

Table S1. Summary of RNA-Seq and mapping results after 48 h and 15 d LK stress.

Time	#SampleID	XZ153-CK	XZ141-CK	ZD9-CK	XZ153-T	XZ141-T	ZD9-T
48 h	Clean reads	29719657	33447266	30666761.5	26506169	22417765.5	23060512
	Clean bases	8894784239	10010482966	9175140638	7929476738	6704719372	6897690494
	GC(%)	58.855	58.545	58.62	58.275	58.815	58.485
	N(%)	0	0	0	0	0	0
	Q20(%)	96.13	96.19	96.075	96.155	95.73	95.86
	Q30(%)	91.02	91.205	91.015	91.215	90.35	90.6
	Mapped Reads(%)	82.71	82.93	82.45	81.26	81.25	80.37
	Uniq Mapped Reads(%)	81.97	82.17	81.71	80.59	80.55	79.70
	Multiple Map Reads(%)	0.74	0.76	0.75	0.68	0.70	0.67
	Reads Map to '+'(%)	41.11	41.25	40.99	40.44	40.40	39.93
15 d	Reads Map to '-'(%)	41.60	41.67	41.46	40.81	40.84	40.42
	Clean reads	27849629.5	24986214.5	33948031	29279850.5	28295976.5	27454594
	Clean bases	8323022336	7465996278	10153168999	8754830062	8448480502	8213049640
	GC(%)	58.475	57.43	57.39	56.8	57.915	57.555
	N(%)	0	0	0.01	0	0.01	0.01
	Q20(%)	97.455	97.435	97.39	97.63	97.64	97.56
	Q30(%)	93.7	93.655	93.675	94.055	94.225	94.055
	Mapped Reads(%)	83.58	84.43	83.23	83.95	84.01	83.89
	Uniq Mapped Reads(%)	82.84	83.69	82.51	83.27	83.21	83.20
	Multiple Map Reads(%)	0.74	0.74	0.72	0.68	0.81	0.69
	Reads Map to '+'(%)	41.73	42.19	41.59	42.04	41.98	41.96
	Reads Map to '-'(%)	41.84	42.22	41.63	41.88	42.02	41.92

Note: CK and T represent control and low K treatment, respectively.

Table S7. Functional classification of LK tolerance related DEGs after 48 h LK stress.

Ontology GO	GO term	Items
Biological process	cellular process	139
	metabolic process	123
	single-organism process	99
	biological regulation	69
	response to stimulus	47
	cellular component organization or biogenesis	40
	developmental process	38
	localization	30
	reproduction	27
	reproductive process	27
	multicellular organismal process	23
	signaling	9
	growth	6
	multi-organism process	5
	detoxification	5
Cellular component	immune system process	2
	biological adhesion	2
Cellular component	cell	166
	cell part	166
	organelle	142
	membrane	73
	organelle part	42
	macromolecular complex	35
	membrane part	32
	membrane-enclosed lumen	9
	extracellular region	7
	cell junction	6
Molecular function	supramolecular complex	1
	binding	155
	catalytic activity	109
	nucleic acid binding transcription factor activity	12
	structural molecule activity	9
	transporter activity	9
	electron carrier activity	4
	antioxidant activity	4
	molecular function regulator	2
	transcription factor activity, protein binding	1
	nutrient reservoir activity	1
	molecular transducer activity	1

Table S8. Functional classification of LK tolerance related DEGs after 15 d LK stress.

Ontology GO	GO term	Items
Biological process	cellular process	251
	metabolic process	226
	single-organism process	192
	biological regulation	103
	cellular component organization or biogenesis	96
	response to stimulus	93
	developmental process	64
	reproduction	53
	reproductive process	53
	localization	52
	multicellular organismal process	43
	multi-organism process	20
	signaling	13
	detoxification	8
	immune system process	5
	growth	5
	biological phase	2
	biological adhesion	1
	locomotion	1
	rhythmic process	1
Cellular component	cell	287
	cell part	287
	organelle	231
	organelle part	100
	membrane	98
	macromolecular complex	82
	membrane part	51
	extracellular region	17
	membrane-enclosed lumen	16
	supramolecular complex	16
	cell junction	6
	nucleoid	5
Molecular function	binding	241
	catalytic activity	204
	transporter activity	21
	antioxidant activity	8
	nucleic acid binding transcription factor activity	7
	structural molecule activity	5
	electron carrier activity	5
	molecular function regulator	4
	transcription factor activity, protein binding	2
	signal transducer activity	1
	molecular transducer activity	1

Table S9. Pathway analysis of LK tolerance related DEGs based on the KEGG data after 48 h of LK stress.

