Table S1. Output from the edgeR analysis. Positive fold-change values indicate genes that are expressed higher in the maize *pbf1* NIL than in the teosinte *pbf1* NIL; negative values genes that are higher in the teosinte NIL. Log2 (counts per million) is based on ~80 million total counts. Only genes with p-values less than 0.05 are shown. False Discovery Rate (FDR) is reported for each locus. Interpro and Gene Ontology terms are listed in the final two columns.

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G134402	8.199501717	0.272589712	6.56E-06	0.160767193	ARP2/3_p21-Arc	cellular_component|intracellular|cell|cytoskeleton|Arp2/3 protein complex|cytoskeleton organization|biological_process|regulation of actin filament polymerization|Arp2/3 complex-mediated actin nucleation|organelle|protein complex
GRMZM2G127850	-8.15556393	0.364152446	6.16E-05	0.754572971	WD40_repeat|WD40_repeat_dom|G-protein_beta_WD-40_rep	molecular_function|protein binding|cellular_component|intracellular|cell|nucleus|nucleolus|organelle
GRMZM2G311756	-1.226080238	4.662804493	0.000108161	0.883640808	Glycosyl_hydrolases_36|Glycoside_hydrolase_SF	molecular_function|catalytic activity|biological_process|metabolic process
GRMZM2G370175	-7.264247534	-0.107767466	0.000144845	0.887498574	Not Annotated	Not Annotated
GRMZM2G094703	-4.881292814	0.04111286	0.000212954	0.937193604	Not Annotated	Not Annotated
GRMZM2G038604	-2.91655158	1.679054152	0.000229433	0.937193604	Not Annotated	Not Annotated
GRMZM5G821869	-1.812841739	2.913053093	0.000377931	1	Not Annotated	Not Annotated
GRMZM2G529658	-1.982236022	2.775380198	0.000504487	1	Not Annotated	Not Annotated
GRMZM2G153675	-2.162762207	0.74288617	0.000507787	1	PP2C-like_dom	molecular_function|catalytic activity|biological_process|metabolic process
GRMZM2G127361	-3.735805934	1.204026244	0.000567348	1	Quin_OxRdtase/zeta-crystal_CS|GroES-like|ADH_GroES-like	nucleotide binding|molecular_function|cellular_component|extracellular region|intracellular|cell|cytoplasm|response to stress|biological_process|zinc ion binding|response to cold|chloroplast|plastid|chloroplast stroma|thylakoid|chloroplast envelope|stromule|oxidoreductase activity|enone reductase activity|2-alkenal reductase (NADP+) activity|ion binding|organelle|apoplast|oxidation-reduction process
GRMZM2G026654	-1.522393404	1.509301167	0.000571693	1	Not Annotated	plasma membrane
GRMZM2G061732	-1.700547596	1.885998416	0.000585992	1	NadA	molecular_function|biological_process|quinolinate synthetase A activity|biosynthetic process|NAD biosynthetic process|cellular nitrogen compound metabolic process|small molecule metabolic process|cofactor metabolic process
GRMZM2G331833	-1.05854083	2.714478319	0.000654094	1	AAA+_ATPase|ATPase_AAA-2|Clp_ATPase_C	nucleotide binding|molecular_function|ATP binding|protein folding|biological_process|nucleoside-triphosphatase activity|unfolded protein binding
GRMZM2G180697	-1.433080229	2.04536531	0.000720598	1	Not Annotated	Not Annotated
GRMZM2G006585	-0.984840779	10.11057173	0.000728688	1	DUF597	Not Annotated
GRMZM2G008341	-0.954259519	5.795302282	0.000780736	1	Zein	molecular_function|nutrient reservoir activity
GRMZM2G036048	-1.625134216	1.362472283	0.000873317	1	Not Annotated	Not Annotated
GRMZM2G169734	7.69342547	-0.531162002	0.000949443	1	Not Annotated	Not Annotated
GRMZM2G075489	-2.596881555	0.119485342	0.001050364	1	Not Annotated	Not Annotated
GRMZM2G021921	-1.036055485	3.877288165	0.001072398	1	Not Annotated	Not Annotated
GRMZM5G864735	-1.315804645	6.21466028	0.001388093	1	Histone_H3|Histone_core_D|Histone-fold	nucleosome|molecular_function|DNA binding|cellular_component|intracellular|cell|nucleus|chromosome|DNA metabolic process|nucleosome assembly|biological_process|cellular component assembly|cellular nitrogen compound metabolic process|organelle|protein heterodimerization activity|chromosome organization|macromolecular complex assembly

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM5G877040	6.731785775	-1.191080492	0.001543696	1	Ribosomal_S12_bac|Ribosomal_S12/S23|NA-bd_OB-fold	molecular_function|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|mitochondrion|ribosome|translation|biological_process|biosynthetic process|small ribosomal subunit|ribonucleoprotein complex|organelle
GRMZM2G353091	1.865247836	2.528356065	0.001559068	1	Znf_RING	molecular_function|protein binding|zinc ion binding|ion binding
GRMZM2G055155	7.928440393	-0.459762611	0.001661546	1	Not Annotated	Not Annotated
GRMZM2G075044	-1.22255831	2.664977655	0.001907838	1	Not Annotated	Not Annotated
GRMZM2G305060	-0.637754318	4.918014516	0.002052422	1	DNA/RNA_helicase_DEAH_CS|Helicase_C|Helicase-assoc_dom|DUF1605|Helicase_ATP-bd	molecular_function|nucleic acid binding|helicase activity|ATP binding|ATP-dependent helicase activity|ATPase activity
GRMZM2G413337	-7.329418719	0.248852193	0.00212943	1	Not Annotated	Not Annotated
GRMZM2G164426	-1.091349858	4.707001473	0.002228122	1	Znf_RING	molecular_function|protein binding|biological_process|zinc ion binding|response to chitin|ion binding|metal ion binding
GRMZM2G042198	6.792620629	-1.165243374	0.002264269	1	Znf_B-box|CCT_domain	molecular_function|protein binding|cellular_component|intracellular|cell|nucleus|plasma membrane|circadian rhythm|biological_process|zinc ion binding|ion binding|organelle|negative regulation of long-day photoperiodism, flowering
GRMZM2G142927	-1.737253345	0.785409223	0.002396933	1	Ndr	Not Annotated
GRMZM2G415228	-1.990172802	0.93949899	0.002435006	1	Not Annotated	Not Annotated
GRMZM2G466993	1.740654467	0.019111133	0.002508421	1	Not Annotated	Not Annotated
GRMZM5G897776	-0.924279384	3.228137708	0.002536282	1	Not Annotated	Not Annotated
GRMZM2G137868	1.122866211	2.746596762	0.00263622	1	Aminotrans_V/Cys_dSase|PyrdxlP-dep_Trfase|Aminotrans_V_PyrdxlP_BS|SP_NH2Trfase/AEP_transaminase	molecular_function|catalytic activity|biological_process|metabolic process|transaminase activity|transferase activity|pyridoxal phosphate binding
GRMZM2G081464	0.692990767	6.006538329	0.002675686	1	Bifunc_inhib/LTP/seed_store	molecular_function|cellular_component|transport|lipid transport|biological_process|lipid binding
GRMZM2G357688	-2.393236284	1.744415687	0.002701765	1	Znf_C2H2|Znf_C2H2-like	molecular_function|cellular_component|intracellular|cell|zinc ion binding|ion binding
GRMZM2G132223	3.619125192	-1.937544079	0.002758414	1	AP2/ERF_dom|DNA-bd_dom	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|cellular_component|intracellular|cell|nucleus|transcription, DNA-templated|regulation of transcription, DNA-templated|biological_process|biosynthetic process|cellular nitrogen compound metabolic process|organelle
GRMZM2G100286	-1.227717733	1.369789949	0.002778861	1	Pumilio_RNA-bd_rpt|ARM-type_fold	molecular_function|RNA binding|binding
GRMZM5G878615	-0.840469455	3.132739683	0.002908867	1	Actin_CS|Actin-related	molecular_function|ATP binding
GRMZM2G331154	-0.753121929	2.42283211	0.002910375	1	WD40_repeat_dom|Znf_RING	molecular_function|protein binding|zinc ion binding|ion binding
GRMZM2G485304	-8.137480626	-0.02003742	0.002935973	1	Not Annotated	Not Annotated
GRMZM2G180691	-0.622900202	4.537023518	0.002936653	1	PEstase_dom|Ser/Thr-sp_prot-phosphatase	molecular_function|phosphoprotein phosphatase activity|cellular_component|intracellular|cell|nucleus|cytoplasm|hydrolase activity|phosphatase activity|organelle
GRMZM2G032145	2.23210574	5.52023696	0.003037864	1	BURP_dom	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G032293	-2.002923843	0.570003303	0.003045982	1	Not Annotated	Not Annotated
GRMZM2G012734	6.532186565	-1.574841175	0.003054616	1	PMR5_N_dom|PC-Esterase	Not Annotated
GRMZM5G880306	-1.837581751	0.430900002	0.003089177	1	OTU|Peptidase_C65_otubain	Not Annotated
GRMZM5G869993	-0.946978091	5.102068078	0.003113959	1	Not Annotated	Not Annotated
GRMZM2G475743	6.850993686	-1.293502364	0.003149886	1	Pentatricopeptide_repeat	Not Annotated
GRMZM2G169782	-1.689944636	0.697370009	0.003157533	1	BTB/POZ-like|BTB/POZ_fold|BTB_POZ|NPH3_dom	molecular_function|protein binding|cellular_component|membrane
GRMZM2G012355	-2.564530681	0.668786001	0.003280473	1	Put_SAM_MeTrfase	molecular_function|methyltransferase activity
GRMZM2G066710	-0.963989348	3.365123035	0.003324191	1	Ser/Thr_dual-sp_kinase_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
AF466202.2_FG007	5.682387865	-1.736009148	0.003327189	1	Aldo/keto_reductase_subgr|NADP_OxRdtase_dom	molecular_function|biological_process|oxidoreductase activity|oxidation-reduction process
GRMZM2G158437	-1.769873937	0.712413903	0.003344138	1	NADP_OxRdtase_dom	Not Annotated
GRMZM5G803419	-1.829349153	0.696585892	0.003408381	1	Not Annotated	Not Annotated
GRMZM2G137596	-2.782723914	-0.105954243	0.003433969	1	Not Annotated	Not Annotated
GRMZM2G180254	-0.554883852	4.237392434	0.003462262	1	NB-ARC|Disease_R	molecular_function|response to stress|defense response|biological_process|ADP binding
GRMZM2G118586	-8.062791785	0.425255432	0.003494101	1	ARPC4	cell morphogenesis|cellular_component|intracellular|cell|cytoskeleton|Arp2/3 protein complex|protein complex assembly|cytoskeleton organization|biological_process|cellular component assembly|actin filament polymerization|Arp2/3 complex-mediated actin nucleation|organelle|protein complex|actin nucleation|anatomical structure development|macromolecular complex assembly
GRMZM2G162119	-4.361565403	-0.514787198	0.003558711	1	Znf_CCCH|RRM_dom|U2_small	molecular_function|nucleic acid binding|zinc ion binding|ion binding
GRMZM2G013563	5.547690956	-1.933974652	0.003565673	1	WD40_repeat|WD40_repeat_dom|WD40_repeat_CS|G-protein_beta_WD-40_rep	molecular_function|protein binding|nucleus|vegetative to reproductive phase transition of meristem|histone binding|Set1C/COMPASS complex
GRMZM2G122199	-0.725210166	3.999792984	0.003580478	1	Not Annotated	Not Annotated
GRMZM2G588223	-0.719080679	3.529829452	0.003608318	1	Not Annotated	molecular_function|RNA binding|double-stranded RNA binding
GRMZM2G403162	-1.130545551	3.776321973	0.003766037	1	Not Annotated	Not Annotated
GRMZM2G039322	-4.008940395	-0.85201388	0.003769297	1	mRNA_splic_Cwf21	Not Annotated
GRMZM5G849275	-6.650356453	-1.059029944	0.004198311	1	Not Annotated	Not Annotated
GRMZM2G150928	-1.045902291	2.894349746	0.004321632	1	Not Annotated	Not Annotated
GRMZM2G318956	-0.753635095	3.190791089	0.004402707	1	TUBGCP	microtubule cytoskeleton organization|spindle pole|cellular_component|intracellular|cell|cytoplasm|microtubule organizing center|cytoskeleton|cytoskeleton organization|biological_process|organelle

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G319573	-0.648338097	3.49817116	0.004430581	1	DNA_helicase_ATP-dep_RecQ|DNA/RNA_helicase_DEAH_CS|Helicase_C|DNA/RNA_helicase_DEAD/DEAH_N|Helicase_ATP-bd|HRDC_dom|HRDC-like	double-strand break repair via homologous recombination|molecular_function|nucleic acid binding|helicase activity|ATP binding|DNA metabolic process|DNA recombination|cellular response to DNA damage stimulus|ATP-dependent helicase activity|biological_process|plasmodesma|ATPase activity|cellular nitrogen compound metabolic process|3'-5' DNA helicase activity|chromosome organization|cellular response to cold|cellular response to abscisic acid stimulus|nucleotide binding|catalytic activity|cellular_component|intracellular|cell|cellular metabolic process
GRMZM2G375249	-2.256002538	-0.283324828	0.004450783	1	Not Annotated	Not Annotated
GRMZM2G030578	-0.507287993	6.334544042	0.004479741	1	Exportin-1/Importin-b-like|ARM-type_fold	molecular_function|binding
GRMZM2G151521	-0.62565326	3.403740165	0.004528161	1	TLC-dom	response to molecule of fungal origin|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|Golgi apparatus|plasma membrane|biological_process|membrane|integral component of membrane|organelle
GRMZM2G346865	-1.428298102	1.343346812	0.004579019	1	Nucleotide_exch_fac_Fes1|ARM-type_fold	molecular_function|binding
GRMZM5G884270	-1.007855253	2.784848479	0.004601078	1	GPI_EtnP_transferase_1_C	molecular_function|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|endoplasmic reticulum membrane|cellular protein modification process|GPI anchor biosynthetic process|lipid metabolic process|biological_process|biosynthetic process|transferase activity|organelle
GRMZM2G075563	-0.948763576	6.421154959	0.00469802	1	TPR_1	molecular_function|protein binding|regulation of sulfur utilization|response to stress|biological_process|cellular response to sulfur starvation
GRMZM2G053120	-0.698665557	8.107038572	0.00477399	1	Zein	molecular_function|nutrient reservoir activity
GRMZM2G457347	-1.162641125	2.131143926	0.004880603	1	Cactin_dom	Not Annotated
GRMZM2G342226	-2.717466493	-0.847470316	0.004897139	1	UDPGP_trans|RNA-helicase_DEAD-box_CS|KOW|Trimer_LpxA-like|DNA/RNA_helicase_DEAD/DEAH_N|Helicase_ATP-bd	molecular_function|nucleic acid binding|helicase activity|ATP binding|ATP-dependent helicase activity|biological_process|metabolic process|transferase activity|nucleotidyltransferase activity|ATPase activity
GRMZM2G513713	-2.096785608	-0.466076276	0.004976986	1	Not Annotated	Not Annotated
GRMZM2G119230	-1.84768278	1.943457872	0.004981909	1	Not Annotated	Not Annotated
GRMZM2G084369	-1.097653261	5.32985546	0.005014999	1	Glutathione-S-Trfase_C-like	protein glutathionylation
GRMZM5G815851	-4.405578184	-0.81112177	0.005073474	1	Not Annotated	Not Annotated
GRMZM5G871297	-0.838329113	3.879749285	0.00509876	1	aa-tRNA-synth_Ia|tRNAsynth_1a_anticodon-bd|tRNA-bd_arm|V/L/I-tRNA-synth_anticodon-bd|Val-tRNA_synth_tRNA-bd	nucleotide binding|molecular_function|aminoacyl-tRNA ligase activity|valine-tRNA ligase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|tRNA metabolic process|translation|tRNA aminoacylation for protein translation|valyl-tRNA aminoacylation|cellular amino acid metabolic process|biological_process|biosynthetic process|ligase activity|cellular nitrogen compound metabolic process|small molecule metabolic process
GRMZM5G844123	-1.584493199	0.811362036	0.005127978	1	Not Annotated	Not Annotated
AC155352.2_FG010	1.34154285	7.240140275	0.005174516	1	Bifunc_inhib/LTP/seed_store	response to auxin|lateral root morphogenesis

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM5G856738	-1.496921073	1.410118126	0.005193382	1	Ser/Thr_dual-sp_kinase_dom|EF_hand_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|EF-hand-dom_pair|Protein_kinase_ATP_BS|EF_Hand_1_Ca_BS	nucleotide binding|molecular_function|protein kinase activity|protein serine/threonine kinase activity|calcium ion binding|ATP binding|cellular_component|intracellular|cell|cytoplasm|vacuole|plasma membrane|cellular protein modification process|protein phosphorylation|response to stress|signal transduction|biological_process|response to salt stress|abscisic acid-activated signaling pathway|regulation of stomatal movement|regulation of anion channel activity|membrane|kinase activity|transferase activity, transferring phosphorus-containing groups|ion binding|organelle
GRMZM2G084513	-0.86846102	2.918328832	0.005268435	1	CENP-O	chromosome, centromeric region|cellular_component|intracellular|cell|nucleus|chromosome|chromosome segregation|biological_process|organelle|cell division
GRMZM2G134439	-0.976829632	1.962952398	0.005310645	1	SANT/Myb|RMMBL|Myb-like_dom	molecular_function|DNA binding|chromatin binding|RNA binding|hydrolase activity, acting on ester bonds|ion binding|metal ion binding
GRMZM2G033348	-0.998239628	3.327205775	0.005341188	1	VPSAP_dom	Not Annotated
GRMZM2G093278	-0.981892733	2.441865524	0.005505016	1	Glycosyl_transferase_4	molecular_function|cellular_component|phospho-N-acetylmuramoyl-pentapeptide-transferase activity|membrane|integral component of membrane
GRMZM2G050939	-0.85679303	3.239276584	0.005582203	1	Znf_C2H2|Znf_C2H2-like	nucleic acid binding transcription factor activity|molecular_function|nucleic acid binding|DNA binding|sequence-specific DNA binding transcription factor activity|RNA binding|cellular_component|intracellular|cell|nucleus|nucleolus|regulation of transcription, DNA-templated|5S rRNA binding|biological_process|zinc ion binding|rRNA binding|ion binding|organelle|5S rDNA binding
GRMZM2G336285	-0.815408037	3.78215941	0.005608752	1	Not Annotated	Not Annotated
GRMZM2G014329	6.850993686	-0.94736682	0.005619042	1	Not Annotated	Not Annotated
GRMZM2G044368	0.504758658	0.862620504	0.00567732	1	Small_GTP-bd_dom|Small_GTPase_Rab_type|Small_GTPase	nucleotide binding|molecular_function|GTP binding|cellular_component|intracellular|cell|nucleus|plasma membrane|transport|response to stress|response to oxidative stress|signal transduction|small GTPase mediated signal transduction|biological_process|response to salt stress|protein transport|organelle
GRMZM2G496821	-1.261218113	3.926853587	0.005739712	1	Not Annotated	Not Annotated
GRMZM2G315730	-1.256735989	2.565929005	0.005805577	1	Not Annotated	Not Annotated
GRMZM2G021369	-1.830545648	2.439008237	0.00585319	1	AP2/ERF_dom|DNA-bd_dom	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|regulation of transcription, DNA-templated|biological_process|cellular_component|intracellular|cell|nucleus|transcription, DNA-templated|biosynthetic process|cellular nitrogen compound metabolic process|organelle
GRMZM2G149132	-1.375893978	0.770321486	0.005867202	1	PP2C-like_dom|PP2C_Mn2_Asp60_BS	molecular_function|catalytic activity|phosphoprotein phosphatase activity|protein serine/threonine phosphatase activity|cellular protein modification process|protein dephosphorylation|biological_process|hydrolase activity|phosphatase activity|ion binding|metal ion binding
GRMZM2G093276	-0.701663969	3.889412214	0.005869644	1	Zn/Fe_permease_fun/pln|ZIP	molecular_function|zinc ion transmembrane transporter activity|cellular_component|intracellular|cell|cytoplasm|transport|biological_process|membrane|integral component of membrane|cytoplasmic membrane-bounded vesicle|transmembrane transporter activity|metal ion transport|organelle|metal ion transmembrane transporter activity|transmembrane transport|zinc ion transmembrane transport

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G151807	-0.996284624	5.09446965	0.00591894	1	Not Annotated	Not Annotated
GRMZM2G155949	-0.645499101	4.096396416	0.005981788	1	SBNO_Helicase_C_dom	regulation of transcription, DNA-templated|biological_process
GRMZM5G842970	-1.57653504	1.801968713	0.006072414	1	Not Annotated	Not Annotated
GRMZM2G548261	-4.170716704	-0.892093244	0.006131152	1	Not Annotated	Not Annotated
GRMZM2G134878	-1.838942014	-0.313580155	0.006137575	1	Not Annotated	Not Annotated
GRMZM2G028928	-0.741070659	3.252538814	0.006181061	1	Small_GTP-bd_dom|Transl_elong_EFTu/EF1A_2|EF_GTP-bd_dom|EFG_V|EF-4|Transl_B-barrel|EFG_III-V|LepA_GTP-bd_C	nucleotide binding|molecular_function|RNA binding|translation elongation factor activity|GTPase activity|GTP binding|cellular_component|intracellular|cell|cytoplasm|mitochondrion|mitochondrial matrix|GTP catabolic process|translation|translational elongation|translation factor activity, nucleic acid binding|biological_process|catabolic process|biosynthetic process|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|ribosome binding|organelle|small molecule metabolic process|positive regulation of translation
GRMZM2G075039	-1.016422836	1.617008769	0.0062205	1	KH_dom_type_1|KH_dom	molecular_function|RNA binding
GRMZM2G045816	-1.962539481	-0.084439632	0.006248536	1	Not Annotated	Not Annotated
GRMZM2G160922	-0.730461985	3.709452615	0.006308183	1	Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|ACT_dom	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|cytosol|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups|metabolic process|chloroplast organization|amino acid binding
GRMZM2G561067	-1.44174242	0.554856639	0.006425871	1	Not Annotated	Not Annotated
GRMZM2G003635	-0.623794609	3.606728437	0.006457238	1	DnaJ_domain|DnaJ_domain_CS	Not Annotated
GRMZM2G005562	-0.63604583	5.112088222	0.006509542	1	Amb_allergen_dom|PbH1|Pectin_lyase_fold/virulence|AmbAllergen	molecular_function|lyase activity
GRMZM2G095810	-0.657318823	2.387520932	0.006534695	1	Znf_Sec23_Sec24|Sec23/24_trunk_dom|Sec23/24_helical_dom|Sec23_24_beta_S	molecular_function|cellular_component|intracellular|cell|cytoplasm|transport|intracellular protein transport|ER to Golgi vesicle-mediated transport|biological_process|zinc ion binding|protein transport|cytoplasmic membrane-bounded vesicle|vesicle-mediated transport|COPII vesicle coat|ion binding|organelle|protein complex
GRMZM2G373527	6.731785775	-1.254670505	0.006556719	1	Not Annotated	Not Annotated
GRMZM2G164413	-0.984845417	3.664500346	0.00657215	1	UPF0136_TM	molecular_function|cellular_component|biological_process|membrane|kinase activity|phosphorylation
GRMZM2G002483	-3.254279308	-0.936057082	0.006697436	1	Not Annotated	Not Annotated
GRMZM2G144254	-0.717340686	3.327151079	0.006814092	1	Mg_trans_NIPA	molecular_function|cellular_component|transport|biological_process|magnesium ion transmembrane transporter activity|magnesium ion transport|membrane|transmembrane transporter activity

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G151227	-0.98187846	1.323884005	0.006849364	1	Chalcone/stilbene_synthase_N|Polyketide_synthase_type-III|Chalcone/stilbene_synth_C|Thiolase-like|Chalcone/stilbene_synthase_AS	molecular_function|catalytic activity|cellular_component|intracellular|cell|nucleus|cytoplasm|vacuole|endoplasmic reticulum|transport|response to stress|response to oxidative stress|biological_process|metabolic process|biosynthetic process|response to wounding|response to gravity|plant-type vacuole membrane|chalcone biosynthetic process|response to auxin|response to jasmonic acid|flavonoid biosynthetic process|auxin polar transport|response to UV-B|naringenin-chalcone synthase activity|transferase activity|transferase activity, transferring acyl groups|transferase activity, transferring acyl groups other than amino-acyl groups|secondary metabolic process|regulation of anthocyanin biosynthetic process|organelle|small molecule metabolic process
GRMZM2G034651	5.547690956	-2.222025228	0.007007718	1	Prp18|PRP4-like	cellular_component|intracellular|cell|nucleus|spliceosomal complex|biological_process|RNA splicing|cellular nitrogen compound metabolic process|organelle
GRMZM2G018080	-0.879221227	2.778483541	0.007065718	1	PsdUridine_synth_cat_dom	maturation of LSU-rRNA from tetracistronic rRNA transcript (SSU-rRNA, LSU-rRNA, 4.5S-rRNA, 5S-rRNA)|maturation of SSU-rRNA from tetracistronic rRNA transcript (SSU-rRNA, LSU-rRNA, 4.5S-rRNA, 5S-rRNA)|pseudouridine synthesis|molecular_function|RNA binding|biological_process|RNA modification|chloroplast|pseudouridine synthase activity|isomerase activity|plastid translation|cellular nitrogen compound metabolic process
GRMZM2G008444	-1.563917081	1.207010507	0.007173516	1	Web	Not Annotated
GRMZM2G134049	-2.522880477	0.628582333	0.007183329	1	Not Annotated	Not Annotated
GRMZM2G007060	-0.814704639	3.741492544	0.007285288	1	Interferon-rel_develop_reg_N|ARM-type_fold	molecular_function|binding|cellular_component|intracellular|cell|nucleus|cytoplasm|response to stress|biological_process|response to salt stress|organelle
AC217897.3_FG010	0.906506319	2.319577259	0.007317323	1	DUF962	cellular_component|integral component of membrane
GRMZM2G115481	-1.092441266	4.753418857	0.007336809	1	LURP1-like|Tubby_C-like	Not Annotated
AC199526.5_FG003	-1.084909445	1.321808792	0.007453762	1	RNA-binding_CRM	Group II intron splicing|molecular_function|RNA binding|cellular_component|intracellular|cell|cytoplasm|mRNA processing|biological_process|RNA splicing|chloroplast|plastid|chloroplast stroma|ribonucleoprotein complex|cellular nitrogen compound metabolic process|organelle
GRMZM5G819302	-0.717303902	6.332227913	0.007456597	1	Not Annotated	Not Annotated
GRMZM2G042278	-1.071771095	1.184562088	0.00747005	1	RWP-RK_dom|GAF|OPR_PB1	molecular_function|protein binding
GRMZM2G150193	-0.458724826	5.517381045	0.007541703	1	DUF3456	Not Annotated
GRMZM2G074423	-0.652572532	3.133856496	0.007552913	1	CHP01589_pln	Not Annotated
GRMZM2G133895	-0.473755917	4.879991773	0.007562363	1	F-box_dom	molecular_function|protein binding
GRMZM2G095094	-0.679731756	2.641190451	0.007600737	1	Pentatricopeptide_repeat	Not Annotated
AC211707.4_FG003	-2.895956836	-1.027818225	0.007615616	1	Not Annotated	Not Annotated
GRMZM2G373738	-1.450227949	2.746227352	0.007656951	1	Small_GTP-bd_dom|Small_GTPase_Rab_type|Small_GTPase	molecular_function|GTP binding|transport|signal transduction|small GTPase mediated signal transduction|biological_process|protein transport

