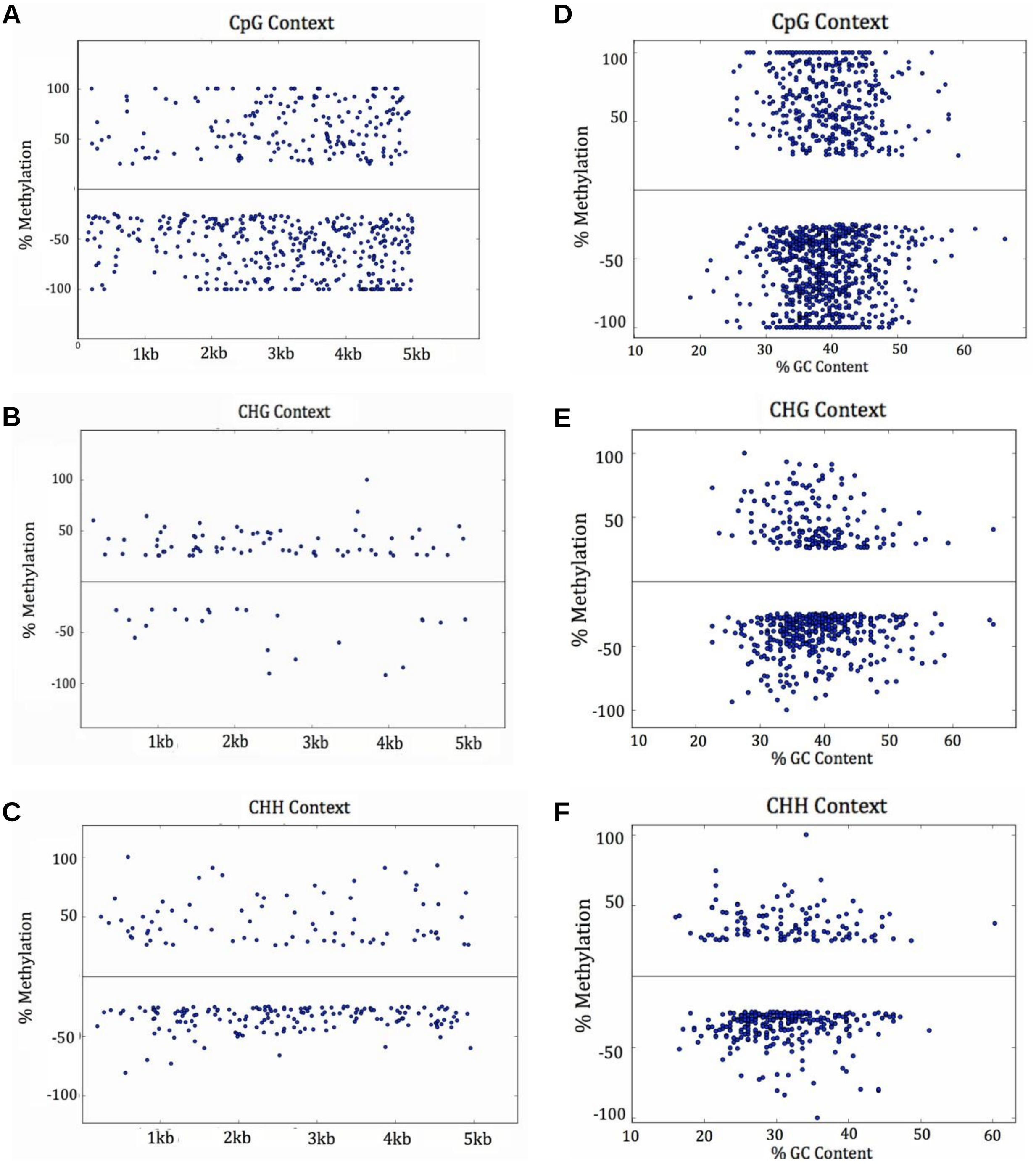

Supplemental Figure 1: Differential methylation levels are independent of gene size and GC content. (A-C) Relationship between gene size and differential methylation in CpG (A), CHG (B), and CHH (C) contexts. (D-F) Relationship between GC content and differential methylation in CpG (D), CHG (E), and CHH (F) contexts.

Supplemental Table1: Summary of cytosine methylation of Methyl-Seq librar

	Methylation context
Paired	Total number of C's analyzed:
	Total C's in CpG context that are methylated
	Total C's in CHG context that are methylated
	Total C's in CHH context that are methylated
	Total C's in unknown context that are methylated
	Total C's in CpG context that are unmethylated
	Total C's in CHG context that are unmethylated
	Total C's in CHH context that are unmethylated
	Total C's in unknown context that are unmethylated
	% C's in CpG context that are methylated
	% C's in CHG context that are methylated
	% C's in CHH context that are methylated
	% C's in unknown context (CN or CHN) that are methylated
Unpaired	Total number of C's analyzed
	Total C's in CpG context that are methylated
	Total C's in CHG context that are methylated
	Total C's in CHH context that are methylated
	Total C's in unknown context that are methylated
	Total C's in CpG context that are unmethylated
	Total C's in CHG context that are unmethylated
	Total C's in CHH context that are unmethylated
	Total C's in unknown context that are unmethylated
	% C's in CpG context that are methylated
	% C's in CHG context that are methylated
	% C's in CHH context that are methylated
	% C's in unknown context (CN or CHN) that are methylated

ries prepared from SCN-infected and control samples.

Control, replication #1	Control, replication #2	Control, replication #3
723,456,481	857156419	293397002
87,767,356	102010655	34398782
63,628,939	75132310	25710478
27,683,854	33567006	11452059
497	598	198
19954680	24381130	8392027
42936454	52191868	17845475
481485198	569873450	195598181
1558	1790	572
81.50%	80.70%	80.40%
59.70%	59.00%	59.00%
5.40%	5.60%	5.50%
24.20%	25.00%	25.70%

5966519	7798697	2637950
733081	930347	314077
529393	683277	232477
270379	355024	123798
13	9	2
187052	251536	86665
365450	490900	166938
3881164	5087613	1713995
22	18	7
79.70%	78.70%	78.40%
59.20%	58.20%	58.20%
6.50%	6.50%	6.70%
37.10%	33.30%	22.20%

SCN-infected, replication #1	**SCN-infected, replication #2**
461144476	894002265
54054778	89931449
39105859	69071527
16549283	31602225
423	540
13377313	26203394
27783614	57164432
310273629	620029238
1227	1521
80.20%	77.40%
58.50%	54.70%
5.10%	4.80%
25.60%	26.20%

4803452	8844841
554858	899974
403668	685436
199520	355432
6	11
165789	300416
306784	595332
3172833	6008251
18	24
77.00%	75.00%
56.80%	53.50%
5.90%	5.60%
25.00%	31.40%

SCN-infected, replication #3
437810581
48290336
35646616
16721866
278
12684354
26211390
298256019
926
79.20%
57.60%
5.30%
23.10%

4222448
464581
342631
191778
8
140767
264589
2818102
6
76.70%
56.40%
6.40%
57.10%

Supplemental Table 2: List of 428 hyper-methylated g

METHYLATED REGIONS
mytileDiff25p200.hyper_CpG.Chr01.422401-422600
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mytileDiff25p200.hyper_CpG.Chr01.5279201-5279400
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jenes in CpG context.

