCAGCGCAGGGCGGCUUGUC
ath-miR1886.2	FexLEA4-01	5	-1	UGAGAUGAAAUCUUUG-AUUGG	UGAAUACAAAGAUUUUGCUUCA
ath-miR416	FexLEA4-01	5	-1	GGUUCGUACGUACACUGUUCA	GUGGCCGGGUGCGUGUGGACC
ath-miR4221	FexLEA4-01	4,5	-1	UUUUCCUCUGUUGAAUUCUUGC	CAAAGGAUACAACAAUGGAAAA
ath-miR4221	FexLEA4-01	5	-1	UUUUCCUCUGUUGAAUUCUUGC	AUAAGGAUUACACGGGGGAGAA
ath-miR4221	FexLEA4-01	5	-1	UUUUCCUCUGUUGAAUUCUUGC	UUGAGAAGGCCGUAGAGGGAAA
ath-miR4239	FexLEA4-01	5	-1	UUUGUUAUUUUCGCAUGCUC	ACAGAAGGCGAAAGAGACGAA
ath-miR4239	FexLEA4-01	5	-1	UUUGUUAUUUUCGCAUGCUC	ACAGAAGGCGAAAGAGACGAA
ath-miR4239	FexLEA4-01	5	-1	UUUGUUAUUUUCGCAUGCUC	ACAGAAGGCGAAAGAGACGAA
ath-miR837-5p	FexLEA4-01	4,5	-1	AUCAGUUUCUUGUUCGUUUA	CAGAAGGCACAAGAAACUUGU
ath-miR838	FexLEA4-01	5	-1	UUUUCUUCUACUUCUUGCACA	GAAGCAAGAAGGAAAAGGGAA
ath-miR157a-3p	FexLEA4-02	5	-1	GCUCUCUAGCCUUCUGUCAUC	CCUCAGAGAAGACUAGGGAGA
ath-miR157b-3p	FexLEA4-02	5	-1	GCUCUCUAGCCUUCUGUCAUC	CCUCAGAGAAGACUAGGGAGA
ath-miR396a-5p	FexLEA4-02	4,5	-1	UUCCACAGCUUUCUUGAACUG	GCAUUAGGCAAAGCUGUGGAA
ath-miR396b-5p	FexLEA4-02	4,5	-1	UUCCACAGCUUUCUUGAACUU	GCAUUAGGCAAAGCUGUGGAA
ath-miR4221	FexLEA4-02	5	-1	UUUUCCUCUGUUGAAUUCUUGC	CUAAGGAUACAACAAUGGAGAA

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR5595a	FexLEA4-02	5	-1	ACAUAUGAUCUGCAUCUUUGC	UGAAAGCGGCUGAUCAAAUGU
ath-miR5995b	FexLEA4-02	5	-1	ACAUAUGAUCUGCAUCUUUGC	UGAAAGCGGCUGAUCAAAUGU
ath-miR836	FexLEA4-02	5	-1	UCCUGUGUUUCCUUUGAUGCGUGG	CCAGAAGGCAAAGGAGACGAAGGA
ath-miR837-5p	FexLEA4-02	5	-1	AUCAGUUUCUUGUUCGUUUCA	CAGAGAGAACAAGAAGGUGAA
ath-miR856	FexLEA4-02	4,5	-1	UAAUCCUACCAUAACUUCAGC	CCUGGUGUUAUUGGAAGCAUUA
ath-miR4221	FexLEA4-03	3,5	-1	UUUUCUCUGUUGAAUUCUUGC	UAAAGAAUGCAGCAAAGGAGAA
ath-miR4221	FexLEA4-03	5	-1	UUUUCUCUGUUGAAUUCUUGC	CAAAGAAUGCAGCCAAGGAGAA
ath-miR831-3p	FexLEA5-01	5	-1	UGAUCUCUUCGUACUCUUCUUG	AGAGAAGGGUAUCAAGAGAUGG
ath-miR169b-3p	FexLEA5-02	5	-1	GGCAAGUUGUCCUUCGGCUACA	CGAGGCCCAAGAACACCUUGCU
ath-miR830-3p	FexLEA5-02	5	-1	UAAUCUUAUUUGAGAAGAAGUG	UCGUUUUACUCAAGGCAGUUA