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G112377	4.876943149	-1.027469125	0.00771517	1	Phos_permease|Sub_transporter|MFS_dom_general_subst_transpt|MFS_dom	molecular_function|inorganic phosphate transmembrane transporter activity|cellular_component|intracellular|cell|nucleus|cytoplasm|vacuole|plasma membrane|transport|phosphate ion transport|response to stress|biological_process|response to abscisic acid|integral component of membrane|cellular response to phosphate starvation|transmembrane transporter activity|organelle|transmembrane transport
GRMZM2G046911	-0.530820501	6.757560522	0.007748356	1	Not Annotated	endosome|Golgi apparatus|trans-Golgi network
GRMZM2G409101	6.300469516	-1.314327898	0.007775047	1	Not Annotated	Not Annotated
GRMZM2G026847	1.318163726	-1.706830568	0.007838225	1	Not Annotated	Not Annotated
GRMZM2G434839	3.363336458	-1.422805039	0.007871278	1	DnaJ_C|HSP_DnaJ_Cys-rich_dom|HSP40/DnaJ_pept-bd	molecular_function|protein folding|biological_process|heat shock protein binding|unfolded protein binding
GRMZM2G303587	6.214150217	-1.470769434	0.007924992	1	Pentatricopeptide_repeat	Not Annotated
GRMZM2G447218	-4.849778971	0.588772886	0.007964178	1	Not Annotated	Not Annotated
GRMZM2G362745	-1.336654018	0.218361396	0.007988236	1	Not Annotated	Not Annotated
GRMZM5G830549	-3.451665735	-0.697524007	0.00804236	1	Not Annotated	Not Annotated
GRMZM2G084421	-1.01836102	3.897547298	0.008090427	1	Not Annotated	Not Annotated
GRMZM2G444743	-1.767696837	4.587913205	0.008122344	1	Not Annotated	Not Annotated
GRMZM2G075974	-0.821957561	5.811928213	0.008156284	1	GATASE	Not Annotated
GRMZM2G013832	-6.969409266	-0.155156664	0.008198658	1	Not Annotated	Not Annotated
GRMZM2G117016	-1.298393056	3.167336702	0.008210344	1	Not Annotated	Not Annotated
GRMZM2G702613	-1.023006543	3.210883768	0.008244888	1	RNA_pol_Rpb8|NA-bd_OB-fold	transcription, DNA-templated|biological_process|biosynthetic process|cellular nitrogen compound metabolic process
GRMZM2G700063	-1.600236864	0.640181954	0.008260628	1	Not Annotated	Not Annotated
GRMZM2G097132	1.049841953	0.410272144	0.008469246	1	Oxoglu/Fe-dep_dioxygenase	molecular_function|biological_process|oxidoreductase activity|oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors|oxidation-reduction process
GRMZM2G485905	-1.179335444	1.070076963	0.008490088	1	Not Annotated	Not Annotated
GRMZM2G049288	-0.616270615	4.04575803	0.008505482	1	DnaJ_domain|ARM-type_fold|DUF4339	molecular_function|binding
GRMZM2G032070	-1.339672828	5.040534427	0.008587047	1	TF_Kbox	nucleic acid binding transcription factor activity|molecular_function|sequence-specific DNA binding transcription factor activity|cellular_component|intracellular|cell|nucleus|regulation of transcription, DNA-templated|biological_process|organelle
GRMZM2G022866	-0.789392038	2.733024809	0.008639132	1	Glutaredoxin|GLR_AS|Thioredoxin-like_fold|Glutathione_S-Trfase_N	molecular_function|biological_process|electron carrier activity|protein disulfide oxidoreductase activity|oxidoreductase activity|homeostatic process|cell redox homeostasis|protein binding|cellular_component|intracellular|cell|cytoplasm|chloroplast|chloroplast thylakoid membrane|plastid|thylakoid|organelle
GRMZM2G397948	-0.848700206	2.614466589	0.008668804	1	BTB/POZ_fold|BACK	molecular_function|protein binding
GRMZM5G832248	-0.664403417	4.472861881	0.00868027	1	RRM_dom|CC1_SF	nucleotide binding|molecular_function|nucleic acid binding|RNA binding|cellular_component|intracellular|cell|nucleus|mRNA processing|biological_process|cellular nitrogen compound metabolic process|organelle
GRMZM2G013970	-0.731385003	3.028588504	0.008734367	1	a-crystallin/Hsp20_dom|HSP20-like_chaperone	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G038973	-1.125067732	2.763073598	0.008760094	1	Gal_mutarotase_SF_dom|Glyco_hydro_38_C	molecular_function|catalytic activity|carbohydrate metabolic process|mannose metabolic process|biological_process|mannosidase activity|hydrolase activity, acting on glycosyl bonds|carbohydrate binding
GRMZM5G816314	-6.097716152	-1.571340689	0.008893162	1	AP2/ERF_dom|DNA-bd_dom	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|regulation of transcription, DNA-templated|biological_process
GRMZM2G068943	-0.504850388	4.502108309	0.008970608	1	Trehalose_PPase|Glyco_trans_20|Trehalose_OtsA|HAD-like_dom	molecular_function|catalytic activity|alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity|carbohydrate metabolic process|trehalose biosynthetic process|biological_process|biosynthetic process|transferase activity, transferring glycosyl groups
GRMZM2G140078	-1.373006347	1.867166211	0.008971858	1	Trehalose_PPase|HAD-SF_hydro_IIB|HAD-like_dom	molecular_function|catalytic activity|carbohydrate metabolic process|trehalose biosynthetic process|biological_process|metabolic process|biosynthetic process
GRMZM2G077258	-0.60002243	4.270083536	0.008985015	1	SET_dom|Rubisco_LSMT_MeTrfase_plant|Rubisco_LSMT_subst-bd	molecular_function|protein binding|cellular_component|intracellular|cell|cytoplasm|biological_process|methyltransferase activity|chloroplast|plastid|transferase activity|[ribulose-bisphosphate carboxylase]-lysine N-methyltransferase activity|methylation|organelle
GRMZM5G871471	-0.776087794	5.6169208	0.009121027	1	ArAA_b-elim_lyase/Thr_aldolase|PyrdxlP-dep_Trfase	molecular_function|cellular amino acid metabolic process|biological_process|lyase activity|small molecule metabolic process
GRMZM2G121495	-1.072268277	1.48262448	0.009124035	1	Glycoside_Hdrlase_35|Galactose-bd-like|Glycoside_hydrolase_SF|Glyco_hydro_35_CS	molecular_function|catalytic activity|hydrolase activity, hydrolyzing O-glycosyl compounds|beta-galactosidase activity|carbohydrate metabolic process|biological_process|metabolic process|hydrolase activity|hydrolase activity, acting on glycosyl bonds|cell wall|plant-type cell wall|plasmodesma
GRMZM2G018573	-0.592458644	3.540566056	0.009159184	1	WD40_repeat|WD40_repeat_dom	molecular_function|protein binding
GRMZM2G467338	-0.723600108	3.035214603	0.009179086	1	Acoase/IPM_deHydtase_lsu_aba|AconitaseA/IPMdHydase_ssu_swvl|Aconitase/Fe_reg_prot_2|Aconitase/3IPM_dehydase_swvl|Aconitase_4Fe-4S_BS	molecular_function|biological_process|metabolic process|4 iron, 4 sulfur cluster binding
GRMZM2G488067	-2.05050308	1.122284268	0.009237387	1	Not Annotated	Not Annotated
GRMZM2G000236	-0.645289033	2.816720561	0.009292368	1	OxRdtase_FMN_N	molecular_function|catalytic activity|cytosol|lipid metabolic process|biological_process|biosynthetic process|response to wounding|jasmonic acid biosynthetic process|response to salicylic acid|FMN binding|oxidoreductase activity|12-oxophytodienoate reductase activity|oxylipin metabolic process|small molecule metabolic process|response to cadmium ion|oxidation-reduction process
AC188838.3_FG005	4.195463902	-1.088467503	0.009321716	1	PRibTrfase_dom|GATase_dom|Amd_phspho_trans|GATase_2_dom	molecular_function|amidophosphoribosyltransferase activity|cell wall|cytosol|purine nucleotide biosynthetic process|'de novo' IMP biosynthetic process|biological_process|metabolic process|biosynthetic process|purine nucleobase biosynthetic process|nucleoside metabolic process|plastid stroma|chloroplast organization|transferase activity|transferase activity, transferring glycosyl groups|cellular nitrogen compound metabolic process|ion binding|small molecule metabolic process|metal ion binding
GRMZM5G886969	-0.884074067	4.755108733	0.009345917	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G087364	-5.66464753	-1.658204622	0.009417217	1	Essential_protein_Yae1_N	Not Annotated
GRMZM5G808787	-1.846880808	0.531896146	0.009427906	1	Not Annotated	Not Annotated
GRMZM2G120091	-0.749202651	1.955056416	0.009437999	1	Not Annotated	Not Annotated
GRMZM2G180155	-0.982974348	1.639409833	0.009517943	1	Not Annotated	molecular_function|glutamine-fructose-6-phosphate transaminase (isomerizing) activity|cellular_component|intracellular|cell|cytoplasm|carbohydrate metabolic process|biological_process|biosynthetic process|carbohydrate biosynthetic process
GRMZM2G163178	-0.902570307	3.337186925	0.009522621	1	Not Annotated	Not Annotated
AC199820.4_FG006	3.129090324	-0.036128946	0.009534284	1	SANT/Myb|Myb_dom_plants|Homeodomain-like|SANT_dom	molecular_function|DNA binding|chromatin binding
GRMZM2G063844	-2.10975519	1.654738738	0.009633814	1	Not Annotated	Not Annotated
GRMZM2G162535	-1.061884524	1.565253161	0.009774104	1	Not Annotated	Not Annotated
GRMZM2G081573	-0.873132711	2.331891913	0.009883864	1	AAA+_ATPase|ABC_transporter-like|ABC_transptr_TM_dom|ABC1_TM_dom|ABC_transporter_CS	nucleotide binding|molecular_function|ATP binding|cellular_component|ATP catabolic process|transport|biological_process|catabolic process|integral component of membrane|ATPase activity|nucleoside-triphosphatase activity|transmembrane transporter activity|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|ATPase activity, coupled to transmembrane movement of substances|small molecule metabolic process|transmembrane transport
GRMZM2G426067	-5.853733089	-1.502187764	0.009901059	1	DUF604	molecular_function|endoplasmic reticulum|transferase activity
GRMZM5G872120	-1.484656723	0.261933147	0.009934576	1	Not Annotated	Not Annotated
GRMZM2G532970	-1.224928243	1.835291948	0.0099487	1	Not Annotated	Not Annotated
GRMZM2G700208	-2.188514363	0.147690609	0.010052505	1	Lipase_GDSL	molecular_function|lipid metabolic process|biological_process|hydrolase activity|hydrolase activity, acting on ester bonds
GRMZM2G024996	-1.012146386	3.117957263	0.010110307	1	Not Annotated	Not Annotated
GRMZM2G031352	-0.488292011	4.365281392	0.010255252	1	Clathrin/coatomer_adapt-like_N|ARM-type_fold	molecular_function|binding|cellular_component|intracellular|cell|cytoplasm|transport|intracellular protein transport|biological_process|vesicle-mediated transport|membrane coat|protein complex
GRMZM2G112792	-1.61772991	0.232870987	0.010269519	1	Oxid_FAD_bind_N|ALO|FAD_OxRdtase_Pln|FAD-linked_Oxase-like_C|FAD-bd_2	molecular_function|catalytic activity|D-arabinono-1,4-lactone oxidase activity|cellular_component|biological_process|UDP-N-acetylmuramate dehydrogenase activity|membrane|oxidoreductase activity|oxidoreductase activity, acting on CH-OH group of donors|flavin adenine dinucleotide binding|oxidation-reduction process
GRMZM2G152888	-0.507801704	3.008390894	0.010369726	1	Aminotransferase_I/II|Aminotrans_II_pyridoxalP_BS|PyrdxlP-dep_Trfase	molecular_function|catalytic activity|cellular_component|intracellular|cell|cytoplasm|vacuole|endoplasmic reticulum|lipid metabolic process|biological_process|metabolic process|biosynthetic process|pollen development|photomorphogenesis|membrane|transferase activity|pyridoxal phosphate binding|cellular nitrogen compound metabolic process|organelle|small molecule metabolic process|sphingosine biosynthetic process
GRMZM2G129232	-1.966336955	-0.726931381	0.010385813	1	Not Annotated	Not Annotated
GRMZM2G106748	-1.058681596	3.521547085	0.010509135	1	LipOase_pln|PLAT/LH2_dom|Lipase_LipOase|LipOase_C|LipOase_CS	molecular_function|iron ion binding|protein binding|lipid metabolic process|fatty acid biosynthetic process|biological_process|biosynthetic process|linoleate 13S-lipoxygenase activity|oxidoreductase activity|oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen|oxylipin biosynthetic process|ion binding|small molecule metabolic process|metal ion binding|oxidation-reduction process

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G411159	-1.041176638	3.677441751	0.010522069	1	PMR5_N_dom|PC-Esterase	response to stress|biological_process|response to cold|response to freezing
GRMZM2G439589	-0.716124414	2.929581996	0.010559514	1	Not Annotated	Not Annotated
GRMZM2G310069	-1.00796365	2.490948067	0.010716253	1	Metal-dep_hydrolase_composite|Amidohydro_3	molecular_function|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|cellular amino acid metabolic process|biological_process|catabolic process|hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds|hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides|histidine catabolic process to glutamate and formamide|small molecule metabolic process|perinuclear region of cytoplasm
GRMZM2G154267	-0.705960969	2.504279784	0.010769513	1	DNA_pol_alpha/epsilon_bsu|DNA_pol_e_bsu|DNA_pol_e_bsu_N	nuclear chromosome|molecular_function|DNA binding|DNA-directed DNA polymerase activity|cellular_component|intracellular|cell|nucleus|chromosome|DNA metabolic process|DNA replication|DNA-dependent DNA replication|biological_process|epsilon DNA polymerase complex|biosynthetic process|nucleotidyltransferase activity|cellular nitrogen compound metabolic process|organelle|protein complex
GRMZM2G518717	-0.534226695	5.543164355	0.010779394	1	Not Annotated	Not Annotated
GRMZM2G089948	-0.717001766	1.994169885	0.010923158	1	Peptidase_S9A|Peptidase_S9	molecular_function|serine-type endopeptidase activity|cellular_component|intracellular|cell|cytoplasm|proteolysis|biological_process|peptidase activity|serine-type peptidase activity|chloroplast|plastid|organelle
GRMZM2G307600	-2.392466064	1.239759681	0.010966894	1	Not Annotated	cellular_component|intracellular|cell|cytoplasm|chloroplast|plastid|organelle
GRMZM2G392101	-0.874143425	1.309749172	0.010989546	1	Sig_transdc_resp-reg_receiver|CheY-like_superfamily	phosphorelay response regulator activity|phosphorelay signal transduction system|molecular_function|signal transducer activity|cellular_component|intracellular|cell|nucleus|cytoplasm|mitochondrion|regulation of transcription, DNA-templated|signal transduction|circadian rhythm|biological_process|plastid|response to cytokinin|response to red light|intracellular signal transduction|organelle
GRMZM2G168002	-2.044574048	0.525145561	0.010998445	1	Myb_CC_LHEQLE|SANT/Myb|Myb_dom_plants|Homeodomain-like	molecular_function|DNA binding|chromatin binding
GRMZM5G839976	-1.586196992	0.229196061	0.011012123	1	Not Annotated	Not Annotated
GRMZM5G805351	-1.586196992	0.229198748	0.011013583	1	Not Annotated	Not Annotated
GRMZM2G168096	-0.408280184	5.474699235	0.011032365	1	Helicase_C|HEAT|SNF2_N|Helicase_ATP-bd|ARM-type_fold|HEAT_type_2|DUF3535	molecular_function|nucleic acid binding|DNA binding|helicase activity|binding|protein binding|ATP binding
GRMZM2G369522	-6.841205151	-0.420142945	0.01104742	1	Cyt_c_oxidase_su3	molecular_function|cellular_component|heme-copper terminal oxidase activity|membrane|oxidoreductase activity
GRMZM2G434572	1.265514305	0.693923816	0.011050036	1	Acireductn_dOase_family|RmlC_Cupin	molecular_function|biological_process|acireductone dioxygenase [iron(II)-requiring] activity|oxidoreductase activity|oxidation-reduction process
GRMZM2G095244	-0.649958789	5.530829098	0.011096081	1	Not Annotated	Not Annotated
GRMZM2G051427	2.380532797	-2.114062355	0.011124972	1	Not Annotated	Not Annotated
GRMZM2G134329	-0.818968679	1.968864009	0.011183391	1	TMEM194	Not Annotated
GRMZM2G158736	-0.957225429	2.670872732	0.011283039	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G456669	-2.96220322	-1.106488695	0.011283165	1	Leu-rich_rpt|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|LRR-contain_N2|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|protein binding|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G176647	-1.161917877	1.710104585	0.011286863	1	WD40_repeat|Lgl_C_dom|WD40_repeat_dom	molecular_function|protein binding
GRMZM2G304638	-0.83886525	3.154590616	0.011382357	1	BEACH_dom|Pep_chain_release_fac_I_II	molecular_function|RNA binding|translation release factor activity|translation|translational termination|translation factor activity, nucleic acid binding|biological_process|biosynthetic process
GRMZM2G087513	-0.746048482	3.047983807	0.011391507	1	GDP-Fuc_O-FucTrfase|FucosylTrfase_pln	cellular_component|intracellular|cell|nucleus|cytoplasm|organelle
GRMZM2G437435	-2.429186513	-0.670402868	0.011409208	1	Peptidase_S8/S53_dom|Inhibitor_I9|Peptidase_S8_subtilisin-rel|Peptidase_S8_Asp-AS	molecular_function|serine-type endopeptidase activity|proteolysis|biological_process|peptidase activity|serine-type peptidase activity|hydrolase activity|identical protein binding|negative regulation of catalytic activity
GRMZM2G049623	-0.636790943	4.730911922	0.011423852	1	Pumilio_RNA-bd_rpt|ARM-type_fold	molecular_function|RNA binding|binding
GRMZM2G448633	-0.897808899	2.87830792	0.011460022	1	Ser/Thr_dual-sp_kinase_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G178919	-0.495625376	3.373834527	0.011509188	1	Not Annotated	Not Annotated
GRMZM2G345081	-1.143785156	3.034195019	0.011537882	1	Not Annotated	Not Annotated
GRMZM2G024476	-1.465478698	0.661039995	0.011546457	1	Oxy_OxRdtase_FAD_BS|Oxid_FAD_bind_N|Cytokinin_DH_FAD/cytokin-bd|FAD-linked_Oxase-like_C|FAD-bd_2	molecular_function|catalytic activity|biological_process|UDP-N-acetylmuramate dehydrogenase activity|cytokinin metabolic process|oxidoreductase activity|oxidoreductase activity, acting on CH-OH group of donors|cytokinin dehydrogenase activity|flavin adenine dinucleotide binding|oxidation-reduction process
GRMZM2G002034	2.028629219	-0.652415686	0.011591587	1	Glyco_hydro_28|PbH1|Pectin_lyase_fold/virulence	molecular_function|polygalacturonase activity|cellular_component|extracellular region|carbohydrate metabolic process|biological_process|metabolic process|hydrolase activity|hydrolase activity, acting on glycosyl bonds
GRMZM2G152011	1.730410483	0.364123387	0.011648307	1	Not Annotated	Not Annotated
GRMZM2G381386	-0.793947054	3.489733311	0.011727501	1	Znf_RING|Helicase_C	molecular_function|nucleic acid binding|helicase activity|protein binding|ATP binding|zinc ion binding|ion binding
GRMZM2G060265	-2.052432252	0.45832584	0.011777379	1	TF_GRAS	Not Annotated
AC209206.3_FG014	1.595069898	3.869983492	0.011788603	1	Tyrosinase|Unchr_di-copper_centre|Polyphenol_oxidase|Polyphenol_oxidase_cen|Polyphenol_oxidase_C	molecular_function|catechol oxidase activity|biological_process|metabolic process|biosynthetic process|oxidoreductase activity|ion binding|pigment biosynthetic process|metal ion binding|oxidation-reduction process

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G474194	0.906550916	3.480932778	0.011854727	1	LolPI|Expansin/allergen_DPBB_dom|Expansin_CBD|Expan_Lol_pI|RlpA-like_DPBB	reproduction|cellular_component|extracellular region|biological_process|sexual reproduction
GRMZM2G343317	0.540641142	-0.234132169	0.01191484	1	Not Annotated	Not Annotated
GRMZM2G346693	-0.726464746	2.873204116	0.011930275	1	Aminotrans_3|PyrdxlP-dep_Trfase	molecular_function|transaminase activity|pyridoxal phosphate binding
GRMZM2G164440	1.055562807	5.647797188	0.012060524	1	Bifunc_inhib/LTP/seed_store	Not Annotated
GRMZM2G340955	-2.139929119	-1.134857897	0.012082472	1	TIM-br_IGPS-like|Pyrv/PenolPyrv_Kinase-like_dom	molecular_function|catalytic activity
GRMZM2G015333	2.485104212	2.478543422	0.01209107	1	Disease-R_pln	Not Annotated
GRMZM2G144662	-1.284408755	1.369859923	0.012119074	1	Ribosomal_L30_N|Lipase_GDSL	molecular_function|lipid metabolic process|biological_process|hydrolase activity, acting on ester bonds
AC195685.3_FG001	2.188585604	-0.964435294	0.012119884	1	Pectin_lyase_fold/virulence|DNA_recomb/repair_Rad51_C|DNA_recomb/repair_RecA-like|RecA_ATP-bd	molecular_function|DNA binding|ATP binding|DNA metabolic process|DNA-dependent ATPase activity|biological_process|ATPase activity|cellular nitrogen compound metabolic process|chiasma assembly
GRMZM2G032887	-0.959068364	3.027717192	0.012132956	1	Transl_elong_EFTu/EF1A_C|Transl_elong_EF1A/Init_IF2_C	molecular_function|GTP binding
GRMZM2G032628	-0.454705708	10.33662228	0.012281289	1	Glyco_hydro_13_N|Glyco_hydro_13_cat_dom|A-amylase_b_C|GlgB|Ig_E-set|Glycoside_hydrolase_SF	molecular_function|catalytic activity|1,4-alpha-glucan branching enzyme activity|hydrolase activity, hydrolyzing O-glycosyl compounds|cellular_component|intracellular|cell|cytoplasm|carbohydrate metabolic process|glycogen biosynthetic process|starch metabolic process|generation of precursor metabolites and energy|biological_process|biosynthetic process|amyloplast|chloroplast|plastid|chloroplast stroma|transferase activity|transferase activity, transferring glycosyl groups|hydrolase activity, acting on glycosyl bonds|starch biosynthetic process|ion binding|cation binding|organelle|cellular response to sucrose stimulus|cellular response to fructose stimulus|cellular response to glucose stimulus|cellular response to light stimulus
GRMZM2G052279	-0.766417814	3.815685069	0.012325034	1	DUF3754	Not Annotated
GRMZM2G090168	2.307470256	2.318092558	0.012455396	1	WD40_repeat|WD40_repeat_dom|WD40_repeat_CS	molecular_function|protein binding
GRMZM2G313327	-1.731221592	0.19630454	0.012535833	1	DUF1005	Not Annotated
GRMZM5G859107	-1.551797997	0.418324986	0.012708584	1	Not Annotated	Not Annotated
GRMZM2G167902	-0.893292728	3.865244943	0.012743885	1	Not Annotated	Not Annotated
GRMZM5G807602	-1.401141714	1.43483568	0.012744222	1	LEA-14	immune system process|cellular_component|cell wall|cell|response to stress|biological_process|plant-type cell wall|external encapsulating structure|defense response to virus
GRMZM2G040158	-0.751037503	3.492307146	0.012754112	1	Cation/H_exchanger	molecular_function|cellular_component|transport|cation transport|biological_process|solute:hydrogen antiporter activity|integral component of membrane|transmembrane transporter activity|transmembrane transport

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G360681	0.491551084	5.828641628	0.012758113	1	Clp_N|ATPase_AAA_core|AAA+_ATPase|ClpA/B|ATPase_AAA-2|ClpA/B_CS1|Clp_ATPase_C	nucleotide binding|molecular_function|ATP binding|response to stress|biological_process|response to heat|chloroplast stroma|response to high light intensity|chloroplast envelope|nucleoside-triphosphatase activity|protein metabolic process|response to hydrogen peroxide|protein unfolding|positive regulation of translation
GRMZM2G448344	1.688172178	1.301116772	0.012786576	1	RuBisCO_lsu_C|RuBisCO_lsu_fd_N|RuBisCO_lsu_N|RuBisCo_large_chain_AS	magnesium ion binding|molecular_function|monooxygenase activity|cellular_component|intracellular|cell|cytoplasm|carbohydrate metabolic process|biological_process|biosynthetic process|chloroplast|plastid|photorespiration|carbon fixation|photosynthesis|oxidoreductase activity|lyase activity|ribulose-bisphosphate carboxylase activity|reductive pentose-phosphate cycle|ion binding|organelle|metal ion binding|oxidation-reduction process
GRMZM2G094532	-0.811843251	3.945785859	0.012819438	1	Zein-bd	Not Annotated
GRMZM2G160685	-2.137686544	0.176675467	0.012825353	1	FAD_bind_dom|Kinesin_motor_dom	molecular_function|microtubule motor activity|ATP binding|cellular_component|intracellular|cell|cytoskeleton|microtubule associated complex|generation of precursor metabolites and energy|microtubule-based movement|biological_process|oxidoreductase activity|oxidoreductase activity, acting on the CH-CH group of donors|electron transport chain|organelle|protein complex|flavin adenine dinucleotide binding|oxidation-reduction process
GRMZM5G825978	-0.944621112	3.092505909	0.012910307	1	Not Annotated	Not Annotated
GRMZM2G083138	-0.832166274	1.356378916	0.012910356	1	Helicase_C	double-strand break repair via homologous recombination|molecular_function|nucleic acid binding|helicase activity|ATP binding|response to gamma radiation|double-strand break repair via synthesis-dependent strand annealing
GRMZM2G103382	-1.345180128	0.135988822	0.012952252	1	GlyceroP-diester-Pdiesterase|PLC-like_Pdiesterase_TIM-brl	molecular_function|carbohydrate metabolic process|glycerol metabolic process|lipid metabolic process|phosphoric diester hydrolase activity|biological_process|glycerophosphodiester phosphodiesterase activity|small molecule metabolic process
GRMZM2G065284	-2.895956836	-1.165479607	0.012993944	1	Znf_CCHC	molecular_function|nucleic acid binding|zinc ion binding|ion binding|metal ion binding
GRMZM2G702406	-1.563244323	1.484715077	0.013000684	1	NA-bd_OB-fold|Rep_factor-A_C	Not Annotated
GRMZM2G332843	1.156136627	1.3655538	0.013014873	1	Pentatricopeptide_repeat	Not Annotated
GRMZM2G067456	-0.833539958	6.129934145	0.013106133	1	Ribosomal_L2|Translation_prot_SH3-like|NA-bd_OB-fold|Rbsml_prot_L2_RNA-bd_dom|Ribosomal_L2_C|Ribosomal_L2_CS	molecular_function|RNA binding|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|nucleus|nucleolus|cytoplasm|vacuole|cytosol|ribosome|plasma membrane|translation|biological_process|biosynthetic process|chloroplast|plastid|large ribosomal subunit|cytosolic large ribosomal subunit|cytosolic ribosome|organelle
GRMZM2G149224	-0.463196619	4.727144149	0.01316066	1	3Beta_OHSteriod_DH/Estase|Reticulon	molecular_function|3-beta-hydroxy-delta5-steroid dehydrogenase activity|lipid metabolic process|steroid biosynthetic process|biological_process|biosynthetic process|oxidoreductase activity|oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor|oxidation-reduction process|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|organelle|nucleotide binding|membrane|sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) activity