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GENE BODY	Glyma.10G160500
PROMOTER	Glyma.10G180400
GENE BODY	Glyma.10G181400
GENE BODY	Glyma.10G182000
GENE BODY	Glyma.10G205500
GENE BODY	Glyma.10G214100
GENE BODY	Glyma.10G222900
GENE BODY	Glyma.10G250500
GENE BODY	Glyma.10G250800
5'UTR	Glyma.10G266600
GENE BODY (174bp); 3'UTR (26bp)	Glyma.10G266600
5' UTR (19); GENE_BODY (181)	Glyma.10G266800
GENE BODY (68bp); 3'UTR (26 bp)	Glyma.10G266800
GENE BODY	Glyma.10G270800
GENE BODY	Glyma.10G274500
GENE BODY	Glyma.11G007200
GENE BODY	Glyma.11G013900
GENE BODY	Glyma.11G024700
GENE BODY	Glyma.11G027000
GENE BODY (44bp); 3'UTR (156bp)	Glyma.11G038500
GENE BODY	Glyma.11G046100
GENE BODY	Glyma.11G047800
GENE BODY	Glyma.11G059600
GENE BODY	Glyma.11G075600
GENE BODY	Glyma.11G077000
GENE BODY	Glyma.11G081200
PROMOTER (170bp); GENE BODY (30bp)	Glyma.11G115900
GENE BODY	Glyma.11G125100
GENE BODY	Glyma.11G131600
GENE BODY	Glyma.11G135300
PROMOTER (134bp); GENE BODY (66bp)	Glyma.11G160300
PROMOTER	Glyma.11G162300
GENE BODY	Glyma.11G170700
GENE BODY	Glyma.11G211200
GENE BODY	Glyma.11G218000
3'UTR	Glyma.11G234200
GENE BODY	Glyma.12G001100
GENE BODY	Glyma.12G001400
5'UTR (95bp); GENE BODY (105bp)	Glyma.12G022400
GENE BODY	Glyma.12G027400

PROMOTER	Glyma.12G028200
GENE BODY	Glyma.12G052000
GENE BODY	Glyma.12G052700
GENE BODY	Glyma.12G052800
GENE BODY	Glyma.12G072900
GENE BODY	Glyma.12G095300
GENE BODY	Glyma.12G101500
GENE BODY	Glyma.12G107000
GENE BODY	Glyma.12G151500
PROMOTER	Glyma.12G152500
GENE BODY	Glyma.12G157700
GENE BODY	Glyma.12G180800
GENE BODY	Glyma.12G188100
GENE BODY	Glyma.12G189100
GENE BODY	Glyma.13G040300
GENE BODY	Glyma.13G048900
GENE BODY	Glyma.13G051300
GENE BODY (76bp); 3'UTR (124bp)	Glyma.13G054500
GENE BODY	Glyma.13G073900
GENE BODY	Glyma.13G080100
GENE BODY	Glyma.13G107100
GENE BODY	Glyma.13G120800
GENE BODY	Glyma.13G124000
GENE BODY (145bp); 3'UTR (55bp)	Glyma.13G127100
PROMOTER (145bp); 5'UTR (55bp)	Glyma.13G139100
GENE BODY (166bp); 3'UTR (34bp)	Glyma.13G145400
GENE BODY	Glyma.13G149200
GENE BODY	Glyma.13G154200
GENE BODY	Glyma.13G163500
GENE BODY	Glyma.13G207200
GENE BODY	Glyma.13G221200
PROMOTER	Glyma.13G222200
GENE BODY	Glyma.13G238000
5'UTR (14bp); GENE BODY (186bp)	Glyma.13G250900
GENE BODY	Glyma.13G297200
PROMOTER (167bp); GENE BODY (33bp)	Glyma.13G320700
GENE BODY	Glyma.13G336200
GENE BODY	Glyma.13G341000
GENE BODY	Glyma.13G342900
GENE BODY (155bp); 3'UTR (45bp)	Glyma.13G344400
GENE BODY	Glyma.13G346900

GENE BODY	Glyma.13G351800
GENE BODY	Glyma.13G362000
GENE BODY	Glyma.13G366100
GENE BODY	Glyma.14G007700
GENE BODY	Glyma.14G012200
GENE BODY	Glyma.14G068900
GENE BODY	Glyma.14G097800
GENE BODY	Glyma.14G123700
GENE BODY (44bp); 3'UTR (156bp)	Glyma.14G127700
5'UTR (89bp); GENEBODY (111bp)	Glyma.14G135900
GENE BODY	Glyma.14G142300
GENE BODY	Glyma.14G146200
GENE BODY	Glyma.14G149700
3'UTR	Glyma.14G149800
GENE BODY	Glyma.14G182400
GENE BODY	Glyma.14G182500
GENE BODY (153bp); 3'UTR (47bp)	Glyma.14G210200
GENE BODY	Glyma.15G013500
GENE BODY	Glyma.15G047100
GENE BODY	Glyma.15G068100
GENE BODY (177bp); 3'UTR (23bp)	Glyma.15G084700
GENE BODY	Glyma.15G086200
GENE BODY	Glyma.15G091000
GENE BODY	Glyma.15G093600
GENE BODY (189bp);3'UTR (11bp)	Glyma.15G094500
3'UTR	Glyma.15G094600
GENE BODY	Glyma.15G115500
GENE BODY	Glyma.15G134800
GENE BODY (181bp); 5'UTR (19bp)	Glyma.15G140300
PROMOTER	Glyma.15G142000
GENE BODY	Glyma.15G171400
GENE BODY	Glyma.15G177000
GENE BODY	Glyma.15G195700
GENE BODY	Glyma.15G230500
GENE BODY	Glyma.15G235500
GENE BODY	Glyma.15G255300
GENE BODY	Glyma.15G275000
GENE BODY	Glyma.16G004800
GENE BODY	Glyma.16G018400
GENE BODY	Glyma.16G022600
GENE BODY	Glyma.16G026000