KEGG-Pathway	ko_ID	Unigene number	Gene
Ribosome	ko03010	7	295
RNA transport	ko03013	6	227
Ribosome biogenesis in eukaryotes	ko03008	6	107
Ubiquitin mediated proteolysis	ko04120	5	192
Plant hormone signal transduction	ko04075	4	271
Spliceosome	ko03040	4	245
DNA replication	ko03030	4	87
Homologous recombination	ko03440	4	81
Phenylpropanoid biosynthesis	ko00940	3	262
Nucleotide excision repair	ko03420	3	97
Mismatch repair	ko03430	3	65
Starch and sucrose metabolism	ko00500	2	271
Purine metabolism	ko00230	2	216
Endocytosis	ko04144	2	191
Pyrimidine metabolism	ko00240	2	171
Glycolysis / Gluconeogenesis	ko00010	2	170
RNA degradation	ko03018	2	168
mRNA surveillance pathway	ko03015	2	153
Galactose metabolism	ko00052	2	108
Base excision repair	ko03410	2	60
Ubiquinone and other terpenoid-quinone biosynthesis	ko00130	2	48
Carbon metabolism	ko01200	1	309
Protein processing in endoplasmic reticulum	ko04141	1	266
Amino sugar and nucleotide sugar metabolism	ko00520	1	172
Oxidative phosphorylation	ko00190	1	149
Peroxisome	ko04146	1	129
Glutathione metabolism	ko00480	1	114
Fatty acid metabolism	ko01212	1	113
Pyruvate metabolism	ko00620	1	105
Phosphatidylinositol signaling system	ko04070	1	102
Aminoacyl-tRNA biosynthesis	ko00970	1	102
Phagosome	ko04145	1	91
Fatty acid degradation	ko00071	1	85
Photosynthesis	ko00195	1	81
Inositol phosphate metabolism	ko00562	1	77
Glycine, serine and threonine metabolism	ko00260	1	76
Glyoxylate and dicarboxylate metabolism	ko00630	1	75
Basal transcription factors	ko03022	1	68
Citrate cycle (TCA cycle)	ko00020	1	67
Pentose and glucuronate interconversions	ko00040	1	62

Ascorbate and aldarate metabolism	ko00053	1	61
Tryptophan metabolism	ko00380	1	56
Fatty acid biosynthesis	ko00061	1	55
Valine, leucine and isoleucine degradation	ko00280	1	53
Circadian rhythm - plant	ko04712	1	51
ABC transporters	ko02010	1	50
Flavonoid biosynthesis	ko00941	1	49
Propanoate metabolism	ko00640	1	30
Photosynthesis - antenna proteins	ko00196	1	25
Linoleic acid metabolism	ko00591	1	21
Brassinosteroid biosynthesis	ko00905	1	18
Sesquiterpenoid and triterpenoid biosynthesis	ko00909	1	17
Non-homologous end-joining	ko03450	1	13

Table S10. Pathway analysis of LK tolerance related DEGs based on the KEGG data after 15 d of LK stress.

KEGG-Pathway	ko_ID	Unigene number	Gene
DNA replication	ko03030	19	87
Ribosome biogenesis in eukaryotes	ko03008	18	107
Purine metabolism	ko00230	12	216
Mismatch repair	ko03430	12	65
Ribosome	ko03010	11	295
Pyrimidine metabolism	ko00240	11	171
Nucleotide excision repair	ko03420	11	97
Homologous recombination	ko03440	11	81
Starch and sucrose metabolism	ko00500	8	271
Phenylpropanoid biosynthesis	ko00940	8	262
RNA transport	ko03013	8	227
Plant hormone signal transduction	ko04075	6	271
RNA degradation	ko03018	6	168
Cysteine and methionine metabolism	ko00270	6	114
Ubiquitin mediated proteolysis	ko04120	5	192
Base excision repair	ko03410	5	60
Plant-pathogen interaction	ko04626	3	197
Endocytosis	ko04144	3	191
Glutathione metabolism	ko00480	3	114
Glycerophospholipid metabolism	ko00564	3	113
Photosynthesis	ko00195	3	81
RNA polymerase	ko03020	3	71
Carbon metabolism	ko01200	2	309
Biosynthesis of amino acids	ko01230	2	282
Spliceosome	ko03040	2	245
Amino sugar and nucleotide sugar metabolism	ko00520	2	172

