Figure S1 The quality score (Q) value of RNA-seq from six samples.

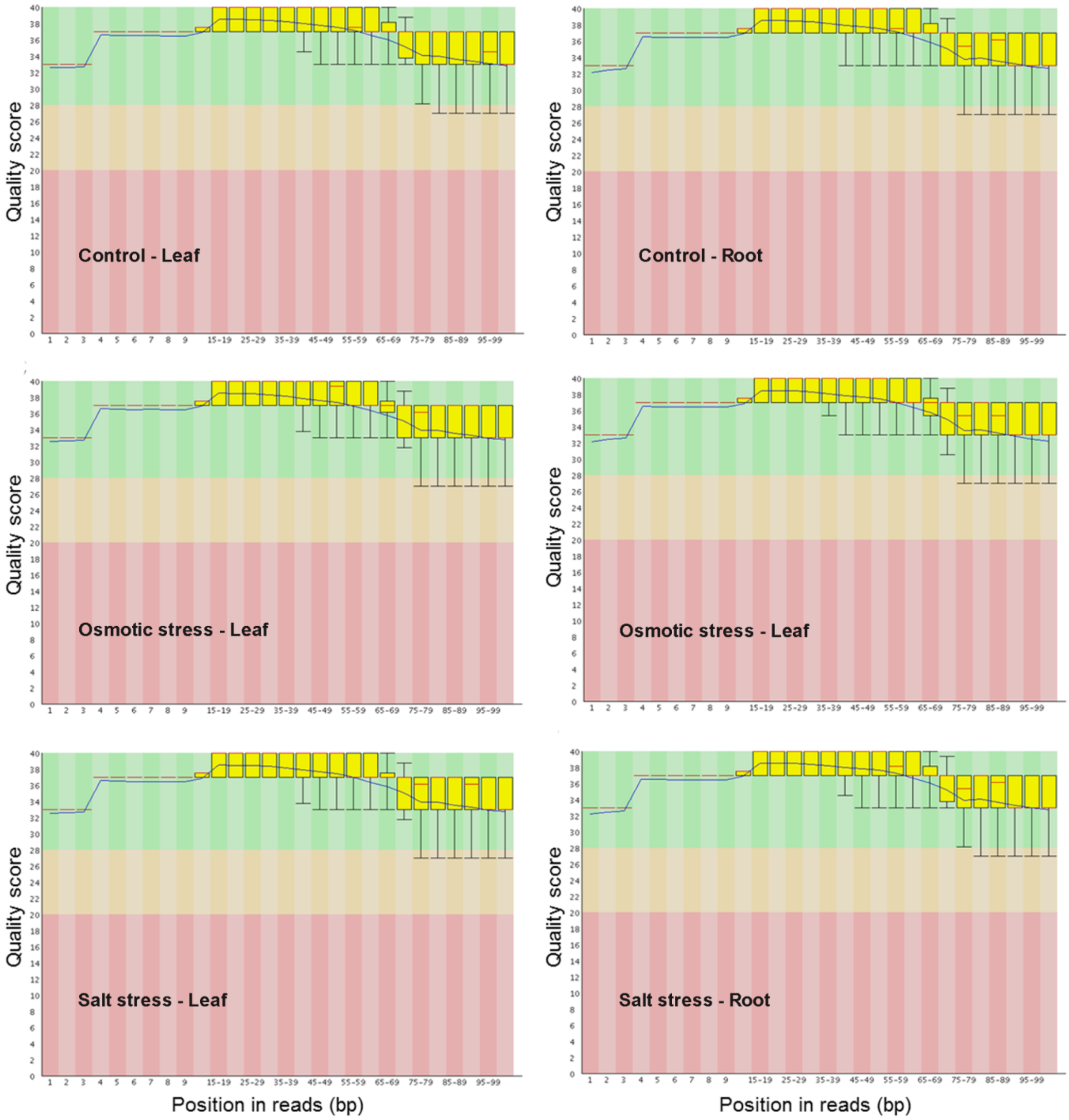

Figure S2 Accumulative frequency of lncRNAs and mRNAs from leaves and roots under osmosis and salt stress.

