

SUPPLEMENTARY APPENDIX

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to:

Genome-wide identification and expression analysis of lipoxygenase genes in Tartary buckwheat

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Biotechnol. Biotechnol. Equip. 2020, **34**

Supplement Data

Table S1 Transcription data.

Accession number	Biosample number	Sample	Tissues	Description
SRP157461	SRR7687373	B48-1	Seedlings 5 days old	Blue light 48h
	SRR7687374	B48-2	Seedlings 5 days old	Blue light 48h
	SRR7687375	B48-3	Seedlings 5 days old	Blue light 48h
	SRR7687376	D48-1	Seedlings 5 days old	Dark 48h
	SRR7687377	D48-2	Seedlings 5 days old	Dark 48h
	SRR7687378	D48-3	Seedlings 5 days old	Dark 48h
	SRR7687379	FR48-1	Seedlings 5 days old	Far red light 48h
	SRR7687380	FR48-2	Seedlings 5 days old	Far red light 48h
	SRR7687381	FR48-3	Seedlings 5 days old	Far red light 48h
	SRR7687382	R48-1	Seedlings 5 days old	Red light 48h
	SRR7687371	R48-2	Seedlings 5 days old	Red light 48h
	SRR7687372	R48-3	Seedlings 5 days old	Red light 48h
SRP141278	SRR7042962	BT18R	Root	Control
	SRR7042961	BT18F1	Flower	Control
	SRR7042960	BT18ST1	Stem	Control
	SRR7042959	L1	Leaf	Control
	SRR7042957	BT18S3	Seed (cell enlargement)	Control
	SRR7042955	BT18S1	Seed (cell division)	Control
	SRR7042953	BT18S5	Seed (deposition of reserves)	Control
	SRR7042952	BT18S9	Seed (desiccation)	Control
	SRR7042950	BT18S7	Seed (maturation)	Control

Table S2 List of primers used for quantitative real-time PCR analysis.

Primer name	Sequence (5'to3')
2300-QF	ATCGAGAAGTAGCGGAAGCA
2300-QR	AGAAGGTATAAGCGCGTCCA
9300-QF	TGTCTCCTTGACGCTCATCA
9300-QR	AAGTATGCTGGCTTCCCTGT
3900-QF	GCCGTACCTGAGTCGGATAA
3900-QR	TTCAATGGCTAGTGGCCTCA
7200-QF	GGTGGCCTAAGCTAAACAGC
7200-QR	TCCTCCAAACGGGTACTGAC
8200-QF	AATGACAGCGGGTACCATCA
8200-QR	GTGAATGGGATGGAGCACAC
4800-QF	ACCCAACTGAAGAGGAGTGG
4800-QR	GTACAACACCGCCATTACCC
5000-QF	CGTTCTCTGCAACGACACTT
5000-QR	ATGGCGGTGAAGTAAGGGAA
2800-QF	GCCACGGAGACAAGAAAGAC
2800-QR	TCTAGCAACAGTTGGTCGGT
actin-F	AAGGAAGCAATTGGCAAC
actin-R	TCACGAAGAGCAACGGTA

Table S3 GO annotations of FtLOXs.

namespace	GOterm	number_of_genes	genes
biological_process	anatomical structure development	6	FtLOX7, FtLOX6c, FtLOX4a, FtLOX4b, FtLOX6b, FtLOX6a
biological_process	anatomical structure formation	6	FtLOX6b, FtLOX6a, FtLOX4a, FtLOX6c, FtLOX7, FtLOX4b
biological_process	involved in morphogenesis		
biological_process	biological_process	11	FtLOX6b, FtLOX6a, FtLOX5, FtLOX2, FtLOX3, FtLOX4a, FtLOX7, FtLOX6c, FtLOX8, FtLOX1, FtLOX4b
biological_process	biosynthetic process	4	FtLOX3, FtLOX2, FtLOX1, FtLOX8
biological_process	lipid metabolic process	11	FtLOX5, FtLOX6a, FtLOX6b, FtLOX4b, FtLOX1, FtLOX6c, FtLOX7, FtLOX8, FtLOX4a, FtLOX3, FtLOX2
biological_process	response to stress	10	FtLOX4a, FtLOX6c, FtLOX7, FtLOX8, FtLOX1, FtLOX4b, FtLOX2, FtLOX3, FtLOX6b, FtLOX6a
biological_process	small molecule metabolic process	4	FtLOX2, FtLOX3, FtLOX8, FtLOX1
cellular_component	cell	11	FtLOX6b, FtLOX6a, FtLOX5, FtLOX2, FtLOX3, FtLOX4a, FtLOX7, FtLOX6c, FtLOX8, FtLOX1, FtLOX4b
cellular_component	cellular_component	11	FtLOX6b, FtLOX6a, FtLOX5, FtLOX2, FtLOX3, FtLOX7, FtLOX6c, FtLOX8, FtLOX4a, FtLOX4b, FtLOX1
cellular_component	cytoplasm	11	FtLOX7, FtLOX6c, FtLOX8, FtLOX4a, FtLOX4b, FtLOX1, FtLOX2, FtLOX3, FtLOX5, FtLOX6b, FtLOX6a
cellular_component	intracellular	11	FtLOX6b, FtLOX6a, FtLOX5, FtLOX2, FtLOX3, FtLOX4a, FtLOX6c, FtLOX7, FtLOX8, FtLOX1, FtLOX4b
cellular_component	organelle	11	FtLOX5, FtLOX6a, FtLOX6b, FtLOX4b, FtLOX1, FtLOX8, FtLOX7, FtLOX6c, FtLOX4a, FtLOX3, FtLOX2
cellular_component	plasma membrane	1	FtLOX5
cellular_component	plastid	11	FtLOX7, FtLOX6c, FtLOX8, FtLOX4a, FtLOX4b, FtLOX1, FtLOX2, FtLOX3, FtLOX5, FtLOX6b, FtLOX6a
cellular_component	thylakoid	4	FtLOX8, FtLOX1, FtLOX2, FtLOX3
molecular_function	molecular_function	11	FtLOX4a, FtLOX6c, FtLOX7, FtLOX8, FtLOX1, FtLOX4b, FtLOX2, FtLOX3, FtLOX5, FtLOX6b, FtLOX6a
molecular_function	oxidoreductase activity	11	FtLOX2, FtLOX3, FtLOX4a, FtLOX7, FtLOX8, FtLOX6c, FtLOX1, FtLOX4b, FtLOX6b, FtLOX6a, FtLOX5

