	Term	Count	P-value	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
Arabidopsis thaliana	GO:0045449~regulation of transcription	76	3.5E-57	81	2024	13998	6.49	8.4E-55	8.4E-55	4.5E-54
	GO:0006350~transcription	55	7.0E-37	81	1311	13998	7.25	1.7E-34	8.3E-35	9.0E-34
	GO:0006355~regulation of transcription, DNA-dependent	40	1.3E-22	81	1089	13998	6.35	3.0E-20	9.9E-21	1.6E-19
	GO:0051252~regulation of RNA metabolic process	40	1.5E-22	81	1095	13998	6.31	3.6E-20	9.1E-21	2.0E-19
	GO:0009791~post-embryonic development	12	8.8E-03	81	851	13998	2.44	8.8E-01	1.0E-01	1.1E+01
	GO:0009651~response to salt stress	8	5.1E-03	81	369	13998	3.75	7.0E-01	8.3E-02	6.4E+00
	GO:0006970~response to osmotic stress	8	7.7E-03	81	399	13998	3.46	8.4E-01	9.7E-02	9.5E+00
	GO:0009908~flower development	7	2.1E-03	81	232	13998	5.21	3.9E-01	6.9E-02	2.7E+00
	GO:0048569~post-embryonic organ development	6	3.5E-03	81	178	13998	5.83	5.7E-01	8.0E-02	4.4E+00
	GO:0048467~gynoecium development	5	2.7E-04	81	55	13998	15.71	6.2E-02	1.3E-02	3.5E-01
	GO:0003002~regionalization	5	1.8E-03	81	91	13998	9.50	3.5E-01	6.9E-02	2.3E+00
	GO:0048438~floral whorl development	5	3.2E-03	81	106	13998	8.15	5.3E-01	8.0E-02	4.0E+00
	GO:0007389~pattern specification process	5	3.7E-03	81	111	13998	7.78	5.9E-01	7.8E-02	4.7E+00
	GO:0048440~carpel development	4	2.7E-03	81	49	13998	14.11	4.8E-01	7.8E-02	3.5E+00
	GO:0045941~positive regulation of transcription	4	3.8E-03	81	55	13998	12.57	6.0E-01	7.3E-02	4.8E+00
	GO:0010628~positive regulation of gene expression	4	4.0E-03	81	56	13998	12.34	6.2E-01	7.1E-02	5.0E+00
	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	4	5.6E-03	81	63	13998	10.97	7.4E-01	8.5E-02	7.0E+00
	GO:0051173~positive regulation of nitrogen compound metabolic process	4	5.6E-03	81	63	13998	10.97	7.4E-01	8.5E-02	7.0E+00
	GO:0010557~positive regulation of macromolecule biosynthetic process	4	5.6E-03	81	63	13998	10.97	7.4E-01	8.5E-02	7.0E+00
	GO:0009891~positive regulation of biosynthetic process	4	6.9E-03	81	68	13998	10.17	8.1E-01	9.8E-02	8.5E+00
	GO:0031328~positive regulation of cellular biosynthetic process	4	6.9E-03	81	68	13998	10.17	8.1E-01	9.8E-02	8.5E+00
	GO:0010604~positive regulation of macromolecule metabolic process	4	7.2E-03	81	69	13998	10.02	8.2E-01	9.6E-02	8.9E+00
Drosophila melanogaster	GO:0045449~regulation of transcription	18	9.6E-18	18	799	7937	9.93	4.1E-15	4.1E-15	1.4E-14
	GO:0006355~regulation of transcription, DNA-dependent	14	5.4E-12	18	612	7937	10.09	2.3E-09	1.2E-09	7.6E-09
	GO:0051252~regulation of RNA metabolic process	14	2.0E-11	18	678	7937	9.11	8.6E-09	2.9E-09	2.8E-08
	GO:0006350~transcription	10	1.1E-07	18	459	7937	9.61	4.6E-05	1.2E-05	1.5E-04
	GO:0030182~neuron differentiation	8	1.1E-05	18	409	7937	8.62	4.9E-03	9.7E-04	1.6E-02
	GO:0002165~instar larval or pupal development	7	1.5E-04	18	418	7937	7.38	6.4E-02	1.1E-02	2.2E-01