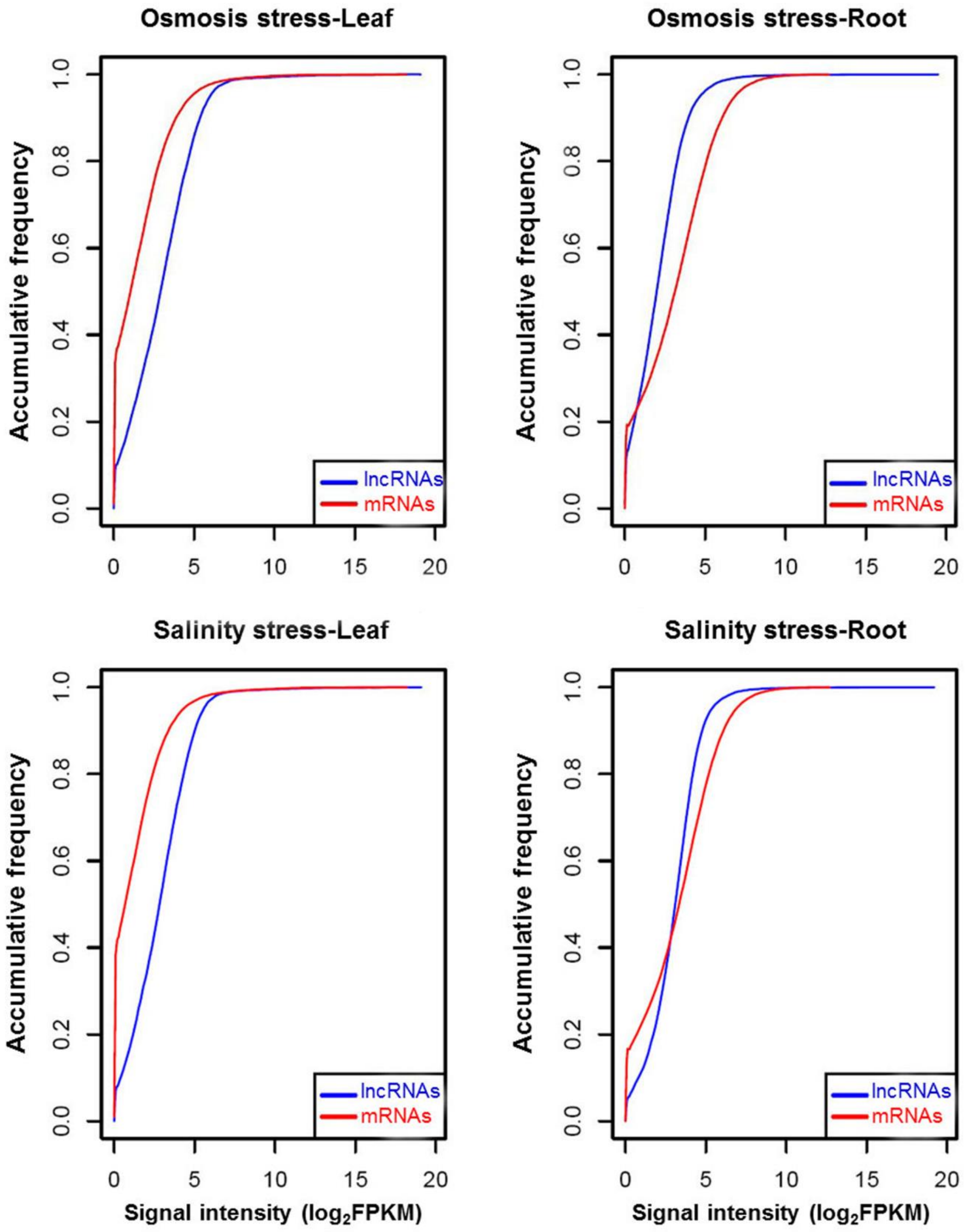

Figure S3 Compare of expressional results between RNA-seq and qRT-PCR.