GENE BODY	Glyma.16G043300
5'UTR (145bp); GENEBODY (55bp)	Glyma.16G069400
GENE BODY	Glyma.16G070900
GENE BODY	Glyma.16G077500
GENE BODY	Glyma.16G082400
GENE BODY	Glyma.16G092500
GENE BODY	Glyma.16G131900
GENE BODY	Glyma.16G131900
PROMOTER (7bp); 5'UTR (193bp)	Glyma.16G144000
GENE BODY	Glyma.16G174700
GENE BODY	Glyma.16G193200
3'UTR	Glyma.16G195300
GENE BODY	Glyma.16G210200
GENE BODY	Glyma.17G006600
GENE BODY	Glyma.17G011500
GENE BODY	Glyma.17G015000
GENE BODY	Glyma.17G015200
GENE BODY (140bp); 3'UTR (60bp)	Glyma.17G022900
GENE BODY	Glyma.17G031900
GENE BODY (190bp); 3'UTR (10bp)	Glyma.17G033700
GENE BODY	Glyma.17G046900
GENE BODY	Glyma.17G052100
GENE BODY	Glyma.17G107600
5'UTR (6); GENE BODY (194)	Glyma.17G120400
GENE BODY	Glyma.17G120900
GENE BODY	Glyma.17G121700
GENE BODY	Glyma.17G122300
GENE BODY	Glyma.17G139100
GENE BODY	Glyma.17G145000
GENE BODY	Glyma.17G146400
GENE BODY	Glyma.17G157100
GENE BODY	Glyma.17G163700
5'UTR (58bp); GENE BODY (142bp)	Glyma.17G166700
3'UTR	Glyma.17G204900
GENE BODY	Glyma.17G220800
PROMOTER	Glyma.17G221300
GENE BODY	Glyma.17G245800
GENE BODY	Glyma.17G249900
GENE BODY	Glyma.18G002400
5'UTR	Glyma.18G016800
GENE BODY	Glyma.18G018300

GENE BODY	Glyma.18G021500
GENE BODY	Glyma.18G039000
GENE BODY	Glyma.18G040400
GENE BODY	Glyma.18G044200
PROMOTER	Glyma.18G047900
GENE BODY	Glyma.18G063000
GENE BODY	Glyma.18G067400
GENE BODY	Glyma.18G085100
GENE BODY	Glyma.18G085200
GENE BODY (52bp); 5'UTR (148bp)	Glyma.18G087100
GENE BODY	Glyma.18G106800
GENE BODY	Glyma.18G136200
GENE BODY	Glyma.18G154700
GENE BODY	Glyma.18G155200
GENE BODY	Glyma.18G181300
PROMOTER	Glyma.18G181400
GENE BODY	Glyma.18G181500
GENE BODY	Glyma.18G184400
GENE BODY (173bp); 3'UTR (27bp)	Glyma.18G197600
GENE BODY	Glyma.18G222100
GENE BODY	Glyma.18G224000
GENE BODY	Glyma.18G228000
GENE BODY	Glyma.18G232900
GENE BODY	Glyma.18G251900
GENE BODY	Glyma.18G298100
GENE BODY	Glyma.19G020200
GENE BODY	Glyma.19G021700
GENE BODY	Glyma.19G026600
GENE BODY	Glyma.19G029100
GENE BODY	Glyma.19G033500
GENE BODY	Glyma.19G039100
GENE BODY	Glyma.19G040800
GENE BODY	Glyma.19G053500
GENE BODY	Glyma.19G073600
PROMOTER	Glyma.19G091700
GENE BODY	Glyma.19G103200
GENE BODY	Glyma.19G125800
PROMOTER	Glyma.19G169700
PROMOTER (51bp); GENE BODY (149bp)	Glyma.19G169800
GENE BODY	Glyma.19G170200
GENE BODY	Glyma.19G175400

PROMOTER (162bp); GENE BODY (38bp)	Glyma.19G184000
GENE BODY	Glyma.19G186900
GENE BODY	Glyma.19G191800
GENE BODY	Glyma.19G191900
3'UTR	Glyma.19G204200
5'UTR	Glyma.19G217200
GENE BODY	Glyma.19G229200
GENE BODY	Glyma.19G237000
GENE BODY	Glyma.19G239700
GENE BODY	Glyma.19G256500
GENE BODY	Glyma.20G005400
GENE BODY	Glyma.20G005400
GENE BODY	Glyma.20G036600
GENE BODY	Glyma.20G087700
GENE BODY	Glyma.20G093200
GENE BODY	Glyma.20G102800
GENE BODY	Glyma.20G111200
GENE BODY	Glyma.20G121600
3'UTR (151bp); GENE BODY (49bp)	Glyma.20G126800
GENE BODY	Glyma.20G130800
PROMOTER	Glyma.20G131200
GENE BODY	Glyma.20G138600
GENE BODY	Glyma.20G161800
GENE BODY	Glyma.20G170500
GENE BODY	Glyma.20G192200
GENE BODY	Glyma.20G239100
GENE BODY	Glyma.20G242400

GENE ANNOTATION	% Methylation Diffe	q value
Regulator of Vps4 activity in the MVB pathway proteir	59.97067449	0.00460124
protein kinase family protein / peptidoglycan-binding	100	2.6925E-08
NSP-interacting kinase 3	100	3.38582E-06
pyruvate dehydrogenase complex E1 alpha subunit	100	0.000703795
peroxisomal adenine nucleotide carrier 1	53.65853659	0.002540759
SNF2 domain-containing protein / helicase domain-co	50.71428571	0.001320947
Nucleoporin autopeptidase	100	0.000115391
Family of unknown function (DUF572)	86.66666667	0.008526819
Disease resistance protein (TIR-NBS-LRR class) family	25.70010973	7.82947E-08
arginase	100	0.005353107
SLOW GROWTH 1	100	0.005353107
N/A	46.2962963	0.005823103
DNA binding;zinc ion binding;nucleic acid binding;nucl	75.91836735	2.4749E-05
Cytochrome P450 superfamily protein	30.5785124	0.002048788
NmrA-like negative transcriptional regulator family pr	67.79661017	2.79341E-06
Protein kinase superfamily protein	69.57328386	0.006793816
RNA-binding (RRM/RBD/RNP motifs) family protein	44.44444444	0.004287198
DNAJ heat shock N-terminal domain-containing protei	90.90909091	1.40706E-05
histone deacetylase 1	100	1.13095E-05
germin-like protein 10	37.25490196	8.05292E-08
ATP binding cassette subfamily B4	81.81818182	0.001920592
nuclear encoded CLP protease 5	63.26530612	0.001455847
CTP synthase family protein	100	0.001240448
Calcium-dependent phosphotriesterase superfamily p	33.33333333	0.001021467
Chaperone DnaJ-domain superfamily protein	57.44680851	0.001337013
NAD(P)-binding Rossmann-fold superfamily protein	50	0.009463526
Protein Transporter, Pam16	27.97131148	0.008193419
ribosomal protein L23AB	90	5.18275E-05
dihydrosphingosine phosphate lyase	85.71428571	0.004907369
Protein kinase superfamily protein	51.2195122	0.000310115
RING/FYVE/PHD zinc finger superfamily protein	27.53623188	0.002670807
Plant protein of unknown function (DUF863)	94.73684211	0.000566467
glutamine synthetase 1;4	55.74712644	0.004907369
ARM repeat superfamily protein	76	0.004550831
fucosyltransferase 11	37.70177839	5.09444E-06
Phox-associated domain;Phox-like;Sorting nexin, C-ter	29.10605847	3.23379E-05
curculin-like (mannose-binding) lectin family protein /	48.38709677	0.001192665
guanylate kinase	44.28571429	0.005131118
auxin F-box protein 5	100	0.001933999