<table>
<tr><th>Gene</th><th>log2 (fold change)</th><th>log2 (count per million)</th><th>P-value</th><th>FDR</th><th>Interpro</th><th>GO</th></tr>
<tr><td>GRMZM2G349062</td><td>-0.686163655</td><td>3.050684368</td><td>0.013192072</td><td>1</td><td>PaO|Rieske_2Fe-2S</td><td>molecular_function|cellular_component|intracellular|cell|cytoplasm|biological_process|chloroplast|plastid|chloroplast envelope|chlorophyllide a oxygenase [overall] activity|oxidoreductase activity|ion binding|organelle|metal ion binding|iron-sulfur cluster binding|2 iron, 2 sulfur cluster binding|oxidation-reduction process</td></tr>
<tr><td>GRMZM2G542170</td><td>-1.626652114</td><td>1.261673984</td><td>0.013242416</td><td>1</td><td>Not Annotated</td><td>Not Annotated</td></tr>
<tr><td>GRMZM2G081380</td><td>-0.623533615</td><td>4.19158706</td><td>0.013453858</td><td>1</td><td>CH-domain|Actinin_actin-bd_CS</td><td>molecular_function|actin binding|protein binding|cytoskeletal protein binding</td></tr>
<tr><td>GRMZM2G074466</td><td>-0.585822488</td><td>5.807779841</td><td>0.013497834</td><td>1</td><td>WD40_repeat|WD40_repeat_dom|WD40_repeat_CS|G-protein_beta_WD-40_rep</td><td>molecular_function|protein binding</td></tr>
<tr><td>GRMZM2G003679</td><td>6.214150217</td><td>-1.732270514</td><td>0.013519394</td><td>1</td><td>Not Annotated</td><td>Not Annotated</td></tr>
<tr><td>GRMZM2G032528</td><td>-1.022968273</td><td>1.66139278</td><td>0.013568815</td><td>1</td><td>Not Annotated</td><td>Not Annotated</td></tr>
<tr><td>GRMZM2G110897</td><td>-0.585334797</td><td>3.181051278</td><td>0.013583497</td><td>1</td><td>CASTOR/POLLUX/SYM8</td><td>nucleotide binding|molecular_function</td></tr>
<tr><td>GRMZM2G126827</td><td>-7.297201094</td><td>-0.16821147</td><td>0.013585083</td><td>1</td><td>Transcpt_factor_SBP-box</td><td>molecular_function|DNA binding|cellular_component|intracellular|cell|nucleus|organelle</td></tr>
<tr><td>GRMZM2G068177</td><td>0.693340104</td><td>1.744068999</td><td>0.013737383</td><td>1</td><td>Znf_DHHC_palmitoyltrfase</td><td>molecular_function|zinc ion binding|ion binding|metal ion binding</td></tr>
<tr><td>GRMZM2G325008</td><td>-0.68917524</td><td>2.770889097</td><td>0.013815406</td><td>1</td><td>Pept_M24_structural-domain|Glyco_hydro_17|X8|Glycoside_hydrolase_SF</td><td>molecular_function|catalytic activity|hydrolase activity, hydrolyzing O-glycosyl compounds|carbohydrate metabolic process|biological_process|metabolic process|cellular process|hydrolase activity|hydrolase activity, acting on glycosyl bonds</td></tr>
<tr><td>GRMZM2G129954</td><td>-0.599570696</td><td>3.454397033</td><td>0.013843586</td><td>1</td><td>Sig_transdc_resp-reg_receiver|CheY-like_superfamily</td><td>phosphorelay response regulator activity|phosphorelay signal transduction system|molecular_function|signal transducer activity|cellular_component|intracellular|cell|nucleus|cytoplasm|regulation of transcription, DNA-templated|signal transduction|circadian rhythm|biological_process|plastid|response to cytokinin|cytokinin-activated signaling pathway|intracellular signal transduction|organelle</td></tr>
<tr><td>GRMZM2G062654</td><td>-1.854824233</td><td>0.527790416</td><td>0.013953283</td><td>1</td><td>Guanylyl_cyclase</td><td>Not Annotated</td></tr>
<tr><td>GRMZM2G071589</td><td>-0.839919095</td><td>5.449091286</td><td>0.014003547</td><td>1</td><td>RRM_dom|CC1_SF</td><td>nucleotide binding|molecular_function|nucleic acid binding|RNA binding|cellular_component|intracellular|cell|nucleus|mRNA processing|biological_process|cellular nitrogen compound metabolic process|organelle</td></tr>
<tr><td>GRMZM2G065899</td><td>-1.413557311</td><td>0.856965521</td><td>0.014082975</td><td>1</td><td>EF_hand_dom|EF_Hand_1_Ca_BS</td><td>molecular_function|calcium ion binding|ion binding</td></tr>
</table>

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G568636	3.058891149	-1.117119388	0.014170201	1	MoCF_OxRdtse_dimer|NADH-Cyt_B5_reductase|Flavoprot_Pyr_Nucl_cyt_Rdtase|OxRdtase_FAD/NAD-bd|Cyt_B5-like_heme/steroid-bd|OxRdtase_Mopterin-bd_dom|OxRdtase_FAD-bd_dom|Mopterin_OxRdtase_euk|Nitr_rd_NADH|Ig_E-set|Fd_Rdtase_FAD-bd|Riboflavin_synthase-like_b-brl|Cyt_B5_heme-BS|OxRdtase_Mopterin_BS	molecular_function|iron ion binding|cellular_component|intracellular|cell|cytoplasm|vacuole|plasma membrane|nitric oxide biosynthetic process|biological_process|nitrate reductase activity|electron carrier activity|biosynthetic process|response to light stimulus|response to symbiotic fungus|nitrate reductase (NADH) activity|oxidoreductase activity|heme binding|molybdenum ion binding|cellular nitrogen compound metabolic process|nitrate assimilation|ion binding|organelle|molybdopterin cofactor binding|oxidoreductase activity, acting on other nitrogenous compounds as donors, with NAD or NADP as acceptor|metal ion binding|flavin adenine dinucleotide binding|oxidation-reduction process|nitrogen cycle metabolic process
AC215201.3_FG008	1.098480556	1.272657426	0.014226016	1	bHLH_dom	molecular_function|DNA binding|cellular_component|intracellular|cell|cytoplasm|mitochondrion|organelle|protein dimerization activity
GRMZM2G126873	-0.683002346	3.650767445	0.014260485	1	Vps16_C	cellular_component|intracellular|cell|cytoplasm|transport|intracellular protein transport|biological_process|plant-type vacuole membrane
AC197150.3_FG003	-6.020883491	-1.607618723	0.014277646	1	K_chnl_volt-dep_EAG/ELK/ERG|cNMP-bd_dom|IQ_motif_EF-hand-BS|Ion_trans_dom|cNMP-bd-like	molecular_function|ion channel activity|protein binding|cellular_component|transport|ion transport|biological_process|membrane|transmembrane transporter activity|response to cadmium ion|transmembrane transport
GRMZM2G162840	-0.656548844	2.338895297	0.014373962	1	Myb-like_dom	molecular_function|DNA binding
GRMZM2G445958	-0.35076555	5.216488192	0.014383903	1	NA-bd_OB-fold|RPA32|RPA_C	Not Annotated
AC233910.1_FG001	-1.61772991	0.298186299	0.014425942	1	Mitochondrial_sb/sol_carrier|Mt_carrier_dom	response to salt stress
GRMZM2G092008	-1.42171831	-0.238866023	0.014471987	1	Phosphotidylethanolamine-bd_CS|PtdEtn-bd_prot_PEBP	reproduction|molecular_function|cellular_component|intracellular|cell|cytoplasm|vacuole|plasma membrane|protein targeting|protein targeting to vacuole|transport|vacuolar transport|biological_process|lipid binding|phosphatidylethanolamine binding|response to sucrose|negative regulation of flower development|inflorescence development|vesicle|organelle|regulation of timing of transition from vegetative to reproductive phase|anatomical structure development|negative regulation of cell aging
GRMZM2G117360	-0.85200884	3.388073636	0.014520095	1	Not Annotated	Not Annotated
GRMZM2G013196	-0.769019538	2.669367372	0.014570018	1	Not Annotated	Not Annotated
GRMZM5G852378	-1.393065149	0.445439462	0.014628723	1	C2_dom|PRibTrfase_C	molecular_function|protein binding|plasma membrane|plasmodesma|organ development
GRMZM5G819204	-0.517942209	3.16761243	0.014637223	1	Not Annotated	Not Annotated
GRMZM2G048567	-0.911456289	1.756295191	0.01465848	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G000264	-0.655868647	5.416628987	0.014748652	1	Cation_transp_P_typ_ATPase|HAD-like_dom	molecular_function|cellular_component|cell|plasma membrane|transport|cation transport|biological_process|integral component of membrane|ATPase activity|cation-transporting ATPase activity|transmembrane transporter activity
GRMZM2G124377	-0.56817299	3.712336751	0.01482004	1	Phosphodiest/P_Trfase|Alkaline_phosphatase_core	molecular_function|catalytic activity|endoplasmic reticulum|biological_process|metabolic process
GRMZM2G092648	-0.623160691	3.003925074	0.014833751	1	DUF789	Not Annotated
GRMZM2G410134	-0.930121604	9.152075285	0.014907205	1	Bifunc_inhib/LTP/seed_store	cellular_component|intracellular|cell|cytoplasm|transport|biological_process|cytoplasmic membrane-bounded vesicle|secretion by cell|organelle
GRMZM2G039610	-0.526396834	5.039401398	0.014920185	1	Not Annotated	cellular_component|intracellular|cell|cytoplasm|plasma membrane|chloroplast|plastid|organelle
GRMZM2G059964	-3.37409334	-1.635432645	0.014954761	1	Bifunc_inhib/LTP/seed_store	Not Annotated
GRMZM2G180951	-0.856948352	2.745657083	0.014996813	1	Glyco_trans_48	1,3-beta-D-glucan synthase complex|molecular_function|1,3-beta-D-glucan synthase activity|cellular_component|cell|plasma membrane|carbohydrate metabolic process|(1->3)-beta-D-glucan biosynthetic process|biological_process|biosynthetic process|membrane|transferase activity, transferring glycosyl groups|protein complex
GRMZM5G826767	1.017495555	2.556555186	0.015001247	1	LEA-14	Not Annotated
GRMZM2G062042	-0.92318188	1.965031347	0.015015036	1	Mlo|Clathrin_H-chain/VPS_repeat|ARM-type_fold	molecular_function|binding|cellular_component|transport|intracellular protein transport|biological_process|cell death|integral component of membrane|vesicle-mediated transport
GRMZM2G017197	-6.488580144	-0.373894035	0.015022348	1	Pentatricopeptide_repeat	Not Annotated
GRMZM2G160178	-1.892042452	1.079392575	0.015084952	1	Not Annotated	Not Annotated
GRMZM2G107540	-0.452789184	4.98616403	0.01512318	1	Histone_H2A|Histone_core_D|Histone-fold	nucleosome|molecular_function|DNA binding|cellular_component|intracellular|cell|nucleus|chromosome|DNA metabolic process|nucleosome assembly|biological_process|cellular component assembly|cellular nitrogen compound metabolic process|organelle|protein heterodimerization activity|chromosome organization|macromolecular complex assembly
GRMZM5G813909	-0.333830422	5.665395352	0.015193193	1	Peptidase_M48	molecular_function|endopeptidase activity|metalloendopeptidase activity|cellular_component|intracellular|cell|cytoplasm|vacuole|endoplasmic reticulum|proteolysis|biological_process|peptidase activity|metallopeptidase activity|membrane|hydrolase activity|organelle|protein maturation|CAAX-box protein processing|CAAX-box protein maturation
GRMZM2G357834	-5.762285887	-1.661253474	0.015196594	1	Wound-induced_Wun1	Not Annotated
GRMZM2G133959	-0.897695052	3.141808352	0.015254548	1	DUF2305	Not Annotated
GRMZM2G389948	-1.34998124	0.388350821	0.015263996	1	Leu-rich_rpt|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|LRR-contain_N2|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|protein binding|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups
GRMZM2G147667	-0.760608338	4.011411699	0.015343225	1	Peptidase_C19/C67|Pept_C19ubi-hydrolase_C_CS	molecular_function|ubiquitin thiolesterase activity|proteolysis|ubiquitin-dependent protein catabolic process|biological_process|peptidase activity|cysteine-type peptidase activity|catabolic process|hydrolase activity

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G090736	0.990493577	4.392488477	0.015370985	1	Monothiol_GRX-rel|Glutaredoxin|Thioredoxin-like_fold|Thioredoxin_domain	molecular_function|biological_process|electron carrier activity|protein disulfide oxidoreductase activity|oxidoreductase activity|homeostatic process|cell redox homeostasis
GRMZM2G169405	-1.532475619	0.15218651	0.0154383	1	Not Annotated	cellular_component|intracellular|cell|cytoplasm|chloroplast|chloroplast thylakoid membrane|plastid|chloroplast stroma|thylakoid|organelle
GRMZM5G863846	-0.605088549	3.121101979	0.015466593	1	Not Annotated	Not Annotated
GRMZM2G017847	-0.678237371	3.630291999	0.015487489	1	Actin_CS|Actin-related	molecular_function|ATP binding
GRMZM2G172011	-0.645027823	4.35706164	0.015519962	1	RRM_dom	nucleotide binding|molecular_function|nucleic acid binding
GRMZM2G059129	-0.559348313	3.245868861	0.01557166	1	GlyceroP-diester-Pdiesterase|PLC-like_Pdiesterase_TIM-brl	molecular_function|carbohydrate metabolic process|glycerol metabolic process|lipid metabolic process|phosphoric diester hydrolase activity|biological_process|glycerophosphodiester phosphodiesterase activity|small molecule metabolic process
GRMZM2G149923	-0.558437557	5.848561008	0.015587827	1	EF_hand_dom|EF-hand-dom_pair|EF_Hand_1_Ca_BS	molecular_function|calcium ion binding|cellular_component|intracellular|cell|nucleus|cytoplasm|cytosol|response to stress|signal transduction|biological_process|response to water deprivation|response to salt stress|response to abscisic acid|calcium-mediated signaling|ion binding|organelle
GRMZM2G353548	-0.631918542	4.510087279	0.015597396	1	WD40_repeat|Quinon protein_ADH-like_supfam|WD40_repeat_dom|WD40_repeat_CS	molecular_function|protein binding
GRMZM2G119079	-0.851840107	2.923358049	0.015648671	1	Tyr/Dual-sp_Pase|Dual-sp_phosphatase_cat-dom|Tyr_Pase_AS|Dual-sp_phosphatase_subgr_cat	molecular_function|protein tyrosine phosphatase activity|cellular protein modification process|protein dephosphorylation|protein tyrosine/serine/threonine phosphatase activity|biological_process|dephosphorylation|hydrolase activity|phosphatase activity|peptidyl-tyrosine dephosphorylation
GRMZM2G469551	-0.652585257	4.108699132	0.015685415	1	START_lipid-bd_dom|Homeobox_dom|Homeodomain-like|MEKHLA	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|regulation of transcription, DNA-templated|biological_process|determination of bilateral symmetry|polarity specification of adaxial/abaxial axis|radial pattern formation|meristem initiation|xylem and phloem pattern formation|cell differentiation|sequence-specific DNA binding|anatomical structure development
GRMZM2G075828	-1.025874429	1.860243113	0.015771141	1	MATE	molecular_function|cellular_component|transport|drug transmembrane transport|biological_process|drug transmembrane transporter activity|antiporter activity|membrane|transmembrane transporter activity|transmembrane transport
GRMZM2G399844	-0.613371111	4.458679292	0.015812929	1	Not Annotated	Not Annotated
GRMZM2G118637	1.070712687	7.193787198	0.015840675	1	Ubiquitin_dom|Ubiquitin_CS|Ubiquitin	molecular_function|protein binding|vacuole|response to UV-B
GRMZM2G013761	-1.014056466	3.568199424	0.015974635	1	GUCT	molecular_function|RNA binding|helicase activity|ATP binding|cellular_component|intracellular|cell|nucleus|organelle
GRMZM5G873635	-1.075467001	2.117966224	0.016072957	1	Not Annotated	Not Annotated
GRMZM2G149175	-0.662392811	3.422562478	0.016087841	1	Not Annotated	Not Annotated
GRMZM2G078124	-1.250878742	0.83480789	0.016124586	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G069098	1.183517605	-0.001651745	0.016142092	1	MATE	molecular_function|cellular_component|intracellular|cell|cytoplasm|vacuole|plasma membrane|transport|drug transmembrane transport|biological_process|response to nematode|drug transmembrane transporter activity|antiporter activity|membrane|transmembrane transporter activity|organelle|transmembrane transport
GRMZM5G870572	-0.457491887	4.439888483	0.016145965	1	BSD	Not Annotated
GRMZM2G405064	-0.924924619	1.282336637	0.016233086	1	Asc_peroxidase|DUF632|Polyketide_cyclase/dehydratase	Not Annotated
GRMZM2G095655	-2.289708685	-1.171935032	0.016236681	1	Universal_stress_UspA|UspA	cellular_component|cell|plasma membrane|response to stress|biological_process|response to cold
GRMZM2G475867	-0.572661101	3.885535303	0.016293602	1	WD40_repeat|Ribosome_control_1	molecular_function|protein binding
GRMZM2G059445	-0.734930359	1.531041383	0.016296909	1	Cyt_trans-like	molecular_function|catalytic activity|biological_process|biosynthetic process
GRMZM2G152194	-0.647640139	4.118924274	0.016503197	1	GPI_mannosylTrfase	alpha-1,6-mannosyltransferase activity|molecular_function|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|carbohydrate metabolic process|translation|cellular protein modification process|protein N-linked glycosylation|GPI anchor biosynthetic process|lipid metabolic process|biological_process|catabolic process|biosynthetic process|transferase activity, transferring glycosyl groups|ER-associated ubiquitin-dependent protein catabolic process|intrinsic component of endoplasmic reticulum membrane|organelle
GRMZM2G464782	-0.798233907	4.367716506	0.016533246	1	Not Annotated	Not Annotated
GRMZM2G134385	-0.44835939	5.413164835	0.016539652	1	BP28_C_dom|ARM-type_fold	molecular_function|binding
GRMZM2G701310	-0.940103213	4.778296407	0.016606365	1	Not Annotated	Not Annotated
GRMZM2G178102	-0.55072616	2.815903883	0.01664256	1	START_lipid-bd_dom|Homeobox_dom|Homeodomain-like|MEKHLA	reproduction|nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|cellular_component|intracellular|cell|nucleus|regulation of transcription, DNA-templated|biological_process|embryo development|determination of bilateral symmetry|embryonic pattern specification|adaxial/abaxial axis specification|polarity specification of adaxial/abaxial axis|adaxial/abaxial pattern specification|meristem initiation|primary shoot apical meristem specification|organelle|sequence-specific DNA binding|anatomical structure development|integument development
GRMZM2G306859	-0.553472266	3.989584304	0.016692463	1	Znf_FYVE_PHD|Acyl_CoA_acyltransferase	Not Annotated
GRMZM2G144705	-1.246702966	1.990041594	0.016788174	1	HNH_nuc|HNH	molecular_function|nucleic acid binding|nuclease activity|endonuclease activity
GRMZM2G043183	-1.110029694	1.068905323	0.016854445	1	Vps52	Not Annotated
GRMZM5G863784	-0.582535368	3.097579649	0.016866309	1	Pept_M3A_M3B	molecular_function|metalloendopeptidase activity|proteolysis|biological_process|peptidase activity|metallopeptidase activity|hydrolase activity|ion binding|metal ion binding
GRMZM2G115772	-0.69283879	2.8673879	0.017005511	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G012685	-2.96220322	-1.172670243	0.017175215	1	Leu-rich_rpt|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|LRR-contain_N2|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|protein binding|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups
GRMZM2G095868	-0.589646774	2.739546832	0.017183049	1	Rab-GTPase-TBC_dom	molecular_function|Rab GTPase activator activity|cellular_component|intracellular|cell|biological_process|enzyme regulator activity|regulation of Rab GTPase activity|positive regulation of Rab GTPase activity
GRMZM2G340359	-0.442101593	4.437550796	0.017192378	1	Pleckstrin_homology|RhoGAP_dom|Rho_GTPase_activation_prot|MIP1_Leuzipper	molecular_function|protein binding|phospholipid binding|cellular_component|intracellular|cell|signal transduction|biological_process|lipid binding
GRMZM2G063316	-0.542251049	3.889733184	0.017240634	1	SET_dom|Rubisco_LSMT_subst-bd	molecular_function|protein binding|cellular_component|intracellular|cell|cytoplasm|chloroplast|plastid|organelle
GRMZM2G155253	-2.924691815	-0.046459015	0.017254818	1	Aldolase_I	molecular_function|catalytic activity|fructose-bisphosphate aldolase activity|cellular_component|extracellular region|intracellular|cell|cytoplasm|cytosol|ribosome|carbohydrate metabolic process|generation of precursor metabolites and energy|glycolysis|biological_process|catabolic process|chloroplast|chloroplast thylakoid|plastid|chloroplast stroma|thylakoid|response to abscisic acid|chloroplast envelope|plastoglobule|membrane|lyase activity|cytosolic ribosome|thylakoid lumen|organelle|response to cadmium ion|apoplast
GRMZM2G152189	2.339597186	1.107860378	0.017255108	1	Not Annotated	Not Annotated
GRMZM2G167243	-1.172124106	1.308506309	0.01729633	1	Not Annotated	chloroplast|photosynthesis
GRMZM2G174449	3.21266024	-2.33298895	0.017462672	1	DUF247_pln	Not Annotated
GRMZM2G158240	-2.429186513	-0.73912757	0.017521783	1	Pectinesterase_cat|Pectinesterase_inhib_dom|Pectin_lyase_fold/virulence|Pectinesterase_AS	molecular_function|enzyme inhibitor activity|cellular_component|cell wall|cell|biological_process|hydrolase activity|enzyme regulator activity|external encapsulating structure|pectinesterase activity|cell wall modification|negative regulation of catalytic activity|aspartyl esterase activity|cell wall organization or biogenesis
GRMZM2G034536	-0.984257686	2.025408497	0.017539013	1	Znf_RING-CH	molecular_function|zinc ion binding|ion binding
GRMZM5G801958	5.919067406	-1.852404395	0.017598128	1	Not Annotated	Not Annotated
GRMZM2G168176	-0.549290056	3.066523375	0.017670502	1	Anticodon-bd|Brix	Not Annotated
GRMZM2G075008	-6.748934336	-0.487109734	0.017757786	1	Not Annotated	Not Annotated
GRMZM2G063369	-0.448187437	5.153721265	0.017759558	1	ARM-type_fold|HEAT_type_2|VAC14_Fig4p-bd	molecular_function|binding|cellular_component|cell|vacuolar membrane|plasma membrane|biological_process|kinase activator activity|enzyme regulator activity|positive regulation of phosphorylation
GRMZM2G569390	-0.52957433	2.458778442	0.017861007	1	DUF868_pln	Not Annotated
GRMZM2G123732	-0.681993819	3.945188906	0.017887785	1	Uncharacterised_TM-40	response to molecule of bacterial origin|root morphogenesis
GRMZM2G147158	-0.632450331	2.065949164	0.017917246	1	Not Annotated	Not Annotated
GRMZM2G177404	-2.769402082	-0.8224568	0.018130942	1	6-PGluconate_DH_C-like	biological_process|oxidation-reduction process
GRMZM2G163247	-0.491849066	4.16398599	0.01816914	1	RRM_dom	nucleotide binding|molecular_function|nucleic acid binding
GRMZM2G178247	-1.961821791	0.039156744	0.018172402	1	Cyclin_N|Cyclin-like|Cyclin_C-dom	cellular_component|intracellular|cell|nucleus|organelle
GRMZM2G401700	-1.185892026	0.580359783	0.018242847	1	Not Annotated	Not Annotated
GRMZM2G053790	-3.625267709	-0.597326258	0.018270124	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM5G882378	-1.03895874	1.76804339	0.01842534	1	Ribosomal_S11|Ribosomal_S11_CS	molecular_function|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|ribosome|translation|biological_process|biosynthetic process|ribonucleoprotein complex|organelle
GRMZM2G076034	5.805575723	-2.032165852	0.018471749	1	WD40_repeat|WD40_repeat_dom|G-protein_beta_WD-40_rep	molecular_function|protein binding
GRMZM2G428391	0.943936899	7.591216809	0.018487488	1	Hsp_70_fam|Heat_shock_70_CS	nucleotide binding|molecular_function|ATP binding|cell wall|mitochondrion|vacuolar membrane|Golgi apparatus|cytosol|plasma membrane|response to stress|biological_process|response to temperature stimulus|response to heat|response to virus|response to bacterium|response to high light intensity|protein ubiquitination|ubiquitin protein ligase binding|response to hydrogen peroxide|response to cadmium ion|apoplast
GRMZM2G107395	-1.041732954	1.721726971	0.018512349	1	14-3-3|14-3-3_CS|14-3-3_domain	Not Annotated
GRMZM2G067853	-0.361586459	5.630414154	0.018514343	1	Cation_transp_P_typ_ATPase|ATPase_P-typ_transduc_dom_A|ATPase_P-typ_P_site|HAD-like_dom|Cation_transp_P-typ_ATPase_IB	nucleotide binding|molecular_function|calcium-transporting ATPase activity|cellular_component|intracellular|cell|cytoplasm|ATP catabolic process|transport|cation transport|calcium ion transport|cellular copper ion homeostasis|biological_process|catabolic process|chloroplast|plastid|response to toxic substance|response to light intensity|chloroplast envelope|cadmium-transporting ATPase activity|zinc transporting ATPase activity|integral component of membrane|ATPase activity|cation-transporting ATPase activity|transmembrane transporter activity|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|homeostatic process|ion binding|organelle|small molecule metabolic process|metal ion binding|zinc ion homeostasis|ATP binding|membrane|hydrolase activity
GRMZM2G135120	-0.57487194	3.489927366	0.018517478	1	Not Annotated	Not Annotated
GRMZM5G869572	-0.995994305	3.177069654	0.018518088	1	ARM-type_fold	molecular_function|binding
GRMZM2G153150	-0.586627631	3.353119796	0.018533088	1	RB_A|RB_B|Cyclin-like|RB_N	cellular_component|intracellular|cell|nucleus|transcription, DNA-templated|regulation of transcription, DNA-templated|cell cycle|biological_process|biosynthetic process|cellular nitrogen compound metabolic process|organelle|regulation of cell cycle
GRMZM2G125441	-0.869717785	3.058262963	0.018533536	1	Not Annotated	Not Annotated
GRMZM2G077307	-0.5824315	5.150449679	0.018724759	1	Znf_RING|Znf_CHY|Znf_CTCHY	molecular_function|protein binding|zinc ion binding|ion binding|metal ion binding
GRMZM2G126808	-0.96647721	2.047648852	0.018739999	1	Leu_zip_homeo|Homeobox_dom|Homeodomain-like|Homeobox_CS	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|cellular_component|intracellular|cell|nucleus|regulation of transcription, DNA-templated|biological_process|response to cytokinin|organelle|sequence-specific DNA binding|transcription, DNA-templated|biosynthetic process|cellular nitrogen compound metabolic process
GRMZM2G451357	-0.426364501	4.710306641	0.01879636	1	Peptidase_C19/C67|Pept_C19ubi-hydrolase_C_CS	molecular_function|ubiquitin thiolesterase activity|ubiquitin-dependent protein catabolic process|biological_process|catabolic process
GRMZM2G462883	1.96554443	-0.170508426	0.018826141	1	AB_hydrolase_3	molecular_function|biological_process|metabolic process|hydrolase activity

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G095851	-3.795187125	4.711031634	0.01882956	1	Small_GTP-bd_dom|Transl_elong_EFTu/EF1A_2|EF_GTP-bd_dom|EFG_V|Transl_elong_EFG/EF2_IV|Transl_B-barrel|EFG_III-V|Ribosomal_S5_D2-typ_fold	nucleotide binding|molecular_function|RNA binding|translation elongation factor activity|GTPase activity|copper ion binding|GTP binding|cellular_component|intracellular|cell|nucleus|nucleolus|cytoplasm|cytosol|plasma membrane|GTP catabolic process|translation|translational elongation|response to stress|translation factor activity, nucleic acid binding|biological_process|catabolic process|biosynthetic process|response to cold|chloroplast|plastid|membrane|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|ion binding|organelle|small molecule metabolic process
GRMZM2G125529	-1.214963223	1.679888675	0.018909951	1	RRM_dom	nucleotide binding|molecular_function|nucleic acid binding
GRMZM2G466938	-1.838942014	-0.486292508	0.018967889	1	TBP	molecular_function|DNA binding|DNA-templated transcription, initiation|biological_process|biosynthetic process|cellular nitrogen compound metabolic process
GRMZM2G319169	-0.670007436	3.713111938	0.018970672	1	ARM-type_fold|DUF3730	molecular_function|binding
GRMZM2G056695	-0.478198406	4.816760266	0.01897297	1	Sec23/24_helical_dom|Gelsolin_dom|Sec23_24_beta_S	cellular_component|intracellular|cell|cytoplasm|transport|intracellular protein transport|ER to Golgi vesicle-mediated transport|biological_process|protein transport|cytoplasmic membrane-bounded vesicle|vesicle-mediated transport|COPII vesicle coat|organelle|protein complex
AC233936.1_FG003	-1.27374877	1.211294173	0.018979038	1	WD40_repeat|WD40_repeat_CS	molecular_function|protein binding
GRMZM2G051138	-0.776511686	1.619874382	0.01902979	1	Not Annotated	cellular_component|intracellular|cell|nucleus|DNA metabolic process|DNA repair|regulation of DNA repair|response to stress|cell cycle|biological_process|cellular nitrogen compound metabolic process|organelle
GRMZM2G022787	-0.699654934	2.27739052	0.01903814	1	Pentatricopeptide_repeat|Znf_CCHC	molecular_function|nucleic acid binding|zinc ion binding|ion binding
GRMZM2G448651	-0.981888204	1.942489322	0.019155375	1	Not Annotated	Not Annotated
GRMZM2G129288	-0.527616187	4.467566209	0.019188308	1	F-box_dom|Tubby_C|Tubby_C_CS|Tubby_C-like	molecular_function|protein binding|cytosol|plasma membrane|plastid|response to fungus
GRMZM2G144674	-1.085106913	0.639535853	0.019198688	1	Not Annotated	Not Annotated
GRMZM2G016866	1.202948054	2.881066027	0.019223872	1	Pentatricopeptide_repeat	Not Annotated
GRMZM2G515667	-2.607625772	-1.049234353	0.019305243	1	Not Annotated	Not Annotated
GRMZM2G007909	-0.663736484	3.618199952	0.019313908	1	Nuc_sug_transpt|UDPgal_transpt	Golgi membrane|molecular_function|sugar:hydrogen symporter activity|cellular_component|intracellular|cell|cytoplasm|endosome|Golgi apparatus|trans-Golgi network|transport|biological_process|carbohydrate transport|integral component of membrane|transmembrane transporter activity|organelle|nucleotide-sugar transmembrane transporter activity|nucleotide-sugar transport
GRMZM2G075077	-1.767278816	-0.609861625	0.019339419	1	Zein-bd	Not Annotated
AC195914.2_FG003	2.865921991	-0.993660172	0.01936639	1	Not Annotated	Not Annotated
GRMZM5G845021	-0.815317387	1.468443532	0.0193676	1	APS_kinase	sulfate assimilation|nucleotide binding|molecular_function|adenylylsulfate kinase activity|ATP binding|sulfur compound metabolic process|biological_process|biosynthetic process|kinase activity|phosphorylation|transferase activity|hydrogen sulfide biosynthetic process