Oxidative phosphorylation	ko00190	2	149
Galactose metabolism	ko00052	2	108
Glycerolipid metabolism	ko00561	2	76
Cyanoamino acid metabolism	ko00460	2	70
Arginine and proline metabolism	ko00330	2	69
Pentose and glucuronate interconversions	ko00040	2	62
Ascorbate and aldarate metabolism	ko00053	2	61
Peroxisome	ko04146	1	129
Fatty acid metabolism	ko01212	1	113
Proteasome	ko03050	1	92
Phagosome	ko04145	1	91
Glycine, serine and threonine metabolism	ko00260	1	76
Glyoxylate and dicarboxylate metabolism	ko00630	1	75
2-Oxocarboxylic acid metabolism	ko01210	1	68
Basal transcription factors	ko03022	1	68
Alanine, aspartate and glutamate metabolism	ko00250	1	67
Terpenoid backbone biosynthesis	ko00900	1	63
Fatty acid biosynthesis	ko00061	1	55
ABC transporters	ko02010	1	50
Sulfur metabolism	ko00920	1	48
N-Glycan biosynthesis	ko00510	1	47
Cutin, suberine and wax biosynthesis	ko00073	1	39
Ether lipid metabolism	ko00565	1	35
Carotenoid biosynthesis	ko00906	1	34
Pantothenate and CoA biosynthesis	ko00770	1	26
Biotin metabolism	ko00780	1	23
Zeatin biosynthesis	ko00908	1	21
Valine, leucine and isoleucine biosynthesis	ko00290	1	20
Brassinosteroid biosynthesis	ko00905	1	18
Sesquiterpenoid and triterpenoid biosynthesis	ko00909	1	17
Non-homologous end-joining	ko03450	1	13

Table S11. Genes encoding TFs showing genotypic difference expression at 48 h and 15 d after LK stress.

Time	Groups	Gene Id	Log ₂ (Fold change)						Seq description
			XZ153		XZ141		ZD9		
48 h	Zinc finger	MLOC_38600	1.02	up	1.46	normal	0.95	normal	Zinc finger protein VAR3
		MLOC_61919	-0.65	normal	-0.43	normal	-1.02	down	Zinc finger protein COL9
		MLOC_33477	1.08	up	0.70	normal	0.60	normal	Zinc finger CCCH domain-containing protein 62
		Hordeum_vulgare_newGene_26949	1.16	up	0.19	normal	0.35	normal	Zinc finger CCCH domain-containing protein 24
		MLOC_20848	-0.56	normal	0.54	normal	-4.21	down	Zinc finger A20 and AN1 domain-containing stress-associated protein 4
		Hordeum_vulgare_newGene_15529	1.02	up	0.48	normal	0.99	normal	zinc finger CCCH domain-containing protein 44-like isoform X2
		MLOC_73724	1.03	up	0.35	normal	0.28	normal	Dof zinc finger protein DOF5.6
		MLOC_37654	1.44	up	--	--	--	--	Dof zinc finger protein DOF5.4
		MLOC_74620	1.32	up	0.55	normal	0.86	normal	Dof zinc finger protein DOF5.1
	bHLH	MLOC_67091	1.05	up	0.20	normal	0.71	normal	Transcription factor bHLH96
		Hordeum_vulgare_newGene_7240	1.25	up	0.33	normal	0.59	normal	Transcription factor bHLH93
		MLOC_26878	1.26	up	0.61	normal	1.37	normal	Transcription factor bHLH93
		MLOC_4876	1.20	up	0.47	normal	0.56	normal	Transcription factor bHLH68
		MLOC_12832	1.03	up	0.73	normal	0.30	normal	Transcription factor bHLH30
		MLOC_66385	1.15	up	0.97	normal	0.67	normal	Transcription factor bHLH30
		MLOC_38887	1.37	up	0.98	normal	0.91	normal	Transcription factor bHLH144
		MLOC_23394	1.18	up	0.95	normal	0.57	normal	Transcription factor bHLH106
		MLOC_69002	--	--	--	--	-1.26	down	Ethylene-responsive transcription factor RAP2-11
15 d	AP2/EREBP	MLOC_55323	2.03	up	0.89	normal	--	--	Ethylene-responsive transcription factor ERF003
		MLOC_58641	1.18	up	0.73	normal	0.79	normal	Ethylene-responsive transcription factor CRF4
		MLOC_75601	-1.01	normal	-1.18	down	-0.91	normal	PREDICTED: ethylene-responsive transcription factor ERF038-like
		Hordeum_vulgare_newGene_28417	1.61	up	0.74	normal	2.10	normal	AP2-like ethylene-responsive transcription factor ANT
		Hordeum_vulgare_newGene_2076	1.38	up	0.44	normal	0.95	normal	AP2-like ethylene-responsive transcription factor AIL5