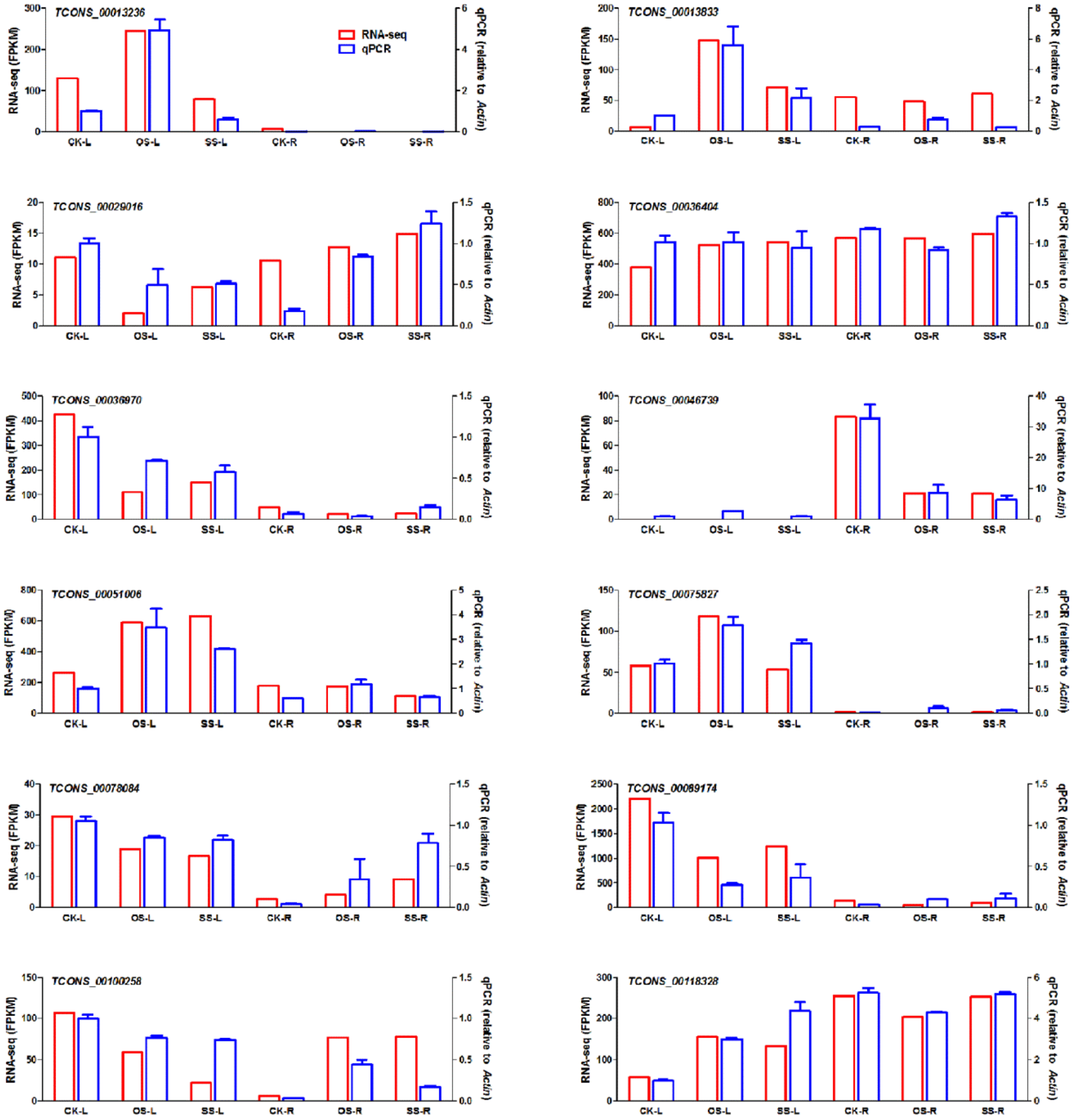

Figure S4 The common and specific lncRNAs identified to be up-regulated (a) and down-regulated (b) in leaves and roots under osmosis and salt stress.

