

Supplemental Table S3. Comparison of GO enrichment analysis for Set 1 versus Set 2 genes in Arabidopsis.

Set 1: Genes associated to *plant embryo globular stage (globular)* but not *mature plant embryo stage (mature)*.

Set 2: Genes associated to *mature plant embryo stage (mature)* but not *plant embryo globular stage (globular)*.

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 1 - globular not mature	Set 2 - mature not globular
GO:0051704	BP	multi-organism process	2.30e-18	---
GO:0009856	BP	pollination	8.10e-17	---
GO:0050896	BP	response to stimulus	1.80e-08	0.0058
GO:0006810	BP	transport	3.00e-07	---
GO:0051234	BP	establishment of localization	1.20e-06	---
GO:0016049	BP	cell growth	1.30e-06	---
GO:0008361	BP	regulation of cell size	1.60e-06	---
GO:0051179	BP	localization	1.80e-06	---
GO:0090066	BP	regulation of anatomical structure size	2.10e-06	---
GO:0032535	BP	regulation of cellular component size	2.10e-06	---
GO:0009719	BP	response to endogenous stimulus	3.20e-06	---
GO:0006950	BP	response to stress	5.40e-06	---
GO:0009607	BP	response to biotic stimulus	7.20e-06	---
GO:0040007	BP	growth	1.60e-05	---
GO:0019748	BP	secondary metabolic process	1.70e-05	---

GO:0022414	BP	reproductive process	2.80e-05	0.0017
GO:0000003	BP	reproduction	3.20e-05	0.0018
GO:0016265	BP	death	4.50e-05	---
GO:0008219	BP	cell death	4.50e-05	---
GO:0030154	BP	cell differentiation	5.80e-05	---
GO:0048869	BP	cellular developmental process	0.00017	---
GO:0003006	BP	reproductive developmental process	0.00023	0.0085
GO:0065007	BP	biological regulation	0.00034	3.80e-06
GO:0065008	BP	regulation of biological quality	0.00064	---
GO:0032502	BP	developmental process	0.0027	0.005
GO:0007165	BP	signal transduction	0.0044	0.0009
GO:0006519	BP	cellular amino acid and derivative metabolic process	0.0044	---
GO:0007275	BP	multicellular organismal development	0.009	0.0021
GO:0009653	BP	anatomical structure morphogenesis	0.01	0.0017
GO:0048856	BP	anatomical structure development	0.015	0.00097
GO:0050794	BP	regulation of cellular process	0.015	1.70e-06
GO:0009605	BP	response to external stimulus	0.015	---
GO:0032501	BP	multicellular organismal process	0.017	0.00059
GO:0008152	BP	metabolic process	0.027	---
GO:0006629	BP	lipid metabolic process	0.039	---
GO:0003824	MF	catalytic activity	6.10e-09	---
GO:0016787	MF	hydrolase activity	1.60e-06	---
GO:0005215	MF	transporter activity	3.90e-06	---
GO:0003700	MF	transcription factor activity	4.80e-05	9.50e-06
GO:0030528	MF	transcription regulator activity	0.00016	7.20e-06
GO:0016788	MF	hydrolase activity, acting on ester bonds	0.00025	---

GO:0030234	MF	enzyme regulator activity	0.0012	---
GO:0005576	CC	extracellular region	1.20e-17	---
GO:0030312	CC	external encapsulating structure	0.00015	---
GO:0005618	CC	cell wall	0.00015	---
GO:0005886	CC	plasma membrane	0.0011	---
GO:0050789	BP	regulation of biological process	---	1.70e-06
GO:0019222	BP	regulation of metabolic process	---	3.80e-06
GO:0009908	BP	flower development	---	3.80e-06
GO:0060255	BP	regulation of macromolecule metabolic process	---	3.50e-05
GO:0006350	BP	transcription	---	6.50e-05
GO:0010468	BP	regulation of gene expression	---	0.00012
GO:0006259	BP	DNA metabolic process	---	0.00051
GO:0048608	BP	reproductive structure development	---	0.0017
GO:0009875	BP	pollen-pistil interaction	---	0.005
GO:0009791	BP	post-embryonic development	---	
GO:0006139	BP	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	---	
GO:0007049	BP	cell cycle	---	
GO:0003677	MF	DNA binding	---	
GO:0016301	MF	kinase activity	---	
GO:0016772	MF	transferase activity, transferring phosphorus-containing groups	---	
GO:0005634	CC	nucleus	---	