Table S4 Statistics of cis-elements in the promoter regions of FtLOX genes.

Name	Start	End	cis	motif
FtLOX1	-1856	-1851	ARE	AAACCA
FtLOX1	-1938	-1933	Box-4	ATTAAT
FtLOX1	-1934	-1927	Box-4	ATTAAT
FtLOX1	-1911	-1906	Box-4	ATTAAT
FtLOX1	-122	-115	CARE	CAACTCAC
FtLOX1	-554	-549	CCAAT-box	CAACGG
FtLOX1	-615	-605	F-BOX	CTATTCTCATT
FtLOX1	-426	-419	GA-motif	ATAGATAA
FtLOX1	-440	-435	GT1-motif	GGTTAA
FtLOX1	-396	-391	GT1-motif	GGTTAA
FtLOX1	-405	-400	LTR	CCGAAA
FtLOX1	-943	-938	MYB	TAACCA
FtLOX1	-768	-763	MYB	TAACCA
FtLOX1	-393	-388	MYB	TAACCA
FtLOX1	-1254	-1249	MYB	CCGTTG
FtLOX1	-1091	-1091	MYC	CAATTG
FtLOX1	-206	-201	MYC	CAATTG
FtLOX1	-1835	-1829	MYC	TCTCTTA
FtLOX1	-443	-439	STRE	AGGGG
FtLOX1	-1889	-1882	TATC-box	TATCCCA
FtLOX1	-736	-731	TGA-element	AACGAC
FtLOX1	-831	-826	TGA-element	AACGAC
FtLOX1	-780	-775	TGA-element	AACGAC
FtLOX1	-130	-124	W-box	TTGACC
FtLOX1	-30	-25	WRE3	CCACCT
FtLOX1	-800	-792	WUN-motif	AAATTTCTT
FtLOX2	-1977	-1972	ABRE	ACGTG
FtLOX2	-1425	-1413	AT1-motif	AATTATTTTTATT
FtLOX2	-1977	-1972	Box-4	ATTAAT
FtLOX2	-1201	-1196	ERE	ATTTTAAA
FtLOX2	-460	-455	G-box	CACGTG
FtLOX2	-322	-317	MYB	TAACCA
FtLOX2	-62	-57	MYB	TAACCA
FtLOX2	-1182	-1173	MYB	TAACCA
FtLOX2	-1894	-1890	MYC	CAATTG
FtLOX2	-1416	-1407	TCA-element	CCATCTTTT
FtLOX2	-424	-417	TGACG-motif	TGACG
FtLOX2	-363	-359	WUN-motif	TTATTACAT
FtLOX2	-346	-342	chs-CMA1a	TTACTTAA
FtLOX3	-1215	-1210	ABRE	ACGTG
FtLOX3	-1407	-1402	ABRE	ACGTG
FtLOX3	-1670	-1663	Box-4	ATTAAT
FtLOX3	-347	-341	Box-4	ATTAAT
FtLOX3	-1685	-1678	Box-4	ATTAAT
FtLOX3	-795	-788	CCAAT-box	CAACGG