ath-miR858a	FexLEA5-02	5	-1	UUUCGUUGUCUGUUCGACCUU	AAGGGAGGACAGACGAGGAAG
ath-miR858b	FexLEA5-02	4,5	-1	UUCGUUGUCUGUUCGACCUUG	UAAGGGAGGACAGACGAGGAA
ath-miR8182	FexLEA6-02	4,5	-1	UUGUGUUGCGUUUCUGUUGAUU	UGGAAAUAGAAGAGCAGCAUAA
ath-miR169b-3p	FexLEAd-01	4,5	-1	GGCAAGUUGUCCUUCGGCUACA	AGAAGGUGAAGGAGAAGUUGCC
ath-miR408-3p	FexLEAd-01	4,5	-1	AUGCACUGCCUCUUCCCUGGC	CUCAAGGAGGAGGCUAUGCAU
ath-miR837-5p	FexLEAd-01	4,5	-1	AUCAGUUUCUUGUUCGUUUCA	UCGGGCCAACAAGGAACUGGA
ath-miR837-5p	FexLEAd-01	5	-1	AUCAGUUUCUUGUUCGUUUCA	ACUGGCCAACAAGGAACUGGA
ath-miR157c-3p	FexLEAd-02	5	-1	GCUCUCUAUACUUCUGUCAC	AUGGCAGAA-UAUGGAGAGA
ath-miR414	FexLEAd-02	4	-1	UCAUCUUCAUCAUCGUCA	GGAGGAUGAUGGGGAAGGUGG
ath-miR4221	FexLEAd-02	5	-1	UUUUCUCUGUUGAAUUCUUGC	CGGAGAAUGCGAC-GAGGAGAA
ath-miR5012	FexLEAd-02	5	-1	UUUUACUGCUACUUGUGUUC	AGUUCACCGGUAGCGGUAAGG
ath-miR838	FexLEAd-02	4,5	-1	UUUUCUUCUACUUCUUGCACA	AAUGCGACGAGGAGAAGAAGG
ath-miR838	FexLEAd-02	5	-1	UUUUCUUCUACUUCUUGCACA	GAUGGGGAAGGUGGAAGGAGA
ath-miR842	FexLEAd-02	4,5	-1	UCAUGGUCAGAUCCGUCAUC	GAAUGAUGGAUAAGAUCAUGG
ath-miR414	FexLEAd-03	5	-1	UCAUCUUCAUCAUCGUCA	AGAAGAGCAUGAUGGAGAAGA

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR4221	FexLEAd-03	5	-1	UUUUCCUCUGUUGAAUUCUUGC	AGGAGAAGUUGACAGGUGGGAA
ath-miR472-3p	FexLEAd-03	5	-1	UUUUUCCUACUCCGCCCAUACC	GGCAAGGUGGGAGGAGGAAGAA
ath-miR834	FexLEAd-03	5	-1	UGGUAGCAGUAGCGGUGGUAA	AUCUUACUGCUGUCGCUACCA
ath-miR472-3p	FexLEAd-04	5	-1	UUUUUCCUACUCCGCCCAUACC	GGCAAGGUGGGAGGAGGAAGAA
ath-miR780.2	FexLEAd-04	5	-1	UUCUUCGUGAAUAUCUGGCAU	AUGGCAGAUAUACGUGAUGAA
ath-miR847	FexLEAd-04	3,5	-1	UCACUCCUCUUCUUCUUGAUG	GCACGAGAAGAAGGGGUGUGA
ath-miR156a-3p	FexLEAd-05	4,5	-1	GCUCACUGCUCUUUCUGUCAGA	AUUGAGAAGAAGAGCGAUGAGC
ath-miR838	FexLEAd-05	3,5	-1	UUUUCUUCUACUUCUUGCACA	UGAGGAAGAAGUGGAAGAAGG
ath-miR838	FexLEAd-05	4	-1	UUUUCUUCUACUUCUUGCACA	GAGGAGAGAAGAAGAAGAAAA
ath-miR847	FexLEAd-05	4,5	-1	UCACUCCUCUUCUUCUUGAUG	CAUUGAGAAGAAGAGCGAUGA
ath-miR865-3p	FexLEAd-05	5	-1	UUUUUCCUCAAUUUAUCCAA	UUAGAAAAAUGUGAGGAAAUA