Restriction endonuclease, type II-like superfamily prot	41.91561845	2.53603E-13
RING/U-box superfamily protein	67.3951049	0.00422635
HEAT/U-box domain-containing protein	97.77777778	2.56349E-09
Protein of unknown function, DUF593	36.81427627	0.00139898
E3 ubiquitin ligase, putative	88.88888889	0.000299513
Sucrase/ferredoxin-like family protein	36.92307692	0.005115318
S-locus lectin protein kinase family protein	46.96969697	1.14187E-08
ENTH/VHS family protein	54.16666667	0.000424206
RNAhelicase-like 8	100	1.41839E-07
growth-regulating factor 9	70.90909091	0.004876312
LOB domain-containing protein 18	47.45762712	0.000581895
GPI transamidase component Gpi16 subunit family pr	86.20689655	7.97829E-06
Vacuolar sorting protein 39	100	3.22217E-05
P-loop containing nucleoside triphosphate hydrolases	70	0.005646129
N/A	100	0.001240448
NIMA-related kinase 5	55.3030303	3.94734E-05
debranching enzyme 1	64.70588235	0.000501408
GroES-like zinc-binding dehydrogenase family protein	100	2.39209E-05
Basic-leucine zipper (bZIP) transcription factor family	47.22222222	0.004284865
Prolyl oligopeptidase family protein	100	0.001933999
glucose-6-phosphate dehydrogenase 4	100	0.005353107
ARM repeat superfamily protein	39.05187835	0.00460124
Esterase/lipase/thioesterase family protein	86.66666667	0.003440723
Ankyrin repeat family protein	88.75	7.33139E-05
Protein of unknown function (DUF3133)	73.33333333	0.005282421
ER lumen protein retaining receptor family protein	30.43478261	0.00319357
switch subunit 3	41.61573213	0.002243341
DNA glycosylase superfamily protein	38.33333333	0.00112567
Protein of unknown function (DUF3223)	61.11111111	0.000713436
glycine-rich protein	39.3764063	0.003161348
CTC-interacting domain 7	97.14285714	2.92739E-06
Pentatricopeptide repeat (PPR) superfamily protein	51.31578947	0.003175057
Peptidyl-tRNA hydrolase II (PTH2) family protein	90.90909091	0.004921546
sequence-specific DNA binding transcription factors;tr	52.10803689	0.008172975
conserved peptide upstream open reading frame 37	52.10803689	0.008172975
O-fucosyltransferase family protein	95.65217391	0.00016351
P-loop containing nucleoside triphosphate hydrolases	100	3.88087E-07
Ribosomal protein S19e family protein	100	0.000703795
Thioredoxin z	67.56756757	0.005375249
Galactose oxidase/kelch repeat superfamily protein	77.14285714	0.006403301
DCD (Development and Cell Death) domain protein	100	0.001933999

N/A	100	6.22335E-07
ribonuclease II family protein	90	0.008505711
ribonuclease II family protein	36.0673847	0.000606269
P-loop containing nucleoside triphosphate hydrolases	26.46587061	0.001970548
NADH-dependent glutamate synthase 1	44.23076923	0.00286027
Protein of unknown function (DUF668)	80.90909091	0.007896428
Protein of unknown function (DUF1644)	25.95866256	1.72831E-07
Smg-4/UPF3 family protein	59.46428571	3.93888E-06
ADP-ribosylation factor A1B	34.14634146	0.006270513
HSP20-like chaperones superfamily protein	100	0.000534009
homolog of nucleolar protein NOP56	28.191246	6.41886E-05
O-fucosyltransferase family protein	100	0.000534009
myb-like transcription factor family protein	91.66666667	9.72954E-05
N/A	86.36363636	0.001058832
N/A	41.17406487	6.64903E-17
N/A	36.91548692	5.906E-10
Phototropic-responsive NPH3 family protein	42.64705882	0.009486365
N/A	85.71428571	0.003645592
Calmodulin-binding transcription activator protein wit	93.33333333	2.45968E-10
chromatin remodeling 4	64.2962963	0.000753828
ENTH/VHS/GAT family protein	95.45454545	2.14973E-05
TRICHOME BIREFRINGENCE-LIKE 23Methylated_Regio	100	1.85987E-10
Tetratricopeptide repeat (TPR)-like superfamily protei	52.94117647	0.006971016
Mitochondrial ATP synthase subunit G protein	86.66666667	0.008526819
Mitochondrial ATP synthase subunit G protein	90	0.000188727
RNApolymerase sigma subunit 2	64.58333333	0.007936784
autoinhibited Ca2+-ATPase 1	66.66666667	0.004711596
N/A	66.66666667	0.004711596
LisH dimerisation motif;WD40/YVTN repeat-like-conta	93.10344828	0.000147771
GATA-type zinc finger protein with TIFY domain	28.52408308	0.00256575
phosphoenolpyruvate carboxylase-related kinase 2	25.32994428	0.001563456
alpha/beta-Hydrolases superfamily protein	87.5	0.005934657
N/A	54.16666667	7.19661E-05
Peptidase C78, ubiquitin fold modifier-specific peptida	100	0.001933999
Protein Transporter, Pam16	58	0.001418149
N/A	100	0.000163436
nudix hydrolase homolog 19	64.28571429	0.00397489
S-locus lectin protein kinase family protein	54.05405405	9.65375E-05
S-locus lectin protein kinase family protein	48.03921569	4.40126E-05
O-methyltransferase family protein	28.7049732	4.50083E-07
Protein kinase superfamily protein	62.16216216	2.58813E-05