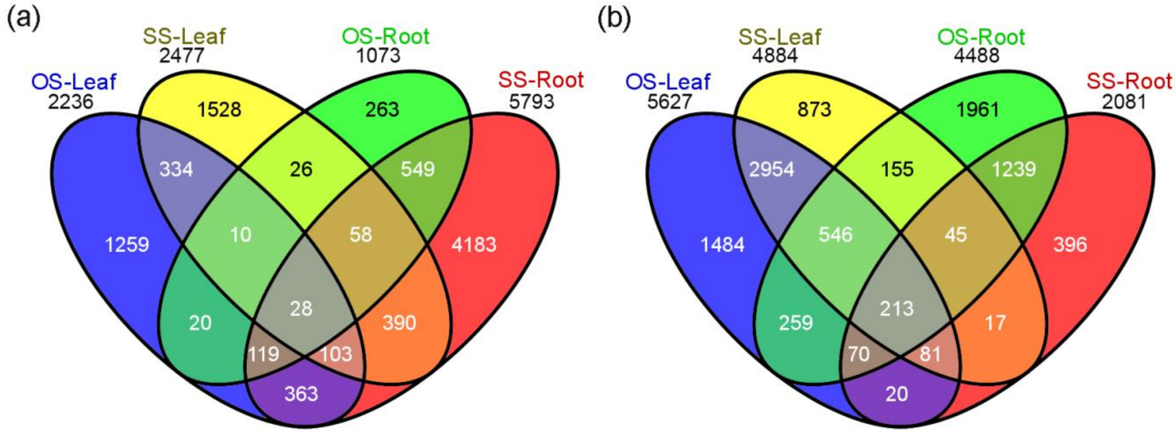

Figure S5 GO enhancements in roots of *M. truncatula* under osmotic stress (a) and salt stress (b). The reliability is calculated by –$\log_{10}$ (*P*-value).