Name	Start	End	cis	motif
FtLOX3	-1802	-1796	CCAAT-box	CAACGG
FtLOX3	-154	-148	CGTCA-motif	CGTCA
FtLOX3	-1047	-1041	CGTCA-motif	CGTCA
FtLOX3	-1417	-1411	ERE	ATTTTAAA
FtLOX3	-1087	-1081	ERE	ATTTTAAA
FtLOX3	-147	-141	G-box	TACGTG
FtLOX3	-1395	-1390	GA-motif	ATAGATAA
FtLOX3	-164	-159	GA-motif	ATAGATAA
FtLOX3	-891	-882	LTR	CCGAAA
FtLOX3	-411	-402	LTR	CCGAAA
FtLOX3	-13	-9	MYB	TAACCA
FtLOX3	-605	-598	MYC	CAATTG
FtLOX3	-1936	-1932	MYC	CAATTG
FtLOX3	-1079	-1075	MYC	CAATTG
FtLOX3	-572	-568	MYC	CAATTG
FtLOX3	-527	-523	STRE	AGGGG
FtLOX3	-117	-113	TCA	TCATCTTCAT
FtLOX3	-1443	-1439	TCA	TCATCTTCAT
FtLOX3	-1510	-1505	TGACG-motif	TGACG
FtLOX3	-1352	-1348	chs-CMA1a	TTACTTAA
FtLOX4	-1238	-1234	ABRE	ACGTG
FtLOX4	-1234	-1230	ABRE	ACGTG
FtLOX4	-416	-409	ABRE	ACGTG
FtLOX4	-358	-353	ABRE	ACGTG
FtLOX4	-1080	-1075	ABRE	ACGTG
FtLOX4	-528	-523	ARE	AAACCA
FtLOX4	-118	-113	Box-4	ATTAAT
FtLOX4	-292	-286	Box-4	ATTAAT
FtLOX4	-619	-613	Box-4	ATTAAT
FtLOX4	-822	-815	Box-4	ATTAAT
FtLOX4	-522	-517	ERE	ATTTTAAA
FtLOX4	-1940	-1931	G-box	CACGTT
FtLOX4	-1456	-1452	G-box	TACGTG
FtLOX4	-757	-748	G-box	TACGTG
FtLOX4	-1270	-1261	G-box	TACGTG
FtLOX4	-1797	-1792	GATA-motif	GATAGGG
FtLOX4	-1938	-1934	GT1-motif	GGTTAAT
FtLOX4	-1099	-1095	I-box	TGATAATG
FtLOX4	-731	-722	MYB	TAACCTG
FtLOX4	-520	-516	O2-site	GTTGACGTGA
FtLOX4	-540	-531	STRE	AGGGG
FtLOX4	-127	-120	TC-rich repeats	ATTCTCTAAC
FtLOX4	-1689	-1684	TCA	TCATCTTCAT
FtLOX4	-36	-31	TCT-motif	TCTTAC
FtLOX4	-1970	-1965	TGACG-motif	TGACG
FtLOX4	-1573	-1958	TGACG-motif	TGACG

Name	Start	End	cis	motif
FtLOX4	-1458	-1453	WUN-motif	AAATTTCTT
FtLOX5	-1557	-1552	ABRE	ACGTG
FtLOX5	-1265	-1258	ACE	CTAACGTATT
FtLOX5	-521	-516	AE-box	AGAAACAA
FtLOX5	-1176	-1171	ARE	AAACCA
FtLOX5	-1201	-1195	ARE	AAACCA
FtLOX5	-198	-193	Box-4	ATTAAT
FtLOX5	-1324	-1319	Box-4	ATTAAT
FtLOX5	-895	-890	Box-4	ATTAAT
FtLOX5	-871	-866	DRE-core	GCCGAC
FtLOX5	-194	-189	ERE	ATTTTAAA
FtLOX5	-685	-680	G-box	TACGTG
FtLOX5	-400	-394	LTR	CCGAAA
FtLOX5	-1434	-1428	MRE	AACCTAA
FtLOX5	-707	-701	MYB	CAACCA
FtLOX5	-626	-622	MYB	CAACCA
FtLOX5	-1280	-1276	MYB	CAACCA
FtLOX5	-262	-253	MYB	CAACCA
FtLOX5	-1560	-1555	MYC	CAATTG
FtLOX5	-1104	-1099	MYC	CAATTG
FtLOX5	-1023	-1018	MYC	CAATTG
FtLOX5	-497	-942	MYB	CAACTG
FtLOX5	-1444	-1439	MYB	TAACTG
FtLOX5	-1502	-1497	MYC	TCTCTTA
FtLOX5	-1708	-1703	P-box	CCTTTTG
FtLOX5	-1070	-1065	P-box	CCTTTTG
FtLOX5	-1870	-1865	STRE	AGGGG
FtLOX5	-1702	-1698	STRE	AGGGG
FtLOX5	-749	-745	TCA-element	CCATCTTTT
FtLOX5	-435	-431	TCT-motif	TCTTAC
FtLOX5	-1715	-1710	W-box	TTGACC
FtLOX5	-668	-663	WRE3	CCACCT
FtLOX5	-1490	-1485	WRE3	CCACCT
FtLOX6	-1210	-1199	ARE	AAACCA
FtLOX6	-1747	-1742	ARE	AAACCA
FtLOX6	-1883	-1878	Box-4	ATTAAT
FtLOX6	-1226	-1221	Box-4	ATTAAT
FtLOX6	-1870	-1865	CAT-box	GCCACT
FtLOX6	-1702	-1698	CGTCA-motif	CGTCA
FtLOX6	-749	-745	CGTCA-motif	CGTCA
FtLOX6	-435	-431	CGTCA-motif	CGTCA
FtLOX6	-1715	-1710	G-box	CACGTT
FtLOX6	-668	-663	G-box	CACGAC
FtLOX6	-1490	-1485	G-box	CACGAC
FtLOX6	-1210	-1199	G-box	ACACGTG(G/t)CACC
FtLOX6	-1747	-1742	MYB	TAACCA