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G098622	-0.372424947	4.770702291	0.019370404	1	Not Annotated	Not Annotated
GRMZM5G864266	-0.416579003	5.371316435	0.019439883	1	MATH|Peptidase_C19/C67|TRAF-like|Pept_C19ubi-hydrolase_C_CS|USP7_ICP0-binding_dom	molecular_function|ubiquitin thiolesterase activity|protein binding|ubiquitin-dependent protein catabolic process|biological_process|catabolic process
GRMZM2G025123	-0.493124879	3.518147767	0.019542567	1	TatC|Sec-indep_translocase_CS	reproduction|molecular_function|cellular_component|intracellular|cell|cytoplasm|lipid metabolic process|transport|biological_process|protein transporter activity|biosynthetic process|protein secretion|chloroplast|chloroplast thylakoid membrane|plastid|double fertilization forming a zygote and endosperm|thylakoid|abscisic acid biosynthetic process|thylakoid membrane organization|protein transport|P-P-bond-hydrolysis-driven protein transmembrane transporter activity|membrane|integral component of membrane|transmembrane transporter activity|integral component of thylakoid membrane|TAT protein transport complex|organelle|protein complex|receptor complex|small molecule metabolic process|membrane organization
GRMZM2G110201	-0.438607122	5.28341912	0.01954337	1	Thiolase|Thiolase-like|Thiolase_AS|Thiolase_CS|Thiolase_acyl_enz_int_AS|Thiolase_N|Thiolase_C	molecular_function|catalytic activity|cellular_component|intracellular|cell|cytoplasm|peroxisome|biological_process|metabolic process|transferase activity|transferase activity, transferring acyl groups|transferase activity, transferring acyl groups other than amino-acyl groups|organelle
GRMZM2G139478	-1.099164549	1.41055323	0.019581461	1	Not Annotated	Not Annotated
GRMZM2G082906	0.769280705	3.75778413	0.01966659	1	Not Annotated	Not Annotated
GRMZM2G030128	-0.724242789	2.678310916	0.019705233	1	Rad50_eukaryotes|Zn_hook_Rad50	telomere maintenance|molecular_function|ATP binding|cellular_component|intracellular|cell|nucleus|cytoplasm|DNA metabolic process|DNA repair|double-strand break repair|mitotic recombination|response to stress|biological_process|telomere capping|Mre11 complex|cellular nitrogen compound metabolic process|organelle|protein complex
GRMZM2G089698	-0.735939286	2.04145975	0.019803264	1	Transferase	molecular_function|transferase activity|transferase activity, transferring acyl groups|transferase activity, transferring acyl groups other than amino-acyl groups
GRMZM2G132095	-1.665539036	1.273214742	0.019850946	1	Not Annotated	Not Annotated
GRMZM2G056419	-0.571449904	3.458641116	0.019936324	1	WD40_repeat|ARPC2/3_su1|WD40_repeat_dom	molecular_function|actin binding|protein binding|cellular_component|intracellular|cell|nucleus|cytoplasm|cytoskeleton|cytoskeletal protein binding|biological_process|regulation of actin filament polymerization|organelle
GRMZM2G440951	-0.628959079	3.191039282	0.019936483	1	Not Annotated	Not Annotated
GRMZM5G800842	-0.668201024	4.718327155	0.019952989	1	UBact_repeat|Molybdenum_cofac_synth_MoeB|Ub-activating_enz_e1_C	nucleotide binding|molecular_function|ATP binding|cellular protein modification process|biological_process|small protein activating enzyme activity
GRMZM2G052586	-1.141820087	1.695992102	0.020047335	1	Ribosomal_L35_non-mt|Ribosomal_L35	molecular_function|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|ribosome|translation|biological_process|biosynthetic process|organelle|ribonucleoprotein complex
GRMZM2G057408	-0.551867251	3.397890391	0.020161785	1	SANT/Myb|Myb_dom_plants|Homeodomain-like|Myb_dom	molecular_function|DNA binding|chromatin binding|response to stress|biological_process|response to salt stress|response to ethylene|response to auxin|response to abscisic acid|response to gibberellin|response to salicylic acid|response to jasmonic acid|response to cadmium ion

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G350265	-0.785401102	2.612803979	0.020187711	1	Not Annotated	Not Annotated
GRMZM2G159890	-0.621007209	3.26239791	0.020234173	1	Plipid/glycerol_acylTrfase|G3P_O-acylTrfase_chlp	molecular_function|glycerol-3-phosphate O-acyltransferase activity|cellular_component|intracellular|cell|cytoplasm|lipid metabolic process|glycerophospholipid metabolic process|phosphatidylglycerol biosynthetic process|biological_process|metabolic process|biosynthetic process|chloroplast|plastid|chloroplast stroma|transferase activity|transferase activity, transferring acyl groups|organelle
GRMZM2G095082	-0.580252176	2.825105584	0.020249326	1	Rhodanese-like_dom	cellular_component|intracellular|cell|cytoplasm|generation of precursor metabolites and energy|response to stress|biological_process|chloroplast|chloroplast thylakoid|chloroplast thylakoid membrane|plastid|thylakoid|photosynthetic electron transport in photosystem II|chloroplast envelope|photosynthesis|defense response to bacterium|organelle
GRMZM2G037146	-1.44209438	-0.361539482	0.020273175	1	a-crystallin/Hsp20_dom|HSP20-like_chaperone	Not Annotated
GRMZM2G704347	-1.468621593	0.27052566	0.020387599	1	Not Annotated	Not Annotated
GRMZM5G872499	-0.396413183	4.455875784	0.020450432	1	EXS_C	cellular_component|integral component of membrane
GRMZM2G149802	-0.296865432	5.123965495	0.020471093	1	DNA-dir_DNA_pol_B_pol2|DNA-dir_DNA_pol_B_exonuc|DNA-dir_DNA_pol_B_multi_dom|DNA-dir_DNA_pol_B|RNaseH-like_dom|Znf_DNA-dir_DNA_pol_B_alpha|DNA-dir_DNA_pol_B_CS|DNA_pol_a_cat_su_N	nucleotide binding|nucleoside binding|molecular_function|nucleic acid binding|DNA binding|DNA-directed DNA polymerase activity|nucleobase-containing compound metabolic process|DNA metabolic process|DNA replication|biological_process|biosynthetic process|nucleotidyltransferase activity|cellular nitrogen compound metabolic process
GRMZM2G088138	-2.549401359	-0.877808196	0.020486611	1	DUF3119	Not Annotated
GRMZM2G077181	-1.309185032	1.437626316	0.020614203	1	Glycosyl_hydrolases_36|Glycoside_hydrolase_SF	Not Annotated
GRMZM2G122954	-1.607752134	-0.371954721	0.020675735	1	BRO1_dom	cellular_component|intracellular|cell|cytoplasm|vacuole|organelle
GRMZM5G893864	-0.638348374	4.717877373	0.020719952	1	Cation_transp_P_typ_ATPase|ATPase_P-typ_cation-transptr_C|HAD-like_dom	molecular_function|cellular_component|transport|cation transport|biological_process|integral component of membrane|ATPase activity|cation-transporting ATPase activity|transmembrane transporter activity
GRMZM2G139846	-2.289708685	-1.192674193	0.020734685	1	Znf_ZZ	molecular_function|zinc ion binding|ion binding
GRMZM2G045259	-0.39728557	4.941507209	0.02079505	1	Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G305096	-0.82820131	0.936800356	0.020805736	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G052670	-0.376115685	4.841361061	0.02080878	1	Sec1-like	transport|vesicle docking involved in exocytosis|biological_process|vesicle-mediated transport|cellular_component|intracellular|cell|cytoplasm|vacuole|trans-Golgi network|intracellular protein transport|plant-type vacuole membrane|organelle
GRMZM2G071208	-0.502717017	5.892222855	0.020923663	1	Aminotrans_IV|B_amino_transII|Aminotrans_IV_CS	molecular_function|catalytic activity|branched-chain-amino-acid transaminase activity|cellular_component|intracellular|cell|cytoplasm|cellular amino acid metabolic process|biological_process|metabolic process|transaminase activity|branched-chain amino acid metabolic process|chloroplast|plastid|transferase activity|organelle|small molecule metabolic process|L-leucine transaminase activity|L-valine transaminase activity|L-isoleucine transaminase activity
GRMZM2G015923	-0.905183903	0.783912279	0.020961579	1	Glyco_trans_8	molecular_function|transferase activity, transferring glycosyl groups
GRMZM2G035821	-0.719720425	2.721787974	0.020977861	1	Znf_RING	molecular_function|protein binding|zinc ion binding|ion binding|metal ion binding
GRMZM2G163954	-1.217218349	2.92168359	0.021020182	1	Not Annotated	Not Annotated
GRMZM2G334239	-2.273244919	-0.781570611	0.021140811	1	Ribosomal_S4e_central_region	molecular_function|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|ribosome|translation|biological_process|biosynthetic process|organelle
GRMZM2G074241	-0.558243185	4.801933231	0.02118867	1	ABC_transporter-like|ABC_transporter_CS|ABC_Peroxi_TM	nucleotide binding|molecular_function|ATP binding|ATP catabolic process|biological_process|catabolic process|ATPase activity|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|small molecule metabolic process|cellular_component|transport|membrane
GRMZM2G335111	6.024278545	-1.546090948	0.021203742	1	Glyco_hydro_17|Glycoside_hydrolase_SF	molecular_function|catalytic activity|hydrolase activity, hydrolyzing O-glycosyl compounds|carbohydrate metabolic process|biological_process|metabolic process|hydrolase activity|hydrolase activity, acting on glycosyl bonds
GRMZM2G465257	-1.345180128	0.088430564	0.021210408	1	Not Annotated	Not Annotated
GRMZM2G105522	-1.408086385	2.366321823	0.021291201	1	DUF506_pln	Not Annotated
GRMZM2G106795	-0.542733425	4.744506626	0.021325344	1	Small_GTP-bd_dom|Small_GTPase_ARF/SAR|Small_GTPase_ARF	nucleotide binding|molecular_function|GTP binding|cellular_component|intracellular|cell|signal transduction|small GTPase mediated signal transduction|biological_process
GRMZM2G037648	-2.289708685	-1.233347303	0.021332325	1	Not Annotated	Not Annotated
GRMZM2G103825	-0.873210695	3.260902438	0.021366607	1	Amidase|Amidase_dom	molecular_function|ligase activity|carbon-nitrogen ligase activity, with glutamine as amido-N-donor
AC210303.3_FG001	-0.806892544	1.963232265	0.021401881	1	Not Annotated	chloroplast|thylakoid membrane organization|vegetative to reproductive phase transition of meristem|chloroplast membrane
AC155352.2_FG001	2.229478942	-1.205838819	0.021466043	1	Cactin_dom	Not Annotated
GRMZM2G023884	-0.523526619	3.304281097	0.021581389	1	Glyco_trans_ALG6/ALG8	molecular_function|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|endoplasmic reticulum membrane|transferase activity, transferring glycosyl groups|transferase activity, transferring hexosyl groups|organelle
GRMZM2G159542	-0.460038063	3.90690684	0.021611703	1	TPR_1|Amidase|TPR-contain_dom|TPR_repeat|Amidase_dom	molecular_function|protein binding|protein targeting to mitochondrion|ligase activity|carbon-nitrogen ligase activity, with glutamine as amido-N-donor
GRMZM2G090505	-0.355442614	4.719856312	0.02161974	1	EF_hand_dom|Caleosin	molecular_function|calcium ion binding|ion binding
GRMZM5G878153	-0.532133693	3.757105795	0.02164844	1	ASCH_domain|PUA-like_domain	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G087479	-0.841824195	1.228809553	0.02166693	1	Sub_transporter|Sugar_transporter_CS|MFS|MFS_dom_general_subst_transpt|MFS_dom	molecular_function|transporter activity|cellular_component|transport|biological_process|membrane|integral component of membrane|transmembrane transporter activity|transmembrane transport
GRMZM2G145012	-1.257654231	2.405727415	0.021699896	1	Not Annotated	Not Annotated
GRMZM2G115162	-0.482907224	2.085522544	0.021723175	1	Ankyrin_rpt|BTB/POZ-like|BTB/POZ_fold|Ankyrin_rpt-contain_dom|NPR1/NIM1-like_C|DUF3420	immune system process|molecular_function|protein binding|cellular_component|intracellular|cell|nucleus|response to stress|biological_process|response to bacterium|response to fungus|defense response to bacterium, incompatible interaction|defense response to fungus, incompatible interaction|defense response to bacterium|organelle|defense response to fungus|effector dependent induction by symbiont of host immune response|salicylic acid binding|regulation of jasmonic acid mediated signaling pathway|regulation of salicylic acid mediated signaling pathway
GRMZM2G123986	-0.489725986	6.897478469	0.021796043	1	TPR_1	molecular_function|protein binding|regulation of sulfur utilization|response to stress|biological_process|cellular response to sulfur starvation
GRMZM5G840699	-0.657318823	2.307754321	0.021859535	1	Cation_transp_P_typ_ATPase|ATPase_P-typ_Plipid-transp|ATPase_P-typ_transduc_dom_A|ATPase_P-typ_P_site|HAD-like_dom|ATPase_P-typ_cyto_domN	nucleotide binding|magnesium ion binding|molecular_function|phospholipid-translocating ATPase activity|ATP binding|cellular_component|transport|cation transport|biological_process|phospholipid transport|integral component of membrane|ATPase activity|cation-transporting ATPase activity|transmembrane transporter activity|ion binding|metal ion binding
GRMZM2G017845	-0.357055211	4.004194091	0.021958505	1	Ubiquitin-int_motif|Znf_LIM|DA1_like	reproduction|molecular_function|plasma membrane|biological_process|zinc ion binding|small conjugating protein binding|ubiquitin binding|ion binding|negative regulation of organ growth|metal ion binding|seed morphogenesis|ovule morphogenesis|anatomical structure development
GRMZM2G024739	-0.53279483	3.501952664	0.021978686	1	Photolyase_FAD-bd/Cryptochr_C|Cryptochrome/DNA_photolyase_1|DNA_photolyase_N|Cryptochrome_pln|DNA_photolyase_1_CS_C|Cryptochrome_C	molecular_function|DNA photolyase activity|protein kinase activity|signal transducer activity|ATP binding|cellular_component|intracellular|cell|nucleus|cytoplasm|DNA metabolic process|DNA repair|cellular protein modification process|response to stress|signal transduction|biological_process|cell death|response to water deprivation|detection of light stimulus|response to blue light|photomorphogenesis|blue light signaling pathway|blue light photoreceptor activity|regulation of meristem growth|stomatal movement|singlet oxygen-mediated programmed cell death|circadian regulation of calcium ion oscillation|kinase activity|lyase activity|secondary metabolic process|cellular nitrogen compound metabolic process|homeostatic process|protein homodimerization activity|organelle|anthocyanin-containing compound metabolic process|protein autophosphorylation|anatomical structure development|regulation of unidimensional cell growth|oxidation-reduction process
GRMZM5G817777	-1.358188787	0.260628547	0.022050097	1	Lipase_GDXG_AS|AB_hydrolase_3	molecular_function|biological_process|metabolic process|hydrolase activity
GRMZM2G088336	-1.457863857	1.123029233	0.022089954	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G179424	-0.425333276	3.774487274	0.022143305	1	WD40_repeat|WD40_repeat_dom|WD40_repeat_CS|DUF3639	molecular_function|protein binding
GRMZM2G348551	-0.454298714	6.69204655	0.022182791	1	Glyco_trans_1|Glycogen/starch_synth|Starch_synth_cat_dom	molecular_function|carbohydrate metabolic process|biological_process|starch synthase activity|biosynthetic process|glucan biosynthetic process|transferase activity, transferring glycosyl groups
GRMZM2G038532	-0.472671393	4.194650943	0.022183874	1	DUF829_TMEM53	Not Annotated
GRMZM2G132810	-0.695449029	4.674141591	0.022270082	1	FH2_Formin	molecular_function|actin binding|cytoskeleton organization|cytoskeletal protein binding|biological_process|cellular component organization|actin cytoskeleton organization
GRMZM2G051270	-0.358354524	5.60458832	0.022279589	1	Sulphate_adenylyltransferase|PUA-like_domain|Sulfurylase_cat_dom|ATP-Sase_PUA-like_dom	sulfate assimilation|molecular_function|sulfate adenylyltransferase (ATP) activity|cellular_component|intracellular|cell|cytoplasm|mitochondrion|plasma membrane|sulfur compound metabolic process|biological_process|chloroplast|plastid|chloroplast stroma|nucleotidyltransferase activity|organelle|response to cadmium ion
GRMZM2G110483	-0.689256367	1.563391976	0.022290442	1	Pentatricopeptide_repeat	Not Annotated
GRMZM2G128056	-0.464923169	7.060276755	0.022298834	1	Peptidase_S10|Peptidase_S10_AS	molecular_function|carboxypeptidase activity|serine-type carboxypeptidase activity|cellular_component|intracellular|cell|cytoplasm|vacuole|proteolysis|biological_process|peptidase activity|organelle
GRMZM2G156356	-0.488135967	4.110057178	0.022337177	1	Not Annotated	maltose metabolic process|molecular_function|maltose transmembrane transporter activity|cellular_component|intracellular|cell|cytoplasm|carbohydrate metabolic process|starch catabolic process|transport|cell communication|multicellular organismal development|biological_process|catabolic process|plastid|response to nematode|response to gravity|chloroplast inner membrane|chloroplast envelope|maltose transport|transmembrane transporter activity|organelle
GRMZM2G038916	-2.098381624	-0.900565958	0.022372163	1	Not Annotated	Not Annotated
GRMZM2G007757	-0.560312819	3.01503066	0.022395777	1	Ketoacyl_synth_N|Ketoacyl_synth_C|Thiolase-like|3-oxoacyl-ACP_synth-2|Ketoacyl_synth_AS	molecular_function|catalytic activity|lipid metabolic process|fatty acid biosynthetic process|biological_process|metabolic process|biosynthetic process|transferase activity|transferase activity, transferring acyl groups|transferase activity, transferring acyl groups other than amino-acyl groups|small molecule metabolic process
GRMZM2G031001	-0.569821881	2.997362294	0.022397387	1	NAC-dom	molecular_function|DNA binding|regulation of transcription, DNA-templated|biological_process
GRMZM2G071076	-0.59900308	4.244207828	0.022431879	1	Choline_transptr-like	cellular_component|membrane|integral component of membrane

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G080603	-0.605332963	13.70922407	0.022534127	1	RRM_dom	reproduction|nucleotide binding|alternative mRNA splicing, via spliceosome|immune system process|molecular_function|nucleic acid binding|DNA binding|double-stranded DNA binding|single-stranded DNA binding|mRNA binding|cellular_component|cell wall|intracellular|cell|nucleus|nucleolus|cytoplasm|peroxisome|cytosol|plasma membrane|DNA metabolic process|mRNA export from nucleus|transport|nucleocytoplasmic transport|response to stress|response to osmotic stress|circadian rhythm|biological_process|response to cold|response to water deprivation|plasmodesma|chloroplast|plastid|response to salt stress|response to abscisic acid|response to zinc ion|regulation of stomatal movement|vegetative to reproductive phase transition of meristem|RNA secondary structure unwinding|external encapsulating structure|DNA duplex unwinding|cellular nitrogen compound metabolic process|organelle|innate immune response|response to cadmium ion|apoplast|anatomical structure development
GRMZM2G358236	-1.280769633	1.277425092	0.0225829	1	DNA-dir_DNA_pol_B_mt/vir|Ribosomal_S12_bac|Ribosomal_S12/S23|NA-bd_OB-fold	nucleotide binding|molecular_function|DNA binding|DNA-directed DNA polymerase activity|nuclease activity|DNA metabolic process|DNA replication|biological_process|3'-5' exonuclease activity|biosynthetic process|nucleotidyltransferase activity|cellular nitrogen compound metabolic process|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|mitochondrion|ribosome|translation|small ribosomal subunit|ribonucleoprotein complex|organelle
GRMZM2G109987	-0.436444797	3.877515878	0.022587792	1	START_lipid-bd_dom|Homeobox_dom|Homeodomain-like|MEKHLA	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|cellular_component|intracellular|cell|nucleus|regulation of transcription, DNA-templated|biological_process|determination of bilateral symmetry|polarity specification of adaxial/abaxial axis|radial pattern formation|meristem initiation|xylem and phloem pattern formation|cell differentiation|organelle|sequence-specific DNA binding|anatomical structure development
GRMZM2G136366	-0.767806178	2.073208825	0.022659259	1	Fmu/NOL1/Nop2p|Fmu/NOL1/Nop2p_CS|RCMT|RCMT_NCL1	molecular_function|RNA binding|methyltransferase activity
GRMZM2G355572	-1.642497133	0.946787949	0.022683639	1	Not Annotated	cellular_component|intracellular|cell|cytoplasm|plasma membrane|chloroplast|plastid|membrane|organelle
GRMZM2G536120	3.440428197	-1.309729367	0.022716754	1	Ankyrin_rpt|TPR_2|TPR_repeat|Ankyrin_rpt-contain_dom	molecular_function|protein binding
GRMZM2G000937	-0.793010899	4.063120986	0.022727989	1	GPI_mannosylTrfase	molecular_function|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|cellular protein modification process|GPI anchor biosynthetic process|lipid metabolic process|biological_process|biosynthetic process|transferase activity, transferring glycosyl groups|intrinsic component of endoplasmic reticulum membrane|organelle
GRMZM2G428676	-7.048957178	-0.895205386	0.022866782	1	Not Annotated	Not Annotated
GRMZM2G086496	-0.509203126	3.529398007	0.022941065	1	POT_fam|MFS_dom_general_subst_transpt|PTR2_symporter_CS	molecular_function|transporter activity|cellular_component|cell|plasma membrane|transport|oligopeptide transport|response to stress|biological_process|response to water deprivation|response to nitrate|nitrate transmembrane transporter activity|nitrate transport|membrane|integral component of membrane|transmembrane transporter activity

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G336337	4.027699685	-1.718568738	0.022948362	1	Cu_oxidase_Cu_BS|Cu-oxidase|Cupredoxin|Cu-oxidase_2|Cu-oxidase_3|Laccase	molecular_function|copper ion binding|cellular_component|extracellular region|biological_process|catabolic process|oxidoreductase activity|secondary metabolic process|ion binding|lignin catabolic process|response to copper ion|metal ion binding|apoplast|hydroquinone:oxygen oxidoreductase activity|oxidation-reduction process
GRMZM2G471529	-0.341943648	2.961430442	0.023009976	1	Sig_transdc_His_kin-like_C|EnvZ-like_dim/P|HATPase_ATP-bd|Sig_transdc_resp-reg_receiver|Sig_transdc_His_kinase_core|CHASE|Sig_transdc_His_kinase_dimeric|CheY-like_superfamily	phosphorelay sensor kinase activity|phosphorelay response regulator activity|phosphorelay signal transduction system|molecular_function|signal transducer activity|osmosensor activity|ATP binding|cellular_component|cell|plasma membrane|regulation of transcription, DNA-templated|response to stress|response to osmotic stress|signal transduction|aging|biological_process|response to cold|response to water deprivation|response to salt stress|regulation of seed germination|leaf senescence|regulation of chlorophyll catabolic process|membrane|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups|signal transduction by phosphorylation|intracellular signal transduction|defense response to bacterium|regulation of shoot system development|anatomical structure development
GRMZM2G102196	-0.400360753	3.455134337	0.023050435	1	Not Annotated	cytosol
GRMZM2G047347	-1.16962564	2.106228702	0.023079672	1	Aminotrans_IV|B_amino_transII|Aminotrans_IV_CS	molecular_function|catalytic activity|branched-chain-amino-acid transaminase activity|cellular_component|intracellular|cell|cytoplasm|cellular amino acid metabolic process|biological_process|metabolic process|transaminase activity|branched-chain amino acid metabolic process|chloroplast|plastid|transferase activity|organelle|small molecule metabolic process|L-leucine transaminase activity|L-valine transaminase activity|L-isoleucine transaminase activity
GRMZM2G007252	1.37577658	1.394229729	0.023243512	1	3Beta_OHSteriod_DH/Estase	nucleotide binding|molecular_function|3-beta-hydroxy-delta5-steroid dehydrogenase activity|lipid metabolic process|steroid biosynthetic process|biological_process|biosynthetic process|oxidoreductase activity|oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor|oxidation-reduction process
GRMZM2G087243	1.035841007	1.842825123	0.023263934	1	Armadillo|ARM-type_fold	molecular_function|binding|protein binding
GRMZM2G088737	-0.403767866	3.611770695	0.023293615	1	Ost-alpha	Not Annotated
GRMZM2G460617	-3.185007782	-1.877044291	0.023311472	1	Not Annotated	Not Annotated
GRMZM2G359365	-0.474915596	4.432360754	0.02332386	1	Cation_transp_P_typ_ATPase|HAD-like_dom	molecular_function|cellular_component|endoplasmic reticulum|plasma membrane|ATP catabolic process|transport|cation transport|cellular metal ion homeostasis|biological_process|catabolic process|pollen germination|meristem maintenance|pollen maturation|integral component of membrane|cellular response to phosphate starvation|ATPase activity|cation-transporting ATPase activity|transmembrane transporter activity|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|small molecule metabolic process|stem cell fate determination

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G441347	0.708380592	5.684284182	0.023334915	1	Aromatic_Lyase|Phe_NH3-lyase|L-Aspartase-like|Phe/His_NH3-lyase_AS	molecular_function|catalytic activity|cellular_component|intracellular|cell|cytoplasm|cellular amino acid metabolic process|L-phenylalanine catabolic process|biological_process|catabolic process|biosynthetic process|phenylpropanoid metabolic process|cinnamic acid biosynthetic process|lyase activity|ammonia-lyase activity|secondary metabolic process|small molecule metabolic process|phenylalanine ammonia-lyase activity
GRMZM2G494514	-0.461283796	4.022948518	0.023368851	1	VWF_A|C2_dom|Copine	molecular_function|protein binding|calcium-dependent phospholipid binding|cellular_component|cell|plasma membrane|biological_process|response to temperature stimulus|response to humidity|plasmodesma|positive regulation of cell size|negative regulation of cell death
GRMZM2G472023	-0.490483828	3.445150415	0.023371254	1	TPR_1|TPR-contain_dom|TPR_repeat	G2/M transition of mitotic cell cycle|molecular_function|protein binding|cell cycle|biological_process|regulation of meristem structural organization|meristem structural organization|membrane|cell division
GRMZM5G873767	0.813175217	3.536042029	0.02337777	1	Lipase_GDSL	molecular_function|lipid metabolic process|biological_process|hydrolase activity|hydrolase activity, acting on ester bonds
GRMZM2G317770	-0.457010079	3.623144351	0.023452583	1	Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	nucleotide binding|immune system process|cell surface pattern recognition receptor signaling pathway|molecular_function|protein kinase activity|protein serine/threonine kinase activity|signal transducer activity|ATP binding|cellular_component|cell|plasma membrane|cellular protein modification process|protein phosphorylation|response to stress|signal transduction|biological_process|defense response to fungus, incompatible interaction|response to chitin|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups|transmembrane receptor protein kinase activity|detection of molecule of fungal origin|detection of peptidoglycan|intracellular signal transduction|defense response to bacterium|protein homodimerization activity|innate immune response|protein autophosphorylation|cellular response to molecule of bacterial origin|cellular response to chitin|chitosan binding
GRMZM5G818431	-0.787726374	1.523930353	0.023467622	1	Kinase-like_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Protein_kinase_ATP_BS|Ser-Thr/Tyr_kinase_cat_dom|UspA	molecular_function|transferase activity, transferring phosphorus-containing groups|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|response to stress
GRMZM2G024615	-0.574496686	3.218657533	0.02354106	1	P_Acid_Pase_2/haloperoxidase	molecular_function|catalytic activity|cellular_component|biological_process|metabolic process|membrane|plasma membrane|phosphatidate phosphatase activity|abscisic acid-activated signaling pathway
GRMZM2G312543	-0.944391991	3.331236182	0.023599165	1	Not Annotated	Not Annotated
GRMZM2G529530	-1.992661944	-0.161751319	0.023638724	1	Not Annotated	Not Annotated
GRMZM2G069201	-0.583535831	2.88512334	0.023820822	1	Leu-rich_rpt|Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|LRR-contain_N2|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|protein binding|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G162369	-0.745093728	2.298340071	0.023883636	1	Not Annotated	cellular_component|intracellular|cell|cytoplasm|ribosome|organelle

