

Table S3 GO enrichment of DEGs in tillers and axillary buds

DEG Categories	GO_Categories	GO_ID	GO_Term	Annotated genes	Significant genes	P-value
Down-regulated DEGs in tillers	Biological process	GO:0032196	transposition	29	4	6.3E-19
	Biological process	GO:0097167	circadian regulation of translation	27	3	0.00011
	Biological process	GO:0009735	response to cytokinin	191	11	0.0004
			proteasome-mediated ubiquitin-			
	Biological process	GO:0043161	dependent protein catabolic process	434	11	0.00041
	Biological process	GO:0016042	lipid catabolic process	320	16	0.00059
	Biological process	GO:0042752	regulation of circadian rhythm	97	5	0.00076
	Biological process	GO:0046686	response to cadmium ion	180	10	0.00077
	Biological process	GO:0007165	signal transduction	2706	85	0.00082
	Biological process	GO:0009626	plant-type hypersensitive response	320	12	0.00139
	Biological process	GO:0046395	carboxylic acid catabolic process	121	9	0.00146
	Biological process	GO:0030163	protein catabolic process	768	25	0.00163
	Biological process	GO:0045037	protein import into chloroplast stroma	27	3	0.00243
	Biological process	GO:0032922	circadian regulation of gene expression	34	3	0.0026
	Biological process	GO:0030243	cellulose metabolic process	83	3	0.00312
	Biological process	GO:0045892	negative regulation of transcription	261	8	0.00373
	Biological process	GO:0051301	cell division	395	11	0.00407
	Biological process	GO:0009755	hormone-mediated signaling pathway	1150	40	0.0043
	Biological process	GO:0042744	hydrogen peroxide catabolic process	175	15	0.00448
	Biological process	GO:0000902	cell morphogenesis	364	21	0.00462
	Biological process	GO:0006412	translation	626	63	0.00469
	Biological process	GO:0006310	DNA recombination	184	4	0.00565
	Biological process	GO:0009909	regulation of flower development	157	3	0.00607
	Biological process	GO:0071396	cellular response to lipid	438	12	0.00854
	Biological process	GO:0009966	regulation of signal transduction	410	15	0.00914
	Biological process	GO:0043170	macromolecule metabolic process	8881	290	0.00945
	Cellular component	GO:0022625	cytosolic large ribosomal subunit	106	23	9.6E-05
	Cellular component	GO:0005886	plasma membrane	4149	148	0.0024
	Cellular component	GO:0022627	cytosolic small ribosomal subunit	56	11	0.0054
	Cellular component	GO:0044432	endoplasmic reticulum part	714	24	0.0082
	Molecular function	GO:0043531	ADP binding	521	20	5.2E-06
	Molecular function	GO:0061630	ubiquitin protein ligase activity	345	6	5.6E-06
	Molecular function	GO:0003735	structural constituent of ribosome	370	55	2.8E-05

Up-regulated DEGs in tillers	Molecular function	GO:0000977	RNA polymerase II regulatory region sequence-specific DNA binding	132	4	8.7E-05
	Molecular function	GO:0005524	ATP binding	3833	118	0.00079
	Molecular function	GO:0016787	hydrolase activity	4705	140	0.00119
	Molecular function	GO:0008270	zinc ion binding	1259	29	0.00228
			serine-type endopeptidase inhibitor activity	59	6	0.00265
	Molecular function	GO:0004867	activity	59	6	0.00265
	Molecular function	GO:0004674	protein serine/threonine kinase activity	1774	56	0.0039
	Molecular function	GO:0046872	metal ion binding	4559	175	0.00395
	Molecular function	GO:0030145	manganese ion binding	59	3	0.00414
	Biological process	GO:0032196	transposition	29	4	7.1E-18
	Biological process	GO:0006310	DNA recombination	184	12	8.5E-05
			proteasome-mediated ubiquitin-dependent protein catabolic process	434	14	0.0001
	Biological process	GO:0043161	dependent protein catabolic process	434	14	0.0001
	Biological process	GO:0007165	signal transduction	2706	116	0.0002
	Biological process	GO:0009735	response to cytokinin	191	9	0.00032
	Biological process	GO:0042752	regulation of circadian rhythm	97	3	0.00044
	Biological process	GO:0009755	hormone-mediated signaling pathway	1150	39	0.00133
	Biological process	GO:0009626	plant-type hypersensitive response	320	27	0.00164
	Biological process	GO:0046686	response to cadmium ion	180	3	0.00182
	Biological process	GO:0030243	cellulose metabolic process	83	3	0.00218
	Biological process	GO:0030163	protein catabolic process	768	18	0.00314
	Biological process	GO:0009407	toxin catabolic process	48	5	0.00355
	Biological process	GO:0071396	cellular response to lipid	438	15	0.00466
	Biological process	GO:0009966	regulation of signal transduction	410	17	0.00469
	Biological process	GO:0009909	regulation of flower development	157	3	0.00489
			regulation of transcription from RNA polymerase II promoter	279	11	0.00593
	Biological process	GO:0006357	positive regulation of cellular biosynthetic process	395	7	0.00597
	Biological process	GO:0031328	biosynthetic process	395	7	0.00597
	Biological process	GO:0045892	negative regulation of transcription	261	6	0.00626
			regulation of post-embryonic root development	15	3	0.00632
	Biological process	GO:2000069	development	15	3	0.00632
	Biological process	GO:0090304	nucleic acid metabolic process	5185	130	0.00671
			regulation of monoatomic ion transmembrane transport	29	4	0.00674
	Biological process	GO:0034765	transmembrane transport	29	4	0.00674