Name	Start	End	cis	motif
FtLOX6	-1875	-1870	MYC	CAATTG
FtLOX6	-1883	-1878	W-box	TTGACC
FtLOX6	-1226	-1221	W-box	TTGACC
FtLOX7	-786	-778	AAGAA-motif	gGTAAAGAAA
FtLOX7	-1768	-1764	ABRE	ACGTG
FtLOX7	-1334	-1330	ABRE	ACGTG
FtLOX7	-129	-125	ABRE	ACGTG
FtLOX7	-885	-878	AE-box	AGAAACTT
FtLOX7	-1473	-1468	ARE	AAACCA
FtLOX7	-1602	-1597	ARE	AAACCA
FtLOX7	-1455	-1450	ARE	AAACCA
FtLOX7	-791	-786	ARE	AAACCA
FtLOX7	-1062	-1057	CAT-box	GCCACT
FtLOX7	-1655	-1648	ERE	ATTTCATA
FtLOX7	-1644	-1637	ERE	ATTTCATA
FtLOX7	-1196	-1191	G-box	CACGTT
FtLOX7	-220	-215	G-box	TACGTG
FtLOX7	-1337	-1330	G-box	TAAACGTG
FtLOX7	-1395	-1390	MBS	CAACTG
FtLOX7	-1304	-1298	MRE	AACCTAA
FtLOX7	-1756	-1751	MYC	CATTTG
FtLOX7	-1265	-1260	MYC	CATTTG
FtLOX7	-1395	-1390	MYB	CAACTG
FtLOX7	-1184	-1178	MYC	TCTCTTA
FtLOX7	-1943	-1939	STRE	AGGGG
FtLOX7	-261	-257	STRE	AGGGG
FtLOX7	-1163	-1157	TCCC-motif	TCTCCCT
FtLOX7	-223	-218	TCT-motif	TCTTAC
FtLOX7	-1770	-1766	TGACG-motif	TGACG
FtLOX7	-1418	-1410	WUN-motif	ACATTACGG
FtLOX7	-1714	-1707	WUN-motif	AAATTACT
FtLOX8	-1182	-1178	ABRE	ACGTG
FtLOX8	-837	-831	ABRE	TACGGTC
FtLOX8	-219	-215	ABRE	ACGTG
FtLOX8	-965	-960	ABRE4	CACGTA
FtLOX8	-23	-18	ARE	AAACCA
FtLOX8	-1442	-1436	Box-4	ATTAAT
FtLOX8	-1159	-1154	Box-4	ATTAAT
FtLOX8	-1803	-1796	CARE	CAACTCAC
FtLOX8	-1395	-1391	CGTCA-motif	CGTCA
FtLOX8	-257	-252	DRE-core	GCCGAC
FtLOX8	-850	-845	G-box	CACGTT
FtLOX8	-966	-959	G-box	CCACGTAA
FtLOX8	-715	-710	G-box	CACGTC
FtLOX8	-1095	-1087	I-box	gGATAAGGTG
FtLOX8	-817	-810	LAMP-element	CTTTATCA

Name	Start	End	cis	motif
FtLOX8	-1822	-1817	LTR	CCGAAA
FtLOX8	-171	-166	MYB	TAACCA
FtLOX8	-1250	-1245	MYB	CAACCA
FtLOX8	-1494	-1489	MYB	CAACCA
FtLOX8	-1540	-1535	MYB	CAACCA
FtLOX8	-1646	-1641	MYB	TAACCA
FtLOX8	-1604	-1599	MYB	CAACCA
FtLOX8	-1696	-1691	MYB	CAACCA
FtLOX8	-1568	-1563	MYC	CAATTG
FtLOX8	-1174	-1169	MYC	CAATTG
FtLOX8	-1208	-1203	MYC	CAATTG
FtLOX8	-1765	-1760	STRE	AGGGG
FtLOX8	-100	-92	TCA	TCATCTTCAT
FtLOX8	-125	-120	TGA-element	AACGAC

Table S5 GO terms for FtLOX co-expression genes.

namespace	GOterm	number_of_genes
biological_process	DNA metabolic process	99
biological_process	aging	7
biological_process	anatomical structure development	82
biological_process	anatomical structure formation involved in morphogenesis	13
biological_process	autophagy	19
biological_process	biological_process	432
biological_process	biosynthetic process	1003
biological_process	carbohydrate metabolic process	361
biological_process	catabolic process	288
biological_process	cell adhesion	2
biological_process	cell cycle	52
biological_process	cell death	10
biological_process	cell differentiation	35
biological_process	cell division	30
biological_process	cell junction organization	1
biological_process	cell morphogenesis	21
biological_process	cell proliferation	9
biological_process	cell wall organization or biogenesis	104
biological_process	cellular amino acid metabolic process	164
biological_process	cellular component assembly	28
biological_process	cellular nitrogen compound metabolic process	741
biological_process	cellular protein modification process	185
biological_process	chromosome organization	70
biological_process	chromosome segregation	16
biological_process	cofactor metabolic process	91
biological_process	cytoskeleton organization	51
biological_process	cytoskeleton-dependent intracellular transport	1
biological_process	developmental maturation	4
biological_process	embryo development	21
biological_process	extracellular matrix organization	6
biological_process	generation of precursor metabolites and energy	81

