

**Supplemental Table S5. Comparison of GO across species for Set 3 and Set 4.**

**Set 3:** Arabidopsis genes whose orthologs have been associated with the *plant embryo coleoptilar stage* (coleoptilar) of maize in the PO, but which have not been associated with the *plant embryo cotyledonary stage* (cotyledonary) in Arabidopsis. **Set 4:** Genes associated with the *plant embryo cotyledonary stage* in Arabidopsis. GO Branches: BP = *biological process*, MF = *molecular function*, and CC = *cellular component*. FDR is the False Discovery Rate of (Benjamini & Yekutieli, 2001). Any reported value is significant at P=0.05 when corrected for multiple tests. Colors correspond to FDR values, with red most significant and dark gray non-significant.

GO Information			FDR	
Term ID	Branch	Term label	Set 3 – coleoptilar not cotyledonary	Set 4 – cotyledonary
GO:0006810	BP	transport	2.20e-05	2.00e-34
GO:0051704	BP	multi-organism process	2.20e-05	1.10e-14
GO:0051234	BP	establishment of localization	2.40e-05	7.40e-38
GO:0051179	BP	localization	2.40e-05	4.50e-40
GO:0009856	BP	pollination	6.20e-05	---
GO:0009719	BP	response to endogenous stimulus	0.00065	1.00e-12
GO:0050896	BP	response to stimulus	0.008	2.00e-75
GO:0016049	BP	cell growth	0.022	0.00093
GO:0090066	BP	regulation of anatomical structure size	0.027	0.00051
GO:0008361	BP	regulation of cell size	0.027	0.00038
GO:0032535	BP	regulation of cellular component size	0.027	0.00051
GO:0003824	MF	catalytic activity	0.00031	1.70e-36
GO:0005215	MF	transporter activity	0.026	3.10e-06
GO:0005576	CC	extracellular region	0.03	---
GO:0009987	BP	cellular process	---	6.70e-165

GO:0044237	BP	cellular metabolic process	---	5.50e-135
GO:0044238	BP	primary metabolic process	---	5.90e-116
GO:0008152	BP	metabolic process	---	2.60e-108
GO:0006807	BP	nitrogen compound metabolic process	---	2.70e-91
GO:0016043	BP	cellular component organization	---	2.70e-86
GO:0006139	BP	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	---	8.90e-73
GO:0043170	BP	macromolecule metabolic process	---	2.90e-71
GO:0009058	BP	biosynthetic process	---	2.70e-70
GO:0044260	BP	cellular macromolecule metabolic process	---	1.30e-69
GO:0044249	BP	cellular biosynthetic process	---	4.20e-65
GO:0065007	BP	biological regulation	---	1.60e-62
GO:0009628	BP	response to abiotic stimulus	---	6.70e-61
GO:0032501	BP	multicellular organismal process	---	7.60e-60
GO:0032502	BP	developmental process	---	8.90e-60
GO:0007275	BP	multicellular organismal development	---	1.10e-56
GO:0050789	BP	regulation of biological process	---	7.40e-56
GO:0009056	BP	catabolic process	---	3.80e-55
GO:0005975	BP	carbohydrate metabolic process	---	4.20e-50
GO:0048856	BP	anatomical structure development	---	4.20e-50
GO:0009791	BP	post-embryonic development	---	1.20e-49
GO:0006950	BP	response to stress	---	1.70e-49
GO:0043412	BP	macromolecule modification	---	3.70e-48
GO:0050794	BP	regulation of cellular process	---	3.90e-40
GO:0006464	BP	protein modification process	---	7.40e-39
GO:0048608	BP	reproductive structure development	---	4.60e-37
GO:0003006	BP	reproductive developmental process	---	1.10e-30
GO:0009607	BP	response to biotic stimulus	---	2.60e-30
GO:0000003	BP	reproduction	---	5.00e-30
GO:0022414	BP	reproductive process	---	7.10e-30