Biological process	GO:0050896	response to stimulus	6874	237	0.00703
Biological process	GO:0035556	intracellular signal transduction	714	24	0.00737
		positive regulation of macromolecule			
Biological process	GO:0010557	biosynthetic process	374	7	0.00848
Biological process	GO:0071495	cellular response to endogenous	1318	46	0.00864
Biological process	GO:0046395	carboxylic acid catabolic process	121	3	0.00865
Biological process	GO:0051301	cell division	395	9	0.00893
Biological process	GO:0034605	cellular response to heat	43	3	0.00924
Biological process	GO:0045491	xylan metabolic process	71	9	0.00991
Cellular component	GO:0005886	plasma membrane	4149	160	0.00099
Cellular component	GO:0005634	nucleus	6444	193	0.00313
Cellular component	GO:0009526	plastid envelope	549	14	0.00801
Molecular function	GO:0003964	RNA-directed DNA polymerase activity	9	4	5.4E-08
Molecular function	GO:0061630	ubiquitin protein ligase activity	345	7	2E-06
Molecular function	GO:0043531	ADP binding	521	62	2.2E-06
Molecular function	GO:0001653	peptide receptor activity	23	3	8.9E-05
Molecular function	GO:0005524	ATP binding	3833	195	0.00011
		RNA polymerase II transcription			
		regulatory region sequence-specific			
Molecular function	GO:0000977	DNA binding	132	6	0.00017
Molecular function	GO:0004674	protein serine/threonine kinase activity	1774	83	0.00047
Molecular function	GO:0008270	zinc ion binding	1259	29	0.00082
Biological process	GO:0032196	transposition	29	6	2.4E-19
		proteasome-mediated ubiquitin-			
Biological process	GO:0043161	dependent protein catabolic process	434	12	0.0002
Biological process	GO:0009626	plant-type hypersensitive response	320	25	0.00047
Biological process	GO:0009735	response to cytokinin	191	5	0.00051
Biological process	GO:0046686	response to cadmium ion	180	6	0.00091
Biological process	GO:0007165	signal transduction	2706	89	0.00108
Biological process	GO:0051301	cell division	395	12	0.00128
Biological process	GO:0016042	lipid catabolic process	320	14	0.00152
Biological process	GO:0030163	protein catabolic process	768	17	0.00194
Biological process	GO:0045892	negative regulation of transcription	261	7	0.00234
Biological process	GO:0006310	DNA recombination	184	8	0.00288
Biological process	GO:0009699	phenylpropanoid biosynthetic process	170	6	0.00348

Down-regulated DEGs in axillary buds	Biological process	GO:0022604	regulation of cell morphogenesis	75	3	0.00406
	Biological process	GO:0044282	small molecule catabolic process	168	7	0.0053
	Biological process	GO:0009746	response to hexose	39	4	0.0056
			positive regulation of cellular			
	Biological process	GO:0031328	biosynthetic process	395	9	0.00593
	Biological process	GO:0009909	regulation of flower development	157	4	0.00718
			regulation of transcription from RNA			
	Biological process	GO:0006357	polymerase II promoter	279	7	0.00749
	Biological process	GO:0071396	cellular response to lipid	438	6	0.00809
	Biological process	GO:0090304	nucleic acid metabolic process	5185	142	0.00813
	Biological process	GO:0009755	hormone-mediated signaling pathway	1150	23	0.0083
	Biological process	GO:0006952	defense response	2129	109	0.00931
			positive regulation of macromolecule			
	Biological process	GO:0010557	biosynthetic process	374	8	0.00961
	Cellular component	GO:0005634	nucleus	6444	174	0.00131
	Cellular component	GO:0005886	plasma membrane	4149	147	0.00156
	Cellular component	GO:0044432	endoplasmic reticulum part	714	26	0.00474
	Molecular function	GO:0061630	ubiquitin protein ligase activity	345	10	3.2E-07
	Molecular function	GO:0043531	ADP binding	521	45	7.9E-07
			RNA polymerase II regulatory region			
	Molecular function	GO:0000977	sequence-specific DNA binding	132	8	2.6E-06
	Molecular function	GO:0005524	ATP binding	3833	167	0.00032
	Biological process	GO:0032196	transposition	29	6	1.6E-17
	Biological process	GO:0006310	DNA recombination	184	15	0.00006
	Biological process	GO:0009735	response to cytokinin	191	6	0.00013
	Biological process	GO:0042752	regulation of circadian rhythm	97	5	0.00015
	Biological process	GO:0030433	ubiquitin-dependent ERAD pathway	45	6	0.00031
	Biological process	GO:0016042	lipid catabolic process	320	13	0.00057
	Biological process	GO:0034605	cellular response to heat	43	6	0.00057
	Biological process	GO:0007165	signal transduction	2706	124	0.00062
	Biological process	GO:0009407	toxin catabolic process	48	11	0.00068
	Biological process	GO:2000012	regulation of auxin polar transport	41	3	0.00069
	Biological process	GO:0009626	plant-type hypersensitive response	320	37	0.00127
	Biological process	GO:0019253	reductive pentose-phosphate cycle	26	10	0.0015
	Biological process	GO:0046686	response to cadmium ion	180	8	0.00151
	Biological process	GO:0030163	protein catabolic process	768	18	0.00189