ath-miR865-3p	FexLEAd-05	5	-1	UUUUUCCUCAAUUUAUCCAA	CAUGAAGAAUCUGAGGAGAAG
ath-miR865-3p	FexLEAd-05	5	-1	UUUUUCCUCAAUUUAUCCAA	GAGAAGAAGUGUGAGGAGGAA
ath-miR838	FexLEAd-06	4,5	-1	UUUUCUUCUACUUCUUGCACA	CGAGGAGGGAGUAGAAGAGGG
ath-miR838	FexLEAd-06	4,5	-1	UUUUCUUCUACUUCUUGCACA	GGAGAAAGAAGAAGAAGAAGG
ath-miR396a-5p	FexLEAd-07	5	-1	UUCCACAGCUUUCUUGAACUG	GGCCACAAGAAGGCUGAGGAA
ath-miR396b-5p	FexLEAd-07	5	-1	UUCCACAGCUUUCUUGAACUU	GGCCACAAGAAGGCUGAGGAA
ath-miR403-3p	FexLEAd-07	5	-1	UUAGAUUCACGCACAAACUCG	AGUGAUUGUGAGUGAGUUUGA
ath-miR8167a	FexLEAd-07	4,5	-1	AGAUGUGGAGAUUCGUGGGGAUG	CACCCCCACCAUAUCCAUAUCA
ath-miR8167b	FexLEAd-07	4,5	-1	AGAUGUGGAGAUUCGUGGGGAUG	CACCCCCACCAUAUCCAUAUCA
ath-miR8167c	FexLEAd-07	4,5	-1	AGAUGUGGAGAUUCGUGGGGAUG	CACCCCCACCAUAUCCAUAUCA
ath-miR8167d	FexLEAd-07	4,5	-1	AGAUGUGGAGAUUCGUGGGGAUG	CACCCCCACCAUAUCCAUAUCA
ath-miR8167e	FexLEAd-07	4,5	-1	AGAUGUGGAGAUUCGUGGGGAUG	CACCCCCACCAUAUCCAUAUCA
ath-miR8167f	FexLEAd-07	4,5	-1	AGAUGUGGAGAUUCGUGGGGAUG	CACCCCCACCAUAUCCAUAUCA
ath-miR838	FexLEAd-07	2,5	-1	UUUUCUUCUACUUCUUGCACA	CAAGGAAGAAGUAGAAGAGAA

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR156a-3p	FexLEAd-08	4,5	-1	GCUCACUGCUCUUUCUGUCAGA	AUCGAGAAGAAGAGCGAUGAGC
ath-miR838	FexLEAd-08	3,5	-1	UUUUCUUCUACUUCUUGCACA	UGAGGAAGAAGUGGAAGAAGG
ath-miR847	FexLEAd-08	4	-1	UCACUCCUCUUCUUCUUGAUG	CAUCGAGAAGAAGAGCGAUGA
ath-miR865-3p	FexLEAd-08	5	-1	UUUUUCCUCAAAUUUAUCCAA	CAUGAAGAAUCUGAGGAGAAG
ath-miR865-3p	FexLEAd-08	5	-1	UUUUUCCUCAAAUUUAUCCAA	GAGAAGAAGUGUGAGGAGGAA
ath-miR832-3p	FexLEAS-01	3,5	-1	UUGAUUCCCAAUCCAAGCAAG	GAUGGAUUGAUUGGGGAUCAA
ath-miR403-5p	FexLEAS-04	5	-1	UGUUUUGUGCUUGAAUCUAAUU	UUAUGGAUGCAAGCUCAAAGUU
ath-miR8182	FexLEAS-04	5	-1	UUGUGUUGCGUUUCUGUUGAUU	UAGCGAUGCAGCCGCAAUACAA
ath-miR8183	FexLEAS-04	5	-1	UUUAGUUGACGGAAUUGUGGC	GACACAAGCCUGUCGACUAUA
ath-miR867	FexLEAS-04	5	-1	UUGAACAUUGGUUUUUAGGAA	UGCCUCAGAAACUAUGUAUGA
ath-miR156a-5p	FexLEAun-01	5	-1	UGACAGAAGAGAGUGAGCAC	AUGCUUACUUUAUUAUUGUUA
ath-miR156b-5p	FexLEAun-01	5	-1	UGACAGAAGAGAGUGAGCAC	AUGCUUACUUUAUUAUUGUUA