namespace	GOterm	number_of_genes
biological_process	Growth	40
biological_process	Homeostatic process	106
biological_process	Immune system process	19
biological_process	Lipid metabolic process	215
biological_process	Mrna processing	41
biological_process	Macromolecular complex assembly	1
biological_process	Membrane organization	47
biological_process	Mitochondrion organization	16
biological_process	Mitotic nuclear division	14
biological_process	Nitrogen cycle metabolic process	6
biological_process	Nucleobase-containing compound catabolic process	20
biological_process	Nucleocytoplasmic transport	48
biological_process	Photosynthesis	53
biological_process	Protein complex assembly	68
biological_process	Protein folding	78
biological_process	Protein maturation	1
biological_process	Protein targeting	38
biological_process	Reproduction	12
biological_process	Response to stress	307
biological_process	Ribonucleoprotein complex assembly	24
biological_process	Ribosome biogenesis	51
biological_process	Secondary metabolic process	33
biological_process	Signal transduction	230
biological_process	Small molecule metabolic process	332
biological_process	Sulfur compound metabolic process	66
biological_process	Symbiosis, encompassing mutualism through parasitism	1
biological_process	tRNA metabolic process	43
biological_process	Translation	181
biological_process	Transmembrane transport	180
biological_process	Transport	338
biological_process	Vacuolar transport	19
biological_process	Vesicle-mediated transport	115
cellular_component	Golgi apparatus	95
cellular_component	Cell	79
cellular_component	Cell wall	55
cellular_component	Cellular_component	2338
cellular_component	Chromosome	65
cellular_component	Cilium	3
cellular_component	Cytoplasm	313
cellular_component	Cytoplasmic membrane-bounded vesicle	28
cellular_component	Cytoskeleton	68
cellular_component	Cytosol	136
cellular_component	Endoplasmic reticulum	114
cellular_component	Endosome	22
cellular_component	External encapsulating structure	1
cellular_component	Extracellular region	101
cellular_component	Extracellular space	5
cellular_component	Intracellular	287
cellular_component	Lipid particle	1

namespace	GOterm	number_of_genes
cellular_component	Lysosome	4
cellular_component	Microtubule organizing center	7
cellular_component	Mitochondrion	116
cellular_component	Nuclear chromosome	9
cellular_component	Nuclear envelope	19
cellular_component	Nucleolus	33
cellular_component	Nucleoplasm	45
cellular_component	Nucleus	666
cellular_component	Organelle	33
cellular_component	Peroxisome	26
cellular_component	Plasma membrane	212
cellular_component	Plastid	198
cellular_component	Protein complex	417
cellular_component	Ribosome	138
cellular_component	Thylakoid	67
cellular_component	Vacuole	52
molecular_function	ATPase activity	172
molecular_function	DNA binding	677
molecular_function	GTPase activity	79
molecular_function	RNA binding	152
molecular_function	Cytoskeletal protein binding	1
molecular_function	Enzyme binding	12
molecular_function	Enzyme regulator activity	81
molecular_function	Helicase activity	67
molecular_function	Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	27
molecular_function	Hydrolase activity, acting on glycosyl bonds	169
molecular_function	Ion binding	2457
molecular_function	Isomerase activity	91
molecular_function	Kinase activity	655
molecular_function	Ligase activity	100
molecular_function	Lipid binding	66
molecular_function	Lyase activity	127
molecular_function	Mrna binding	6
molecular_function	Methyltransferase activity	125
molecular_function	Molecular function	1478
molecular_function	Nuclease activity	55
molecular_function	Nucleic acid binding transcription factor activity	230
molecular_function	Nucleotidyltransferase activity	77
molecular_function	Oxidoreductase activity	700
molecular_function	Peptidase activity	192
molecular_function	Phosphatase activity	110
molecular_function	Protein binding transcription factor activity	32
molecular_function	Protein binding, bridging	1
molecular_function	Protein transporter activity	24
molecular_function	rRNA binding	18
molecular_function	Signal transducer activity	68
molecular_function	Structural constituent of ribosome	136
molecular_function	Structural molecule activity	20
molecular_function	Transcription factor binding	3

namespace	GOterm	number_of_genes
molecular_function	Transferase activity, transferring acyl groups	132
molecular_function	Transferase activity, transferring alkyl or aryl (other than methyl) groups	37
molecular_function	Transferase activity, transferring glycosyl groups	210
molecular_function	Translation factor activity, RNA binding	51
molecular_function	Transmembrane transporter activity	343
molecular_function	Ubiquitin-like protein binding	1