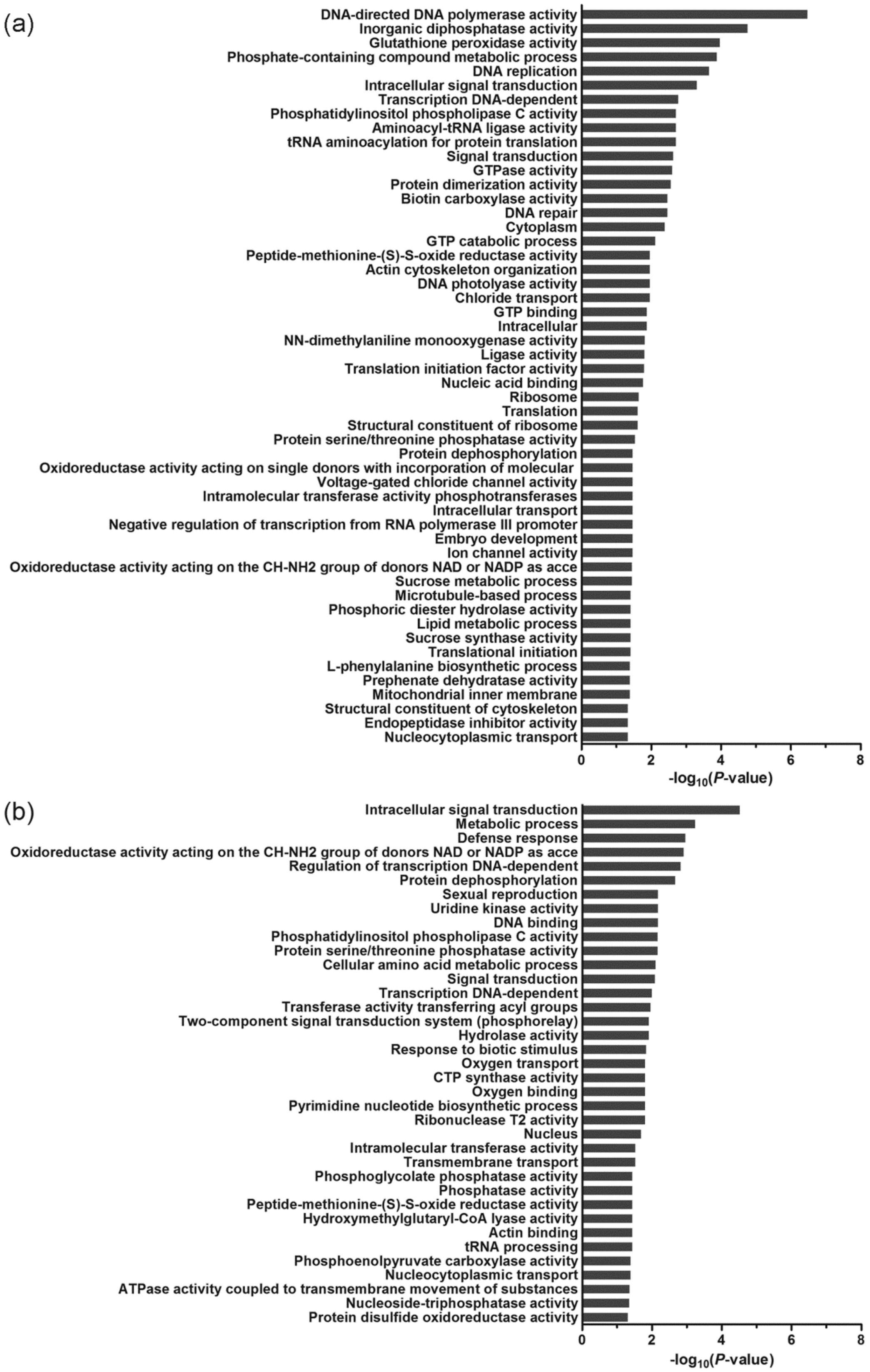

Figure S6 The interaction networks among lncRNAs and protein-coding genes.