ath-miR156c-5p	FexLEAun-01	5	-1	UGACAGAAGAGAGUGAGCAC	AUGCUUACUUUAUUAUUGUUA
ath-miR156d-5p	FexLEAun-01	5	-1	UGACAGAAGAGAGUGAGCAC	AUGCUUACUUUAUUAUUGUUA
ath-miR156e	FexLEAun-01	5	-1	UGACAGAAGAGAGUGAGCAC	AUGCUUACUUUAUUAUUGUUA
ath-miR156f-5p	FexLEAun-01	5	-1	UGACAGAAGAGAGUGAGCAC	AUGCUUACUUUAUUAUUGUUA
ath-miR173-5p	FexLEAun-01	3	-1	UUCGCUUGCAGAGAGAAAUCAC	UUUUUUUCUCUCUGAAAGUGAA
ath-miR396a-5p	FexLEAun-01	5	-1	UUCCACAGCUUUCUUGAACUG	AAGUUUAAUGAGGUGGUGGAA
ath-miR396b-5p	FexLEAun-01	5	-1	UUCCACAGCUUUCUUGAACUU	AAGUUUAAUGAGGUGGUGGAA
ath-miR414	FexLEAun-01	4,5	-1	UCAUCUUCAUCAUCAUCGUCA	AGGUGGAGCUGAUGAAGGUGA
ath-miR3434-5p	FexLEAun-02	4,5	-1	ACUUGGCUGAUUCUAUUUAUU	UGUAAUGGAGACGGCCAAGA
ath-miR5654-5p	FexLEAun-02	5	-1	AUAAAUCCCAACAUCUCCA	UGAAAGAUGUUGGGAGUGAA
ath-miR773a	FexLEAun-02	5	-1	UUUGCUUCCAGCUUUUGUCUC	GUGAAAGAUGUUGGGAGUGAA
ath-miR8177	FexLEAun-02	5	-1	GUGUGAUGAUGUGUCAUUUAUA	CUGAGAUCUCAAUAUCAUCGUAC
ath-miR847	FexLEAun-02	5	-1	UCACUCCUCUUCUUCUUGAUG	AUUAAAGGAGAGGCGGAGAGA

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR862-5p	FexLEAun-02	5	-1	UCCAAUAGGUCGAGCAUGUGC	AUUUAUGUUUGACGUAUUGGC
ath-miR865-3p	FexLEAun-02	5	-1	UUUUUCCUCAAUUUAUCCAA	AAGGAGAAAUUUGAACGAGAA
ath-miR870-3p	FexLEAun-02	5	-1	UAAUUUGGUGUUUCUUCGAUC	GAUGGUGGAAACACCAAAGUU
ath-miR2937	FexLEAun-03	4,5	-1	AUAAGAGCUGUUGAAGGAGUC	GUUUUCUGCAAGAGUUCUUGU
ath-miR426	FexLEAun-03	4,5	-1	UUUUGGAAAUUUGUCCUACG	GUUGAGGCCAAAUUGCUAGGA
ath-miR826b	FexLEAun-03	5	-1	UGGUUUUGGACACGUGAAAAU	UCUUUGCCGUGUUUCAAACUA
ath-miR837-5p	FexLEAun-03	4,5	-1	AUCAGUUUCUUGUUCGUUUA	CAAGAAGAAGAAGAGACUGAA
ath-miR838	FexLEAun-03	5	-1	UUUUCUUCUACUUCUUGCACA	AGCUCAAGAAGAAGAAGAGAC
ath-miR2937	FexLEAun-04	5	-1	AUAAGAGCUGUUGAAGGAGUC	GUUUACUGCAAGAGUUCUUGU
ath-miR390a-5p	FexLEAun-04	5	-1	AAGCUCAGGAGGGAUAGCGCC	AUUGCUAUCUUUGCUGUGUUU
ath-miR390b-5p	FexLEAun-04	5	-1	AAGCUCAGGAGGGAUAGCGCC	AUUGCUAUCUUUGCUGUGUUU
ath-miR837-5p	FexLEAun-04	4,5	-1	AUCAGUUUCUUGUUCGUUUA	CAAGAAGAAGAAGAGACUGAA