	GO:0009791~post-embryonic development	7	1.9E-04	18	434	7937	7.11	7.9E-02	1.2E-02	2.7E-01
	GO:0007548~sex differentiation	4	2.6E-04	18	60	7937	29.40	1.1E-01	1.4E-02	3.6E-01
	GO:0007552~metamorphosis	6	7.5E-04	18	362	7937	7.31	2.8E-01	3.5E-02	1.1E+00
	GO:0045165~cell fate commitment	5	1.3E-03	18	232	7937	9.50	4.2E-01	5.2E-02	1.8E+00
	GO:0001751~compound eye photoreceptor cell differentiation	4	1.6E-03	18	111	7937	15.89	4.9E-01	5.9E-02	2.2E+00
	GO:0001754~eye photoreceptor cell differentiation	4	1.8E-03	18	116	7937	15.20	5.3E-01	6.2E-02	2.5E+00
	GO:0048813~dendrite morphogenesis	4	1.8E-03	18	117	7937	15.08	5.4E-01	5.9E-02	2.5E+00
	GO:0016358~dendrite development	4	1.8E-03	18	117	7937	15.08	5.4E-01	5.9E-02	2.5E+00
	GO:0000902~cell morphogenesis	6	1.9E-03	18	442	7937	5.99	5.5E-01	5.5E-02	2.6E+00
	GO:0046530~photoreceptor cell differentiation	4	2.4E-03	18	128	7937	13.78	6.4E-01	6.5E-02	3.3E+00
	GO:0045137~development of primary sexual characteristics	3	2.6E-03	18	36	7937	36.75	6.7E-01	6.8E-02	3.6E+00
	GO:0048812~neuron projection morphogenesis	5	2.7E-03	18	286	7937	7.71	6.9E-01	6.6E-02	3.8E+00
	GO:0031175~neuron projection development	5	2.7E-03	18	287	7937	7.68	6.9E-01	6.3E-02	3.8E+00
	GO:0048667~cell morphogenesis involved in neuron differentiation	5	2.8E-03	18	288	7937	7.66	7.0E-01	6.1E-02	3.8E+00
	GO:0000904~cell morphogenesis involved in differentiation	5	3.3E-03	18	303	7937	7.28	7.6E-01	6.9E-02	4.6E+00
	GO:0003006~reproductive developmental process	6	3.4E-03	18	506	7937	5.23	7.6E-01	6.6E-02	4.6E+00
	GO:0032989~cellular component morphogenesis	6	3.7E-03	18	518	7937	5.11	8.0E-01	7.0E-02	5.1E+00
	GO:0048858~cell projection morphogenesis	5	4.1E-03	18	320	7937	6.89	8.3E-01	7.3E-02	5.6E+00
	GO:0032990~cell part morphogenesis	5	4.6E-03	18	331	7937	6.66	8.6E-01	7.9E-02	6.3E+00
	GO:0048707~instar larval or pupal morphogenesis	5	5.4E-03	18	347	7937	6.35	9.0E-01	8.9E-02	7.4E+00
	GO:0048666~neuron development	5	5.4E-03	18	347	7937	6.35	9.0E-01	8.9E-02	7.4E+00
	GO:0009886~post-embryonic morphogenesis	5	5.8E-03	18	353	7937	6.25	9.2E-01	9.1E-02	7.8E+00
	GO:0030030~cell projection organization	5	6.5E-03	18	365	7937	6.04	9.4E-01	9.8E-02	8.8E+00
	GO:0051146~striated muscle cell differentiation	3	8.3E-03	18	65	7937	20.35	9.7E-01	1.2E-01	1.1E+01
	GO:0007423~sensory organ development	5	9.8E-03	18	410	7937	5.38	9.9E-01	1.4E-01	1.3E+01
Mus musculus	GO:0045449~regulation of transcription	29	2.7E-20	31	2227	13588	5.71	6.0E-18	6.0E-18	3.4E-17
	GO:0006355~regulation of transcription, DNA-dependent	21	4.1E-13	31	1465	13588	6.28	9.2E-11	4.6E-11	5.3E-10
	GO:0051252~regulation of RNA metabolic process	21	5.6E-13	31	1488	13588	6.19	1.2E-10	4.1E-11	7.1E-10
	GO:0006350~transcription	20	1.8E-10	31	1772	13588	4.95	4.1E-08	1.0E-08	2.4E-07
	GO:0010629~negative regulation of gene expression	8	2.4E-05	31	410	13588	8.55	5.3E-03	1.1E-03	3.1E-02
	GO:0010605~negative regulation of macromolecule metabolic process	8	9.2E-05	31	506	13588	6.93	2.0E-02	3.4E-03	1.2E-01
	GO:0016481~negative regulation of transcription	7	1.4E-04	31	372	13588	8.25	3.0E-02	4.4E-03	1.8E-01
	GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	7	2.0E-04	31	397	13588	7.73	4.3E-02	5.4E-03	2.5E-01