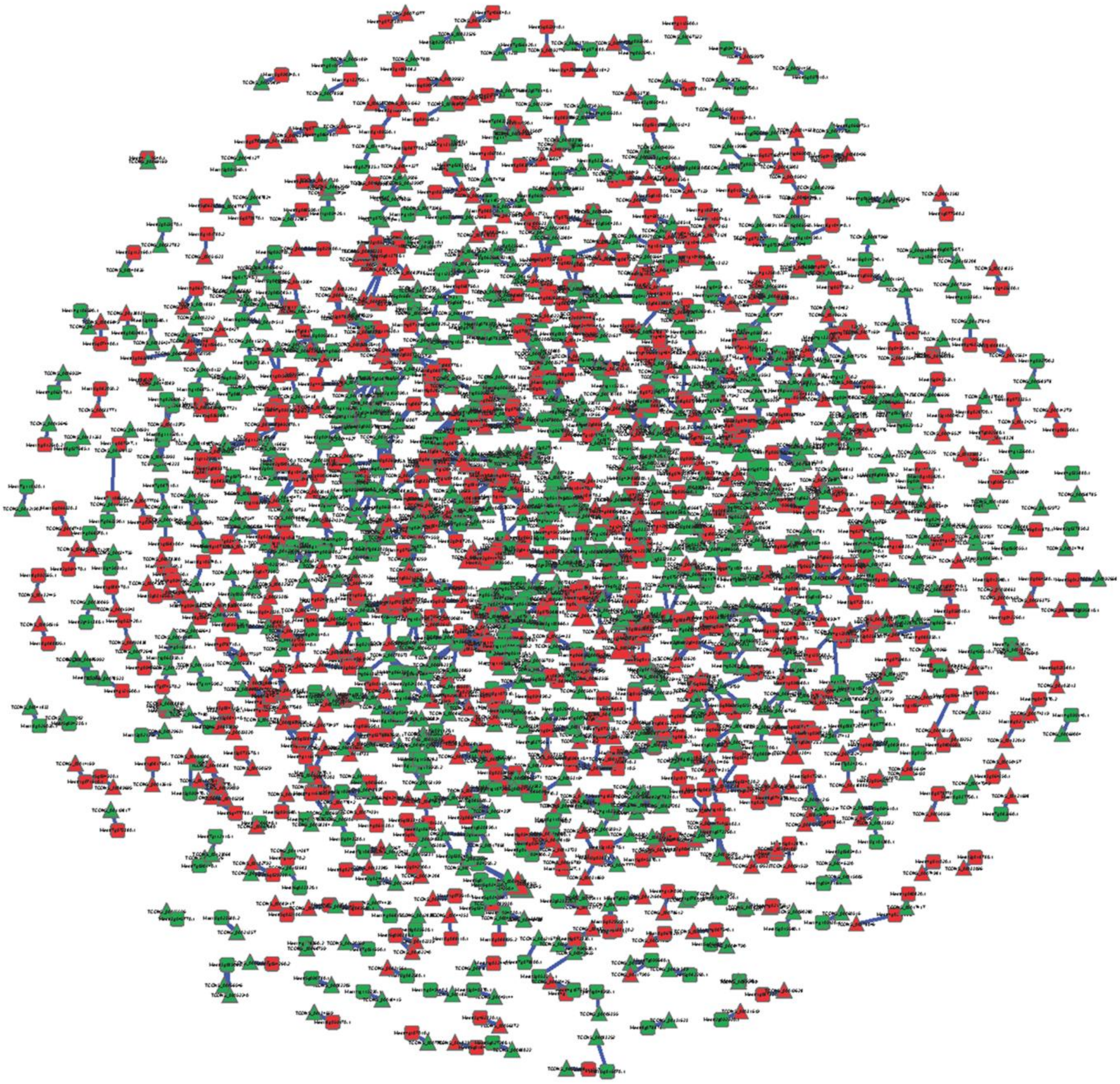

Table S2 The GO enhancements in leaves under osmotic stress

GO term	Description	$-\log_{10}(P\text{-value})$
GO:0004089	Carbonate dehydratase activity	5.53
GO:0015976	Carbon utilization	5.53
GO:0016887	ATPase activity	3.51
GO:0000156	Two-component response regulator activity	3.39
GO:0000160	Two-component signal transduction system (phosphorelay)	3.34
GO:0055085	Transmembrane transport	2.43
GO:0016874	Ligase activity	2.24
GO:0004075	Biotin carboxylase activity	2.12
GO:0004435	Phosphatidylinositol phospholipase C activity	2.12
GO:0006412	Translation	1.92
GO:0003735	Structural constituent of ribosome	1.78
GO:0006629	Lipid metabolic process	1.71
GO:0008081	Phosphoric diester hydrolase activity	1.71
GO:0009607	Response to biotic stimulus	1.7
GO:0042218	1-aminocyclopropane-1-carboxylate biosynthetic process	1.7
GO:0016847	1-aminocyclopropane-1-carboxylate synthase activity	1.7
GO:0006979	Response to oxidative stress	1.69
GO:0051537	2 iron, 2 sulfur cluster binding	1.51
GO:0006535	Cysteine biosynthetic process from serine	1.51
GO:0004602	Glutathione peroxidase activity	1.51
GO:0005840	Ribosome	1.49
GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	1.48
GO:0009058	Biosynthetic process	1.44
GO:0004871	Signal transducer activity	1.44
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	1.41
GO:0015935	Small ribosomal subunit	1.4