	MYB	MLOC_7426	-0.38	normal	-1.06	down	-1.09	normal	Transcription factor MYB44
		MLOC_63964	-0.07	normal	-2.09	down	-1.31	down	Transcription factor MYB44
		MLOC_68698	1.38	up	--	--	--	--	Transcription factor MYB39
		MLOC_62877	-0.38	normal	0.11	normal	-1.01	down	Myb-like protein G
		MLOC_74184	0.03	normal	0.11	normal	-1.05	down	MYB-related protein
	WRKY	MLOC_66345	1.16	up	0.92	normal	--	--	Probable WRKY transcription factor 12
		MLOC_12078	1.36	up	--	--	--	--	Probable WRKY transcription factor 12
	Homeodomain	MLOC_18272	1.60	up	--	--	--	--	BEL1-like homeodomain protein 11
	HMG	MLOC_7518	1.36	up	0.74	normal	0.87	normal	HMG-Y-related protein A
15 d	AP2/EREBP	Hordeum_vulgare_newGene_2076	0.30	normal	-0.54	normal	-1.02	down	AP2-like ethylene-responsive transcription factor AIL5
		MLOC_10221	0.34	normal	-0.86	normal	-1.82	down	AP2-like ethylene-responsive transcription factor ANT
		MLOC_63425	-0.29	normal	-0.26	normal	-1.14	down	AP2-like ethylene-responsive transcription factor ANT
		Hordeum_vulgare_newGene_28417	-0.37	normal	-0.93	normal	-1.35	down	AP2-like ethylene-responsive transcription factor ANT
		MLOC_10878	1.24	up	0.20	normal	0.55	normal	Ethylene-responsive transcription factor ERF113
	MYB	MLOC_71066	-0.43	normal	-1.76	normal	-1.22	down	Transcription factor MYB44
		MLOC_67317	0.27	normal	-0.69	normal	-1.16	down	Myb-related protein 3R-1 GN=MYB3R-1
		MLOC_10556	0.06	normal	-1.06	normal	-1.10	down	Myb-related protein 3R-1 GN=MYB3R-1
		MLOC_67081	0.06	normal	-0.49	normal	-1.53	down	Putative Myb family transcription factor At1g14600
	WRKY	MLOC_66345	0.29	normal	-1.45	normal	-1.36	down	Probable WRKY transcription factor 12
	bHLH	MLOC_26878	0.56	normal	-0.34	normal	-1.31	down	Transcription factor bHLH93
	HSF	MLOC_70567	0.21	normal	-0.32	normal	-1.21	down	Heat stress transcription factor B-4b
	MADS-box	MLOC_38061	--	--	--	--	-1.54	down	MADS-box transcription factor 18
	HMG	MLOC_36749	0.13	normal	-0.75	normal	-1.07	down	WD repeat and HMG-box DNA-binding protein 1

Note: '--' and 'normal' presented in the table means no detection and without significant gene expression in this study, respectively.

Table S12. Genes encoding protein transporters and kinases showing genotypic difference expression at 48 h and 15 d after LK stress.