glutamate receptor 3.4	90	0.004165018
WPP domain interacting protein 1	32.88299935	5.92326E-06
SNARE-like superfamily protein	46.55172414	0.003404756
O-fucosyltransferase family protein	92.30769231	0.001904087
exocyst subunit exo70 family protein G1	42.37891738	0.000137185
glucose-6-phosphate dehydrogenase 1	100	0.000277356
actin binding protein family	90	4.31948E-05
NAD(P)-binding Rossmann-fold superfamily protein	40.15151515	0.001323216
Calcineurin-like metallo-phosphoesterase superfamily	78.66666667	3.79056E-05
ribosomal protein L5 B	100	0.001933999
Copper transport protein family	30	1.88168E-05
NF-X-like 1	66.46766169	0.001753712
Protein kinase superfamily protein	77.01149425	0.001735936
Phosphoribosyltransferase family protein	54.54545455	0.005925316
delta 1-pyrroline-5-carboxylate synthase 2	65.43478261	0.000740742
DNAJ heat shock family protein	100	0.000796198
SU(VAR)3-9 homolog 9	49.89316239	0.00837369
basic helix-loop-helix (bHLH) DNA-binding superfamily	46.66666667	0.007949013
SERINE CARBOXYPEPTIDASE-LIKE 49	25.34040518	8.32659E-06
receptor kinase 1	30.74176104	0.0089048
Fumarylacetoacetate (FAA) hydrolase family	44.68267581	0.001749681
CBS domain-containing protein with a domain of unkr	39.53488372	0.005008332
RNA-binding (RRM/RBD/RNP motifs) family protein	45.90163934	0.003910739
alpha/beta-Hydrolases superfamily protein	52.82258065	0.001574405
tRNA/rRNA methyltransferase (SpoU) family protein	100	0.000703795
Sec1/munc18-like (SM) proteins superfamily	73.21428571	0.003456358
starch synthase 4	71.23287671	0.003865571
Minichromosome maintenance (MCM2/3/5) family pr	100	9.19326E-05
Transketolase family protein	76.66666667	0.002979043
Chalcone and stilbene synthase family protein	28.18035427	0.000254749
Protein of unknown function (DUF1644)	92.59259259	1.99309E-05
RAB GDP dissociation inhibitor 2	66.66666667	0.000107792
leucine-rich repeat transmembrane protein kinase far	60.95571096	0.001687678
aspartate aminotransferase	72.22222222	0.008968817
nuclear pore anchor	91.66666667	0.000531226
ubiquinol-cytochrome C chaperone family protein	88.23529412	0.000181199
N/A	100	4.77422E-10
DEA(D/H)-box RNA helicase family protein	100	4.77422E-10
ATP-dependent peptidases;nucleotide binding;serine-	27.16384739	0.005579319
auxin transport protein (BIG)	45.45454545	0.000389249
male gametophyte defective 3	38.85714286	4.70906E-06

Kinase interacting (KIP1-like) family protein	36.40254341	5.94932E-05
RNA-binding CRS1 / YhbY (CRM) domain-containing pr	67.85714286	0.003062832
TATA BOX ASSOCIATED FACTOR II 59	100	9.291E-06
Protein of unknown function (DUF1644)	95.55555556	1.65597E-07
pentatricopeptide (PPR) repeat-containing protein	90.90909091	0.002195562
tubulin folding cofactor E / Pfifferling (PFI)	90	0.000150272
Intron maturase, type II family protein	91.89189189	8.92381E-05
hercules receptor kinase 2	83.33333333	0.002153108
GTP binding	54.54545455	0.001442614
toprim domain-containing protein	92.30769231	0.004921546
Translation initiation factor SUI1 family protein	44.92753623	4.56951E-05
Protein kinase superfamily protein	33.65732369	0.000760638
Pentatricopeptide repeat (PPR-like) superfamily prote	61.8556701	2.22958E-06
N/A	62.87878788	2.19395E-05
N/A	72.95238095	9.0706E-06
ATP-dependent Clp protease	84.59459459	0.000427669
protein tyrosine kinase family protein	60.60606061	0.005062639
zinc finger protein-related	56.66666667	0.000128408
Protein of unknown function, DUF538	100	0.000175386
NSP (nuclear shuttle protein)-interacting GTPase	50	0.003675254
sugar transporter 14	49.31677019	0.000229292
N/A	65.46610169	5.63119E-06
sister chromatid cohesion 1 protein 4	100	9.19326E-05
LUC7 related protein	81.81818182	0.007012912
GRIP-related ARF-binding domain-containing protein 1	68.75	0.000299513
titan9	82.22222222	0.000229292
myosin XI D	100	0.000534009
ribonuclease Ps	50	0.005183954
Galactose oxidase/kelch repeat superfamily protein	72.36842105	7.96564E-06
NIMA-related kinase 4	90.90909091	0.00016351
chloroplast RNA-binding protein 29	77.27272727	0.000499771
KCBP-interacting protein kinase	81.81818182	0.001485491
SERINE CARBOXYPEPTIDASE-LIKE 49	100	6.21853E-10
INO80 ortholog	84.61538462	0.00023892
N/A	31	3.16655E-05
10-formyltetrahydrofolate synthetase	31	3.16655E-05
Transcriptional coactivator/pterin dehydratase	35.38461538	0.005353107
S-adenosyl-L-methionine-dependent methyltransferas	91.30434783	0.000152866
anaphase-promoting complex/cyclosome 11	92.85714286	0.00327541
TOPLESS-related 3	78.65497076	1.104E-05
N/A	100	0.000534009

HSP20-like chaperones superfamily protein	72.72727273	8.96769E-05
zeta-carotene desaturase	57.14285714	0.005146361
CAMV movement protein interacting protein 7	30.76761525	0.009714209
S-adenosyl-L-methionine-dependent methyltransferas	72.15189873	0.006029944
N/A	56	0.008180794
phosphoenolpyruvate carboxylase 4	68.11594203	0.008002959
N/A	58.65102639	0.00170456
DHHC-type zinc finger family protein	82.5	1.43495E-12
Homeotic gene regulator	40.55258467	0.006311455
NPK1-related protein kinase 3	84.61538462	0.0016582
Endosomal targeting BRO1-like domain-containing prc	80	0.008552
Endosomal targeting BRO1-like domain-containing prc	77.5862069	0.002492172
N/A	80	0.008552
N/A	77.5862069	0.002492172
trehalose phosphatase/synthase 5	96	3.94723E-05
N/A	34.11329137	2.29387E-06
N/A	78	0.000292927
KH domain-containing protein	80	0.007299149
Leucine-rich repeat protein kinase family protein	90.90909091	0.002195562
hydroxymethylglutaryl-CoA synthase / HMG-CoA synt	100	0.000796198
Restriction endonuclease, type II-like superfamily prot	32.67973856	0.008596793
Carbohydrate-binding protein	40.38461538	0.001806186
plant U-box 49	62.71186441	0.005164617
Pentatricopeptide repeat (PPR) superfamily protein	90	0.000120058
N/A	75.51020408	0.005173153
Phosphatidylinositol 3- and 4-kinase family protein wi	67.85714286	5.74583E-05
RNA polymerase II large subunit	33.79120879	0.000664113
Chloroplast Ycf2;ATPase, AAA type, core	40.24435394	0.000837685
P-loop containing nucleoside triphosphate hydrolases	72.72727273	0.003077442
Putative glycosyl hydrolase of unknown function (DUF	100	0.000175386
Tetratricopeptide repeat (TPR)-like superfamily protei	76.92307692	0.004905666
Insulinase (Peptidase family M16) family protein	60.38647343	0.000776284
homolog of histone chaperone HIRA	35.48387097	0.001920592
cleavage and polyadenylation specificity factor 100	100	0.001240448
transcription factor-related	25.05145798	2.23026E-05
DegP protease 7	47.43961353	0.000227945
N/A	58.20895522	0.002774689
Pentatricopeptide repeat (PPR) superfamily protein	90	0.000150272
Methylthiotransferase	80	0.001078742
N/A	29.6875	0.005960506
nucleolin like 2	51.45424837	1.35949E-07