Table S3 The GO enhancements in leaves under salt stress

GO term	Description	-log$_{10}$(P-value)
GO:0004089	Carbonate dehydratase activity	4.38
GO:0015976	Carbon utilization	4.38
GO:0015934	Large ribosomal subunit	2.11
GO:0006412	Translation	1.96
GO:0004075	Biotin carboxylase activity	1.74
GO:0003735	Structural constituent of ribosome	1.72
GO:0008270	Zinc ion binding	1.61
GO:0019843	rRNA binding	1.5

Table S4 The GO enhancements in roots under osmotic stress

GO term	Description	$-\log_{10}(P\text{-value})$
GO:0003887	DNA-directed DNA polymerase activity	6.52
GO:0004427	Inorganic diphosphatase activity	4.8
GO:0004602	Glutathione peroxidase activity	4.01
GO:0006796	Phosphate-containing compound metabolic process	3.92
GO:0006260	DNA replication	3.69
GO:0035556	Intracellular signal transduction	3.35
GO:0006351	Transcription, DNA-dependent	2.81
GO:0006418	tRNA aminoacylation for protein translation	2.74
GO:0004812	Aminoacyl-trna ligase activity	2.74
GO:0004435	Phosphatidylinositol phospholipase C activity	2.74
GO:0007165	Signal transduction	2.66
GO:0003924	Gtpase activity	2.64
GO:0046983	Protein dimerization activity	2.59
GO:0006281	DNA repair	2.5
GO:0004075	Biotin carboxylase activity	2.5
GO:0005737	Cytoplasm	2.42
GO:0006184	GTP catabolic process	2.15
GO:0006821	Chloride transport	2
GO:0003913	DNA photolyase activity	2
GO:0030036	Actin cytoskeleton organization	2
GO:0008113	Peptide-methionine-(S)-S-oxide reductase activity	2
GO:0005525	GTP binding	1.91
GO:0005622	Intracellular	1.91
GO:0004499	N,N-dimethylaniline monooxygenase activity	1.86
GO:0016874	Ligase activity	1.84
GO:0003743	Translation initiation factor activity	1.83
GO:0003676	Nucleic acid binding	1.81
GO:0005840	Ribosome	1.68
GO:0003735	Structural constituent of ribosome	1.65
GO:0006412	Translation	1.65
GO:0004722	Protein serine/threonine phosphatase activity	1.57
GO:0006470	Protein dephosphorylation	1.51
GO:0005216	Ion channel activity	1.5
GO:0009790	Embryo development	1.5
GO:0016480	Negative regulation of transcription from RNA polymerase III promoter	1.5
GO:0046907	Intracellular transport	1.5
GO:0016868	Intramolecular transferase activity, phosphotransferases	1.5
GO:0005247	Voltage-gated chloride channel activity	1.5
GO:0016701	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	1.5

GO:0005985	Sucrose metabolic process	1.49
GO:0016639	Oxidoreductase activity, acting on the CH-NH_2 group of donors, NAD or NADP as acceptor	1.49
GO:0006629	Lipid metabolic process	1.45
GO:0008081	Phosphoric diester hydrolase activity	1.45
GO:0007017	Microtubule-based process	1.45
GO:0006413	Translational initiation	1.45
GO:0016157	Sucrose synthase activity	1.45
GO:0005743	Mitochondrial inner membrane	1.43
GO:0004664	Prephenate dehydratase activity	1.43
GO:0009094	L-phenylalanine biosynthetic process	1.43
GO:0006913	Nucleocytoplasmic transport	1.37
GO:0004866	Endopeptidase inhibitor activity	1.37
GO:0005200	Structural constituent of cytoskeleton	1.37