GO:0006629	BP	lipid metabolic process	---	3.10e-29
GO:0007049	BP	cell cycle	---	1.80e-27
GO:0019222	BP	regulation of metabolic process	---	6.90e-27
GO:0019538	BP	protein metabolic process	---	7.80e-27
GO:0044267	BP	cellular protein metabolic process	---	2.20e-25
GO:0006091	BP	generation of precursor metabolites and energy	---	3.00e-24
GO:0006519	BP	cellular amino acid and derivative metabolic process	---	1.20e-23
GO:0009653	BP	anatomical structure morphogenesis	---	1.90e-21
GO:0009908	BP	flower development	---	2.20e-21
GO:0006259	BP	DNA metabolic process	---	2.50e-21
GO:0060255	BP	regulation of macromolecule metabolic process	---	1.90e-19
GO:0019748	BP	secondary metabolic process	---	1.90e-19
GO:0015979	BP	photosynthesis	---	5.80e-19
GO:0009059	BP	macromolecule biosynthetic process	---	1.00e-18
GO:0065008	BP	regulation of biological quality	---	1.40e-17
GO:0006350	BP	transcription	---	2.00e-17
GO:0034645	BP	cellular macromolecule biosynthetic process	---	5.40e-17
GO:0010468	BP	regulation of gene expression	---	6.40e-16
GO:0009790	BP	embryonic development		5.50e-14
GO:0040029	BP	regulation of gene expression, epigenetic		6.80e-14
GO:0048869	BP	cellular developmental process		7.70e-14
GO:0007165	BP	signal transduction		1.10e-12
GO:0009605	BP	response to external stimulus		1.40e-10
GO:0010467	BP	gene expression		2.00e-10
GO:0042592	BP	homeostatic process		9.90e-10
GO:0030154	BP	cell differentiation		6.00e-09
GO:0016265	BP	death		7.00e-09
GO:0008219	BP	cell death		7.00e-09
GO:0040007	BP	growth		1.10e-08
GO:0009606	BP	tropism		1.90e-06

GO:0019725	BP	cellular homeostasis		2.20e-06
GO:0007154	BP	cell communication		0.00053
GO:0005515	MF	protein binding		4.70e-39
GO:0005488	MF	binding		2.00e-29
GO:0000166	MF	nucleotide binding		2.20e-22
GO:0016740	MF	transferase activity		2.10e-13
GO:0016787	MF	hydrolase activity		2.30e-11
GO:0016817	MF	hydrolase activity, acting on acid anhydrides		2.50e-09
GO:0016818	MF	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides		2.70e-09
GO:0016462	MF	pyrophosphatase activity		3.90e-09
GO:0016772	MF	transferase activity, transferring phosphorus-containing groups		2.70e-08
GO:0017111	MF	nucleoside-triphosphatase activity		3.00e-08
GO:0005198	MF	structural molecule activity		1.70e-06
GO:0016301	MF	kinase activity		1.50e-05
GO:0003677	MF	DNA binding		0.00012
GO:0016788	MF	hydrolase activity, acting on ester bonds		0.008
GO:0003774	MF	motor activity		0.015
GO:0004518	MF	nuclease activity		0.02
GO:0008135	MF	translation factor activity, nucleic acid binding		0.047
GO:0044464	CC	cell part		2.30e-170
GO:0005623	CC	cell		2.30e-170
GO:0005622	CC	intracellular		5.70e-124
GO:0044424	CC	intracellular part		2.90e-122
GO:0044446	CC	intracellular organelle part		6.00e-94
GO:0044422	CC	organelle part		6.00e-94
GO:0043229	CC	intracellular organelle		4.60e-89
GO:0043226	CC	organelle		4.80e-89
GO:0005737	CC	cytoplasm		2.90e-88

GO:0044444	CC	cytoplasmic part		1.30e-84
GO:0043227	CC	membrane-bounded organelle		4.80e-84
GO:0043231	CC	intracellular membrane-bounded organelle		8.60e-84
GO:0016020	CC	membrane		2.60e-60
GO:0009536	CC	plastid		2.60e-56
GO:0005829	CC	cytosol		1.90e-46
GO:0005886	CC	plasma membrane		4.80e-33
GO:0031975	CC	envelope		6.30e-30
GO:0031967	CC	organelle envelope		6.30e-30
GO:0032991	CC	macromolecular complex		6.70e-29
GO:0009579	CC	thylakoid		1.40e-19
GO:0043232	CC	intracellular non-membrane-bounded organelle		9.70e-19
GO:0043228	CC	non-membrane-bounded organelle		9.70e-19
GO:0005773	CC	vacuole		6.50e-18
GO:0031974	CC	membrane-enclosed lumen		6.30e-17
GO:0043233	CC	organelle lumen		1.20e-16
GO:0070013	CC	intracellular organelle lumen		1.20e-16
GO:0005794	CC	Golgi apparatus		1.90e-16
GO:0044428	CC	nuclear part		4.60e-16
GO:0005634	CC	nucleus		3.40e-15
GO:0031981	CC	nuclear lumen		2.70e-12
GO:0005783	CC	endoplasmic reticulum		1.80e-11
GO:0005768	CC	endosome		3.30e-09
GO:0005730	CC	nucleolus		4.70e-09
GO:0005840	CC	ribosome		5.10e-07
GO:0012505	CC	endomembrane system		7.50e-07
GO:0005777	CC	peroxisome		1.60e-05
GO:0042579	CC	microbody		1.60e-05
GO:0030529	CC	ribonucleoprotein complex		4.60e-05
GO:0005654	CC	nucleoplasm		0.00015

GO:0030312	CC	external encapsulating structure		0.0017
GO:0005635	CC	nuclear envelope		0.002
GO:0005618	CC	cell wall		0.002
GO:0005856	CC	cytoskeleton		0.0021