Calcium-dependent lipid-binding (CaLB domain) famil	33.01127214	0.002262668
Far-red impaired responsive (FAR1) family protein	76	0.001056985
ARM repeat superfamily protein	100	0.000356554
cell division cycle protein 48-related / CDC48-related	100	1.79916E-05
N/A	100	1.80662E-05
BRI1 suppressor 1 (BSU1)-like 2	100	0.005353107
Protein of unknown function (DUF604)	100	0.000534009
NAD(P)H dehydrogenase B1	100	2.76356E-05
Nucleotide-diphospho-sugar transferases superfamily	58.33333333	0.004382042
purine permease 5	43.65576284	4.8246E-08
phosphoesterase	100	0.000175386
DNA/RNA helicase protein	61.52829191	6.15235E-07
Leucine-rich repeat protein kinase family protein	71.42857143	0.000954694
mitochondrial editing factor 20	51.12299465	5.77753E-08
plastid division1	100	7.77969E-06
glycosyl hydrolase family 81 protein	67.27272727	0.006637634
N/A	57.26227795	0.003828761
ARM repeat superfamily protein	100	0.000703795
protein kinase 2A	36.1025641	0.005131118
Tetratricopeptide repeat (TPR)-like superfamily protei	71.02272727	0.006329252
Ribosomal protein L18ae family	71.875	0.003804626
P-loop containing nucleoside triphosphate hydrolases	43.63636364	0.000340295
Rho termination factor	70.50092764	0.009132855
Leucine-rich repeat transmembrane protein kinase fa	52.10803689	0.008172975
Transducin/WD40 repeat-like superfamily protein	68.88888889	2.29387E-06
ACT-like superfamily protein	42.22222222	2.62633E-05
ser/arg-rich protein kinase 4	81.03448276	0.000429508
Ubiquitin C-terminal hydrolases superfamily protein	71.42857143	0.005353107
Leucine-rich repeat family protein	64	0.000343098
NAD(P)-binding Rossmann-fold superfamily protein	51.46871009	0.009468768
Phototropic-responsive NPH3 family protein	90.90909091	0.004921546
Protein of unknown function (DUF1000)	48.14814815	7.79233E-06
Telomerase activating protein Est1	100	0.001240448
Ribonuclease E inhibitor RraA/Dimethylmenaquinone	85.71428571	0.003645592
Protein of unknown function (DUF1421)	94.44444444	0.000775974
ARM repeat superfamily protein	80.85106383	2.49223E-05
triosephosphate isomerase	56.41025641	0.007970342
A20/AN1-like zinc finger family protein	86.36363636	0.001440019
topoisomerase 6 subunit B	66.66666667	3.08821E-05
crinkly4	29.78723404	7.14707E-05
CTC-interacting domain 4	100	1.65617E-05

Protein phosphatase 2A, regulatory subunit PR55	94.44444444	5.62741E-05
pleiotropic drug resistance 12	48.93617021	0.00195593
Pre-mRNA-processing-splicing factor	90	0.000312342
HEAT SHOCK PROTEIN 89.1	70.76923077	0.00244009
Kinase-related protein of unknown function (DUF129	100	0.005353107
ARM repeat superfamily protein	65.83333333	0.000664113
S-adenosyl-L-methionine-dependent methyltransfera	37.14285714	0.008730732
plastid division1	40.90909091	0.000785474
Ribosomal protein L33 family protein	87.5	0.00077132
N/A	42.36641221	0.000406439
Sulfite exporter TauE/SafE family protein	100	0.005353107
N/A	77.36842105	0.000903423
long chain acyl-CoA synthetase 9	28.74006453	2.20084E-06
N/A	28.74006453	2.20084E-06
hydroxyproline-rich glycoprotein family protein	90.90909091	0.000566467
Restriction endonuclease, type II-like superfamily prot	90.90909091	0.000566467
autophagy protein Apg5 family	91.30434783	0.000325828
CASC3/Barentsz eIF4AIII binding	36.69172932	0.003705057
Plant protein of unknown function (DUF639)	95.65217391	1.61342E-06
Tetratricopeptide repeat (TPR)-like superfamily protei	58.97435897	0.00412992
Pentatricopeptide repeat (PPR) superfamily protein	47.61904762	0.001314704
plant U-box 17	65.625	0.000464513
auxin response factor 8	76.19047619	0.002126331
cullin4	31.27548049	0.000375798
alpha-mannosidase 3	93.33333333	0.000116803
potassium channel in Arabidopsis thaliana 1	93.33333333	0.000116803
Inositol monophosphatase family protein	68.29268293	2.16506E-05
Ribosomal protein L12/ ATP-dependent Clp protease	100	0.000115391
ATP-citrate lyase B-1	25.49019608	0.001933999
N/A	92.30769231	5.87593E-05
N/A	88.23529412	0.004244872
Mob1/phocein family protein	53.84615385	0.008698249
N/A	53.08641975	2.39209E-05
Polynucleotidyl transferase, ribonuclease H-like super	60.41666667	0.008827127
PREFOLDIN 1	52.17391304	0.003546663
Trypsin family protein	53.03030303	0.002618347
Cellulose synthase family protein	80	0.00218781
ATPases;nucleotide binding;ATP binding;nucleoside-tr	26.66666667	0.005771093
transducin family protein / WD-40 repeat family prot	100	0.000796198
Protein kinase superfamily protein	54.54545455	3.56531E-05
pentatricopeptide (PPR) repeat-containing protein	86.14718615	0.00139578