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G061910	-2.826521499	-1.342885699	0.024126274	1	LEA-14	Not Annotated
GRMZM2G044472	6.214150217	-1.796008288	0.024214392	1	LACT/PDAT_acylTrfase	molecular_function|lipid metabolic process|biological_process|O-acyltransferase activity|transferase activity, transferring acyl groups
GRMZM2G037478	-5.762285887	-1.844264417	0.024249838	1	AB_hydrolase_3	molecular_function|biological_process|metabolic process|hydrolase activity
GRMZM2G017193	-2.188514363	-0.094835559	0.024323261	1	Pyridine_nuc-diS_OxRdtase_2|FAD_pyr_nucl-diS_OxRdtase|Flavin_mOase-like	molecular_function|N,N-dimethylaniline monooxygenase activity|biological_process|biosynthetic process|auxin biosynthetic process|oxidoreductase activity|flavin adenine dinucleotide binding|NADP binding|oxidation-reduction process
GRMZM2G036872	-0.450007624	4.012553519	0.024337484	1	Pleckstrin_homology|RhoGAP_dom|Rho_GTPase_activation_prot|MIP1_Leuzipper	molecular_function|protein binding|phospholipid binding|cellular_component|intracellular|cell|signal transduction|biological_process|lipid binding
GRMZM2G464572	6.532186565	-1.609474061	0.024487255	1	UBQ-conjugat_E2|UBQ conjugating_enzyme/RWD	molecular_function|transport|phosphate ion transport|response to stress|biological_process|cellular response to phosphate starvation|ligase activity|acid-amino acid ligase activity|homeostatic process|phosphate ion homeostasis
GRMZM2G041847	-0.526378591	2.939539859	0.024519157	1	Not Annotated	Not Annotated
GRMZM2G044697	-0.443066025	3.305537882	0.024570227	1	Peptidase_M50	molecular_function|metalloendopeptidase activity|proteolysis|biological_process|peptidase activity|cellular_component|intracellular|cell|cytoplasm|chloroplast|chloroplast thylakoid membrane|plastid|thylakoid|organelle
GRMZM2G038722	-2.359144022	-1.030240221	0.024656997	1	SANT/Myb|Homeodomain-like|Myb_dom	molecular_function|DNA binding|chromatin binding
GRMZM2G177532	-0.608958612	3.818722294	0.024662403	1	Cation_efflux	molecular_function|cellular_component|transport|cation transport|biological_process|cation transmembrane transporter activity|integral component of membrane|transmembrane transporter activity|transmembrane transport
GRMZM2G079823	-0.591469165	5.201609739	0.024720447	1	KH_dom	molecular_function|RNA binding|protein binding|cellular_component|intracellular|cell|nucleus|organelle
GRMZM5G854948	-0.735227556	2.555065591	0.024796594	1	NOTUM	Not Annotated
GRMZM2G053766	-0.425247216	4.008970067	0.024811534	1	APC4_long_dom|WD40_repeat|WD40_repeat_dom|Apc4_WD40_dom	cellular_component|intracellular|cell|nucleus|anaphase-promoting complex|biological_process|catabolic process|embryo development|regulation of mitotic metaphase/anaphase transition|anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process|organelle|protein complex|ovule development|molecular_function|protein binding
GRMZM2G029243	-0.73858826	4.122270425	0.024895144	1	Glyco_hydro_31|Gal_mutarotase_SF_dom|Glycoside_hydrolase_SF	molecular_function|catalytic activity|hydrolase activity, hydrolyzing O-glycosyl compounds|carbohydrate metabolic process|biological_process|hydrolase activity, acting on glycosyl bonds|carbohydrate binding
GRMZM2G174782	-1.767278816	-0.675765693	0.024907833	1	Lipase_GDSL	molecular_function|lipid metabolic process|biological_process|hydrolase activity|hydrolase activity, acting on ester bonds
GRMZM2G123969	-5.66464753	-1.842930537	0.024923745	1	Ribosomal_L7Ae/L30e/S12e/Gad45|Ribosomal_L30e_CS	plasma membrane|plasmodesma|response to fungus|cytosolic large ribosomal subunit|cytosolic ribosome
AC202185.4_FG004	-0.898381211	2.136841437	0.024955052	1	a-crystallin/Hsp20_dom|HSP20-like_chaperone	Not Annotated
GRMZM2G434514	-1.112880329	2.914501235	0.02500821	1	LysM_dom	biological_process|catabolic process|cell wall macromolecule catabolic process|cell wall organization or biogenesis

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G015955	-0.518292029	5.681577553	0.025025983	1	Zn/Fe_permease_fun/pln|ZIP	molecular_function|copper ion transmembrane transporter activity|iron ion transmembrane transporter activity|zinc ion transmembrane transporter activity|cellular_component|cell|vacuolar membrane|plasma membrane|transport|iron ion transport|zinc ion transport|biological_process|response to nematode|response to zinc ion|membrane|integral component of membrane|transmembrane transporter activity|metal ion transport|iron ion transmembrane transport|copper ion transmembrane transport|metal ion transmembrane transporter activity|transmembrane transport|zinc ion transmembrane transport
GRMZM2G463167	-1.658304763	2.995875078	0.025124657	1	Not Annotated	Not Annotated
GRMZM2G158647	-0.561664526	3.124442616	0.025159453	1	Not Annotated	Not Annotated
GRMZM2G147619	-0.471603279	3.232185208	0.025198694	1	Post-SET_dom|SET_dom|AWS	molecular_function|protein binding|cellular_component|intracellular|cell|nucleus|methyltransferase activity|histone-lysine N-methyltransferase activity|organelle|reproduction|DNA repair|cellular protein modification process|biological_process|response to UV-B|vegetative to reproductive phase transition of meristem|histone methylation|transferase activity|methylation|histone lysine methylation|anatomical structure development|chromosome organization
GRMZM2G055219	-0.607962638	2.962833396	0.025199956	1	Golgin_subfamily_A_member_5	cellular_component|intracellular|cell|cytoplasm|Golgi apparatus|organelle
GRMZM2G362021	-2.170387635	0.23815453	0.025260073	1	D-isomer_2_OHA_DH_cat_dom|D-isomer_2_OHA_DH_NAD-bd	nucleotide binding|molecular_function|biological_process|metabolic process|oxidoreductase activity|oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor|cofactor binding|NAD binding|oxidation-reduction process
GRMZM2G099984	1.735134872	1.302120687	0.02537094	1	PMP3	cellular_component|response to stress|biological_process|response to cold|integral component of membrane|hyperosmotic salinity response
GRMZM2G119867	-0.597045211	3.751968318	0.025427671	1	Not Annotated	Not Annotated
GRMZM2G041527	-0.94072921	0.986600296	0.025439997	1	RNase_P/MRP_POP1|POPLD	tRNA 5'-leader removal|molecular_function|nuclease activity|ribonuclease P activity|rRNA processing|RNA processing|tRNA metabolic process|biological_process|cellular nitrogen compound metabolic process
GRMZM2G139977	-0.440255506	4.546585358	0.025461229	1	Znf_ZZ|Znf_TAZ|Znf_FYVE_PHD|Histone_H3-K56_AcTrfase_RTT109|Zinc_finger_PHD-type_CS	protein binding transcription factor activity|molecular_function|transcription cofactor activity|histone acetyltransferase activity|cellular_component|intracellular|cell|nucleus|regulation of transcription, DNA-templated|cellular protein modification process|protein acetylation|biological_process|zinc ion binding|flower development|histone acetylation|transferase activity, transferring acyl groups|ion binding|organelle|chromosome organization
GRMZM2G038252	-6.306344777	-0.48937641	0.025462648	1	Homeobox_dom|Homeodomain-like	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|cellular_component|intracellular|cell|nucleus|regulation of transcription, DNA-templated|biological_process|organelle|sequence-specific DNA binding
GRMZM2G304926	5.919067406	-1.999071664	0.025462818	1	Not Annotated	Not Annotated
GRMZM2G304548	-0.752808504	11.62784874	0.02552234	1	Allergen/tryp_amyl_inhib_CS|Allergen/soft/tryp_amyl_inhib|Bifunc_inhib/LTP/seed_store	molecular_function|serine-type endopeptidase inhibitor activity|cellular_component|extracellular region|biological_process|negative regulation of peptidase activity|enzyme regulator activity|peptidase inhibitor activity

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G019177	-2.216761781	-1.209109358	0.025622764	1	Beta-lactamas-like	molecular_function|biological_process|hydrolase activity|response to arsenic-containing substance
GRMZM2G103070	-0.659857925	2.605137626	0.025639262	1	Leu-rich_rpt|Prot_kinase_dom|Kinase-like_dom|LRR-contain_N2	molecular_function|protein kinase activity|protein binding|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM5G885445	-1.112221242	2.294655082	0.025743292	1	Not Annotated	Not Annotated
GRMZM2G162640	0.56466241	3.801515446	0.025861071	1	BTB/POZ-like|BTB/POZ_fold	molecular_function|protein binding
GRMZM2G341405	-0.959895528	4.416661988	0.025900751	1	UBQ-conjugat_E2|RWD-domain|UBQ-conjugating_enzyme/RWD|PPase-energised_H-pump|Sig_transdc_resp-reg_receiver|CheY-like_superfamily|Alfin	molecular_function|protein binding|ligase activity|acid-amino acid ligase activity|phosphorelay response regulator activity|phosphorelay signal transduction system|inorganic diphosphatase activity|signal transducer activity|cellular_component|regulation of transcription, DNA-templated|transport|signal transduction|biological_process|hydrogen-translocating pyrophosphatase activity|proton transport|membrane|transmembrane transporter activity
GRMZM2G026203	-1.368096432	0.518077816	0.025922588	1	Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G450659	-0.629297826	3.329119769	0.025984753	1	Pept_M3A_M3B	molecular_function|metalloendopeptidase activity|proteolysis|biological_process|peptidase activity|cellular_component|intracellular|cell|cytoplasm|metallopeptidase activity|chloroplast|chloroplast thylakoid membrane|plastid|thylakoid|hydrolase activity|ion binding|organelle|metal ion binding
GRMZM2G171068	-0.525875509	3.20908313	0.026071125	1	Znf_CW	molecular_function|zinc ion binding|ion binding
GRMZM5G848838	3.837828013	-1.895590415	0.026143058	1	Not Annotated	Not Annotated
GRMZM2G016281	-0.846192224	1.139933772	0.026233281	1	DnaJ_C|HSP40/DnaJ_pept-bd	molecular_function|protein folding|biological_process|unfolded protein binding
GRMZM2G175423	-0.498101761	11.89289719	0.02623579	1	ADH_Zn_CS|GroES-like|ADH_C|ADH_GroES-like	nucleotide binding|molecular_function|L-iditol 2-dehydrogenase activity|cytoplasm|biological_process|zinc ion binding|plasmodesma|oxidoreductase activity|ion binding|metal ion binding|oxidation-reduction process
GRMZM5G862101	-0.597505335	2.182680536	0.026314817	1	TB2_DP1_HVA22	response to stress|biological_process|response to cold|response to water deprivation|response to abscisic acid|hyperosmotic salinity response
GRMZM2G301553	-1.209559776	0.631493606	0.026406922	1	aa-tRNA-synth_I_CS|DUF1279|NA-bd_OB-fold	nucleotide binding|molecular_function|aminoacyl-tRNA ligase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|tRNA metabolic process|translation|tRNA aminoacylation for protein translation|cellular amino acid metabolic process|biological_process|biosynthetic process|ligase activity|cellular nitrogen compound metabolic process|small molecule metabolic process
GRMZM2G451366	-0.37430401	5.502736486	0.026492111	1	Nicastrin|Nicalin|EF_Hand_1_Ca_BS	cellular_component|intracellular|cell|cytoplasm|mitochondrion|vacuole|endoplasmic reticulum|plasma membrane|biological_process|regulation of signal transduction|membrane|integral component of membrane|protein processing|organelle|protein maturation

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G051406	-1.245752356	2.512565755	0.026533596	1	Not Annotated	Not Annotated
GRMZM2G323754	-0.431943988	4.862718539	0.026543555	1	Uncharacterised_FPL	Not Annotated
GRMZM2G158024	-0.397760511	3.813606749	0.026577181	1	KH_dom_type_2|GTP-bd_Era|KH_prok-type|Small_GTP-bd_dom|GTP_binding_domain	nucleotide binding|molecular_function|RNA binding|GTP binding|cellular_component|intracellular|cell|cytoplasm|chloroplast|plastid|organelle
GRMZM2G376959	-6.969409266	-1.357117882	0.026618124	1	WD40_repeat|WD40_repeat_dom|WD40_repeat_CS|G-protein_beta_WD-40_rep	molecular_function|protein binding
GRMZM2G127230	-0.749176671	1.868373891	0.026688122	1	SRP_Ffh|Signal_recog_particle_SRP54_M|AAA+_ATPase|SRP54_GTPase_dom|Signal_recog_particl_SRP54_hlx	nucleotide binding|molecular_function|RNA binding|GTPase activity|GTP binding|cellular_component|intracellular|cell|cytoplasm|GTP catabolic process|protein targeting|SRP-dependent cotranslational protein targeting to membrane|transport|biological_process|7S RNA binding|catabolic process|nucleoside-triphosphatase activity|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|small molecule metabolic process|signal recognition particle
GRMZM2G130064	-0.433794702	4.218881085	0.026786772	1	Bac_surfAg_D15|Surface_Ag_variable_number	cellular_component|mitochondrion|chloroplast organization|chloroplast envelope|outer membrane
GRMZM2G026143	-1.088206334	1.112476982	0.02686043	1	Not Annotated	Not Annotated
GRMZM2G421256	-0.643017549	2.009285603	0.026901958	1	SANT/Myb|Myb_dom_plants|Homeodomain-like	molecular_function|DNA binding|chromatin binding
GRMZM2G405476	5.919067406	-1.706369139	0.026947065	1	Ribosomal_L2_bac/org-type|Translation_prot_SH3-like|Ribosomal_L2_C|Ribosomal_L2_CS	molecular_function|RNA binding|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|ribosome|translation|biological_process|biosynthetic process|chloroplast|plastid|large ribosomal subunit|membrane|transferase activity|rRNA binding|ribonucleoprotein complex|organelle
GRMZM2G099238	-1.39489665	3.524433471	0.026984877	1	Znf_RING	molecular_function|protein binding|zinc ion binding|ion binding|metal ion binding
GRMZM2G004412	-0.782325147	1.173480759	0.027001448	1	NB-ARC|Disease_R	molecular_function|response to stress|defense response|biological_process|ADP binding
GRMZM5G846506	-1.972778718	-1.37223668	0.027008246	1	SANT/Myb|Myb_dom_plants|Homeodomain-like|Myb_dom	molecular_function|DNA binding|chromatin binding
GRMZM2G067028	-0.421183358	3.232667772	0.027151553	1	Glyas_Fos-R_dOase_dom	molecular_function|cellular_component|intracellular|cell|cytoplasm|chloroplast|plastid|oxidoreductase activity|oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen|organelle
GRMZM2G347743	-0.409486048	4.022121407	0.02725666	1	Peptidase_S10|Peptidase_S10_AS	molecular_function|carboxypeptidase activity|serine-type carboxypeptidase activity|proteolysis|biological_process|peptidase activity
GRMZM2G117612	-0.516785434	4.624566845	0.027401102	1	CUE|Znf_RING	molecular_function|protein binding|zinc ion binding|ion binding
GRMZM2G098828	-0.375347362	3.189541465	0.027563412	1	Ser/Thr_dual-sp_kinase_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G398288	-0.439983753	4.186100301	0.027711291	1	Cation_transp_P_typ_ATPase|ATPase_P-typ_Plipid-transp|ATPase_P-typ_transduc_dom_A|ATPase_P-typ_P_site|HAD-like_dom|ATPase_P-typ_cyto_domN	nucleotide binding|magnesium ion binding|molecular_function|phospholipid-translocating ATPase activity|ATP binding|cellular_component|transport|cation transport|biological_process|phospholipid transport|membrane|integral component of membrane|hydrolase activity|ATPase activity|cation-transporting ATPase activity|transmembrane transporter activity|ion binding|metal ion binding
GRMZM2G060886	-0.614476872	5.325276226	0.027801546	1	Methyltransf_11|Phosphoethanolamine_N-MeTrfase	molecular_function|biological_process|metabolic process|methyltransferase activity|methylation|reproduction|phosphoethanolamine N-methyltransferase activity|cell morphogenesis|lipid metabolic process|phosphatidylcholine biosynthetic process|biosynthetic process|pollen development|unidimensional cell growth|pollen tube growth|pollen tube guidance|transferase activity|cell differentiation|cellular nitrogen compound metabolic process|growth|locomotion|choline biosynthetic process|small molecule metabolic process|post-embryonic root development|anatomical structure development
GRMZM2G056612	-0.322316535	3.937569415	0.02790537	1	Ser/Thr_dual-sp_kinase_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|calcium ion binding|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups|ion binding
GRMZM2G046681	-0.430272148	3.452866029	0.02797513	1	MFS|MFS_dom_general_subst_transpt|MFS_dom	molecular_function|inorganic phosphate transmembrane transporter activity|cellular_component|intracellular|cell|cytoplasm|transport|biological_process|chloroplast|plastid|chloroplast envelope|integral component of membrane|transmembrane transporter activity|organelle|transmembrane transport
GRMZM2G120047	-0.572967104	4.80304653	0.028031523	1	Proteasome_sua/b|Proteasome_asu_N|Proteasome_suA-type	proteasome complex|molecular_function|endopeptidase activity|threonine-type endopeptidase activity|cellular_component|intracellular|cell|nucleus|cytoplasm|vacuole|cytosol|proteasome core complex|ribosome|proteolysis|ubiquitin-dependent protein catabolic process|biological_process|peptidase activity|catabolic process|hydrolase activity|proteasome core complex, alpha-subunit complex|cytosolic ribosome|organelle|protein complex|response to cadmium ion|proteolysis involved in cellular protein catabolic process
GRMZM2G145063	-0.535371127	5.503725248	0.028047294	1	Peptidase_M28	molecular_function|proteolysis|biological_process|peptidase activity
GRMZM2G047851	-2.273244919	-0.876291198	0.028053167	1	Cdc6_C_dom	Not Annotated
GRMZM5G830932	-0.476555549	3.397557935	0.028066819	1	RNA_pol_sigma70|RNA_pol_sigma70_r3|RNA_pol_sigma70_r2|RNA_pol_sigma70_r4|RNA_pol_sigma_r3_r4|RNA_pol_sigma_r2|RNA_pol_sigma-70_dom|RNA_pol_sigma_SigB/C/D_plastid	protein binding transcription factor activity|nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|DNA-templated transcription, initiation|regulation of transcription, DNA-templated|biological_process|biosynthetic process|sigma factor activity|cellular nitrogen compound metabolic process|plastid sigma factor activity|DNA-directed RNA polymerase activity|cellular response to light stimulus|regulation of RNA biosynthetic process
GRMZM2G023946	-0.737995417	2.220225281	0.028102713	1	DUF1624	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G071626	-0.459673257	3.96727008	0.02813311	1	Mediator_Med11	protein binding transcription factor activity|RNA polymerase II transcription cofactor activity|molecular_function|cellular_component|intracellular|cell|nucleus|nucleoplasm|regulation of transcription from RNA polymerase II promoter|biological_process|mediator complex|organelle|protein complex
GRMZM2G112030	-6.306344777	-1.637543974	0.028151587	1	Cyt_b/b6_N|Cyt_b/b6_C|Di-haem_cyt_TM	molecular_function|cellular_component|intracellular|cell|cytoplasm|mitochondrion|mitochondrial inner membrane|mitochondrial respiratory chain complex III|generation of precursor metabolites and energy|mitochondrial electron transport, ubiquinol to cytochrome c|ubiquinol-cytochrome-c reductase activity|biological_process|electron carrier activity|membrane|integral component of membrane|oxidoreductase activity|transmembrane transporter activity|electron transport chain|respiratory electron transport chain|ion binding|organelle|protein complex|metal ion binding|respiratory chain
GRMZM2G058039	-0.361672009	5.823374326	0.028244415	1	RRM_dom	molecular_function|nucleic acid binding
GRMZM2G128809	-0.518331333	3.423674577	0.028244751	1	RRM_dom	nucleotide binding|molecular_function|nucleic acid binding
GRMZM2G001853	0.426996331	4.291772553	0.0282895	1	Not Annotated	Not Annotated
GRMZM5G823629	-0.412758153	4.473676776	0.028299084	1	Tpt_PEP_trans_dom|UAA	Golgi membrane|molecular_function|nucleotide-sugar transmembrane transporter activity|cellular_component|intracellular|cell|cytoplasm|Golgi apparatus|plasma membrane|transport|biological_process|nucleotide-sugar transport|membrane|integral component of membrane|transmembrane transporter activity|organelle|transmembrane transport
GRMZM2G005844	-0.742272614	2.546426419	0.028302381	1	DNA_methylase_N6_adenine_CS|MT-A70-like	molecular_function|nucleic acid binding|nucleobase-containing compound metabolic process|biological_process|methyltransferase activity|methylation|cellular nitrogen compound metabolic process
GRMZM2G488726	-2.425390406	-1.215854047	0.028302735	1	Not Annotated	Not Annotated
GRMZM2G408598	-0.619735802	4.143571725	0.028371703	1	ARM-type_fold|IPI1/TEX10	molecular_function|binding
GRMZM2G119411	-0.31904299	4.999938316	0.028450059	1	Peptidase_M28	molecular_function|endoplasmic reticulum|proteolysis|biological_process|peptidase activity
GRMZM2G162093	-1.393065149	0.518050204	0.028688634	1	Not Annotated	Not Annotated
GRMZM2G054378	-0.920543216	2.560231495	0.028713191	1	tRNA_(Gua-N-7)_MeTrfase|Coatomer/clathrin_app_Ig-like	molecular_function|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|Golgi apparatus|Golgi-associated vesicle|tRNA metabolic process|tRNA modification|transport|intracellular protein transport|biological_process|methyltransferase activity|tRNA (guanine-N7-)-methyltransferase activity|cytoplasmic membrane-bounded vesicle|vesicle-mediated transport|cellular nitrogen compound metabolic process|organelle|RNA (guanine-N7)-methylation
GRMZM5G831887	-0.652290106	2.159088018	0.028717195	1	HATPase_ATP-bd|Heat_shock_protein_90_CS|Hsp90_N	molecular_function|ATP binding|protein folding|response to stress|biological_process|unfolded protein binding
GRMZM2G050460	-0.510117126	5.366934231	0.028756102	1	Ribosomal_L7Ae/L30e/S12e/Gad45|Ribosomal_L30e_CS	molecular_function|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|cytosol|ribosome|translation|biological_process|biosynthetic process|cytosolic large ribosomal subunit|cytosolic ribosome|organelle

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G001799	-0.865551734	2.147125338	0.028879713	1	AUX_IAA|AuxIAA_ARF_dimer	molecular_function|cellular_component|intracellular|cell|nucleus|transcription, DNA-templated|regulation of transcription, DNA-templated|signal transduction|biological_process|biosynthetic process|auxin-activated signaling pathway|cellular nitrogen compound metabolic process|organelle|protein dimerization activity
GRMZM2G003979	-0.499647231	5.075091189	0.028924356	1	Znf_RING	molecular_function|protein binding|zinc ion binding|ion binding
GRMZM2G115564	-0.530752432	2.731752825	0.028948413	1	DNA-dir_Rpol_phage-type	molecular_function|DNA binding|DNA-directed RNA polymerase activity|cellular_component|intracellular|cell|cytoplasm|mitochondrion|transcription, DNA-templated|biological_process|biosynthetic process|transferase activity|nucleotidyltransferase activity|cellular nitrogen compound metabolic process|organelle
GRMZM2G078274	-1.013952119	3.098220605	0.028951218	1	B3_DNA-bd|AUX_IAA|Auxin_resp|AuxIAA_ARF_dimer|DNA-bd_pseudobarrel	reproduction|molecular_function|DNA binding|cellular_component|intracellular|cell|nucleus|transcription, DNA-templated|regulation of transcription, DNA-templated|signal transduction|biological_process|biosynthetic process|response to hormone|response to auxin|auxin-activated signaling pathway|flower development|cellular nitrogen compound metabolic process|organelle|protein dimerization activity|anatomical structure development
GRMZM2G129448	-0.696285168	1.940774706	0.029121686	1	ENT_N	Not Annotated
GRMZM2G148913	-0.716580694	3.98359893	0.029263428	1	Lipase_3	molecular_function|triglyceride lipase activity|lipid metabolic process|biological_process|hydrolase activity
GRMZM2G094168	-0.973103309	1.396806405	0.029368659	1	DUF597	Not Annotated
GRMZM2G052206	-0.4695928	3.563374019	0.029410562	1	Ser/Thr_dual-sp_kinase_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups|nucleotide binding
GRMZM2G130043	-0.530529945	3.39492301	0.029423583	1	Starch_synth_cat_dom	Not Annotated
GRMZM2G041258	0.492958986	5.552021681	0.029532105	1	DUF538	Not Annotated
GRMZM2G110997	-3.817350266	4.153506563	0.029596493	1	Not Annotated	Not Annotated
GRMZM2G337819	-0.598873653	2.566486178	0.029602711	1	Reg_chr_condens|RCC1/BLIP-II	Not Annotated
GRMZM2G027331	-0.298436195	4.517888414	0.029616422	1	HAD-like_dom	cellular_component|intracellular|cell|cytoplasm|chloroplast|plastid|chloroplast stroma|organelle
GRMZM2G467717	-0.375073071	3.364052018	0.029656703	1	ARM-type_fold	molecular_function|binding
GRMZM2G047791	-0.589135226	2.279655198	0.029722351	1	Not Annotated	Not Annotated
GRMZM2G400961	-1.456245974	0.280202917	0.029742205	1	Not Annotated	Not Annotated
GRMZM2G506602	-1.333639536	4.810977108	0.02976832	1	Not Annotated	Not Annotated
GRMZM2G081822	-1.010426162	0.715266881	0.02994943	1	a-crystallin/Hsp20_dom|HSP20-like_chaperone	Not Annotated
GRMZM2G122941	-1.123588479	1.159991867	0.029959758	1	Not Annotated	Not Annotated
GRMZM5G825935	-0.97988874	2.254788952	0.029998349	1	Not Annotated	Not Annotated
GRMZM2G133746	-1.099816294	1.247377187	0.030008306	1	Not Annotated	Not Annotated
GRMZM2G475349	1.188637462	2.120206658	0.030181051	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G109560	-0.517937907	4.689640552	0.030184315	1	Lon_bac/euk-typ|ATPase_AAA_core|AAA+_ATPase|Pept_S16_N|Peptidase_S16_AS|Pept_S16_C|PUA-like_domain|Ribosomal_S5_D2-typ_fold|ClpA/B	nucleotide binding|molecular_function|ATP-dependent peptidase activity|serine-type endopeptidase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|peroxisome|peroxisomal matrix|protein complex assembly|proteolysis|misfolded or incompletely synthesized protein catabolic process|protein targeting|transport|biological_process|peptidase activity|serine-type peptidase activity|catabolic process|protein import into peroxisome matrix, docking|hydrolase activity|ATPase activity|nucleoside-triphosphatase activity|cellular component assembly|growth|organelle|organelle lumen|lateral root development|anatomical structure development|macromolecular complex assembly
GRMZM2G117971	-5.559918443	-2.083657087	0.030230817	1	Barwin|RlpA-like_DPBB|Barwin_CS	immune system process|response to stress|biological_process|response to virus|systemic acquired resistance|response to salt stress|response to ethylene|defense response to fungus, incompatible interaction|defense response to bacterium|defense response to fungus|response to herbivore
GRMZM2G072526	-0.359978661	4.219052965	0.03026237	1	Glyco_hydro_17|X8|Glycoside_hydrolase_SF	molecular_function|catalytic activity|hydrolase activity, hydrolyzing O-glycosyl compounds|carbohydrate metabolic process|biological_process|hydrolase activity|hydrolase activity, acting on glycosyl bonds
AC202435.3_FG003	-5.446987515	-1.881023278	0.030278026	1	PEstase_dom	molecular_function|hydrolase activity
GRMZM5G879527	-0.444780914	3.079041264	0.030281321	1	bHLH_dom	molecular_function|protein dimerization activity
GRMZM5G846314	2.099808753	-0.841055317	0.030295044	1	Not Annotated	Not Annotated
GRMZM2G462422	-0.504064852	2.642254646	0.030422496	1	Not Annotated	Not Annotated
GRMZM2G451147	-0.828745997	0.315020738	0.030531732	1	Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	nucleotide binding|molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G113662	-4.170716704	-1.141019883	0.030587668	1	Not Annotated	Not Annotated
GRMZM2G430675	-0.759240358	1.12001882	0.030662988	1	AAA+_ATPase|ABC_transporter-like|ABC_transporter_CS	nucleotide binding|molecular_function|ATP binding|plasma membrane|ATPase activity|nucleoside-triphosphatase activity
GRMZM2G062577	0.405563286	5.358346526	0.030665349	1	Lipase_GDSL	molecular_function|lipid metabolic process|biological_process|hydrolase activity|hydrolase activity, acting on ester bonds
GRMZM2G165383	-0.318729213	5.447289099	0.030777691	1	SerB|HAD-SF_hydro_IB_PSP-like|HAD-like_dom	molecular_function|phosphoserine phosphatase activity|cellular_component|intracellular|cell|cytoplasm|cellular amino acid metabolic process|L-serine biosynthetic process|biological_process|metabolic process|biosynthetic process|chloroplast|plastid|pollen development|embryo development|dephosphorylation|phosphatase activity|organelle|small molecule metabolic process|root development
GRMZM5G854146	3.125330034	-1.015790968	0.030777902	1	Ribosomal_L2_bac/org-type|Translation_prot_SH3-like|Ribosomal_L2_C|Ribosomal_L2_CS	molecular_function|RNA binding|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|mitochondrion|ribosome|translation|biological_process|biosynthetic process|chloroplast|plastid|large ribosomal subunit|membrane|transferase activity|organelle