Up-regulated DEGs in axillary buds	Biological process	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	434	10	0.00236
	Biological process	GO:0006438	valyl-tRNA aminoacylation	10	3	0.00338
	Biological process	GO:0097164	ammonium ion metabolic process	52	6	0.00436
	Biological process	GO:0051301	cell division	395	10	0.00493
	Biological process	GO:0009765	photosynthesis, light harvesting	28	7	0.00507
	Biological process	GO:0016045	detection of bacterium	16	3	0.00535
	Biological process	GO:0048608	reproductive structure development	1140	27	0.00624
	Biological process	GO:0050896	response to stimulus	6874	291	0.00631
	Biological process	GO:0009966	regulation of signal transduction	410	24	0.00654
	Biological process	GO:0071396	cellular response to lipid regulation of transcription from RNA	438	15	0.00657
	Biological process	GO:0006357	polymerase II promoter	279	13	0.00887
	Biological process	GO:0009755	hormone-mediated signaling pathway	1150	36	0.00889
	Biological process	GO:0045892	negative regulation of transcription	261	4	0.00924
	Cellular component	GO:0005886	plasma membrane	4149	206	0.0011
	Cellular component	GO:0009501	amyloplast	32	7	0.0018
	Cellular component	GO:0009941	chloroplast envelope	544	29	0.0029
	Cellular component	GO:0005819	spindle integral component of endoplasmic	181	9	0.0036
	Cellular component	GO:0030176	reticulum membrane	67	8	0.0061
	Cellular component	GO:0009526	plastid envelope	549	30	0.0073
	Cellular component	GO:0009524	phragmoplast	210	8	0.0078
	Cellular component	GO:0005789	endoplasmic reticulum membrane	667	42	0.0096
	Cellular component	GO:0005634	nucleus	6444	199	0.0098
	Molecular function	GO:0003964	RNA-directed DNA polymerase activity	9	4	7.5E-08
	Molecular function	GO:0043531	ADP binding	521	79	5.3E-07
	Molecular function	GO:0061630	ubiquitin protein ligase activity	345	3	1.6E-05
	Molecular function	GO:0000977	RNA polymerase II regulatory region sequence-specific DNA binding	132	8	4.2E-05
	Molecular function	GO:0005524	ATP binding	3833	217	0.00013
	Molecular function	GO:0016984	ribulose-bisphosphate carboxylase activity	7	5	0.00018
	Molecular function	GO:0016788	hydrolase activity, acting on ester bonds	2462	109	0.00096
	Molecular function	GO:0016866	intramolecular transferase activity	50	5	0.00162

Molecular function	GO:0004674	protein serine/threonine kinase activity	1774	75	0.00171
Molecular function	GO:0030234	enzyme regulator activity	393	17	0.00222
Molecular function	GO:0004190	aspartic-type endopeptidase activity	128	6	0.00248
Molecular function	GO:0008270	zinc ion binding	1259	33	0.00306
Molecular function	GO:0004832	valine-tRNA ligase activity	10	3	0.00342
Molecular function	GO:0008135	translation factor activity, RNA binding	132	6	0.00492
Molecular function	GO:0043167	ion binding	8671	412	0.00505
Molecular function	GO:0004842	ubiquitin-protein transferase activity <i>glyceraldehyde-3-phosphate</i> <i>dehydrogenase (NAD(P)+)</i>	583	13	0.00599
Molecular function	GO:0043891	<i>(phosphorylating) activity</i>	8	4	0.00704
Molecular function	GO:0004386	helicase activity	243	10	0.00734