apyrase 2	74.46428571	7.49529E-05
S-adenosyl-L-methionine-dependent methyltransferas	71.52777778	1.80691E-11
RNA-binding (RRM/RBD/RNP motifs) family protein	76.59574468	0.004387699
golgin candidate 1	88.57142857	1.04662E-06
Sec23/Sec24 protein transport family protein	100	0.001933999
N/A	100	0.001933999
compromised recognition of TCV 1	61.53846154	0.002461367
compromised recognition of TCV 1	100	1.15987E-09
Protein kinase superfamily protein	51.2195122	0.001098386
disease resistance family protein / LRR family protein	35.75989783	0.005071096
CAP160 protein	52.38095238	0.002365643
F-box/RNI-like superfamily protein	44.11764706	0.00432082
hydroxyproline-rich glycoprotein family protein	72.80701754	0.001484791
microtubule-associated proteins 70-5	28.57699805	0.007765513
Saposin-like aspartyl protease family protein	100	0.000115391
tobamovirus multiplication 1	52.38095238	0.001724632
phospholipases;galactolipases	30.80467919	0.005009981
N/A	45.65217391	0.008725044
calmodulin binding;transcription regulators	64.28571429	2.84235E-06
PAS domain-containing protein tyrosine kinase family	100	0.001933999
ARM repeat superfamily protein	71.42857143	0.006163469
Transducin/WD40 repeat-like superfamily protein	54.23728814	0.000379699
N/A	33.30395829	0.00037888
fatty acyl-ACP thioesterases B	28.38612368	0.007118315
histone deacetylase 15	47.54299754	0.008669534
Transcription factor TFIIE, alpha subunit	57.89473684	0.001262576
arogenate dehydrogenase	29.15662651	0.002726993
Phosphatidic acid phosphatase (PAP2) family protein	68.75	0.007623546
PPPDE putative thiol peptidase family protein	91.66666667	0.000531226
Plant VAMP (vesicle-associated membrane protein) fa	75	0.001377202
N/A	37.67292127	1.67271E-13
casein kinase alpha 1	69.49152542	0.00716723
MRG family protein	63.08243728	0.0002397
mitotic-like cyclin 3B from Arabidopsis	100	0.000703795
histidine kinase 5	25.83476027	0.00795685
Protein of unknown function (DUF1336)	38.98305085	0.000788107
N/A	86.42857143	0.000603677
GYF domain-containing protein	56	0.004902405
DNA repair-recombination protein (RAD50)	43.44086022	0.000813972
ubiquitin-specific protease 4	52	0.002856708
Protein of unknown function (DUF630 and DUF632)	45.27272727	4.18656E-05

Uroporphyrinogen decarboxylase	55.69620253	0.000102596
DegP protease 7	92.30769231	0.001904087
ALWAYS EARLY 4	40.47354791	0.001643595
Homeodomain-like superfamily protein	37.89431384	0.000137899
nodulin MtN21 /EamA-like transporter family protein	29.69866418	0.002513721
smr (Small MutS Related) domain-containing protein	95.23809524	2.50298E-08
RNA helicase, ATP-dependent, SK12/DOB1 protein	60	0.005907747
beta-1,2-xylosyltransferase	51.66666667	0.000105925
beta-1,2-xylosyltransferase	51.66666667	0.000105925
N/A	52.07017544	0.009832971
MAP kinase 20	29.78723404	0.004711596
trehalose phosphate synthase	100	2.29387E-06
Phototropic-responsive NPH3 family protein	40.36697248	0.001244221
plant U-box 9	100	0.000534009
myb-like HTH transcriptional regulator family protein	45.47088426	0.008806789
N/A	45.47088426	0.008806789
protein kinase 1B	92.85714286	0.001904087
Sulfite exporter TauE/SafE family protein	27.42470296	0.000407564
sulfoquinovosyldiacylglycerol 2	41.19743407	3.16655E-05
zinc finger protein-related	54.28571429	0.007693472
Calcium-dependent lipid-binding (CaLB domain) family	100	0.000703795
5\'-3\' exonuclease family protein	75	0.000244744
RNA polymerase II transcription mediators	56	0.006489924
Protein of unknown function (DUF630 and DUF632)	100	1.15987E-09
TCP-1/cpn60 chaperonin family protein	39.0625	0.009395572
Pectate lyase family protein	55	0.000441067
N/A	78.33333333	0.001959434
purple acid phosphatase 23	61.11111111	0.001369449
PHD finger family protein	100	5.68891E-07
COBRA-like extracellular glycosyl-phosphatidyl inosito	78.57142857	0.00338527
NSP-interacting kinase 1	75.97402597	2.47622E-10
Proline-rich spliceosome-associated (PSP) family prote	77.27272727	0.006226358
NAD-dependent glycerol-3-phosphate dehydrogenase	54.16666667	0.005138627
NAD+ transporter 2	73.21428571	0.005836783
zinc ion binding;nucleic acid binding;zinc ion binding	88.46153846	0.000464062
Glycosyl hydrolase family 38 protein	76.47058824	0.000150717
disproportionating enzyme 2	100	0.00014754
response regulator 24	25.33151059	0.009895324
ENTH/VHS/GAT family protein	25.33151059	0.009895324
plus-3 domain-containing protein	84.84848485	0.001249711
ankyrin repeat family protein	63.0952381	0.006619382

Ribosomal protein L4/L1 family	49.14021164	6.03721E-06
ARM repeat superfamily protein	54.54545455	0.009312357
ENTH/VHS family protein	38.55421687	0.001574215
ENTH/VHS family protein	100	5.45404E-07
Cleavage and polyadenylation specificity factor (CPSF)	42.82296651	0.00197301
HIT zinc finger ;PAPA-1-like conserved region	30.6122449	0.003545459
N/A	32.14101904	0.005228525
D-aminoacid aminotransferase-like PLP-dependent en	65.78947368	0.002174657
DNAJ heat shock N-terminal domain-containing protei	92.85714286	0.000709141
zinc knuckle (CCHC-type) family protein	100	0.000534009
SU(VAR)3-9 homolog 9	39.9897855	0.000586613
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Protein of unknown function (DUF1666)	100	8.63345E-08
Protein of unknown function (DUF668)	92.30769231	0.000709141
Protein kinase superfamily protein	57.77777778	0.001304542
Nucleotidylyl transferase superfamily protein	100	0.001240448
clathrin adaptor complexes medium subunit family pr	90.47619048	0.000310043
Ubiquitin-like superfamily protein	45.90301003	0.001927119
Cyclase family protein	92	8.79837E-06
Homeodomain-like protein with RING/FYVE/PHD-type	70	0.006629474
transducin family protein / WD-40 repeat family prote	36.71096346	0.006801176
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	25.71022727	0.005353107
Methyltransferase MT-A70 family protein	35.17412698	2.46415E-09
DNAse I-like superfamily protein	27.99422799	0.00674261
lactate/malate dehydrogenase family protein	100	0.000356554
syntaxin of plants 43	68.88888889	0.006458536
N/A	100	0.001933999

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2.06864E-05
1.0806E-08
2.11353E-05
6.23179E-06
4.19359E-06
3.34038E-06
1.1973E-05
8.74075E-07
1.75962E-08
1.79811E-06

4.51821E-08
1.28533E-15
8.16793E-06
2.7272E-10
2.83514E-06
2.83514E-06
3.88079E-06
1.26737E-13
1.31234E-06
9.99996E-06
3.68476E-06
8.01981E-06
1.95779E-06
1.76766E-05
7.66995E-08
2.36878E-06
9.83903E-06
2.07821E-05
8.65029E-10
2.83514E-06
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1.72863E-05
5.03324E-07
1.76844E-06
6.86935E-18
1.59888E-05
1.87884E-07
7.39602E-07
1.83222E-05
8.55946E-07
5.94415E-07
9.50562E-06
9.03138E-07
4.69267E-06
2.15109E-08