Time	Groups	Gene Id	Log ₂ (Fold change)					Seq description	
			XZ153	XZ141	ZD9				
LRR	LRR	MLOC_7595	1.08	up	0.24	normal	0.03	normal	LRR receptor-like serine/threonine-protein kinase ERECTA
		MLOC_49313	1.05	up	0.32	normal	0.83	normal	Inactive leucine-rich repeat receptor-like protein kinase CORYNE
		MLOC_63615	1.07	up	0.82	normal	0.48	normal	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1
		MLOC_15202	1.04	up	-0.32	normal	-0.51	normal	Probable inactive leucine-rich repeat receptor-like protein kinase At3g03770
		MLOC_15706	1.50	up	1.18	normal	1.24	normal	Probable leucine-rich repeat receptor-like protein kinase At1g68400
		MLOC_65197	1.12	up	1.09	normal	1.21	normal	Probable leucine-rich repeat receptor-like protein kinase At1g68400
		MLOC_55492	1.98	up	--	--	--	--	Probable LRR receptor-like serine/threonine-protein kinase At1g34110
		MLOC_39231	1.06	up	0.27	normal	0.20	normal	Probable LRR receptor-like serine/threonine-protein kinase At1g67720
		MLOC_15083	1.28	up	--	--	--	--	Probable LRR receptor-like serine/threonine-protein kinase At4g26540
		Hordeum_vulgare_newGene_24024	1.25	up	0.25	normal	0.65	normal	F-box/LRR-repeat protein 4
CRK	CRK	MLOC_57098	1.51	up	1.12	normal	0.85	normal	Probable LRR receptor-like serine/threonine-protein kinase At4g37250
		MLOC_23221	--	--	--	--	-1.07	down	Cysteine-rich receptor-like protein kinase 10
Yellow-strike	Yellow-strike	MLOC_38009	1.20	up	0.54	normal	0.41	normal	Cysteine-rich receptor-like protein kinase 7
		MLOC_16235	1.21	up	0.15	normal	0.37	normal	Probable metal-nicotianamine transporter YSL1
15 d	LRR	MLOC_39156	1.15	up	0.29	normal	0.13	normal	MATE family: Protein TRANSPARENT TESTA 12
		MLOC_13594	-0.55	normal	-1.22	normal	-1.07	down	LRR receptor-like serine/threonine-protein kinase GSO1
		MLOC_65917	0.03	normal	-3.99	down	-1.78	down	LRR receptor-like serine/threonine-protein kinase GSO1
		MLOC_62236	-0.38	normal	-1.43	normal	-1.43	down	LRR receptor-like serine/threonine-protein kinase RCH1
		Hordeum_vulgare_newGene_26246	0.07	normal	-0.74	normal	-1.03	down	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM3
		MLOC_65197	-0.04	normal	-0.67	normal	-1.11	down	Probable leucine-rich repeat receptor-like protein kinase At1g68400
		MLOC_55492	-0.25	normal	--	--	-1.30	down	Probable LRR receptor-like serine/threonine-protein kinase At1g34110
		MLOC_54885	0.16	normal	-1.14	down	-0.62	normal	Probable LRR receptor-like serine/threonine-protein kinase At1g67720

	Hordeum_vulgare_newGene_28613	1.53	up	--	--	--	--	Probable LRR receptor-like serine/threonine-protein kinase At1g67720
	Hordeum_vulgare_newGene_18275	1.19	up	-0.06	normal	--	--	Probable LRR receptor-like serine/threonine-protein kinase
	MLOC_37098	0.13	normal	-0.40	normal	-1.13	down	Probable LRR receptor-like serine/threonine-protein kinase At4g36180
	MLOC_57098	0.11	normal	-0.36	normal	-1.01	down	Probable LRR receptor-like serine/threonine-protein kinase At4g37250
	Hordeum_vulgare_newGene_13780	1.02	up	0.38	normal	--	--	Probable LRR receptor-like serine/threonine-protein kinase At5g10290
	Hordeum_vulgare_newGene_21089	0.03	normal	-1.13	down	--	--	Probable LRR receptor-like serine/threonine-protein kinase At5g65240
	MLOC_13076	-0.14	normal	-0.65	normal	-1.05	down	Probably inactive leucine-rich repeat receptor-like protein kinase At3g28040
	MLOC_70904	0.26	normal	-0.43	normal	-1.21	down	Probably inactive leucine-rich repeat receptor-like protein kinase IMK2
	MLOC_71159	0.30	normal	-0.35	normal	-1.03	down	Probably inactive leucine-rich repeat receptor-like protein kinase IMK2
	MLOC_9122	0.41	normal	-0.44	normal	-1.13	down	Probably inactive leucine-rich repeat receptor-like protein kinase IMK2
	MLOC_23846	--	--	--	--	-1.42	down	F-box/FBD/LRR-repeat protein At2g04230
Yellow-strike	MLOC_16235	0.29	normal	-0.04	normal	-1.06	down	Probable metal-nicotianamine transporter YSL1
	MLOC_71596	0.33	normal	0.17	normal	-1.91	down	Nicotianamine synthase 9 GN=NAS9
Ammonium	MLOC_33834	--	--	--	--	-2.60	down	Ammonium transporter 1 member 2
Nitrate	Hordeum_vulgare_newGene_4161	1.34	up	0.26	normal	0.80	normal	Probable peptide/nitrate transporter At3g43790

Note: '--' and 'normal' presented in the table means no detection and without significant gene expression in this study, respectively.