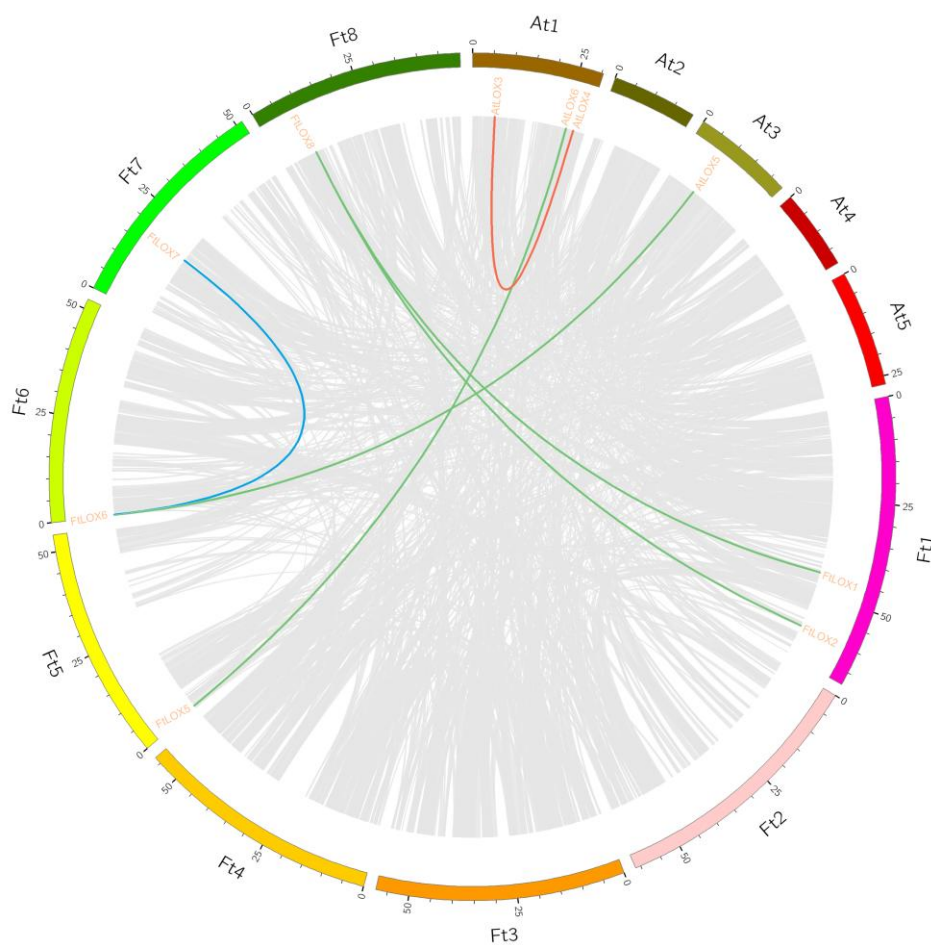
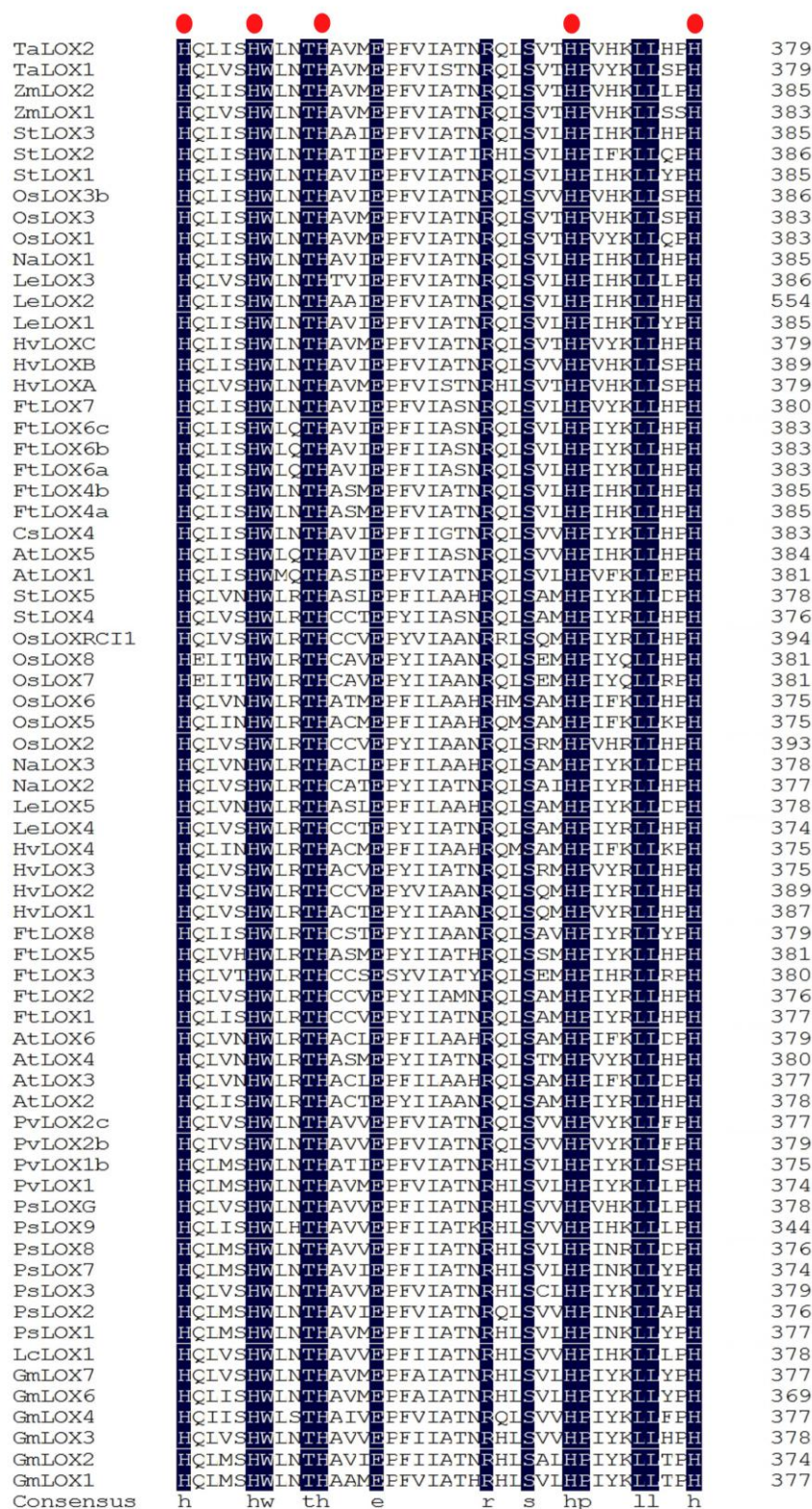


Figure S1 Synteny analysis of LOX genes between Tartary buckwheat and Arabidopsis.

Note: Green lines indicate colinear gene pairs; blue line indicates segmental duplication pairs in Tartary; red line indicates segmental duplication pairs in Arabidopsis. The chromosome number is indicated at the bottom of each chromosome.