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G129209	-1.062102084	1.763980355	0.030858023	1	Fatty_acid_desaturase-1|DUF3474	molecular_function|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|lipid metabolic process|fatty acid biosynthetic process|unsaturated fatty acid biosynthetic process|response to stress|biological_process|biosynthetic process|response to temperature stimulus|response to cold|chloroplast|plastid|chloroplast envelope|oxidoreductase activity|oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water|omega-3 fatty acid desaturase activity|organelle|small molecule metabolic process|oxidation-reduction process|response to karrikin
GRMZM2G180639	-0.833859849	1.39282643	0.030863259	1	RRM_dom	nucleotide binding|molecular_function|nucleic acid binding
GRMZM2G425920	-0.73010241	2.502724014	0.030877386	1	bZIP	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|regulation of transcription, DNA-templated|biological_process|sequence-specific DNA binding
GRMZM2G433117	-0.47421032	3.999839247	0.03095964	1	Not Annotated	Not Annotated
GRMZM2G133483	-5.66464753	-1.523922095	0.030987376	1	Not Annotated	Not Annotated
GRMZM2G454189	-1.368096432	0.448317737	0.031106108	1	Not Annotated	Not Annotated
GRMZM2G367459	-1.368096432	0.448317774	0.03111113	1	Not Annotated	Not Annotated
GRMZM2G075690	-0.480114234	4.875093499	0.031153137	1	JAB_MPN_dom|USP8_dimer	molecular_function|protein binding
AC203424.3_FG001	-0.413923296	4.652725934	0.031304362	1	DUF1620	cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|organelle|protein complex|ER membrane protein complex
GRMZM2G343713	-6.885217933	-1.381808902	0.031340644	1	Ribosomal_L2_bac/org-type|Translation_prot_SH3-like|Ribosomal_L2_C|Ribosomal_L2_CS	molecular_function|RNA binding|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|ribosome|translation|biological_process|biosynthetic process|large ribosomal subunit|transferase activity|organelle
GRMZM2G034430	-0.437161173	4.689248992	0.031347879	1	Endo/exonuclease/phosphatase	Not Annotated
GRMZM2G072034	-1.121027976	0.695645954	0.031356017	1	Lipocln_cytosolic_FA-bd_dom|Calycin-like|Lipocalin_ApoD|Lipocalin_CS	cellular_component|intracellular|cell|cytoplasm|mitochondrion|vacuole|vacuolar membrane|endoplasmic reticulum|Golgi apparatus|plasma membrane|response to stress|biological_process|response to heat|response to cold|response to light stimulus|plasmodesma|hyperosmotic salinity response|organelle
GRMZM5G847302	-5.446987515	-1.886161656	0.031446996	1	Not Annotated	Not Annotated
GRMZM2G318860	-0.481627977	3.715947906	0.031559215	1	DDHD	molecular_function|ion binding|metal ion binding|cellular_component|intracellular|cell|cytoplasm|vacuole|biological_process|detection of gravity|gravitropism|amyloplast organization|plant-type vacuole membrane|negative gravitropism|organelle
GRMZM2G032711	-0.327107337	4.237565613	0.031573319	1	WD40_repeat|WD40_repeat_dom|WD40_repeat_CS|G-protein_beta_WD-40_rep|Histone-bd_RBBP4_N	molecular_function|protein binding|cellular_component|intracellular|cell|nucleus|organelle|protein complex|Cul4-RING ubiquitin ligase complex|cytosol
GRMZM2G059700	-0.541247344	3.788284333	0.031591854	1	Aminotrans_V/Cys_dSase|PyrdxlP-dep_Trfase	molecular_function|catalytic activity|biological_process|metabolic process|pyridoxal phosphate binding

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G017365	-0.604445371	3.401041304	0.03185294	1	Cation_efflux	molecular_function|cellular_component|transport|cation transport|biological_process|cation transmembrane transporter activity|integral component of membrane|transmembrane transporter activity|transmembrane transport|response to nematode
GRMZM2G041167	-5.762285887	-1.901853826	0.032197047	1	Sphingomyelin_synth-like_dom	Not Annotated
GRMZM2G516387	-0.674029381	4.041165153	0.032257231	1	Not Annotated	Not Annotated
GRMZM5G814771	2.6737445	1.117846892	0.032266358	1	Not Annotated	Not Annotated
GRMZM2G031802	-0.412180391	5.021248124	0.032288306	1	ER_ret_rcpt	immune system process|molecular_function|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|Golgi apparatus|protein retention in ER lumen|transport|signal transduction|biological_process|defense response signaling pathway, resistance gene-independent|protein transport|membrane|integral component of membrane|organelle|ER retention sequence binding
GRMZM2G034811	-1.016422836	1.552031192	0.032307992	1	RNA-helicase_DEAD-box_CS|DNA/RNA_helicase_DEAD/DEAH_N|Helicase_ATP-bd	molecular_function|nucleic acid binding|helicase activity|ATP binding|ATP-dependent helicase activity|biological_process|FMN binding|oxidoreductase activity|ATPase activity|oxidation-reduction process
GRMZM2G062197	-0.89695234	4.483606892	0.032366357	1	Pyrophosphatase	magnesium ion binding|molecular_function|inorganic diphosphatase activity|cellular_component|intracellular|cell|cytoplasm|phosphate-containing compound metabolic process|biological_process|ion binding
GRMZM2G462080	-1.100801487	1.704453245	0.032387565	1	Not Annotated	Not Annotated
GRMZM2G092916	-1.38776329	1.264035691	0.032408561	1	TBP	molecular_function|DNA binding|DNA-templated transcription, initiation|biological_process|biosynthetic process|cellular nitrogen compound metabolic process
GRMZM2G419852	-5.190552506	-2.027025911	0.032477348	1	DUF966|DHR-1_domain	Not Annotated
GRMZM2G037343	1.476372342	0.690781521	0.032482261	1	Cation/H_exchanger	molecular_function|cellular_component|transport|cation transport|biological_process|solute:hydrogen antiporter activity|integral component of membrane|transmembrane transporter activity|transmembrane transport
GRMZM5G897604	-0.571097585	3.000879579	0.03267419	1	Not Annotated	Not Annotated
GRMZM2G092991	-0.630292969	3.633449288	0.032737044	1	Mg_trans_NIPA	molecular_function|cellular_component|plasma membrane|transport|biological_process|magnesium ion transmembrane transporter activity|magnesium ion transport|membrane|transmembrane transporter activity
GRMZM5G892247	2.76106725	2.101634538	0.032757157	1	RNA_pol_Rpb1_5|RNA_pol_Rpb1_4|DNA-dir_RpoC2_beta_pp	molecular_function|DNA binding|DNA-directed RNA polymerase activity|cellular_component|intracellular|cell|cytoplasm|transcription, DNA-templated|biological_process|biosynthetic process|chloroplast|plastid|transferase activity|nucleotidyltransferase activity|cellular nitrogen compound metabolic process|organelle
GRMZM2G386923	-1.096771699	2.236732571	0.032760352	1	Rcd1	Not Annotated
GRMZM2G029531	-0.877428517	1.052212826	0.032775181	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G060163	-0.982634733	4.72536617	0.03280052	1	RNR_small|Ferritin-like_SF	molecular_function|ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor|cellular_component|intracellular|cell|cytoplasm|ribonucleoside-diphosphate reductase complex|DNA metabolic process|DNA replication|multicellular organismal development|biological_process|cell death|biosynthetic process|deoxyribonucleoside diphosphate metabolic process|programmed cell death|oxidoreductase activity|cellular nitrogen compound metabolic process|ion binding|protein complex|small molecule metabolic process|transition metal ion binding|regulation of cell cycle|oxidation-reduction process
GRMZM2G094083	-0.739379478	4.412149167	0.032807592	1	Cyclophilin-like_PPIase_dom	molecular_function|RNA binding|translation initiation factor activity|translation|translational initiation|translation factor activity, nucleic acid binding|biological_process|biosynthetic process|protein peptidyl-prolyl isomerization|peptidyl-prolyl cis-trans isomerase activity|protein folding|cellular protein modification process|isomerase activity
GRMZM2G091449	-0.747734232	3.965290506	0.032813489	1	Cleavage/polyA-sp_fac_asu_C	molecular_function|nucleic acid binding|cellular_component|intracellular|cell|nucleus|organelle
GRMZM2G397661	-3.46008794	-1.72955567	0.032876881	1	Not Annotated	peroxisome
GRMZM2G009080	-1.337526977	-0.3079385	0.032986098	1	DUF581	Not Annotated
GRMZM5G806638	2.694379503	2.066431709	0.033026204	1	Not Annotated	Not Annotated
GRMZM2G110531	-0.483794075	2.751101518	0.033140058	1	MATH|BTB/POZ-like|TRAF-like|BTB/POZ_fold|BTB_POZ	molecular_function|protein binding
GRMZM5G857930	-0.702488402	2.539662592	0.033142809	1	Telomer_end-bd_POT1/Cdc13|NA-bd_OB-fold	nuclear chromosome|telomere maintenance|nuclear chromosome, telomeric region|molecular_function|DNA binding|cellular_component|intracellular|cell|nucleus|chromosome|DNA metabolic process|biological_process|cellular nitrogen compound metabolic process|homeostatic process|organelle|chromosome organization
GRMZM2G146097	-6.170663056	-0.638088269	0.033165879	1	Glc/ribitol_DH	Not Annotated
GRMZM2G007715	-0.31468058	4.315175746	0.033168224	1	Peptidase_M16_C|L-Aspartase-like|Metalloenz_LuxS/M16|Fumarate_lyase_N	molecular_function|catalytic activity|ion binding|metal ion binding
GRMZM2G048117	-0.375760482	5.199593993	0.033199459	1	DUF846_euk	cellular_component|trans-Golgi network|Golgi organization|protein secretion|unidimensional cell growth|integral component of membrane
GRMZM2G118766	-0.672629259	2.335935255	0.033325511	1	Not Annotated	Not Annotated
GRMZM2G066538	-2.867979965	-0.792225402	0.03337042	1	Not Annotated	Not Annotated
GRMZM2G096171	-1.095300868	1.766477944	0.033394791	1	Sig_transdc_resp-reg_receiver|CheY-like_superfamily	phosphorelay response regulator activity|phosphorelay signal transduction system|molecular_function|signal transducer activity|regulation of transcription, DNA-templated|signal transduction|biological_process|intracellular signal transduction
GRMZM2G133943	-0.252945305	3.912211825	0.033432686	1	PLipase_D/transphosphatidylase|C2_dom|PLipase_D_C	molecular_function|catalytic activity|protein binding|biological_process|metabolic process

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
AC196475.3_FG004	1.280048931	4.231255215	0.033659469	1	O_MeTrfase_2|Plant_MeTrfase_dimerisation|COMT|De-COase2_CS	molecular_function|cellular_component|intracellular|cell|nucleus|cytoplasm|plasma membrane|biological_process|methyltransferase activity|O-methyltransferase activity|biosynthetic process|phenylpropanoid biosynthetic process|lignin biosynthetic process|transferase activity|secondary metabolic process|quercetin 3-O-methyltransferase activity|methylation|myricetin 3'-O-methyltransferase activity|organelle|protein dimerization activity|caffeate O-methyltransferase activity|flavonol biosynthetic process
GRMZM2G113476	-0.572357677	3.244527783	0.033672952	1	UbiA_prenyltransferase	molecular_function|prenyltransferase activity|cellular_component|integral component of membrane|transferase activity|transferase activity, transferring alkyl or aryl (other than methyl) groups|plastid|chloroplast envelope|plastoquinone biosynthetic process|homogentisate farnesyltransferase activity|homogentisate geranylgeranyltransferase activity|homogentisate solanesyltransferase activity|carotenoid biosynthetic process
GRMZM2G461948	-0.548105461	3.882075625	0.03368838	1	HECT	molecular_function|ubiquitin-protein ligase activity|cellular_component|intracellular|cell|cellular protein modification process|biological_process|ligase activity
GRMZM2G086294	-0.94016996	12.40761968	0.033828878	1	Not Annotated	molecular_function|cellular_component|intracellular|cell|cytoplasm|vacuole|cytoplasmic membrane-bounded vesicle|aleurone grain|organelle|nutrient reservoir activity
GRMZM2G381933	-0.715825306	3.914879245	0.03390227	1	PAPS_reduct|Mopterin-bd_dom	molecular_function|catalytic activity|Mo-molybdopterin cofactor biosynthetic process|biological_process|metabolic process|biosynthetic process|cellular nitrogen compound metabolic process|cofactor metabolic process
GRMZM2G010740	-1.342687958	0.466147246	0.03397766	1	VWF_A	molecular_function|protein binding
GRMZM2G045507	-0.515217712	2.4579871	0.03404221	1	Not Annotated	Not Annotated
AC208346.3_FG004	2.33381893	0.163910803	0.034044879	1	Exo70|Cullin_repeat-like_dom	exocyst|cellular_component|intracellular|cell|cytoplasm|transport|exocytosis|biological_process|vesicle-mediated transport|protein complex
GRMZM2G107651	-0.722433286	1.520225114	0.034058171	1	DENN_dom	Not Annotated
GRMZM5G814310	-0.340357023	5.793636691	0.03424436	1	Not Annotated	endoplasmic reticulum
GRMZM2G055437	-1.342687958	0.432973551	0.034315322	1	WD40_repeat|WD40_repeat_dom|WD40_repeat_CS|G-protein_beta_WD-40_rep	molecular_function|protein binding
GRMZM2G121063	-0.441872305	5.709497568	0.034351799	1	K+_transporter	plant-type vacuole|molecular_function|cellular_component|intracellular|cell|cytoplasm|vacuole|vacuolar membrane|plasma membrane|transport|biological_process|potassium ion transmembrane transporter activity|membrane|transmembrane transporter activity|organelle|transmembrane transport|potassium ion transmembrane transport

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G162748	-0.426257106	5.684275519	0.034395025	1	Rieske_Fe-S_prot_C|Cyt_b6-f_cplx_Fe-S_su|Rieske_2Fe-2S	molecular_function|cellular_component|intracellular|cell|cytoplasm|plasma membrane|generation of precursor metabolites and energy|response to stress|ubiquinol-cytochrome-c reductase activity|biological_process|plastoquinol--plastocyanin reductase activity|chloroplast|chloroplast thylakoid|plastid|thylakoid|chloroplast envelope|nonphotochemical quenching|photosynthesis|membrane|integral component of membrane|oxidoreductase activity|oxidoreductase activity, acting on diphenols and related substances as donors|transmembrane transporter activity|electron transport chain|thylakoid membrane|defense response to bacterium|ion binding|organelle|electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II activity|metal ion binding|iron-sulfur cluster binding|2 iron, 2 sulfur cluster binding|oxidation-reduction process|response to karrikin
GRMZM2G073026	-5.446987515	-2.089364341	0.034598124	1	Ribosomal_L5|Ribosomal_L5_domain	molecular_function|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|vacuole|ribosome|translation|biological_process|biosynthetic process|membrane|cytosolic large ribosomal subunit|cytosolic ribosome|organelle
GRMZM5G842695	-0.409508032	2.973877167	0.034617391	1	MATE	molecular_function|cellular_component|transport|drug transmembrane transport|biological_process|drug transmembrane transporter activity|antiporter activity|membrane|transmembrane transporter activity|transmembrane transport
GRMZM2G034947	-0.5539882	2.809927632	0.034651853	1	Znf_GRF	molecular_function|zinc ion binding|ion binding
GRMZM2G142875	-0.538207274	4.507157383	0.034679797	1	DUF566	Not Annotated
GRMZM5G864414	-0.621885537	5.95199965	0.034687526	1	Ser/Thr_dual-sp_kinase_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	nucleotide binding|molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G590771	0.928190612	2.579569744	0.034862971	1	Not Annotated	Not Annotated
GRMZM2G176474	-0.734455239	3.981747097	0.035010448	1	Not Annotated	Not Annotated
GRMZM2G046436	-0.675500431	3.769998434	0.035016866	1	RGP_fam	molecular_function|carbohydrate metabolic process|biological_process|biosynthetic process|isomerase activity|intramolecular transferase activity|cellulose biosynthetic process
GRMZM2G512616	-1.467034179	-0.56346846	0.035032279	1	Not Annotated	Not Annotated
GRMZM2G041039	2.139445598	-1.907573821	0.03516087	1	Not Annotated	Not Annotated
GRMZM2G101060	-2.55584726	0.415680846	0.035301856	1	F-box_dom	molecular_function|protein binding
GRMZM2G547542	-0.180216883	4.384928905	0.035427045	1	Spermidine/spermine_synthase|Methyltransf_11	molecular_function|catalytic activity|biological_process|metabolic process|methyltransferase activity|methylation
GRMZM2G354834	-0.871745122	1.411305566	0.035441878	1	Not Annotated	Not Annotated
GRMZM5G876520	-0.487304845	5.2358218	0.035550852	1	Not Annotated	origin recognition complex|molecular_function|DNA binding|ATP binding|cellular_component|intracellular|cell|nucleus|chromosome|DNA metabolic process|DNA replication|biological_process|biosynthetic process|cellular nitrogen compound metabolic process|identical protein binding|organelle|protein complex
GRMZM2G581326	-2.379055769	-0.905775865	0.035599026	1	Not Annotated	Not Annotated
GRMZM2G397391	2.082631722	-0.744142419	0.035629817	1	Glycosyltransferase_AER61	molecular_function|transferase activity, transferring glycosyl groups

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G148896	-0.580669223	3.76330161	0.035691943	1	Thiaminase-2/PQQC|Haem_Oase-like_multi-hlx|HAD-like_dom	Not Annotated
GRMZM2G106974	-0.465018133	4.892160268	0.035716575	1	Valyl-tRNA_ligase|aa-tRNA-synth_Ia|Val/Leu/Ile-tRNA-synth_edit|tRNAsynth_1a_anticodon-bd|tRNA-bd_arm|V/L/I-tRNA-synth_anticodon-bd	nucleotide binding|aminoacyl-tRNA editing activity|molecular_function|aminoacyl-tRNA ligase activity|valine-tRNA ligase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|mitochondrion|cytosol|tRNA metabolic process|translation|tRNA aminoacylation for protein translation|valyl-tRNA aminoacylation|regulation of translational fidelity|cellular amino acid metabolic process|biological_process|biosynthetic process|chloroplast|embryo development ending in seed dormancy|ligase activity|cellular nitrogen compound metabolic process|small molecule metabolic process
GRMZM2G456603	1.782222137	2.094716251	0.035749082	1	NADH_UbQ_OxRdtase_su10	cellular_component|intracellular|cell|cytoplasm|mitochondrion|mitochondrial respiratory chain complex I|mitochondrial membrane|organelle|protein complex|respiratory chain complex I
GRMZM5G831795	-0.591562113	2.470666702	0.035819922	1	Peptidase_M20|Peptidase_M20_dimer|Amidohydrolase	molecular_function|biological_process|metabolic process|hydrolase activity
GRMZM2G446170	1.009033139	0.976588536	0.035834097	1	BURP_dom	Not Annotated
GRMZM2G082180	-0.512776404	1.98923858	0.035845502	1	Small_GTP-bd_dom|GTPase_MnmE|GTP_binding_domain|GTP-bd_TrmE_N|GTPase_MnmE_C_dom	nucleotide binding|molecular_function|GTPase activity|GTP binding|cellular_component|intracellular|cell|GTP catabolic process|tRNA metabolic process|tRNA modification|tRNA processing|biological_process|catabolic process|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|small molecule metabolic process
GRMZM2G121826	-0.383271915	4.16709997	0.035901991	1	Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Kinase-like_dom	molecular_function|protein kinase activity|ATP binding|cellular_component|cell|plasma membrane|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G129399	1.77046045	0.789706989	0.035912115	1	HeavyMe-assoc_HMA	molecular_function|transport|biological_process|metal ion transport|ion binding|metal ion binding
GRMZM2G167999	-0.448615329	5.266570989	0.036046461	1	WD40_repeat|WD40_repeat_dom|WD40_repeat_CS|G-protein_beta_WD-40_rep|DUF3337	molecular_function|protein binding|lateral root formation
GRMZM2G158069	-0.621890846	1.965385754	0.036172779	1	Smr/MutS2_C|DUF1771	cytoplasm
GRMZM2G162388	-0.560295886	6.416033319	0.036233207	1	Cyclophilin-like_PPIase_dom|Cyclophilin-type_PPIase_CS|Cyclophilin-type_PPIase	protein peptidyl-prolyl isomerization|molecular_function|peptidyl-prolyl cis-trans isomerase activity|cytosol|plasma membrane|protein folding|cellular protein modification process|biological_process|isomerase activity
GRMZM2G140016	-0.415057468	3.206170167	0.036234115	1	Znf_C2H2|Znf_C2H2-like	molecular_function|nucleic acid binding|cellular_component|intracellular|cell|zinc ion binding|ion binding|sequence-specific DNA binding

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G451792	-1.298872964	0.654153707	0.036236278	1	AAA+_ATPase|ABC_transporter-like|ABC_2_trans|PDR_assoc|ABC_transporter_CS	nucleotide binding|molecular_function|ATP binding|cellular_component|ATP catabolic process|biological_process|catabolic process|membrane|ATPase activity|nucleoside-triphosphatase activity|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|small molecule metabolic process
GRMZM2G113415	-0.578169723	3.696593169	0.036301092	1	Not Annotated	Not Annotated
GRMZM2G158252	-0.926048637	1.51812897	0.036348834	1	Sig_transdc_His_kin-like_C|EnvZ-like_dim/P|HATPase_ATP-bd|Sig_transdc_resp-reg_receiver|Sig_transdc_His_kinase_core|CHASE|Sig_transdc_His_kinase_dimeric|CheY-like_superfamily	phosphorelay sensor kinase activity|phosphorelay response regulator activity|phosphorelay signal transduction system|molecular_function|signal transducer activity|osmosensor activity|ATP binding|cellular_component|regulation of transcription, DNA-templated|response to stress|response to osmotic stress|signal transduction|biological_process|response to water deprivation|response to toxic substance|response to salt stress|response to abscisic acid|regulation of flower development|regulation of seed germination|phloem or xylem histogenesis|regulation of chlorophyll catabolic process|membrane|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups|kinase binding|signal transduction by phosphorylation|negative regulation of iron ion transport|intracellular signal transduction|identical protein binding|protein histidine kinase binding|regulation of meristem development|regulation of shoot system development|cellular response to cold|cellular response to abscisic acid stimulus|secondary growth
GRMZM2G016447	-0.712691513	5.301539747	0.036386031	1	Not Annotated	Not Annotated
GRMZM2G165390	-0.750926045	1.940318586	0.036569632	1	UDP_glucos_trans	molecular_function|biological_process|metabolic process|biosynthetic process|anthocyanin-containing compound biosynthetic process|transferase activity|transferase activity, transferring glycosyl groups|transferase activity, transferring hexosyl groups|secondary metabolic process|UDP-glucosyltransferase activity|anthocyanidin 3-O-glucosyltransferase activity|quercetin 3-O-glucosyltransferase activity|flavonol 3-O-arabinosyltransferase activity|response to karrikin
GRMZM2G079348	2.101564679	0.260696789	0.03659828	1	Catalase_haem_BS|Catalase_immune_responsive|Catalase_core|Catalase|Catalase-like_dom|Catalase_AS|Catalase_clade1/3	molecular_function|catalase activity|peroxidase activity|response to stress|response to oxidative stress|biological_process|catabolic process|oxidoreductase activity|heme binding|hydrogen peroxide catabolic process|ion binding|metal ion binding|oxidation-reduction process|cell wall|mitochondrion|cellular response to nitrogen starvation|response to light stimulus|response to abscisic acid|chloroplast envelope|cellular response to sulfate starvation|cellular response to phosphate starvation|cytosolic ribosome|response to hydrogen peroxide|response to cadmium ion|cobalt ion binding|cellular_component|intracellular|cell|cytoplasm|organelle
GRMZM2G126956	-0.792163788	0.707859977	0.036700611	1	Znf_CCHC|WD40_repeat|WD40_repeat_dom|WD40_repeat_CS	molecular_function|nucleic acid binding|protein binding|cellular_component|intracellular|cell|nucleus|DNA metabolic process|DNA repair|response to stress|biological_process|zinc ion binding|response to UV-B|cellular nitrogen compound metabolic process|ion binding|organelle
GRMZM5G857327	-2.330678439	0.026611475	0.036706063	1	Not Annotated	Not Annotated
GRMZM5G819140	-1.299631648	0.610075338	0.036896686	1	Not Annotated	Not Annotated
GRMZM5G881996	-0.554682316	3.787419408	0.036929265	1	Sec63-dom|Ig_E-set	Not Annotated
GRMZM2G095254	0.906237631	0.273074831	0.036980956	1	ATPase_AAA_CS|ATPase_AAA_core|AAA+_ATPase|AAA_N_dom	nucleotide binding|molecular_function|ATP binding|nucleoside-triphosphatase activity