Table S5 The GO enhancements in roots under salt stress

GO term	Description	$-\log_{10}(P\text{-value})$
GO:0035556	Intracellular signal transduction	4.56
GO:0008152	Metabolic process	3.28
GO:0006952	Defense response	3
GO:0016639	Oxidoreductase activity, acting on the CH-NH_2 group of donors, NAD or NADP as acceptor	2.95
GO:0006355	Regulation of transcription, DNA-dependent	2.86
GO:0006470	Protein dephosphorylation	2.71
GO:0004849	Uridine kinase activity	2.21
GO:0019953	Sexual reproduction	2.21
GO:0003677	DNA binding	2.21
GO:0004435	Phosphatidylinositol phospholipase C activity	2.21
GO:0004722	Protein serine/threonine phosphatase activity	2.2
GO:0006520	Cellular amino acid metabolic process	2.14
GO:0007165	Signal transduction	2.13
GO:0006351	Transcription, DNA-dependent	2.03
GO:0016746	Transferase activity, transferring acyl groups	2
GO:0000160	Two-component signal transduction system (phosphorelay)	1.95
GO:0016787	Hydrolase activity	1.95
GO:0009607	Response to biotic stimulus	1.87
GO:0033897	Ribonuclease T2 activity	1.84
GO:0006221	Pyrimidine nucleotide biosynthetic process	1.84
GO:0019825	Oxygen binding	1.84
GO:0003883	CTP synthase activity	1.84
GO:0015671	Oxygen transport	1.84
GO:0005634	Nucleus	1.73
GO:0016866	Intramolecular transferase activity	1.57
GO:0055085	Transmembrane transport	1.56
GO:0008033	tRNA processing	1.48
GO:0003779	Actin binding	1.48
GO:0004419	Hydroxymethylglutaryl-coa lyase activity	1.48
GO:0008113	Peptide-methionine-(S)-S-oxide reductase activity	1.48
GO:0016791	Phosphatase activity	1.48
GO:0008967	Phosphoglycolate phosphatase activity	1.48
GO:0006913	Nucleocytoplasmic transport	1.43
GO:0008964	Phosphoenolpyruvate carboxylase activity	1.43
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	1.4
GO:0017111	Nucleoside-triphosphatase activity	1.39
GO:0015035	Protein disulfide oxidoreductase activity	1.35

Table S6 Sequences of primes using in this study

LncRNAs/Actin	Sense primes (5’-3’)	Antisense primes (5’-3’)
TCONS_00013236	ACAGGCCCTCAATAGAA	CGAGGAGCTTCAGAAAGA
TCONS_00013833	TCAATGTGGTCGTAGCGT	CTTGCGATGAGTTGGGTT
TCONS_00029016	TCTTCCCATGACAATACA	AATAGCCAAAGCTCTAAC
TCONS_00036404	GAGCCCTGCTTTACCTTT	GTGTCGCTAATGCGTTGC
TCONS_00036970	ATTTCATAGGCTGTGGAT	TTTACTCGGTCTGTCTCC
TCONS_00046739	CAACTCCTCCTGCAATCA	TCCAAACCTAAGACCCTA
TCONS_00051006	TCCACCACTTGGGTAGAC	TACCTGGATGGGGTCAAT
TCONS_00075827	CAGTATCAATTTAGGTGGGC	CAAATGACCGAAGTAGCG
TCONS_00078084	AGAGTGTAGCCCTGAACG	TCACTGCCGAAAGAGGAG
TCONS_00089174	TTGAGGTCGGGCAAGTAT	TGGATTTGAACCAGCGTA
TCONS_00100258	CCTTACTGGTGCTTTGTC	TTCATACCTGTTTCTCCC
TCONS_00118328	TCCGAGATTTAACCTTTAC	CTATGTTTGGGTATCTGTAT
Actin	ACGAGCGTTTCAGATG	ACCTCCGATCCAGACA