

Table S2 GO enrichment analysis of upregulated and downregulated co-DEGs

Biological process GO terms						Cellular components						Molecular functions					
upregulated co-DEGs						upregulated						upregulated					
#term ID	term description	observ ed gene count	backgr ound gene count	strengt h	false discove ry rate	#term ID	term description	obser ved gene count	backgr ound gene count	strengt h	false discove ry rate	#term ID	term description	obse rved gene count	back gr ound gene count	strengt h	false discove ry rate
GO:0050896	Response to stimulus	222	6678	0.15	#####	GO:00480:Apoplast	48	396	0.46	1.59E-07	GO:00302:Carbohydrate binding	33	424	0.35	0.0062		
GO:0042221	Response to chemical	128	3176	0.23	#####	GO:01101:Cellular anatomical entity	1067	23375	0.04	1.59E-07	GO:00038:Catalytic activity	524	####	0.12	4.71E-12		
GO:0009628	Response to abiotic stimulus	100	1915	0.34	#####	GO:00055:Extracellular region	160	1792	0.33	3.35E-15	GO:00431:Cation binding	253	4912	0.17	3.47E-08		
GO:0100333	Response to organic substance	81	2197	0.19	0.0205	GO:00095:Photosystem	13	91	0.53	0.0216	GO:00200:Heme binding	57	512	0.51	1.40E-10		
GO:0019700	Response to oxygen-containing compound	78	1600	0.31	#####	GO:00095:Photosystem i	10	37	0.81	0.0017	GO:00055:Iron ion binding	37	444	0.38	0.00072		
GO:0009719	Response to endogenous stimulus	71	1696	0.25	0.0016	GO:00719:Cell periphery	280	4866	0.14	3.93E-06	GO:00468:Metal ion binding	251	4876	0.17	3.75E-08		
GO:0009725	Response to hormone	69	1638	0.25	0.0017	GO:00056:Cell wall	58	692	0.3	0.00026	GO:00044:Monooxygenase activity	40	428	0.43	2.35E-05		
GO:0009266	Response to temperature stimulus	47	567	0.54	#####	GO:00160:Integral component of me	305	5316	0.14	1.12E-06	GO:00164:Oxidoreductase activity	167	2078	0.37	1.80E-19		
GO:0009416	Response to light stimulus	41	622	0.45	#####	GO:00312:Intrinsic component of me	323	5544	0.15	1.52E-07	GO:00166:Oxidoreductase activity, acting on ch-c	24	303	0.36	0.0367		
GO:0010035	Response to inorganic substance	40	809	0.32	0.0063	GO:00312:Intrinsic component of pla	37	424	0.32	0.0055	GO:00167:Oxidoreductase activity, acting on pair	48	524	0.42	2.43E-06		
GO:0009408	Response to heat	36	285	0.73	#####	GO:00160:Membrane	440	8895	0.07	0.0027	GO:00166:Oxidoreductase activity, acting on the	23	277	0.38	0.0288		
GO:0006979	Response to oxidative stress	36	484	0.5	#####	GO:00058:Plasma membrane	226	4198	0.11	0.0055	GO:00046:Peroxidase activity	18	157	0.52	0.0054		
GO:0006970	Response to osmotic stress	34	500	0.46	#####	GO:00057:Vacuole	72	1067	0.21	0.0086	GO:00436:Protein self-association	17	144	0.53	0.0059		
GO:0009651	Response to salt stress	31	405	0.51	#####	downregulated						GO:00469:Tetrapyrrole binding	65	552	0.53	4.87E-13	
GO:0006457	Protein folding	30	309	0.61	#####	GO:00480:Apoplast	37	396	0.43	8.61E-05	GO:00167:Transferase activity, transferring alkyl	18	176	0.47	0.0158		
GO:0015979	Photosynthesis	27	223	0.71	#####	GO:01101:Cellular anatomical entity	885	23375	0.04	6.47E-06	GO:00469:Transition metal ion binding	77	1420	0.2	0.0195		
GO:0097305	Response to alcohol	27	510	0.35	0.0384	GO:00055:Extracellular region	120	1792	0.29	2.41E-08	GO:00055:Calmodulin binding	24	305	0.36	0.0383		
GO:0003032	Response to reactive oxygen species	25	209	0.7	#####	GO:00095:Photosystem	16	91	0.71	0.00012	GO:00168:Carbon-oxygen lyase activity, acting on	9	55	0.67	0.0341		