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G434696	-0.508056024	4.912097202	0.036981455	1	WD40_repeat_dom|WD40_repeat|Synaptobrevin	molecular_function|protein binding|cellular_component|plasma membrane|transport|biological_process|integral component of membrane|vesicle-mediated transport
GRMZM2G306345	-0.283539757	10.76383198	0.037105529	1	PPDK_PEP-bd|PEP_util_C|PEP-util_enz_mobile_dom|Pyruvate_phosphate_dikinase|Pyrv/PenolPyrv_Kinase-like_dom|PEP_util_AS|PEP_util_CS	molecular_function|catalytic activity|ATP binding|nucleus|cytosol|pyruvate metabolic process|biological_process|chloroplast stroma|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups|small molecule metabolic process|pyruvate, phosphate dikinase activity
GRMZM5G840560	-0.322970439	5.845757724	0.037149377	1	Glyco_trans_48	1,3-beta-D-glucan synthase complex|molecular_function|1,3-beta-D-glucan synthase activity|cellular_component|cell|plasma membrane|carbohydrate metabolic process|(1->3)-beta-D-glucan biosynthetic process|biological_process|biosynthetic process|membrane|transferase activity, transferring glycosyl groups|protein complex
GRMZM2G119175	-0.398514141	7.317363586	0.037281129	1	Pyr_Knase|Pyrv_Knase-like_insert_dom|Pyrv_Knase_brl|Pyrv_Knase_C|Pyrv/PenolPyrv_Kinase-like_dom	magnesium ion binding|molecular_function|catalytic activity|pyruvate kinase activity|cellular_component|cell|cytosol|plasma membrane|carbohydrate metabolic process|generation of precursor metabolites and energy|glycolysis|biological_process|catabolic process|membrane|kinase activity|phosphorylation|transferase activity|potassium ion binding|ion binding|response to cadmium ion
GRMZM2G054210	-0.503265996	4.619575496	0.037305231	1	Clathrin/coatomer_adapt-like_N|Clathrin_a/b/g-adaptin_app_Ig|Clathrin_g-adaptin_app|Coatomer/clathrin_app_Ig-like|ARM-type_fold|AP1_complex_gsu	molecular_function|binding|cellular_component|intracellular|cell|cytoplasm|Golgi apparatus|transport|intracellular protein transport|biological_process|protein transporter activity|protein transport|membrane|vesicle-mediated transport|membrane coat|clathrin adaptor complex|organelle|protein complex|Golgi apparatus part
GRMZM2G047255	-0.385825364	3.982482352	0.037415434	1	FH2_Formin	Not Annotated
GRMZM2G035098	-0.950488664	0.918129476	0.037525863	1	RIO_kinase|Kinase-like_dom|RIO-like_kinase	molecular_function|catalytic activity|protein serine/threonine kinase activity|ATP binding|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM5G851130	2.119099508	1.276983924	0.037600472	1	Ribosomal_S2|Stathmin_fam|Ribosomal_S2_flav_dom	molecular_function|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|mitochondrion|ribosome|translation|biological_process|biosynthetic process|small ribosomal subunit|regulation of microtubule polymerization or depolymerization|organelle
GRMZM2G025132	-0.440394901	2.315350578	0.037784978	1	Not Annotated	Not Annotated
GRMZM2G022310	-0.394015671	4.397479176	0.037816291	1	Glyco_trans_1|PIGA_GPI_anchor_biosynthesis	cellular protein modification process|GPI anchor biosynthetic process|lipid metabolic process|biological_process|biosynthetic process
GRMZM2G120833	1.770546462	-0.578650485	0.037893769	1	Thr_synthase_like|Trp_syn_b_sub_like_PLP_eny_SF|Ser/Thr_deHydtase_PyrdxlP-BS	molecular_function|cellular amino acid metabolic process|biological_process|pyridoxal phosphate binding|small molecule metabolic process
GRMZM5G883100	-1.749582807	-1.311614241	0.037899042	1	Not Annotated	Not Annotated
GRMZM2G590885	-1.986178083	0.12891193	0.037913733	1	Not Annotated	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G350658	2.731571738	-0.803350503	0.037974576	1	PSS	cellular amino acid metabolic process|lipid metabolic process|phosphatidylserine biosynthetic process|biological_process|biosynthetic process|small molecule metabolic process
GRMZM2G415433	-0.333141694	3.933371494	0.03800249	1	FH2_Formin	cellular_component|intracellular|cell|nucleus|organelle
GRMZM5G869635	-1.122351933	-0.140025957	0.038141502	1	F-box_dom	molecular_function|protein binding
GRMZM2G475882	-0.839694375	1.819999095	0.038220915	1	AUX_IAA|Auxin_resp|AuxIAA_ARF_dimer|DNA-bd_pseudobarrel	reproduction|molecular_function|DNA binding|cellular_component|intracellular|cell|nucleus|transcription, DNA-templated|regulation of transcription, DNA-templated|signal transduction|biological_process|biosynthetic process|response to hormone|response to auxin|auxin-activated signaling pathway|flower development|cellular nitrogen compound metabolic process|organelle|protein dimerization activity|anatomical structure development
GRMZM2G118183	1.979319474	-1.238079257	0.038373029	1	Not Annotated	Not Annotated
GRMZM5G873675	-1.488830761	0.531385239	0.038432505	1	Not Annotated	Not Annotated
GRMZM2G058568	-0.499948289	3.200387814	0.038444074	1	Not Annotated	Not Annotated
GRMZM2G155837	-0.701833719	2.601487047	0.038463459	1	Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Kinase-like_dom|Protein_kinase_ATP_BS|Malectin|Ser/Thr_kinase_AS	molecular_function|protein kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups|nucleotide binding|protein serine/threonine kinase activity
GRMZM2G086403	-1.030346581	1.068951555	0.038498066	1	DUF597	Not Annotated
GRMZM2G046025	-0.303673602	4.869051652	0.03857926	1	Yip1	cellular_component|cell|endosome|Golgi apparatus|trans-Golgi network|cytosol|plasma membrane|membrane
GRMZM2G466281	-0.239695601	5.494697328	0.038609291	1	CDP-OH_P_trans|CHOPT	molecular_function|cellular_component|Golgi apparatus|lipid metabolic process|biological_process|phospholipid biosynthetic process|biosynthetic process|membrane|transferase activity|phosphotransferase activity, for other substituted phosphate groups
GRMZM2G097736	-2.39938158	0.356783606	0.038623107	1	Not Annotated	Not Annotated
GRMZM2G031628	-0.800035641	3.122700889	0.0386463	1	Glyco_hydro_1|Glycoside_hydrolase_SF	molecular_function|catalytic activity|hydrolase activity, hydrolyzing O-glycosyl compounds|carbohydrate metabolic process|biological_process|hydrolase activity, acting on glycosyl bonds
GRMZM2G038801	1.188201305	2.546602922	0.038765696	1	HSP_DnaJ_Cys-rich_dom	molecular_function|heat shock protein binding|unfolded protein binding
GRMZM2G371793	2.070942286	-1.272788952	0.038775146	1	Acid_phosphat_B|HAD-like_dom	molecular_function|acid phosphatase activity|phosphatase activity
GRMZM2G474236	-0.386662402	4.252537557	0.038856267	1	Galactose-bd-like|Rad4/PNGase_transGLS-fold	molecular_function|DNA binding|damaged DNA binding|cellular_component|intracellular|cell|nucleus|DNA metabolic process|nucleotide-excision repair|response to stress|biological_process|cellular nitrogen compound metabolic process|organelle
GRMZM5G823111	2.579393465	-1.48022399	0.038864758	1	Not Annotated	Not Annotated
GRMZM2G172829	-0.368602421	4.99145905	0.038923375	1	Clp_protease_ATP-bd_su_ClpX|AAA+_ATPase|ATPase_AAA-2|Clp_ATPase_C	nucleotide binding|molecular_function|ATP binding|protein folding|biological_process|nucleoside-triphosphatase activity|unfolded protein binding
GRMZM2G062657	-0.440645664	2.615102827	0.039111401	1	BRCT_dom|GNAT_dom|Acyl_CoA_acyltransferase	molecular_function|N-acetyltransferase activity|transferase activity, transferring acyl groups

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G172787	-0.682058507	0.73715295	0.039122185	1	Topo_IA_DNA-bd|Topo_IA_2|Topo_IA|TopoI_bac-type|Toprim_domain|Topo_IA_cen|Topo_IA_core_domain|Topo_IA_AS	molecular_function|DNA binding|DNA topoisomerase activity|DNA topoisomerase type I activity|cellular_component|intracellular|cell|chromosome|DNA metabolic process|DNA topological change|biological_process|isomerase activity|cellular nitrogen compound metabolic process|organelle
GRMZM5G878607	-2.139929119	-1.259800528	0.039128505	1	Epimerase_deHydtase	nucleotide binding|molecular_function|catalytic activity|cytosol|biological_process|plasmodesma|UDP-rhamnose biosynthetic process|UDP-L-rhamnose synthase activity|auxin efflux|cellular metabolic process|UDP-glucose 4,6-dehydratase activity|coenzyme binding|flavonol biosynthetic process
GRMZM2G364178	-0.658602819	4.585976577	0.03913708	1	Not Annotated	Not Annotated
GRMZM2G114692	-0.281458932	4.978708281	0.039147713	1	Pumilio_RNA-bd_rpt|ARM-type_fold	molecular_function|RNA binding|binding|cellular_component|intracellular|cell|nucleus|nucleolus|organelle
GRMZM2G434317	-0.567576643	2.955066544	0.039190222	1	DUF707	Not Annotated
GRMZM2G155729	-0.527174836	2.79324254	0.039275573	1	UDPGP_trans	molecular_function|UDP-N-acetylglucosamine diphosphorylase activity|UTP:glucose-1-phosphate uridylyltransferase activity|cellular_component|cell|cytosol|plasma membrane|UDP-glucose metabolic process|UDP-N-acetylglucosamine metabolic process|biological_process|metabolic process|nucleotidyltransferase activity|UDP-N-acetylgalactosamine metabolic process|cellular nitrogen compound metabolic process|small molecule metabolic process|UDP-N-acetylgalactosamine diphosphorylase activity
GRMZM2G162758	2.783625559	-0.985629366	0.03943662	1	Cyt_P450_E_grp-I|Cyt_P450|Cyt_P450_CS	molecular_function|monooxygenase activity|iron ion binding|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|lipid metabolic process|biological_process|electron carrier activity|biosynthetic process|suberin biosynthetic process|oxidoreductase activity|oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen|secondary metabolic process|heme binding|very long-chain fatty acid biosynthetic process|ion binding|organelle|small molecule metabolic process|metal ion binding|oxidation-reduction process
GRMZM2G040326	-0.463463557	5.191540654	0.039511931	1	Peptidase_S9	molecular_function|proteolysis|biological_process|peptidase activity|serine-type peptidase activity
GRMZM2G565441	-1.529695997	1.003792171	0.03951209	1	Not Annotated	Not Annotated
GRMZM5G867512	1.488448704	0.48697787	0.039515994	1	Cyt_c_biogenesis_CcbS|Cyt_c_biogenesis|Cyt_c_assembly	molecular_function|cellular_component|intracellular|cell|cytoplasm|mitochondrion|protein complex assembly|transport|biological_process|respiratory chain complex IV assembly|heme transporter activity|heme transport|membrane|cytochrome complex assembly|cellular component assembly|organelle|macromolecular complex assembly
GRMZM2G347645	-0.520931853	4.735504568	0.039532035	1	Membrane_Tatp1/CMV_rcpt	embryo development|pollen tube guidance|maintenance of protein localization in endoplasmic reticulum
GRMZM2G154574	-0.643935671	2.867687984	0.039548941	1	tRNA_yW-synthesising|tRNA_Trfase_Trm5/Tyw2|Kelch_1	molecular_function|protein binding|transferase activity
AC213463.3_FG002	-0.26614386	4.595387707	0.039566171	1	Tscrpt_elong_fac_Eaf_N	cellular_component|intracellular|cell|nucleus|nucleoplasm|regulation of transcription, DNA-templated|biological_process|ELL-EAF complex|organelle|protein complex
GRMZM2G098721	-0.344868703	3.457639628	0.039570641	1	Elf1	Not Annotated

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G102754	-0.573924148	1.782938237	0.039664493	1	NRAMP-like	establishment of planar polarity|response to molecule of bacterial origin|molecular_function|transporter activity|cellular_component|transport|response to osmotic stress|biological_process|response to heat|response to salt stress|positive regulation of abscisic acid-activated signaling pathway|auxin polar transport|regulation of stomatal movement|leaf senescence|membrane|negative regulation of defense response|defense response to bacterium|root hair cell differentiation|defense response to fungus|defense response by callose deposition in cell wall|cellular response to iron ion
GRMZM5G861479	-2.021807725	4.399155121	0.039668877	1	Proteasome_suA-type	molecular_function|threonine-type endopeptidase activity|peptidase activity
GRMZM2G361120	-2.273244919	-0.524691689	0.039693168	1	PEP_carboxykinase_N	molecular_function|phosphoenolpyruvate carboxykinase activity|carbohydrate metabolic process|gluconeogenesis|biological_process|biosynthetic process|lyase activity|purine nucleotide binding
GRMZM2G063262	-0.349827123	4.115686265	0.039727385	1	Not Annotated	Not Annotated
GRMZM2G136146	-0.855487852	3.217549324	0.03986267	1	Not Annotated	Not Annotated
GRMZM2G086971	-0.554978433	4.639438899	0.039877037	1	Glutathione_S-Trfase_N|Thioredoxin-like_fold|Small_GTP-bd_dom|Small_GTPase_Rab_type|Small_GTPase	molecular_function|protein binding|cellular_component|intracellular|cell|cytoplasm|chloroplast|plastid|organelle|nucleotide binding|GTP binding|plasma membrane|transport|signal transduction|small GTPase mediated signal transduction|biological_process|protein transport|membrane
GRMZM2G394212	-0.824197523	3.601825526	0.039918124	1	mOase_FAD-bd|Rng_hydrolase-like	Not Annotated
GRMZM5G899151	-2.826521499	-1.350659452	0.039923994	1	Not Annotated	Not Annotated
GRMZM2G016382	-0.474917194	1.688723805	0.040000079	1	Pentatricopeptide_repeat	Not Annotated
GRMZM2G007854	-0.192689527	4.665499352	0.040048859	1	Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM5G804708	1.870514762	0.50880231	0.04006658	1	ClpP|ClpP_AS|ClpP/TepA	nucleotide binding|molecular_function|serine-type endopeptidase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|proteolysis|biological_process|peptidase activity|serine-type peptidase activity|chloroplast|plastid stroma|chloroplast thylakoid membrane|plastid|chloroplast stroma|thylakoid|chloroplastic endopeptidase Clp complex|hydrolase activity|organelle|protein complex
GRMZM2G372928	-0.97901813	0.413114693	0.040075875	1	Znf_PHD|PWWP_dom|Znf_FYVE_PHD|Zinc_finger_PHD-type_CS|Znf_PHD-finger	molecular_function|protein binding|zinc ion binding|DNA mediated transformation|plasmodesma|ion binding|metal ion binding
GRMZM5G814985	-0.38690209	4.272068394	0.040357627	1	Helicase/UvrB_dom|Helicase_ATP-bd|RNase_III_dom	molecular_function|DNA binding|ATP binding|hydrolase activity|RNA binding|nuclease activity|ribonuclease III activity|RNA processing|biological_process|cellular nitrogen compound metabolic process

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM5G881077	-2.710912757	-2.215005859	0.0404411	1	PP2C_Mn2_Asp60_BS	molecular_function|protein serine/threonine phosphatase activity|cellular protein modification process|protein dephosphorylation|biological_process|phosphatase activity
GRMZM2G164224	-0.8373127	0.952971009	0.040481926	1	Prot_kinase_dom|MSP_dom|Ser/Thr_kinase_AS|PapD-like|Kinase-like_dom|TPR-contain_dom	molecular_function|protein kinase activity|protein serine/threonine kinase activity|structural molecule activity|protein binding|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G552793	-1.257113712	0.644205021	0.040518602	1	Not Annotated	Not Annotated
GRMZM5G884407	-0.903878861	1.15118024	0.040538096	1	Not Annotated	Not Annotated
GRMZM2G160430	-1.244594024	1.137072301	0.040609678	1	Sugar/inositol_transpt|Sub_transporter|Sugar_transporter_CS|MFS_dom_general_subst_transpt|MFS_dom	molecular_function|transporter activity|cellular_component|intracellular|cell|cytoplasm|vacuole|plasma membrane|transport|biological_process|membrane|integral component of membrane|transmembrane transporter activity|substrate-specific transmembrane transporter activity|organelle|transmembrane transport
GRMZM2G114772	-1.086482148	0.736512483	0.040643924	1	Glyco_trans_8	molecular_function|transferase activity, transferring glycosyl groups
GRMZM2G368411	-6.020883491	-1.817687946	0.040686118	1	Oxoglu/Fe-dep_dioxygenase|Isopenicillin-N_synthase|DIOX_N	molecular_function|biological_process|oxidoreductase activity|oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors|oxidation-reduction process
GRMZM2G172800	2.454378154	-0.299404566	0.04068656	1	Pentatricopeptide_repeat	Not Annotated
GRMZM2G111898	-4.118781116	-1.201231898	0.040737013	1	Not Annotated	Not Annotated
GRMZM2G465046	2.605487928	-1.074109877	0.040762962	1	Lipase_GDSL	molecular_function|lipid metabolic process|biological_process|hydrolase activity|hydrolase activity, acting on ester bonds
GRMZM2G008305	-0.943358613	-0.258930842	0.040777154	1	DUF868_pln	Not Annotated
GRMZM2G077202	-0.270396055	3.64582059	0.040909571	1	Glyco_hydro_14|Glycoside_hydrolase_SF	polysaccharide catabolic process|molecular_function|catalytic activity|carbohydrate metabolic process|biological_process|catabolic process|beta-amylase activity|hydrolase activity, acting on glycosyl bonds
GRMZM2G389881	-0.726308563	1.383905916	0.041153526	1	Not Annotated	Not Annotated
GRMZM2G178960	0.786994657	2.680296447	0.041227263	1	Ribul_P_3_epim-like|RibuloseP-bd_barrel|Ribul_P_3_epim	molecular_function|catalytic activity|ribulose-phosphate 3-epimerase activity|cellular_component|extracellular region|intracellular|cell|cytoplasm|carbohydrate metabolic process|pentose-phosphate shunt|response to stress|biological_process|metabolic process|catabolic process|response to cold|chloroplast|plastid|chloroplast stroma|thylakoid|response to nematode|chloroplast envelope|stromule|isomerase activity|racemase and epimerase activity, acting on carbohydrates and derivatives|cellular nitrogen compound metabolic process|ion binding|organelle|small molecule metabolic process|metal ion binding|apoplast|cofactor metabolic process
GRMZM2G022090	-0.538703474	2.795207838	0.041268494	1	Not Annotated	Not Annotated
GRMZM2G075387	-0.285865845	3.838505293	0.041278641	1	UDP_glucos_trans	molecular_function|biological_process|metabolic process|transferase activity, transferring glycosyl groups|transferase activity, transferring hexosyl groups

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G130927	-0.678131964	2.853361034	0.041308025	1	Ser/Thr_dual-sp_kinase_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	MAPK cascade|nucleotide binding|activation of MAPKK activity|molecular_function|DNA binding|protein kinase activity|protein serine/threonine kinase activity|MAP kinase kinase kinase activity|signal transducer activity|ATP binding|cellular_component|intracellular|cell|nucleus|cellular protein modification process|protein phosphorylation|response to stress|response to osmotic stress|signal transduction|biological_process|response to cold|response to wounding|response to salt stress|kinase activity|transferase activity, transferring phosphorus-containing groups|enzyme binding|kinase binding|organelle|response to cadmium ion
GRMZM5G853305	2.083906771	1.359468029	0.041308044	1	Ribosomal_L16|Ribosomal_L10e/L16|Ribosomal_L16_CS	molecular_function|RNA binding|structural constituent of ribosome|structural molecule activity|cellular_component|intracellular|cell|cytoplasm|ribosome|translation|biological_process|biosynthetic process|chloroplast|plastid|rRNA binding|ribonucleoprotein complex|organelle
GRMZM5G887345	-0.474702361	4.682685158	0.0413354	1	Not Annotated	Not Annotated
GRMZM2G314934	-2.844820352	-2.115746682	0.041481503	1	Not Annotated	Not Annotated
GRMZM2G100988	-0.920189563	1.478895996	0.041500209	1	Not Annotated	Not Annotated
GRMZM2G158446	-0.532482074	3.410616462	0.041512031	1	Not Annotated	Not Annotated
GRMZM2G409430	-0.239925187	3.998668074	0.041570334	1	Nucleoporin_Nup85	nuclear envelope
GRMZM2G063647	-1.361519041	-1.146569737	0.041614451	1	Not Annotated	Not Annotated
GRMZM2G091494	-0.26145807	4.225359656	0.041622856	1	Anoctamin	Not Annotated
GRMZM2G312661	-0.710924846	1.360481234	0.041654728	1	EF_hand_dom|EF-hand-dom_pair|EF_Hand_1_Ca_BS	molecular_function|calcium ion binding|ion binding
GRMZM2G124593	-0.355668068	4.831334316	0.041668236	1	Pyr_Knase|Pyrv_Knase-like_insert_dom|Pyrv_Knase_brl|Pyrv_Knase_C|Pyrv/PenolPyrv_Kinase-like_dom	magnesium ion binding|molecular_function|catalytic activity|pyruvate kinase activity|carbohydrate metabolic process|generation of precursor metabolites and energy|glycolysis|biological_process|catabolic process|kinase activity|phosphorylation|transferase activity|potassium ion binding|ion binding
GRMZM2G099239	-5.446987515	-2.136409904	0.041698105	1	Remorin_C	Not Annotated
GRMZM2G019621	-0.640171775	2.506135721	0.041711585	1	ATPase_AAA_CS|ATPase_AAA_core|AAA+_ATPase|ClpA/B	nucleotide binding|molecular_function|ATP binding|nucleoside-triphosphatase activity
GRMZM5G852338	-0.764553277	4.378966668	0.041727854	1	Dilute|Dil_domain	molecular_function|protein binding
GRMZM2G151406	-0.54426654	2.164961146	0.041744425	1	Cation_transp_P_typ_ATPase|ATPase_P-typ_transduc_dom_A|ATPase_P-typ_P_site|HAD-like_dom|Cation_transp_P-typ_ATPase_IB	nucleotide binding|molecular_function|ATP binding|cellular_component|transport|cation transport|copper ion transport|biological_process|integral component of membrane|hydrolase activity|ATPase activity|cation-transporting ATPase activity|transmembrane transporter activity|ion binding|copper-transporting ATPase activity|metal ion binding
GRMZM2G080116	0.577465798	1.117161662	0.041809097	1	Dynein_light_chain_typ-1/2	cellular_component|intracellular|cell|cytoskeleton|microtubule associated complex|microtubule-based process|biological_process|organelle|protein complex
GRMZM2G062453	-2.289708685	-1.039112221	0.04186766	1	Glyco_trans_14|Cyclin_N|Cyclin-like|Cyclin_A/B/D/E	regulation of cyclin-dependent protein serine/threonine kinase activity|molecular_function|cellular_component|biological_process|acetylglucosaminyltransferase activity|membrane|transferase activity, transferring glycosyl groups|enzyme binding|protein kinase binding|regulation of cell cycle

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G133660	1.182876815	3.609485938	0.041932274	1	Not Annotated	Not Annotated
GRMZM2G124718	-0.799872984	2.152720729	0.041936814	1	Poly(ADP-ribose)pol_reg_dom|Poly(ADP-ribose)pol_cat_dom	molecular_function|NAD+ ADP-ribosyltransferase activity|carbohydrate metabolic process|translation|cellular protein modification process|protein ADP-ribosylation|biological_process|biosynthetic process|transferase activity, transferring glycosyl groups
GRMZM2G103236	-0.522579923	4.642745943	0.042014898	1	GroES-like|Chaperonin_Cpn10	cellular_component|intracellular|cell|cytoplasm|protein folding|biological_process|chloroplast|plastid|chloroplast stroma|chloroplast envelope|organelle
GRMZM2G100946	-0.508119011	5.150068886	0.042017393	1	Armadillo|BTB/POZ-like|BTB/POZ_fold|BTB_POZ|ARM-type_fold	molecular_function|binding|protein binding
GRMZM2G377115	-0.282660717	3.790933787	0.042058102	1	UbiB_dom|Prot_kinase_dom|Kinase-like_dom	molecular_function|protein kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|chlorophyll catabolic process|kinase activity|transferase activity, transferring phosphorus-containing groups|response to photooxidative stress
GRMZM2G180435	0.772779502	1.487962245	0.0420622	1	Not Annotated	Not Annotated
GRMZM2G036829	-0.395461354	3.932060645	0.04210935	1	Split_barrel_FMN-bd|DUF2470	molecular_function|cellular_component|intracellular|cell|cytoplasm|generation of precursor metabolites and energy|biological_process|chloroplast|chloroplast thylakoid|plastid|chloroplast stroma|photosynthetic electron transport chain|post-embryonic development|FMN binding|photosynthesis|oxidoreductase activity|tetrapyrrole biosynthetic process|organelle|protein anchor|oxidation-reduction process|positive regulation of heme biosynthetic process
GRMZM2G155974	-0.50136963	2.913807984	0.042172269	1	Glutathione_synth_subst-bd_euk|Glutathione_synthase_euk|PreATP-grasp_dom	molecular_function|glutathione synthase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|cytosol|cellular amino acid metabolic process|glutathione biosynthetic process|sulfur compound metabolic process|biological_process|biosynthetic process|chloroplast|plastid|response to jasmonic acid|ligase activity|organelle|small molecule metabolic process
GRMZM2G305332	-0.735711046	2.099129879	0.042230771	1	Actin-related	molecular_function|ATP binding|cellular_component|intracellular|cell|cytoskeleton|Arp2/3 protein complex|cytoskeleton organization|biological_process|regulation of actin filament polymerization|Arp2/3 complex-mediated actin nucleation|organelle|protein complex|cell morphogenesis|actin filament organization|multidimensional cell growth|trichome morphogenesis|cell differentiation|growth|anatomical structure development
GRMZM2G142964	-0.493284794	2.605388863	0.042271488	1	JmjC_dom	core promoter proximal region sequence-specific DNA binding|molecular_function|protein binding|nucleus|positive regulation of seed germination|histone demethylase activity (H3-R2 specific)|histone demethylase activity (H4-R3 specific)|histone H4-R3 methylation|histone H3-R2 demethylation|histone H4-R3 demethylation
GRMZM2G079389	-0.250935589	3.6620976	0.042423761	1	Dymeclin	Not Annotated
GRMZM2G126774	-0.414587676	3.157833663	0.042428966	1	Helicase_C|SNF2_N|HARP_dom|Helicase_ATP-bd	molecular_function|nucleic acid binding|DNA binding|helicase activity|ATP binding|cellular_component|intracellular|cell|nucleus|biological_process|chromatin modification|organelle|chromosome organization

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G029396	-0.231225271	5.288843408	0.042513245	1	Squ/phyt_synthse|Squal_synth|Terpenoid_synth|Squalene/phytoene_synthase_CS	molecular_function|farnesyl-diphosphate farnesyltransferase activity|cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|plasma membrane|lipid metabolic process|biological_process|lipid biosynthetic process|biosynthetic process|integral component of membrane|transferase activity|transferase activity, transferring alkyl or aryl (other than methyl) groups|organelle
GRMZM2G058573	-0.485365798	5.300315247	0.04262586	1	Sirtuin|Ssirtuin_cat_dom	molecular_function|NAD+ binding
GRMZM2G165746	-0.77421556	1.507573735	0.042696641	1	Mit_carrier|Mitochondrial_sb/sol_carrier|Mt_carrier_dom	cellular_component|transport|biological_process|membrane|integral component of membrane|transmembrane transport
GRMZM2G005061	-0.455990243	3.916275385	0.042748867	1	Not Annotated	double-strand break repair via homologous recombination|molecular_function|double-stranded DNA binding|single-stranded DNA binding|nucleus|mitochondrion|DNA repair|ion binding|cobalt ion binding
GRMZM2G150834	-0.853445276	1.539053635	0.042830236	1	SAC3/GANP/Nin1/mts3/eIF-3-p25	Not Annotated
GRMZM2G121264	-1.776278403	-0.269066763	0.042852671	1	Cyt_P450_E_grp-I|Cyt_P450|Cyt_P450_CS	molecular_function|monooxygenase activity|iron ion binding|biological_process|electron carrier activity|oxidoreductase activity|oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen|heme binding|ion binding|metal ion binding|oxidation-reduction process
GRMZM2G302891	-1.243381455	-0.081958389	0.042861884	1	Znf_C2H2|Znf_C2H2-like	molecular_function|cellular_component|intracellular|cell|zinc ion binding|ion binding
GRMZM2G386824	-0.483761772	3.996727647	0.042881423	1	Glycoside_Hdrlase_35|Lectin_gal-bd_dom|Galactose-bd-like|Glycoside_hydrolase_SF|Glyco_hydro_35_CS	molecular_function|hydrolase activity, hydrolyzing O-glycosyl compounds|carbohydrate metabolic process|biological_process|hydrolase activity, acting on glycosyl bonds|carbohydrate binding
GRMZM2G129413	0.772865605	2.716117533	0.042888474	1	AA_transpt_TM	cellular_component|biological_process|response to nematode|cotyledon vascular tissue pattern formation|membrane|integral component of membrane|root cap development|anatomical structure development
GRMZM2G439448	-5.762285887	-1.953363896	0.042900942	1	Remorin_C	Not Annotated
GRMZM2G117544	-0.541800634	3.950735168	0.042902613	1	Proteasome_sua/b|Proteasome_bsu_CS|Proteasome_suB-type	proteasome complex|molecular_function|endopeptidase activity|threonine-type endopeptidase activity|cellular_component|intracellular|cell|nucleus|cytoplasm|vacuolar membrane|cytosol|proteasome core complex|plasma membrane|proteolysis|biological_process|peptidase activity|catabolic process|hydrolase activity|organelle|protein complex|proteolysis involved in cellular protein catabolic process
GRMZM2G404207	-0.510666771	2.823075241	0.042933506	1	Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM5G833032	-0.580482926	3.0147714	0.043052654	1	SANT/Myb|Myb_dom_plants|Homeodomain-like|Myb_dom	molecular_function|DNA binding|chromatin binding|response to stress|biological_process|response to salt stress|response to ethylene|response to auxin|response to abscisic acid|response to gibberellin|response to salicylic acid|response to jasmonic acid|response to cadmium ion
GRMZM2G456023	-0.262339798	4.103267583	0.043066596	1	START_lipid-bd_dom|Pleckstrin_homology|DUF1336	molecular_function|protein binding|phospholipid binding|lipid binding
GRMZM2G168519	-0.526206866	2.590489571	0.043092603	1	Longin_dom|Longin-like_dom|Synaptobrevin	cellular_component|transport|biological_process|membrane|integral component of membrane|vesicle-mediated transport
GRMZM2G157677	0.892375306	1.111328794	0.043122586	1	Not Annotated	Not Annotated
GRMZM2G011655	-0.625202435	2.341598123	0.043134068	1	Squ/phyt_synthse|Terpenoid_synth	molecular_function|biological_process|biosynthetic process|transferase activity
GRMZM2G131476	-0.639627722	3.568654842	0.043260781	1	Leu_zip_homeo|Homeobox_dom|Homeodomain-like|Homeobox_CS	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|cellular_component|intracellular|cell|nucleus|transcription, DNA-templated|regulation of transcription, DNA-templated|biological_process|biosynthetic process|response to cytokinin|cellular nitrogen compound metabolic process|organelle|sequence-specific DNA binding
GRMZM2G033767	-0.547671439	1.976120665	0.043293176	1	Plipid/glycerol_acylTrfase	molecular_function|biological_process|metabolic process|transferase activity, transferring acyl groups
GRMZM5G858653	-0.719777406	3.665854905	0.043358304	1	ALMT	transport|biological_process|malate transport
GRMZM2G004349	-0.416689939	4.265785083	0.043396777	1	Reticulon	cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|organelle
GRMZM2G174048	1.972526441	-0.645844524	0.043406105	1	Plcyanin-like|Cupredoxin	molecular_function|copper ion binding|electron carrier activity|ion binding
GRMZM2G701058	-0.632566384	2.150453077	0.043514435	1	Not Annotated	Not Annotated
GRMZM2G011078	-0.445939508	3.605900247	0.043542688	1	SCAMP	cellular_component|cell|plasma membrane|transport|biological_process|protein transport|membrane|integral component of membrane
GRMZM2G111679	-0.660655908	2.079191723	0.043564472	1	LEA-14	Not Annotated
GRMZM2G011631	-0.54749725	4.527083995	0.043611183	1	DNA-dir_DNA_pol_B_exonuc|DNA-dir_DNA_pol_B_multi_dom|DNA-dir_DNA_pol_B|RNase H-like_dom|DNA_pol_e_suA_C	nucleotide binding|molecular_function|nucleic acid binding|DNA binding|DNA-directed DNA polymerase activity|cellular_component|intracellular|cell|nucleus|nucleobase-containing compound metabolic process|DNA metabolic process|DNA replication|biological_process|zinc ion binding|epsilon DNA polymerase complex|biosynthetic process|nucleotidyltransferase activity|cellular nitrogen compound metabolic process|ion binding|organelle
GRMZM2G168228	-0.541675593	4.204176245	0.043729395	1	ATPase_AAA_CS|ATPase_AAA_core	molecular_function|ATP binding

