

Supplemental Table 4 Gene Ontology classification of differentially expressed genes (DEGs) in *Arabidopsis*. DEGs identified in the polysomal RNA fraction (FDR ≤ 5% and fold change ≥ 2) were included. AgriGO categories were considered significant and are presented in bold if represented by 5 or more transcripts and $p \leq 0.05$. The first number in each column header represents the total number of probe sets meeting these criteria in the gene list, while the number below in parentheses represents the number of probe sets in this list with AgriGO annotation(s). Bgitem refers to total number of genes with the corresponding annotation in this genome, GO_acc is the Gene Ontology accession, Poly is Polyribosomal RNA, and Total is Total RNA.

GO_acc	Term	bgitem	Poly Induced (318)	Total Induced (432)	Poly Repressed (220)	Total Repressed (384)
GO:0003756	protein disulfide isomerase activity	22	5	5	0	0
GO:0003824	catalytic activity	9638	139	165	84	165
GO:0004089	carbonate dehydratase activity	30	0	0	1	5
GO:0005515	protein binding	2944	53	60	12	21
GO:0005576	extracellular region	285	5	13	12	19
GO:0005618	cell wall	403	16	20	8	16
GO:0005622	intracellular	9671	107	130	91	190
GO:0005623	cell	15217	209	260	147	280
GO:0005737	cytoplasm	6822	78	98	75	162
GO:0005773	vacuole	383	15	15	2	6
GO:0005783	endoplasmic reticulum	466	25	25	3	3
GO:0005886	plasma membrane	1456	54	62	12	21
GO:0005984	disaccharide metabolic process	45	2	1	3	6
GO:0006464	protein modification process	1474	35	37	12	25
GO:0006497	protein amino acid lipidation	31	8	7	2	6
GO:0006950	response to stress	2320	54	70	23	37
GO:0006952	defense response	766	20	29	7	14
GO:0006979	response to oxidative stress	332	12	13	7	10
GO:0008152	metabolic process	10614	126	163	81	162
GO:0009311	oligosaccharide metabolic process	52	2	1	3	6
GO:0009408	response to heat	161	5	10	1	1
GO:0009505	plant-type cell wall	254	10	10	6	10
GO:0009507	chloroplast	2740	20	27	59	140
GO:0009521	photosystem	66	0	0	2	6
GO:0009523	photosystem II	45	0	0	2	5
GO:0009526	plastid envelope	331	1	2	14	35
GO:0009532	plastid stroma	322	0	2	14	24
GO:0009534	chloroplast thylakoid	290	0	0	15	35
GO:0009535	chloroplast thylakoid membrane	231	0	0	13	32
GO:0009536	plastid	2965	20	27	59	140
GO:0009543	chloroplast thylakoid lumen	89	0	0	4	9
GO:0009570	chloroplast stroma	249	0	2	14	24
GO:0009579	thylakoid	376	1	2	20	43
GO:0009607	response to biotic stimulus	638	20	26	7	13
GO:0009617	response to bacterium	247	11	13	6	9
GO:0009627	systemic acquired resistance	54	0	7	0	0
GO:0009628	response to abiotic stimulus	1471	29	38	16	31
GO:0009941	chloroplast envelope	265	1	2	14	32
GO:0010035	response to inorganic substance	279	14	20	7	7
GO:0010038	response to metal ion	238	10	15	6	4
GO:0010218	response to far red light	57	2	1	3	6
GO:0010876	lipid localization	24	1	6	4	4
GO:0012505	endomembrane system	3416	56	72	34	55
GO:0015979	photosynthesis	162	0	0	6	20
GO:0016020	membrane	4068	84	105	45	90
GO:0016052	carbohydrate catabolic process	128	8	4	1	4
GO:0016301	kinase activity	1641	34	39	7	13
GO:0016491	oxidoreductase activity	1463	22	24	23	41
GO:0016667	oxidoreductase activity, acting on sulfur group of do	109	1	2	8	8
GO:0016772	transferase activity, transferring phosphorus-contain	1887	37	40	9	15
GO:0016860	intramolecular oxidoreductase activity	60	6	0	0	0
GO:0016862	intramolecular oxidoreductase activity, interconverti	22	5	0	0	0
GO:0016862	intramolecular oxidoreductase activity, interconverti	22	0	5	0	0
GO:0016864	intramolecular oxidoreductase activity, transposing	22	5	5	0	0
GO:0018130	heterocycle biosynthetic process	123	0	0	4	9
GO:0018193	peptidyl-amino acid modification	35	8	7	3	8
GO:0019684	photosynthesis, light reaction	103	0	0	0	9
GO:0030246	carbohydrate binding	162	9	0	0	0
GO:0030312	external encapsulating structure	407	16	20	8	16
GO:0031090	organelle membrane	842	7	10	15	39
GO:0031225	anchored to membrane	272	2	2	6	10
GO:0031226	intrinsic to plasma membrane	74	4	3	4	7
GO:0031365	N-terminal protein amino acid modification	8	8	7	2	6
GO:0031967	organelle envelope	595	2	5	15	37
GO:0031975	envelope	595	2	5	15	37
GO:0031976	plastid thylakoid	293	0	0	15	35
GO:0031977	thylakoid lumen	95	0	0	4	9
GO:0031978	plastid thylakoid lumen	89	0	0	4	9
GO:0031984	organelle subcompartment	295	0	0	15	35
GO:0034357	photosynthetic membrane	273	0	0	13	33
GO:0034641	cellular nitrogen compound metabolic process	506	9	15	11	18
GO:0042157	lipoprotein metabolic process	31	8	7	2	6
GO:0042158	lipoprotein biosynthetic process	31	8	7	2	6
GO:0042221	response to chemical stimulus	2085	52	60	31	43
GO:0042651	thylakoid membrane	244	0	0	13	32
GO:0043167	ion binding	2087	35	48	14	31
GO:0043169	cation binding	2087	35	48	14	31

GO:0043226	organelle	8155	87	108	82	174
GO:0043227	membrane-bounded organelle	7622	85	106	81	173
GO:0043229	intracellular organelle	8149	87	108	82	174
GO:0043231	intracellular membrane-bounded organelle	7615	85	106	81	173
GO:0043412	macromolecule modification	1636	35	38	12	25
GO:0043543	protein amino acid acylation	10	7	6	2	6
GO:0044275	cellular carbohydrate catabolic process	125	8	4	1	4
GO:0044422	organelle part	2562	18	26	38	75
GO:0044424	intracellular part	9302	105	126	90	186
GO:0044425	membrane part	1360	20	24	13	29
GO:0044432	endoplasmic reticulum part	75	6	8	0	0
GO:0044434	chloroplast part	746	1	4	33	68
GO:0044435	plastid part	867	1	4	33	69
GO:0044436	thylakoid part	307	0	0	15	35
GO:0044444	cytoplasmic part	6289	74	91	73	160
GO:0044446	intracellular organelle part	2561	18	26	38	75
GO:0044459	plasma membrane part	222	11	7	5	8
GO:0044464	cell part	15217	209	260	147	280
GO:0046658	anchored to plasma membrane	36	2	1	4	6
GO:0046686	response to cadmium ion	178	9	12	6	4
GO:0048046	apoplast	182	4	11	9	14
GO:0050896	response to stimulus	4057	88	104	48	74
GO:0051082	unfolded protein binding	93	7	0	0	0
GO:0051704	multi-organism process	776	19	26	7	13
GO:0051707	response to other organism	599	16	23	7	13
GO:0055035	plastid thylakoid membrane	231	0	0	13	32