TaLOX2	HQLISHWLNTFAVMEFFVIATNRQLSVTHFVHKLLHFFH	379
TaLOX1	HQLVSHWLNTFAVMEFFVISTNRQLSVTHFVYKLLSPH	379
ZmLOX2	HQLISHWLNTFAVMEFFVIATNRQLSVTHFVHKLLLPH	385
ZmLOX1	HQLVSHWLNTFAVMEFFVIATNRQLSVTHFVHKLLSSH	383
StLOX3	HQLISHWLNTFAAIEFFVIATNRQLSVLHFIHKLLHFFH	385
StLOX2	HQLISHWLNTFATIEFFVIATNRHLSVLHFIKLLQPH	386
StLOX1	HQLISHWLNTFAVIEFFVIATNRQLSVLHFIHKLLYPH	385
OsLOX3b	HQLISHWLNTFAVIEFFVIATNRQLSVVHFEVHKLLSPH	386
OsLOX3	HQLISHWLNTFAVMEFFVIATNRQLSVTHFVHKLLSPH	383
OsLOX1	HQLISHWLNTFAVMEFFVIATNRQLSVTHFVYKLLQPH	383
NaLOX1	HQLISHWLNTFAVIEFFVIATNRQLSVLHFIHKLLHFFH	385
LeLOX3	HQLVSHWLNTFTVIEFFVIATNRQLSVLHFIHKLLLPH	386
LeLOX2	HQLISHWLNTFAAIEFFVIATNRQLSVLHFIHKLLHFFH	554
LeLOX1	HQLISHWLNTFAVIEFFVIATNRQLSVLHFIHKLLYPH	385
HvLOXC	HQLISHWLNTFAVMEFFVIATNRQLSVTHFVYKLLHFFH	379
HvLOXB	HQLISHWLNTFAVIEFFVIATNRQLSVVHFEVHKLLSPH	389
HvLOXA	HQLVSHWLNTFAVMEFFVISTNRHLSVLTHFVHKLLSPH	379
FtLOX7	HQLISHWLNTFAVIEFFVIASNRQLSVLHFEYKLLHFFH	380
FtLOX6c	HQLISHWLQTFHAVIEFFIIASNRQLSVLHFIYKLLHFFH	383
FtLOX6b	HQLISHWLQTFHAVIEFFIIASNRQLSVLHFIYKLLHFFH	383
FtLOX6a	HQLISHWLQTFHAVIEFFIIASNRQLSVLHFIYKLLHFFH	383
FtLOX4b	HQLISHWLNTFASMEFFVIATNRQLSVLHFIHKLLHFFH	385
FtLOX4a	HQLISHWLNTFASMEFFVIATNRQLSVLHFIHKLLHFFH	385
CsLOX4	HQLISHWLNTFAVIEFFIIIGTNRQLSVVHFIYKLLHFFH	383
AtLOX5	HQLISHWLQTFHAVIEFFIIASNRQLSVVHFIHKLLHFFH	384
AtLOX1	HQLISHWLQTFASIEFFVIATNRQLSVLHFEVFKLLHFFH	381
StLOX5	HQLVNHWLRTFASIEFFIIAAHRLSAMHFIYKLLDPH	378
StLOX4	HQLVSHWLRTFECCTEFPYIIASNRQLSAMHFIYRLHFFH	376
OsLOXRCI1	HQLVSHWLRTFCCVEFPYIIAANRISQMHEFYRLHFFH	394
OsLOX8	HELITHWLRTFCAVEFPYIIAANRQLSEMHEFYQLHFFH	381
OsLOX7	HELITHWLRTFCAVEFPYIIAANRQLSEMHEFYQLHFFH	381
OsLOX6	HQLVNHWLRTFATMEFFIIAAHRLSAMHFIKLLHFFH	375
OsLOX5	HQLINHWLRTFACMEFFIIAAHRLSAMHFIKLLKPH	375
OsLOX2	HQLVSHWLRTFCCVEFPYIIAANRQLSRMHEVHFLHFFH	393
NaLOX3	HQLVNHWLRTFACIEFFIIAAHRLSAMHFIYKLLDPH	378
NaLOX2	HQLVSHWLRTFCATEFPYIIATNRQLSAIHEFYRLHFFH	377
LeLOX5	HQLVNHWLRTFASIEFFIIAAHRLSAMHFIYKLLDPH	378
LeLOX4	HQLVSHWLRTFCCCTEFPYIIATNRQLSAMHFIYRLHFFH	374
HvLOX4	HQLINHWLRTFACMEFFIIAAHRLSAMHFIKLLKPH	375
HvLOX3	HQLVSHWLRTFACVEFPYIIATNRQLSRMHEVYRLHFFH	375
HvLOX2	HQLVSHWLRTFCCVEFPYIIAANRQLSQMHEFYRLHFFH	389
HvLOX1	HQLVSHWLRTFACTEFPYIIAANRQLSQMHEVYRLHFFH	387
FtLOX8	HQLISHWLRTFCSTEFPYIIAANRQLSAVHEFYRLYPH	379
FtLOX5	HQLVHHWLRTFASMEFPYIIATNRQLSSMHEFYKLLHFFH	381
FtLOX3	HQLVTHWLRTFCCSESYVIATYRQLSEMHEFIHFLHFFH	380
FtLOX2	HQLVSHWLRTFCCVEFPYIIAMNRQLSAMHFIYRLHFFH	376
FtLOX1	HQLISHWLRTFCCVEFPYIIATNRQLSAMHFIYRLHFFH	377
AtLOX6	HQLVNHWLRTFACIEFFIIAAHRLSAMHFIKLLDPH	379
AtLOX4	HQLVNHWLRTFASMEFPYIIATNRQLSTMHEVYKLLHFFH	380
AtLOX3	HQLVNHWLRTFACIEFFIIAAHRLSAMHFIKLLDPH	377
AtLOX2	HQLISHWLRTFACTEFPYIIAANRQLSAMHFIYRLHFFH	378
PvLOX2c	HQLVSHWLNTFAVVEFFVIATNRQLSVVHFEYKLLFFH	377
PvLOX2b	HQLVSHWLNTFAVVEFFVIATNRQLSVVHFEYKLLFFH	379
PvLOX1b	HQLMSHWLNTFATIEFFVIATNRHLSVLHFIYKLLSPH	375
PvLOX1	HQLMSHWLNTFAVMEFFVIATNRHLSVLHFIYKLLLPH	374
PsLOXG	HQLVSHWLNTFAVVEFFIIATNRHLSVHFEVHKLLLPH	378
PsLOX9	HQLISHWLRTFAVVEFFIIATNRHLSVHFIHKLLLPH	344
PsLOX8	HQLMSHWLNTFAVVEFFIIATNRHLSVLHFINKLLDPH	376
PsLOX7	HQLMSHWLNTFAVIEFFIIATNRHLSVLHFINKLLYPH	374
PsLOX3	HQLVSHWLNTFAVVEFFVIATNRHLSVHFIYKLLYPH	379
PsLOX2	HQLMSHWLNTFAVIEFFVIATNRQLSVVHFINKLLAPH	376
PsLOX1	HQLMSHWLNTFAVMEFFIIATNRHLSVLHFINKLLYPH	377
LcLOX1	HQLVSHWLNTFAVVEFFIIATNRHLSVHFIHKLLLPH	378
GmLOX7	HQLVSHWLNTFAVMEFFAIATNRHLSVLHFIYKLLYPH	377
GmLOX6	HQLISHWLNTFAVMEFFAIATNRHLSVLHFIYKLLYPH	369
GmLOX4	HQLISHWLSTFAIVEFFVIATNRQLSVVHFIYKLLFFH	377
GmLOX3	HQLVSHWLNTFAVVEFFIIATNRHLSVHFIYKLLHFFH	378
GmLOX2	HQLMSHWLNTFAVIEFFIIATNRHLSVHFIYKLLTFH	374
GmLOX1	HQLMSHWLNTFAAMEFFVIATNRHLSVLHFIYKLLTFH	377
Consensus	h h w t h e r s h p l l h	