GO:0042542	Response to hydrogen peroxide	22	113	0.92	#####	GO:00095:Photosystem i	11	37	0.93	0.00011	GO:00719:FAD binding	11	65	0.69	0.0074		
GO:0019748	Secondary metabolic process	22	287	0.51	0.0014	GO:00095:Chloroplast	103	2010	0.17	0.007	GO:00053:Inorganic phosphate transmembrane t	7	29	0.84	0.0232		
GO:0051259	Protein complex oligomerization	21	106	0.92	#####	GO:00095:Chloroplast thylakoid	33	414	0.36	0.0025	GO:00431:Ion binding	371	8664	0.09	0.00049		
GO:0044550	Secondary metabolite biosynthetic process	15	192	0.52	0.0272	GO:00095:Chloroplast thylakoid men	28	355	0.36	0.0086	GO:00480:Monosaccharide binding	9	59	0.64	0.0465		
GO:0019684	Photosynthesis, light reaction	12	108	0.67	0.0068	GO:00095:Photosystem i reaction ce	4	8	1.16	0.0353	GO:00166:Oxidoreductase activity, acting on perc	19	165	0.52	0.0034		
GO:0009642	Response to light intensity	11	97	0.68	0.012	GO:00095:Photosystem ii	12	71	0.69	0.0025	GO:00198:Vitamin binding	17	184	0.43	0.0465		
GO:0010345	Suberin biosynthetic process	10	33	1.11	#####	GO:00095:Plastid	117	2294	0.17	0.0029	downregulated						
GO:0048582	Positive regulation of post-embryonic develp	9	72	0.72	0.0272	GO:00095:Thylakoid	37	460	0.37	0.0011	GO:00302:Carbohydrate binding	33	424	0.27	0.0445		
GO:0009765	Photosynthesis, light harvesting	8	37	0.96	0.0026	GO:00426:Thylakoid membrane	32	376	0.39	0.0014	GO:00038:Catalytic activity	608	####	0.1	2.69E-10		
downregulated												GO:00431:Cation binding	259	4912	0.1	0.0043	
GO:0008152	Metabolic process	677	13896	0.07	#####	GO:00200:Heme binding	74	512	0.54	2.11E-15	GO:00055:Iron ion binding	53	444	0.46	4.22E-08		
GO:0050896	Response to stimulus	364	6678	0.11	#####	GO:00468:Metal ion binding	258	4876	0.1	0.0039	GO:00044:Monooxygenase activity	53	428	0.47	1.62E-08		
GO:0006950	Response to stress	246	3733	0.2	#####	GO:00164:Oxidoreductase activity	190	2078	0.34	2.45E-19	GO:00166:Oxidoreductase activity, acting on ch-c	32	303	0.4	0.00064		
GO:0055114	Oxidation-reduction process	225	2314	0.37	#####	GO:00480:Monosaccharide binding	60	524	0.44	1.62E-08	GO:00166:Oxidoreductase activity, acting on pair	60	524	0.44	1.62E-08		
GO:0042221	Response to chemical	223	3176	0.22	#####	GO:00046:Peroxidase activity	24	157	0.56	5.18E-05	GO:00166:Oxidoreductase activity, acting on the	29	277	0.4	0.0017		
GO:0044281	Small molecule metabolic process	153	2184	0.22	#####	GO:00436:Protein self-association	21	144	0.54	0.00035	GO:00046:Peroxidase activity	24	157	0.56	5.18E-05		
GO:0070887	Cellular response to chemical stimulus	138	1943	0.23	#####	GO:00469:Tetrapyrrole binding	81	552	0.55	3.30E-17	GO:00436:Protein self-association	21	144	0.54	0.00035		
GO:0050685	Transmembrane transport	130	1668	0.27	#####	GO:00469:Transition metal ion binding	96	1420	0.21	0.0007	GO:00469:Tetrapyrrole binding	81	552	0.55	3.30E-17		
GO:0006952	Defense response	123	1532	0.28	#####	GO:00469:Transition metal ion binding	96	1420	0.21	0.0007	GO:00167:Transferase activity, transferring alkyl	25	176	0.53	9.06E-05		
GO:0009605	Response to external stimulus	118	1478	0.28	#####	GO:00228:Active ion transmembrane transporter	32	352	0.34	0.0068	GO:00469:Transition metal ion binding	96	1420	0.21	0.0007		
GO:0043436	Oxoacid metabolic process	117	1432	0.29	#####	GO:00228:Active transmembrane transporter acti	73	752	0.37	8.13E-08	GO:00228:Active transmembrane transporter acti	73	752	0.37	8.13E-08		