ath-miR838	FexLEAun-04	5	-1	UUUUCUUCUACUUCUUGCACA	AGCUCAAGAAGAAGAAGAGAC
ath-miR414	FexLEAun-05	5	-1	UCAUCUUCAUCAUCAUCGUA	GGAAGACAGAGAUGAAGAUGA
ath-miR5012	FexLEAun-05	5	-1	UUUUACUGCUACUUGUGUUC	AAAACAGAGGUAGUAGAGAGG
ath-miR779.2	FexLEAun-05	5	-1	UGAUUGGAAAUUCGUUGACU	GAGCAAUGAAGUUACCCAUA
ath-miR865-3p	FexLEAun-05	5	-1	UUUUUCCUCAAUUUAUCCAA	GGUGAGAAAAUUGAGGAAACA
ath-miR5998a	FexLEAun-06	5	-1	ACAGUUUGUGUUUUGUUUUGU	ACAAAACAAGGACCAAACUGG
ath-miR5998b	FexLEAun-06	5	-1	ACAGUUUGUGUUUUGUUUUGU	ACAAAACAAGGACCAAACUGG
ath-miR836	FexLEAun-06	5	-1	UCCUGUGUUUCCUUUGAUGCGUGG	UGAAACGGCCGAGGAGACAAAGGA
ath-miR858a	FexLEAun-06	5	-1	UUUCGUUGUCUGUUCGACCUU	CUGCUCAGCAGGCAAGGAGA
ath-miR5025	FexLEAun-07	5	-1	ACUGUAUAUAUGUAAGUGACA	GGUUAUUGUCAUGUAUACAGA
ath-miR5658	FexLEAun-07	4,5	-1	AUGAUGAUGAUGAUGAUGAAA	AUUCUUCUCGUCAUCAUUUU
ath-miR773b-5p	FexLEAun-07	5	-1	GGCAAUAACUUGAGCAAACA	CAUUUGCUGGUGUUAUUGCU
ath-miR843	FexLEAun-07	4	-1	UUUAGGUCGAGCUUCAUUGGA	CAUAAUGAAGGUUGAUUUGAA

Table S4. (continued)

miRNA name	Target gene name	Expectation	UPE	miRNA aligned fragment	Target aligned fragment
ath-miR167a-5p	FexLEAun-08	4,5	-1	UGAAGCUGCCAGCAUGAUCUA	UGGAUUGCGGUGGUAGUUUCA
ath-miR167b	FexLEAun-08	4,5	-1	UGAAGCUGCCAGCAUGAUCUA	UGGAUUGCGGUGGUAGUUUCA
ath-miR167d	FexLEAun-08	4,5	-1	UGAAGCUGCCAGCAUGAUCUGG	GUGGAUUGCGGUGGUAGUUUCA
ath-miR4240	FexLEAun-08	5	-1	UGACUAGACCCGUAA-CAUUAC	CGGAUGCUUAUGGAUUUAGUCA
ath-miR426	FexLEAun-08	3,5	-1	UUUUGGAAAUUUGUCCUUACG	GCUAAGGAGACAUUUUCAAAA
ath-miR5648-5p	FexLEAun-08	4,5	-1	UUUGGAAAUUUUGGCUUGACU	GGCCAAGCAAAGUGCUUCCGAG
ath-miR5998a	FexLEAun-08	4	-1	ACAGUUUGUGUUUUGUUUUGU	AAAAGACAAAGCUCAAAAUGU
ath-miR5998a	FexLEAun-08	5	-1	ACAGUUUGUGUUUUGUUUUGU	GAAAGGUAAAGCACAGAAUGC
ath-miR5998b	FexLEAun-08	4	-1	ACAGUUUGUGUUUUGUUUUGU	AAAAGACAAAGCUCAAAAUGU
ath-miR5998b	FexLEAun-08	5	-1	ACAGUUUGUGUUUUGUUUUGU	GAAAGGUAAAGCACAGAAUGC
ath-miR829-5p	FexLEAun-08	4,5	-1	ACUUUGAAGCUUUGAUUUGAA	GCCAAGUCAAGCUUCGGGAA
ath-miR870-3p	FexLEAun-08	5	-1	UAAUUUGGUGUUUCUUCGAUC	AUCCGCAGAUACACCGAAUUC