Figure S2 Sequence alignments of 38-residue motifs in 69 LOX members.

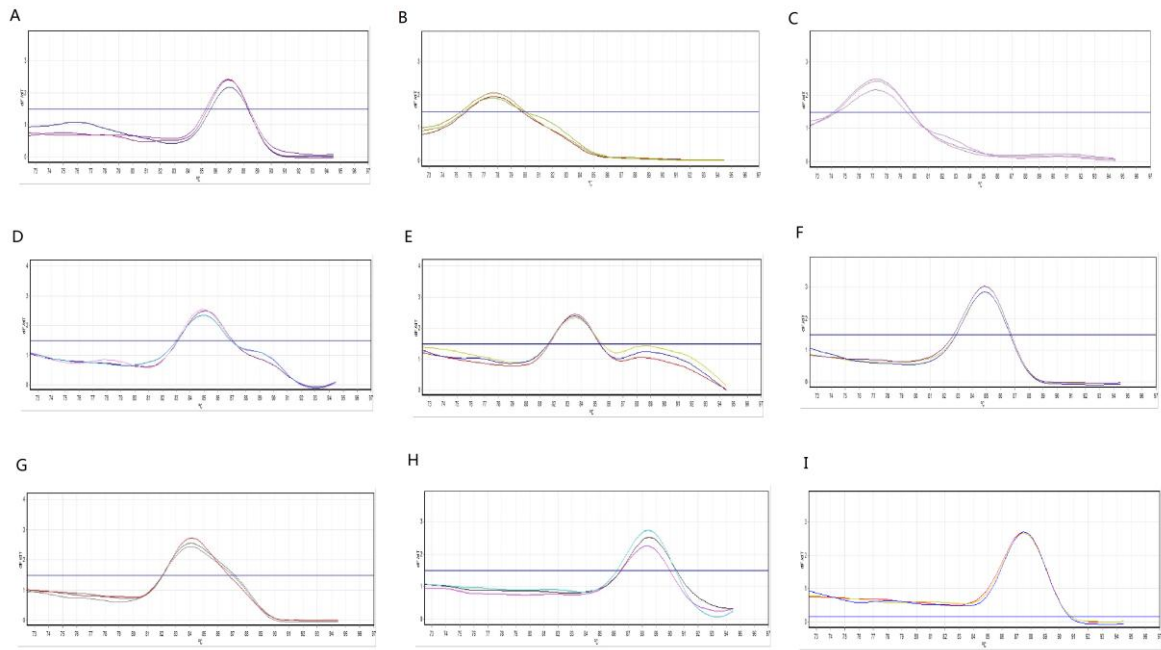


Figure S3 Melting curve analyses for qPCR of the eight candidate LOX genes of Tartary buckwheat. (A–I) Melting curves of *FtLOX1*, *FtLOX2*, *FtLOX3*, *FtLOX4*, *FtLOX5*, *FtLOX6*, *FtLOX7*, *FtLOX8* and actin of *Fagopyrum tartaricum*.