GO:1901700	Response to oxygen-containing compound	110	1600	0.22	0.0001	GO:00085:Anion transmembrane transporter acti	32	377	0.31	0.0181	GO:00085:Anion transmembrane transporter acti	32	377	0.31	0.0181		
GO:0019752	Carboxylic acid metabolic process	106	1318	0.28	#####	GO:00162:Antioxidant activity	26	200	0.49	0.00018	GO:00162:Antioxidant activity	26	200	0.49	0.00018		
GO:0009607	Response to biotic stimulus	102	1076	0.36	#####	GO:00152:Antipporter activity	24	251	0.36	0.0205	GO:00152:Antipporter activity	24	251	0.36	0.0205		
GO:0044119	Interspecies interaction between organisms	99	1146	0.31	#####	GO:00426:ATPase-coupled transmembrane trans	22	224	0.37	0.0237	GO:00426:ATPase-coupled transmembrane trans	22	224	0.37	0.0237		
GO:0006811	Ion transport	95	1288	0.25	#####	GO:00151:Carbohydrate transmembrane transpo	14	97	0.54	0.011	GO:00151:Carbohydrate transmembrane transpo	14	97	0.54	0.011		
GO:0051707	Response to other organism	94	1031	0.34	#####	GO:00053:Carbohydrate:proton symporter activity	10	55	0.64	0.018	GO:00053:Carbohydrate:proton symporter activity	10	55	0.64	0.018		
GO:0005975	Carbohydrate metabolic process	92	1418	0.19	0.0045	GO:00800:Chitin binding	7	29	0.76	0.0277	GO:00800:Chitin binding	7	29	0.76	0.0277		
GO:0098542	Defense response to other organism	77	801	0.36	#####	GO:00045:Chitinase activity	9	43	0.7	0.015	GO:00045:Chitinase activity	9	43	0.7	0.015		
GO:0034220	Ion transmembrane transport	74	996	0.25	0.0006	GO:00512:Dioxygenase activity	25	262	0.36	0.018	GO:00512:Dioxygenase activity	25	262	0.36	0.018		
GO:0044283	Small molecule biosynthetic process	72	973	0.25	0.0009	GO:00037:DNA-binding transcription factor activit	109	1705	0.19	0.0015	GO:00037:DNA-binding transcription factor activit	109	1705	0.19	0.0015		
GO:1901135	Carbohydrate derivative metabolic process	64	997	0.19	0.0463	GO:00465:Glucosyltransferase activity	31	262	0.45	0.00012	GO:00465:Glucosyltransferase activity	31	262	0.45	0.00012		
GO:0010035	Response to inorganic substance	62	809	0.26	0.0013	GO:00043:Glutathione transferase activity	18	67	0.81	1.50E-06	GO:00043:Glutathione transferase activity	18	67	0.81	1.50E-06		
GO:0046394	Carboxylic acid biosynthetic process	61	716	0.31	0.0001	GO:00167:Hydrolase activity, acting on glycosyl t	45	630	0.23	0.0347	GO:00167:Hydrolase activity, acting on glycosyl t	45	630	0.23	0.0347		
GO:0071554	Cell wall organization or biogenesis	58	819	0.23	0.0117	GO:00045:Hydrolase activity, hydrolyzing o-glyco	15	124	0.46	0.0274	GO:00045:Hydrolase activity, hydrolyzing o-glyco	15	124	0.46	0.0274		
GO:0006820	Anion transport	53	520	0.39	#####	GO:00151:Inorganic anion transmembrane trans	63	947	0.2	0.0234	GO:00151:Inorganic anion transmembrane trans	63	947	0.2	0.0234		
GO:0032787	Monocarboxylic acid metabolic process	51	692	0.25	0.0117	GO:00301:Manganese ion binding	11	76	0.54	0.0358	GO:00301:Manganese ion binding	11	76	0.54	0.0358		
GO:0045229	External encapsulating structure organizatio	50	704	0.23	0.0243	GO:00167:Oxidoreductase activity, acting on pair	23	204	0.43	0.004	GO:00167:Oxidoreductase activity, acting on pair	23	204	0.43	0.004		
GO:0071555	Cell wall organization	48	679	0.23	0.0331	GO:00800:Quercetin 3-o-glucosyltransferase acti	10	62	0.59	0.0312	GO:00800:Quercetin 3-o-glucosyltransferase acti	10	62	0.59	0.0312		