	GO:0051172~negative regulation of nitrogen compound metabolic process	7	2.1E-04	31	401	13588	7.65	4.5E-02	5.1E-03	2.6E-01
	GO:0010558~negative regulation of macromolecule biosynthetic process	7	2.6E-04	31	418	13588	7.34	5.6E-02	5.7E-03	3.3E-01
	GO:0031327~negative regulation of cellular biosynthetic process	7	3.0E-04	31	430	13588	7.14	6.5E-02	6.1E-03	3.8E-01
	GO:0009890~negative regulation of biosynthetic process	7	3.2E-04	31	434	13588	7.07	6.8E-02	5.9E-03	4.0E-01
	GO:0045892~negative regulation of transcription, DNA-dependent	5	4.5E-03	31	308	13588	7.12	6.3E-01	7.3E-02	5.5E+00
	GO:0051253~negative regulation of RNA metabolic process	5	4.6E-03	31	310	13588	7.07	6.4E-01	7.0E-02	5.7E+00
	GO:0010551~regulation of specific transcription from RNA polymerase II promoter	3	5.6E-03	31	51	13588	25.78	7.1E-01	8.0E-02	6.9E+00
	GO:0032583~regulation of gene-specific transcription	3	9.5E-03	31	67	13588	19.63	8.8E-01	1.2E-01	1.1E+01
Homo sapiens	GO:0045449~regulation of transcription	34	1.8E-18	40	2601	13528	4.42	5.7E-16	1.9E-16	2.5E-15
	GO:0006355~regulation of transcription, DNA-dependent	32	7.1E-21	40	1773	13528	6.10	2.2E-18	2.2E-18	9.6E-18
	GO:0051252~regulation of RNA metabolic process	32	1.4E-20	40	1813	13528	5.97	4.4E-18	2.2E-18	1.9E-17
	GO:0006350~transcription	28	7.2E-14	40	2101	13528	4.51	2.3E-11	5.7E-12	9.7E-11
	GO:0010629~negative regulation of gene expression	9	7.8E-05	40	504	13528	6.04	2.4E-02	4.9E-03	1.0E-01
	GO:0006357~regulation of transcription from RNA polymerase II promoter	9	9.3E-04	40	727	13528	4.19	2.5E-01	2.4E-02	1.2E+00
	GO:0010605~negative regulation of macromolecule metabolic process	9	9.9E-04	40	734	13528	4.15	2.7E-01	2.2E-02	1.3E+00
	GO:0016481~negative regulation of transcription	8	3.0E-04	40	459	13528	5.89	8.9E-02	1.5E-02	4.0E-01
	GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	8	5.7E-04	40	512	13528	5.28	1.7E-01	2.0E-02	7.7E-01
	GO:0051172~negative regulation of nitrogen compound metabolic process	8	6.2E-04	40	519	13528	5.21	1.8E-01	1.9E-02	8.3E-01
	GO:0010558~negative regulation of macromolecule biosynthetic process	8	8.5E-04	40	547	13528	4.95	2.3E-01	2.4E-02	1.1E+00
	GO:0031327~negative regulation of cellular biosynthetic process	8	9.8E-04	40	561	13528	4.82	2.7E-01	2.4E-02	1.3E+00
	GO:0009890~negative regulation of biosynthetic process	8	1.1E-03	40	573	13528	4.72	3.0E-01	2.3E-02	1.5E+00
	GO:0045892~negative regulation of transcription, DNA-dependent	7	5.0E-04	40	356	13528	6.65	1.5E-01	2.2E-02	6.7E-01
	GO:0051253~negative regulation of RNA metabolic process	7	5.4E-04	40	362	13528	6.54	1.6E-01	2.1E-02	7.3E-01
	GO:0045893~positive regulation of transcription, DNA-dependent	7	2.3E-03	40	477	13528	4.96	5.1E-01	4.4E-02	3.0E+00

	GO:0051254~positive regulation of RNA metabolic process	7	2.4E-03	40	481	13528	4.92	5.2E-01	4.3E-02	3.1E+00
	GO:0045941~positive regulation of transcription	7	5.2E-03	40	564	13528	4.20	8.0E-01	8.2E-02	6.7E+00
	GO:0010628~positive regulation of gene expression	7	6.0E-03	40	581	13528	4.07	8.5E-01	9.0E-02	7.7E+00
	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	7	8.4E-03	40	624	13528	3.79	9.3E-01	1.1E-01	1.1E+01
	GO:0051173~positive regulation of nitrogen compound metabolic process	7	9.7E-03	40	644	13528	3.68	9.5E-01	1.2E-01	1.2E+01
	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	6	4.0E-03	40	371	13528	5.47	7.2E-01	6.8E-02	5.3E+00
	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	5	7.0E-03	40	266	13528	6.36	8.9E-01	1.0E-01	9.0E+00

Supplemental Table 2. Gene Ontology enrichment analysis.

The table shows enrichments of Gene Ontology annotations in *A. thaliana*, *D. melanogaster*, *M. musculus*, and *H. sapiens* TFs predicted to be targeted by miPs.