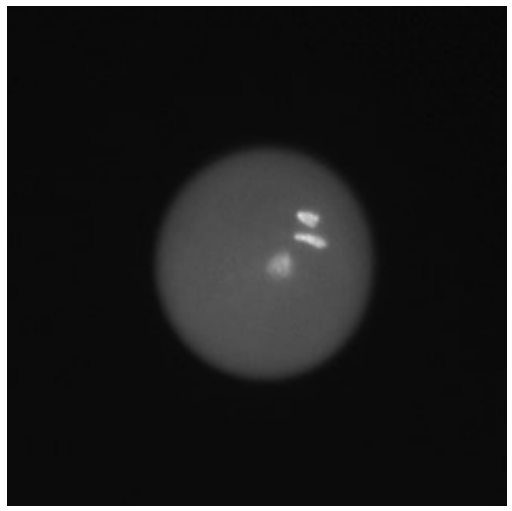
Mature Pollen



Sperm Cell

Differentially expressed genes

Top significantly overrepresented GO terms

GO Term	Description	p-value
GO:0043687	Post-translational protein modification	3.50E-17
GO:0046686	Response to cadmium ion	5.70E-16
GO:0051788	Response to misfolded protein	1.40E-15
GO:0044710	Single-organism metabolic process	5.20E-15
GO:0080129	Proteasome core complex assembly	3.40E-14
GO:0061025	Membrane fusion	1.50E-12
GO:0033121	Regulation of purine nucleotide catabolism	1.50E-11
GO:0009118	Regulation of nucleoside metabolic processes	1.50E-11
GO:0006511	Ubiquitin-dependent protein catabolic processes	1.90E-11
GO:0006886	Intracellular protein transport	2.90E-11
GO:0035295	Tube development	8.80E-11
GO:0009853	Photorespiration	1.30E-10
GO:0006487	Protein N-linked glycosylation	3.80E-10
GO:0009860	Pollen tube growth	1.70E-09
GO:0016926	Protein desumoylation	3.60E-09
GO:0006623	Protein targeting to vacuole	5.20E-09
GO:0050665	Hydrogen peroxide biosynthetic process	5.40E-09
GO:0006897	Endocytosis	6.30E-09

GO Term	Description	p-value
GO:0007062	Sister chromatid cohesion	1.30E-14
GO:0009154	Purine ribonucleotide catabolic process	5.70E-14
GO:0042138	Meiotic DNA double-strand break formation	4.70E-09
GO:0000278	Mitotic cell cycle	5.00E-09
GO:0031048	Chromatin silencing by small RNA	1.60E-08
GO:0000911	Cytokinesis by cell plate formation	1.80E-08
GO:0009630	Gravitropism	2.90E-08
GO:0035196	Production of miRNAs involved in gene silencing	5.50E-08
GO:0006396	RNA processing	9.80E-08
GO:0010228	Vegetative to reproductive phase transition	1.00E-07
GO:0006635	Fatty acid beta-oxidation	1.60E-07
GO:0000724	Double-strand break repair	2.40E-07
GO:0045132	Meiotic chromosome segregation	2.80E-07
GO:0010267	Production of ta-siRNAs involved in RNA interference	4.40E-07
GO:0019563	Glycerol catabolic process	2.20E-06
GO:0031338	Regulation of vesicle fusion	2.30E-06
GO:0010564	Regulation of cell cycle process	4.10E-06
GO:0000398	mRNA splicing, via spliceosome	5.80E-06

Heading paragraph (revised slightly):

Gene ontology (GO) analysis of mRNA transcripts highlights contrasting cellular processes in mature pollen (containing sperm cells as well as the vegetative cell) and sperm cells alone, consistent with the distinct roles of the sperm cells and the vegetative cell in reproduction.

Figure description paragraph:

GO annotations were assigned to highly differentially expressed genes (q-value < 0.01) using the R package topGO (Alexa, et al. (2016)) in combination with maize-GAMER, a recent maize gene functional annotation (Wimalanathan, et al. (2017)). GO annotations associated with genes highly-expressed in mature pollen are shown in yellow, while those associated with genes highly-expressed in sperm cells are shown in blue.

References:

Alexa, et al (2016)

To cite package 'topGO' in publications use: Adrian Alexa and Jorg Rahnenfuhrer (2016). topGO: Enrichment Analysis for Gene Ontology. R package version 2.28.0.

BibTeX:

@Manual{, title = {topGO: Enrichment Analysis for Gene Ontology}, author = {Adrian Alexa and Jorg Rahnenfuhrer}, year = {2016}, note = {R package version 2.28.0}, }

Wimalanathan, et al. (2017)

BibTex:

@article {Wimalanathan222836, author = {Wimalanathan, Kokulapalan and Friedberg, Iddo and Andorf, Carson M. and Lawrence-Dill, Carolyn J.}, title = {Maize GO Annotation - Methods, Evaluation, and Review (maize-GAMER)}, year = {2017}, doi = {10.1101/222836}, publisher = {Cold Spring Harbor Laboratory}, abstract = {We created a new high-coverage, robust, and reproducible functional annotation of maize protein coding genes based on Gene Ontology (GO) term assignments. Whereas the existing Phytozome and Gramene maize GO annotation sets only cover 41\% and 56\% of maize protein coding genes, respectively, this study provides annotations for 100\% of the genes. We also compared the quality of our newly-derived annotations with the existing Gramene and Phytozome functional annotation sets by comparing all three to a manually annotated gold standard set of 1,619 genes where annotations were primarily inferred from direct assay or mutant phenotype. Evaluations based on the gold standard indicate that our new annotation set is measurably more accurate than those from Phytozome and Gramene. To derive this new high-coverage, high-confidence annotation set we used sequence-similarity and protein-domain-presence methods as well as mixed-method pipelines that developed for the Critical Assessment of Function Annotation (CAFA) challenge. Our project to improve maize annotations is called maize-GAMER (GO Annotation Method, Evaluation, and Review) and the newly-derived annotations are accessible via MaizeGDB (http://download.maizegdb.org/maize-GAMER) and CyVerse (B73 RefGen_v3 5b+ at doi.org/10.7946/P2S62P and B73 RefGen_v4 Zm00001d.2 at doi.org/10.7946/P2M925).}, URL = {https://www.biorxiv.org/content/early/2017/11/21/222836}, eprint = {https://www.biorxiv.org/content/early/2017/11/21/222836.full.pdf}, journal = {bioRxiv}}