GO:0005976	Polysaccharide metabolic process	45	588	0.26	0.0124	GO:00800:Quercetin 7-o-glucosyltransferase acti	10	61	0.59	0.0284	GO:00800:Quercetin 7-o-glucosyltransferase acti	10	61	0.59	0.0284		
GO:0098656	Anion transmembrane transport	44	383	0.44	#####	GO:00152:Secondary active transmembrane tran	50	487	0.39	7.48E-06	GO:00152:Secondary active transmembrane tran	50	487	0.39	7.48E-06		
GO:0006520	Cellular amino acid metabolic process	44	493	0.33	0.0009	GO:00152:Solute:cation symporter activity	16	143	0.43	0.0352	GO:00152:Solute:cation symporter activity	16	143	0.43	0.0352		
GO:0006790	Sulfur compound metabolic process	43	379	0.43	#####	GO:00465:Glucosyltransferase activity	31	262	0.45	0.00012	GO:00465:Glucosyltransferase activity	31	262	0.45	0.00012		
GO:0006979	Response to oxidative stress	41	484	0.31	0.0043	GO:00043:Glutathione transferase activity	18	67	0.81	1.50E-06	GO:00043:Glutathione transferase activity	18	67	0.81	1.50E-06		
GO:0009723	Response to ethylene	39	343	0.43	#####	GO:01401:Transcription regulator activity	111	1862	0.15	0.0181	GO:01401:Transcription regulator activity	111	1862	0.15	0.0181		
GO:0016052	Carbohydrate catabolic process	38	409	0.35	0.0015	GO:00167:Transferase activity, transferring glyco	65	756	0.31	3.25E-05	GO:00167:Transferase activity, transferring glyco	65	756	0.31	3.25E-05		
GO:1901605	Alpha-amino acid metabolic process	37	368	0.38	0.0005	GO:00167:Transferase activity, transferring hexo	46	474	0.37	9.06E-05	GO:00167:Transferase activity, transferring hexo	46	474	0.37	9.06E-05		
GO:0071369	Cellular response to ethylene stimulus	35	278	0.48	#####	GO:00228:Transmembrane transporter activity	123	1619	0.26	1.87E-07	GO:00228:Transmembrane transporter activity	123	1619	0.26	1.87E-07		
GO:0009636	Response to toxic substance	35	294	0.45	#####	GO:00052:Transporter activity	125	1726	0.24	1.59E-06	GO:00052:Transporter activity	125	1726	0.24	1.59E-06		
GO:0009620	Response to fungus	34	329	0.39	0.0007	GO:00352:UDP-glucosyltransferase activity	25	213	0.45	0.0012	GO:00352:UDP-glucosyltransferase activity	25	213	0.45	0.0012		
GO:0009873	Ethylene-activated signaling pathway	33	271	0.46	#####	GO:00081:UDP-glucosyltransferase activity	41	403	0.39	0.0001	GO:00081:UDP-glucosyltransferase activity	41	403	0.39	0.0001		
GO:0019748	Secondary metabolic process	33	287	0.44	0.0001	GO:00429:Xenobiotic transmembrane transporter	15	98	0.56	0.004	GO:00429:Xenobiotic transmembrane transporter	15	98</				

GO:0009251	Glucan catabolic process	10	58	0.62	0.0226
GO:0044247	Cellular polysaccharide catabolic process	9	49	0.64	0.0276
GO:0030245	Cellulose catabolic process	8	27	0.85	0.0053
GO:0006568	Tryptophan metabolic process	8	30	0.8	0.0088
GO:0080029	Cellular response to boron-containing subst	7	12	1.14	0.0008
GO:0019288	Isopentenyl diphosphate biosynthetic proces	7	14	1.08	0.0014
GO:0071281	Cellular response to iron ion	7	18	0.97	0.0043
GO:0016137	Glycoside metabolic process	7	33	0.71	0.0495
GO:0006949	Syncytium formation	6	13	1.04	0.0062
GO:0000162	Tryptophan biosynthetic process	6	18	0.9	0.0192
GO:1901806	Beta-glucoside biosynthetic process	6	22	0.81	0.0408
GO:0019756	Cyanogenic glycoside biosynthetic process	6	23	0.79	0.047
GO:0010055	Atrichoblast differentiation	5	5	1.38	0.0024
GO:0080169	Cellular response to boron-containing subst	5	5	1.38	0.0024
GO:0032107	Regulation of response to nutrient levels	5	10	1.08	0.0151