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G063851	-0.343920198	6.740767795	0.043743909	1	Citrate_synthase-like|Citrate_synthase_euk|Citrate_synthase-like_core|Citrate_synthase_AS	molecular_function|citrate (Si)-synthase activity|ATP binding|cellular_component|cell wall|intracellular|cell|cytoplasm|mitochondrion|carbohydrate metabolic process|generation of precursor metabolites and energy|tricarboxylic acid cycle|biological_process|zinc ion binding|catabolic process|chloroplast|plastid|transferase activity|transferase activity, transferring acyl groups|external encapsulating structure|ion binding|organelle|cellular carbohydrate metabolic process|response to cadmium ion|transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer|cofactor metabolic process
GRMZM2G476902	5.682387865	-2.342306726	0.043789497	1	Armadillo|ARM-rpt_dom|ARM-type_fold	molecular_function|binding|protein binding
GRMZM2G091973	-2.509591532	-1.503578777	0.043926062	1	Reticulon	cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|organelle
GRMZM2G089767	-0.505946146	2.90326228	0.043929868	1	Carboh/pur_kinase_PfkB_CS|Adenokinase|PfkB_dom	molecular_function|phosphotransferase activity, alcohol group as acceptor
GRMZM2G496477	-2.215776886	-1.518722823	0.044162916	1	Not Annotated	Not Annotated
GRMZM2G055905	-0.354898605	5.698587791	0.044219097	1	PEstase_dom|Ser/Thr-sp_prot-phosphatase	molecular_function|phosphoprotein phosphatase activity|cellular_component|intracellular|cell|nucleus|cytoplasm|biological_process|negative regulation of flower development|hydrolase activity|phosphatase activity|organelle
GRMZM5G864412	-2.844820352	-2.155573489	0.044299288	1	PCRF|Pep_chain_release_fac_I_II|Cyclin-like	molecular_function|RNA binding|translation release factor activity|cellular_component|intracellular|cell|cytoplasm|translation|translational termination|translation factor activity, nucleic acid binding|biological_process|biosynthetic process|translation release factor activity, codon specific
GRMZM2G462760	-1.968797709	-1.112498219	0.044338937	1	Auxin_inducible_ARG7	molecular_function|calmodulin binding|cellular_component|intracellular|cell|cytoplasm|mitochondrion|signal transduction|biological_process|auxin-activated signaling pathway|organelle|response to stimulus
GRMZM2G150952	-0.323893029	3.325034558	0.044357983	1	Prot_kinase_dom|PAP/fibrillin_dom|Kinase-like_dom	molecular_function|protein kinase activity|structural molecule activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|cellular protein modification process|protein phosphorylation|biological_process|chloroplast|plastid|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups|organelle
GRMZM2G007038	-0.498896148	4.38508151	0.044569008	1	Small_GTP-bd_dom|Transl_elong_EFTu/EF1A_2|EF_GTP-bd_dom|TF_IF2_bacterial-like|Transl_B-barrel|TIF_IF2_dom3	nucleotide binding|molecular_function|RNA binding|translation initiation factor activity|GTPase activity|GTP binding|cellular_component|intracellular|cell|GTP catabolic process|translation|translational initiation|translation factor activity, nucleic acid binding|biological_process|catabolic process|biosynthetic process|cellular nitrogen compound metabolic process|nucleobase-containing compound catabolic process|small molecule metabolic process|chloroplast stroma|chloroplast envelope
GRMZM2G171229	-1.145434831	-0.512947915	0.044575824	1	Cyt_trans-like	molecular_function|catalytic activity|biological_process|biosynthetic process|transferase activity|nucleotidyltransferase activity
GRMZM2G138997	-0.494483456	2.175580266	0.044673374	1	Znf_RING	molecular_function|protein binding|zinc ion binding|ion binding|metal ion binding

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G092813	-2.967347766	-2.102487771	0.044894994	1	AMP-dep_Synth/Lig|AMP-binding_CS|AMP-bd_C	molecular_function|catalytic activity|sulfur compound metabolic process|biological_process|metabolic process|biosynthetic process|ligase activity|benzoate-CoA ligase activity|secondary metabolic process|glucosinolate biosynthetic process
GRMZM2G088896	-1.243750343	4.298287707	0.04493238	1	Not Annotated	Not Annotated
GRMZM5G837841	-1.185521095	2.349387819	0.044983155	1	EXOV	Not Annotated
GRMZM2G328356	5.547690956	-2.374940888	0.045008725	1	Not Annotated	Not Annotated
GRMZM2G047705	-0.351197026	4.42044131	0.045012706	1	Not Annotated	Not Annotated
GRMZM2G318033	-6.650356453	-1.631813185	0.045082706	1	Uncharacterised_Cys-rich|DUF2985	cellular_component|cell|plasma membrane
GRMZM2G114503	-5.190552506	-1.853191931	0.045128457	1	SANT/Myb|Homeodomain-like	molecular_function|DNA binding|chromatin binding
GRMZM2G335287	-0.280378548	5.165644155	0.045133455	1	Sec7_dom|DUF1981_Sec7_assoc|ARM-type_fold	molecular_function|ARF guanyl-nucleotide exchange factor activity|binding|biological_process|enzyme regulator activity|regulation of ARF protein signal transduction
GRMZM2G399284	-0.586519108	5.898120446	0.045158227	1	GroES-like|Chaperonin_21_chloroplast|Chaprnonin_Cpn10_CS|Chaperonin_Cpn10	molecular_function|copper ion binding|ATP binding|cellular_component|extracellular region|intracellular|cell|cytoplasm|mitochondrion|protein folding|response to stress|biological_process|response to cold|chloroplast|chloroplast thylakoid membrane|plastid|chloroplast stroma|thylakoid|chloroplast envelope|ion binding|organelle|response to cadmium ion|apoplast|positive regulation of superoxide dismutase activity
GRMZM2G020508	-0.985454012	2.588694343	0.045204484	1	Not Annotated	Not Annotated
GRMZM2G087482	-0.36789281	4.573285761	0.045228775	1	Znf_PHD|Znf_FYVE_PHD|Zinc_finger_PHD-type_CS|Znf_PHD-finger|GNAT_dom|Acyl_CoA_acyltransferase	molecular_function|protein binding|zinc ion binding|ion binding|N-acetyltransferase activity|transferase activity, transferring acyl groups
GRMZM2G093766	-0.410870772	3.791262059	0.045231419	1	Not Annotated	Not Annotated
AC194272.3_FG003	1.068004259	-1.814322818	0.045304229	1	Not Annotated	Not Annotated
GRMZM2G035405	-0.560218293	4.875579027	0.045316785	1	B3_DNA-bd|AUX_IAA|Auxin_resp|AuxIAA_ARF_dimer|DNA-bd_pseudobarrel	reproduction|molecular_function|DNA binding|cellular_component|intracellular|cell|nucleus|transcription, DNA-templated|regulation of transcription, DNA-templated|signal transduction|biological_process|biosynthetic process|response to hormone|response to auxin|auxin-activated signaling pathway|flower development|cellular nitrogen compound metabolic process|organelle|protein dimerization activity|anatomical structure development
GRMZM2G071448	-0.259401091	3.744970936	0.04536761	1	WD40_repeat|WD40_repeat_dom|WD40_repeat_CS|G-protein_beta_WD-40_rep	molecular_function|protein binding
GRMZM2G081907	-1.266374302	0.249270749	0.045386211	1	ARM-type_fold|CLASP_N_dom	molecular_function|binding
GRMZM2G078297	-0.875394386	1.778230529	0.045449902	1	Not Annotated	Not Annotated
GRMZM2G096008	-1.467034179	-0.519070432	0.045534968	1	HeavyMe-assoc_HMA	molecular_function|transport|biological_process|metal ion transport|ion binding|metal ion binding
GRMZM2G465728	-0.509064072	1.727536564	0.045578847	1	Not Annotated	Not Annotated
GRMZM2G167766	-0.85741877	1.926258017	0.045587004	1	Uncharacterised_Ycf19	cellular_component|chloroplast|chloroplast thylakoid membrane|cytochrome b6f complex assembly|membrane

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G093598	-0.27653008	4.042793049	0.045646322	1	UDPgal_transpt|Nuc_sug_transpt|UDP/CMP-sugar_transptr	Golgi membrane|molecular_function|nucleotide-sugar transmembrane transporter activity|sugar:hydrogen symporter activity|cellular_component|intracellular|cell|cytoplasm|Golgi apparatus|transport|biological_process|carbohydrate transport|nucleotide-sugar transport|membrane|integral component of membrane|transmembrane transporter activity|organelle|sialic acid transmembrane transporter activity|sialic acid transport
GRMZM2G035848	-0.558296638	1.750407534	0.045656638	1	Not Annotated	Not Annotated
GRMZM2G177215	1.583851225	-0.194491679	0.045737036	1	Not Annotated	Not Annotated
GRMZM2G088539	-0.507011956	4.967568935	0.045786218	1	Znf_RanBP2	molecular_function|cellular_component|intracellular|cell|zinc ion binding|ion binding
GRMZM2G074208	-1.091972963	0.775795154	0.04581431	1	DNA_methylase_N6_adenine_CS|N6_adenine_Mtase-rel_euk|ATPase_P-typ_cyto_domN	molecular_function|nucleic acid binding|biological_process|methyltransferase activity|methylation
GRMZM2G363554	6.122335732	-2.099706959	0.045874985	1	UDP_glucos_trans	molecular_function|biological_process|metabolic process|transferase activity, transferring glycosyl groups|transferase activity, transferring hexosyl groups
GRMZM2G124061	-1.345180128	0.011082506	0.045895038	1	VWF_A	molecular_function|protein binding
GRMZM2G428201	-0.780917992	2.307999913	0.045903319	1	Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Kinase-like_dom|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G106028	-0.416591446	4.921843667	0.046014313	1	MAP65_Ase1_PRC1	microtubule cytoskeleton organization|cytokinesis|molecular_function|cytoskeleton organization|microtubule binding|cytoskeletal protein binding|biological_process|cell division
GRMZM2G146280	-0.345495604	5.776497621	0.046045128	1	WD40_repeat|WD40_repeat_dom	molecular_function|protein binding|autophagy|response to stress|aging|biological_process|catabolic process|leaf senescence|response to starvation|anatomical structure development
GRMZM2G351454	-0.799127579	0.996286295	0.04609683	1	APO_dom	molecular_function|RNA binding
GRMZM2G326643	-0.402729204	7.332244022	0.046102842	1	Glyco_trans_48|FKS1-like_dom1	reproduction|1,3-beta-D-glucan synthase complex|molecular_function|1,3-beta-D-glucan synthase activity|cellular_component|cell|plasma membrane|carbohydrate metabolic process|(1->3)-beta-D-glucan biosynthetic process|cell cycle|biological_process|biosynthetic process|pollen development|microsporogenesis|membrane|transferase activity, transferring glycosyl groups|growth|protein complex|developmental growth
GRMZM2G011355	-0.740792087	6.513230409	0.046189629	1	Small_GTPase_ARF/SAR|Small_GTPase_ARF	nucleotide binding|molecular_function|GTP binding|cellular_component|intracellular|cell|signal transduction|small GTPase mediated signal transduction|biological_process
GRMZM2G029055	-0.292754995	4.66345302	0.046216179	1	tRNAsynth_1a_anticodon-bd|Met-tRNA_synth|Methionyl/Leucyl_tRNA_Synth	nucleotide binding|molecular_function|aminoacyl-tRNA ligase activity|methionine-tRNA ligase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|mitochondrion|tRNA metabolic process|translation|tRNA aminoacylation for protein translation|methionyl-tRNA aminoacylation|cellular amino acid metabolic process|biological_process|biosynthetic process|chloroplast|chloroplast stroma|ligase activity|cellular nitrogen compound metabolic process|small molecule metabolic process|ovule development

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G003225	-1.299631648	0.268388718	0.046346373	1	Nse4_C	cellular_component|intracellular|cell|nucleus|chromosome|DNA metabolic process|DNA repair|response to stress|biological_process|Smc5-Smc6 complex|cellular nitrogen compound metabolic process|organelle|protein complex
GRMZM2G009849	-0.37475848	5.561982478	0.046406061	1	ARM-type_fold	molecular_function|binding|microtubule binding|plasmodesma|preprophase band|cell plate formation involved in plant-type cell wall biogenesis|cortical microtubule cytoskeleton
GRMZM2G471670	1.108353859	-0.48242015	0.046415997	1	Clp_N	biological_process|protein metabolic process
GRMZM2G006452	-0.384170121	4.645974905	0.046567052	1	RecF/RecN/SMC_N|SMC_hinge	molecular_function|protein binding|ATP binding|cellular_component|intracellular|cell|chromosome|biological_process|organelle|chromosome organization
GRMZM2G057416	0.927848439	2.670548226	0.046578147	1	Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	nucleotide binding|molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|phosphorylation|transferase activity, transferring phosphorus-containing groups|cytoplasm
GRMZM2G163159	-0.377378214	2.633482394	0.04660464	1	Not Annotated	Not Annotated
GRMZM2G161641	-1.112647767	0.79752435	0.046687856	1	AA_transpt_TM	Not Annotated
GRMZM2G021885	0.599473732	4.697740903	0.046808093	1	Not Annotated	Not Annotated
GRMZM2G085939	-0.730912506	2.273321879	0.047052368	1	Lipase_3|Mono/diacylglycerol_lipase_N	molecular_function|triglyceride lipase activity|lipid metabolic process|biological_process|catabolic process|lipid catabolic process|hydrolase activity
GRMZM2G089676	-0.309896977	5.334626137	0.047130436	1	NTF2|RRM_dom|Nuclear_transport_factor_2_euk	nucleotide binding|molecular_function|nucleic acid binding|cellular_component|intracellular|cell|transport|biological_process
GRMZM2G070394	-1.3802367	-0.239700256	0.047171437	1	Not Annotated	Not Annotated
GRMZM2G465764	-0.512711668	3.353586362	0.047200405	1	Glyco_trans_48	1,3-beta-D-glucan synthase complex|molecular_function|1,3-beta-D-glucan synthase activity|cellular_component|cell|plasma membrane|carbohydrate metabolic process|(1->3)-beta-D-glucan biosynthetic process|biological_process|biosynthetic process|membrane|transferase activity, transferring glycosyl groups|protein complex
GRMZM2G497523	-5.66464753	-2.068141419	0.047212499	1	Not Annotated	Not Annotated
GRMZM2G386714	-0.252961929	5.062437523	0.047213481	1	NA-bd_OB_tRNA|aa-tRNA-synt_II|Lys-tRNA-ligase_II|aa-tRNA-synth_II|NA-bd_OB-fold|Lys-tRNA-synth_II_C	nucleotide binding|molecular_function|nucleic acid binding|aminoacyl-tRNA ligase activity|lysine-tRNA ligase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|tRNA metabolic process|translation|tRNA aminoacylation for protein translation|lysyl-tRNA aminoacylation|cellular amino acid metabolic process|biological_process|biosynthetic process|ligase activity|cellular nitrogen compound metabolic process|small molecule metabolic process
GRMZM2G003289	-0.828745997	0.347877178	0.047228572	1	Trp_syn_b_sub_like_PLP_eny_SF	Not Annotated
GRMZM2G306771	-0.771506469	0.950964139	0.047307153	1	Leu-rich_rpt|Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|protein binding|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G112895	-0.387457417	3.347037116	0.047340862	1	Not Annotated	Not Annotated
GRMZM2G086841	-1.3802367	-0.22140044	0.047403271	1	DnaJ_domain	nucleus|response to light stimulus|chloroplast stroma

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G179215	-0.645932338	4.008732995	0.047522562	1	Small_GTPase_Rab_type|Small_GTPase|Small_GTP-bd_dom	nucleotide binding|molecular_function|GTP binding|transport|signal transduction|small GTPase mediated signal transduction|biological_process|protein transport
GRMZM2G037413	6.024278545	-2.082511678	0.047533833	1	Cellulose_synth|Znf_RING	molecular_function|protein binding|cellular_component|carbohydrate metabolic process|biological_process|zinc ion binding|biosynthetic process|membrane|transferase activity, transferring glycosyl groups|cellulose synthase (UDP-forming) activity|cellulose biosynthetic process|ion binding|cell wall|cell|response to stress|response to osmotic stress|response to water deprivation|secondary cell wall biogenesis|positive regulation of abscisic acid biosynthetic process|integral component of membrane|transferase activity|external encapsulating structure|defense response to bacterium|defense response to fungus|cell wall organization or biogenesis
GRMZM2G165272	-0.953812672	4.442567619	0.047651617	1	HSF_DNA-bd	nucleic acid binding transcription factor activity|molecular_function|DNA binding|sequence-specific DNA binding transcription factor activity|cellular_component|intracellular|cell|nucleus|regulation of transcription, DNA-templated|biological_process|organelle|sequence-specific DNA binding
GRMZM2G092968	-0.968259159	1.227760896	0.047672335	1	Not Annotated	Not Annotated
GRMZM2G446625	-0.575758035	3.51123781	0.047721194	1	DUF1350	Not Annotated
GRMZM2G053117	-1.437149867	3.476650092	0.047804801	1	Kinase-like_dom|Methionyl/Leucyl_tRNA_Synth|LACT/PDAT_acylTrfase	nucleotide binding|molecular_function|aminoacyl-tRNA ligase activity|ATP binding|cellular_component|intracellular|cell|cytoplasm|tRNA metabolic process|translation|tRNA aminoacylation for protein translation|cellular amino acid metabolic process|biological_process|biosynthetic process|transferase activity, transferring phosphorus-containing groups|ligase activity|cellular nitrogen compound metabolic process|small molecule metabolic process|lipid metabolic process|O-acyltransferase activity|transferase activity, transferring acyl groups
GRMZM2G006759	-1.393065149	0.70262899	0.047814611	1	Not Annotated	Not Annotated
GRMZM2G416322	-1.408956345	-0.97984116	0.047846466	1	Ser-Thr/Tyr_kinase_cat_dom|Prot_kinase_dom|Kinase-like_dom	molecular_function|protein kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G059212	-0.34486811	6.892070917	0.047864949	1	Glyco_trans_48	1,3-beta-D-glucan synthase complex|molecular_function|1,3-beta-D-glucan synthase activity|cellular_component|cell|plasma membrane|carbohydrate metabolic process|(1->3)-beta-D-glucan biosynthetic process|biological_process|biosynthetic process|cell plate|plasmodesma|membrane|transferase activity, transferring glycosyl groups|protein complex
GRMZM5G833066	-1.255758727	4.054225152	0.047894042	1	Not Annotated	Not Annotated
GRMZM2G342254	-2.122278548	-0.693109287	0.047927047	1	Not Annotated	Not Annotated
GRMZM5G891295	-0.527145896	3.222353383	0.047929014	1	PIG-U	cellular_component|intracellular|cell|cytoplasm|endoplasmic reticulum|endoplasmic reticulum membrane|plasma membrane|cellular protein modification process|GPI anchor biosynthetic process|lipid metabolic process|biological_process|biosynthetic process|integral component of membrane|organelle
AC233864.1_FG014	-1.416903436	-0.357843906	0.047945188	1	DUF616	Not Annotated
GRMZM2G158333	1.237318858	6.257243892	0.048317442	1	Ribosomal_S7_CS|Ribosomal_S7_dom	molecular_function|RNA binding|structural constituent of ribosome|structural molecule activity|translation|biological_process|biosynthetic process

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G364901	-0.376207389	3.672529926	0.048339102	1	Protoporphyrinogen_oxidase|Amino_oxidase	reproduction|nucleotide binding|molecular_function|oxygen-dependent protoporphyrinogen oxidase activity|cellular_component|intracellular|cell|cytoplasm|mitochondrion|porphyrin-containing compound biosynthetic process|biological_process|biosynthetic process|chloroplast|plastid|embryo development|embryo development ending in seed dormancy|chloroplast envelope|oxidoreductase activity|cellular nitrogen compound metabolic process|organelle|anatomical structure development|cofactor metabolic process|oxidation-reduction process
GRMZM2G032337	-0.548737502	3.56078436	0.048393636	1	Prot_kinase_dom|UspA|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	nucleotide binding|molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|response to stress|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G037585	-0.287929269	4.650093051	0.048627275	1	Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	nucleotide binding|molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular_component|cell|plasma membrane|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G472382	-0.800184591	1.152046081	0.048643461	1	PCRF|PrfB|Pep_chain_release_fac_I_II	molecular_function|RNA binding|translation release factor activity|cellular_component|intracellular|cell|cytoplasm|RNA processing|translation|translational termination|translation factor activity, nucleic acid binding|biological_process|biosynthetic process|chloroplast|plastid|plastid organization|translation release factor activity, codon specific|cellular nitrogen compound metabolic process|organelle
GRMZM5G846198	-0.476117623	5.024919139	0.048648169	1	Glyco_trans_8	molecular_function|transferase activity, transferring glycosyl groups
GRMZM2G082330	-0.321068968	5.964458426	0.048724067	1	Protease-assoc_domain|Preselin/SPP|Peptidase_A22B_SPP	molecular_function|aspartic-type endopeptidase activity|cellular_component|cell|vacuolar membrane|plasma membrane|peptidase activity|integral component of membrane
GRMZM2G093623	-0.536414453	3.601141585	0.048727538	1	DNA_mismatch_repair_MutS_C	molecular_function|DNA binding|damaged DNA binding|ATP binding|DNA metabolic process|mismatch repair|response to stress|biological_process|mismatched DNA binding|cellular nitrogen compound metabolic process
GRMZM2G075463	-2.159055047	-1.011168898	0.048779948	1	Not Annotated	Not Annotated
AC211175.3_FG005	-0.451984752	2.785958505	0.048856241	1	Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom|Protein_kinase_ATP_BS	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G058862	-0.679656373	1.330529459	0.048858707	1	TatD_family|DNase_TatD-rel_CS	molecular_function|nuclease activity|endodeoxyribonuclease activity, producing 5'-phosphomonoesters
GRMZM2G059669	-0.39842888	3.485502678	0.048888787	1	Aminotrans_IV	molecular_function|catalytic activity|biological_process|metabolic process
GRMZM2G147112	-5.559918443	-2.117798471	0.048966566	1	Prot_kinase_dom|Kinase-like_dom	molecular_function|protein kinase activity|ATP binding|nucleus|nucleolus|cytoplasm|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G116785	-0.27370797	4.043809229	0.048989197	1	bHLH_dom	molecular_function|DNA binding|regulation of transcription, DNA-templated|biological_process|protein dimerization activity

Gene	log2 (fold change)	log2 (count per million)	P-value	FDR	Interpro	GO
GRMZM2G128477	-0.239680947	3.949183401	0.049024132	1	WD40_repeat|WD40_repeat_dom|WD40_repeat_CS|G-protein_beta_WD-40_rep	molecular_function|protein binding|negative regulation of shoot apical meristem development
GRMZM2G120151	2.372306186	-0.982577197	0.049117446	1	Transcription_factor_TCP|TF_TCP_subgr	Not Annotated
GRMZM2G524711	-0.453033782	2.37559633	0.049120128	1	Not Annotated	molecular_function|protein binding
GRMZM2G313553	-0.468922505	3.80828704	0.049126565	1	HNH_nuc|HNH|Helicase_C	molecular_function|nucleic acid binding|helicase activity|nuclease activity|endonuclease activity|ATP binding
GRMZM2G146446	-0.830924395	4.417841541	0.049182243	1	EGF-like_CS|DUF3522	Not Annotated
GRMZM2G147724	-0.47405868	1.946560911	0.049227749	1	Sphingomyelin_synth-like_dom	molecular_function|lipid metabolic process|biological_process|biosynthetic process|transferase activity, transferring glycosyl groups|sphingolipid biosynthetic process|inositol phosphoceramide synthase activity
AC209987.4_FG010	-0.350867263	3.137847684	0.049232919	1	Plcyanin-like|Cupredoxin	molecular_function|copper ion binding|electron carrier activity|ion binding
GRMZM2G446213	0.753628378	2.688704418	0.04927013	1	DUF1005	cellular_component|cell|plasma membrane|plastid
GRMZM2G136926	-1.110029694	1.081243232	0.049445521	1	Not Annotated	Not Annotated
GRMZM2G143182	-5.324460101	-2.17758658	0.049519285	1	DUF223|NA-bd_OB-fold|Rep_factor-A_C	Not Annotated
GRMZM5G865999	-0.342588811	4.781687994	0.049520823	1	Ser/Thr_dual-sp_kinase_dom|AGC-kinase_C|Prot_kinase_dom|Ser/Thr_kinase_AS|Kinase-like_dom	molecular_function|protein kinase activity|protein serine/threonine kinase activity|ATP binding|cellular protein modification process|protein phosphorylation|biological_process|kinase activity|transferase activity, transferring phosphorus-containing groups
GRMZM2G140728	-1.215049476	1.839073437	0.049554636	1	Glyoxalase-like_dom	Not Annotated
GRMZM2G127478	-1.164114798	0.547393633	0.049572143	1	Not Annotated	Not Annotated
GRMZM2G109354	-0.23238028	4.299193318	0.049637099	1	Transcpt_factor_SBP-box	molecular_function|DNA binding|cellular_component|intracellular|cell|nucleus|organelle
GRMZM2G065498	-3.410580217	6.093521688	0.049649496	1	Plcyanin-like|Cupredoxin	molecular_function|copper ion binding|electron carrier activity|ion binding
GRMZM2G406588	-0.738428715	2.124157676	0.049760731	1	Not Annotated	Not Annotated
GRMZM2G336745	1.772926957	-0.132041302	0.049798285	1	NIF_FeS_clus_asmbl_NifU_N|DUF1084	molecular_function|iron ion binding|biological_process|iron-sulfur cluster assembly|cellular component assembly|ion binding|iron-sulfur cluster binding
GRMZM2G156648	-0.600010587	3.178643898	0.04983792	1	OTU	cellular_component|cell|plasma membrane
GRMZM2G052750	-0.598197969	2.585034449	0.049858712	1	Ribosome_control_1|Quino_amine_DH_bsu	Golgi apparatus
GRMZM2G035213	0.895495728	1.816169497	0.04990849	1	Methyltransf_11|Tocopherol_O-MeTrfase	molecular_function|biological_process|metabolic process|methyltransferase activity|biosynthetic process|vitamin E biosynthetic process|transferase activity|methylation|small molecule metabolic process|tocopherol O-methyltransferase activity
GRMZM2G397836	-0.719662455	3.870243571	0.049936534	1	Cl-channel_volt-gated|CBS_dom|Cl-channel_core	molecular_function|ion channel activity|voltage-gated chloride channel activity|protein binding|cellular_component|transport|chloride transport|biological_process|membrane|transmembrane transporter activity|transmembrane transport|trans-Golgi network|unidimensional cell growth
GRMZM2G177227	-0.756979623	0.743969858	0.049946541	1	Exo70|Cullin_repeat-like_dom	exocyst|cellular_component|intracellular|cell|cytoplasm|transport|exocytosis|biological_process|vesicle-mediated transport|protein complex