6.59081E-08
2.69215E-06
2.22863E-06
9.47969E-08
3.97809E-06
3.74449E-12
1.2333E-05
6.86686E-08
6.86686E-08
2.43585E-05
8.99044E-06
6.77352E-10
1.55571E-06
5.09877E-07
2.10672E-05
2.10672E-05
2.69215E-06
3.63144E-07
1.50702E-08
1.74787E-05
7.39602E-07
1.9366E-07
1.39829E-05
1.26737E-13
2.29579E-05
4.01728E-07
2.88392E-06
1.75748E-06
1.36839E-10
5.83931E-06
2.21541E-14
1.31913E-05
1.0201E-05
1.21562E-05
4.25735E-07
1.06659E-07
1.03544E-07
2.45492E-05
2.45492E-05
1.56624E-06
1.43394E-05

2.12069E-09
2.26932E-05
2.11146E-06
1.30389E-10
2.91114E-06
6.21927E-06
1.04484E-05
3.31392E-06
7.4782E-07
5.09877E-07
5.72673E-07
2.98129E-08
1.57648E-11
7.4782E-07
1.65313E-06
1.54644E-06
2.5647E-07
2.74309E-06
3.26481E-09
1.43753E-05
1.4878E-05
1.07817E-05
2.85516E-13
1.47182E-05
3.05926E-07
1.38654E-05
2.83514E-06

Supplemental Table 3: List of 180 hyper-methylated genes

METHYLATED REGIONS
mytileDiff25p200.hyper_merged_CHG.Chr01.3247801-3248000
mytileDiff25p200.hyper_merged_CHG.Chr01.3809801-3810000
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mytileDiff25p200.hyper_merged_CHG.Chr01.27947801-27948000
mytileDiff25p200.hyper_merged_CHG.Chr01.28296001-28296200
mytileDiff25p200.hyper_merged_CHG.Chr01.39914801-39915000
mytileDiff25p200.hyper_merged_CHG.Chr01.51419601-51419800
mytileDiff25p200.hyper_merged_CHG.Chr01.54098201-54098400
mytileDiff25p200.hyper_merged_CHG.Chr01.56514201-56514400
mytileDiff25p200.hyper_merged_CHG.Chr02.3944201-3944400
mytileDiff25p200.hyper_merged_CHG.Chr02.4705401-4705600
mytileDiff25p200.hyper_merged_CHG.Chr02.8446601-8446800
mytileDiff25p200.hyper_merged_CHG.Chr02.8836201-8836400
mytileDiff25p200.hyper_merged_CHG.Chr02.11813801-11814000
mytileDiff25p200.hyper_merged_CHG.Chr02.13182001-13182200
mytileDiff25p200.hyper_merged_CHG.Chr02.13256601-13256800
mytileDiff25p200.hyper_merged_CHG.Chr02.13400201-13400400
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mytileDiff25p200.hyper_merged_CHG.Chr02.21064601-21064800
mytileDiff25p200.hyper_merged_CHG.Chr02.24762401-24762600
mytileDiff25p200.hyper_merged_CHG.Chr02.26134801-26135000
mytileDiff25p200.hyper_merged_CHG.Chr02.26356201-26356400
mytileDiff25p200.hyper_merged_CHG.Chr02.35290201-35290400
mytileDiff25p200.hyper_merged_CHG.Chr02.35678401-35678600
mytileDiff25p200.hyper_merged_CHG.Chr02.38833001-38833200
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mytileDiff25p200.hyper_merged_CHG.scaffold_197.12001-12200
mytileDiff25p200.hyper_merged_CHG.scaffold_28.78801-79000
mytileDiff25p200.hyper_merged_CHG.scaffold_361.7201-7400

in CHG context.

REGION	GENE ID	GENE ANNOT
PROMOTER	Glyma.01G031200	N/A
GENE BODY	Glyma.01G036200	RNI-like supe
GENE BODY	Glyma.01G073400	SNF2 domain
GENE BODY	Glyma.01G092400	tRNA arginine
GENE BODY	Glyma.01G093200	Metal-depen
GENE BODY	Glyma.01G115300	Plant protein
GENE BODY	Glyma.01G177700	aminopeptid
GENE BODY	Glyma.01G209300	RGPR-related
GENE BODY	Glyma.01G241300	target of rapa
GENE BODY	Glyma.02G041800	disease resist
GENE BODY	Glyma.02G051700	beta-galactos
GENE BODY	Glyma.02G094200	mitochondria
GENE BODY	Glyma.02G097900	bZIP transcrip
PROMOTER	Glyma.02G119900	N/A
PROMOTER	Glyma.02G129000	ARM repeat s
GENE BODY	Glyma.02G129400	N/A
GENE BODY	Glyma.02G130400	Chalcone and
GENE BODY	Glyma.02G137000	5\'-3\' exonu
GENE BODY	Glyma.02G162300	protein kinas
GENE BODY	Glyma.02G165800	Protein kinas
GENE BODY	Glyma.02G169200	protein phos
GENE BODY	Glyma.02G170100	Phosphofruct
GENE BODY	Glyma.02G188900	AGAMOUS-lik
PROMOTER	Glyma.02G190100	amino acid pe
PROMOTER	Glyma.02G203000	C-terminal do
PROMOTER	Glyma.02G215200	Restriction er
PROMOTER(3bp) ; GENE BODY (197bp)	Glyma.02G252400	beta HLH pro
PROMOTER	Glyma.02G291300	calmodulin-d
GENE BODY	Glyma.03G008100	cytochrome P
GENE BODY	Glyma.03G014400	NAD(P)-bindi
GENE BODY	Glyma.03G052800	Disease resist
GENE BODY	Glyma.03G059100	nodulin MtN2
GENE BODY	Glyma.03G061000	glycoprotease
PROMOTER	Glyma.03G101500	N/A
GENE BODY	Glyma.03G102100	IQ-domain 18
GENE BODY	Glyma.03G133000	RECA homolo
PROMOTER (102bp); 5'UTR (98bp)	Glyma.03G141100	N/A
GENE BODY	Glyma.04G089400	N/A
PROMOTER	Glyma.04G129400	N/A
GENE BODY	Glyma.04G135000	nudix hydrola
GENE BODY	Glyma.04G138200	glutathione S

GENE BODY	Glyma.04G155100	FAD/NAD(P)-
3'UTR	Glyma.04G162800	gamma subu
GENE BODY	Glyma.04G211000	Copine (Calci
GENE BODY	Glyma.04G256700	O-fucosyltran
PROMOTER	Glyma.05G058200	YbaK/aminoa
3'UTR (138bp)	Glyma.05G067200	Histone H3 K
GENE BODY	Glyma.05G084600	N/A
3'UTR	Glyma.05G096300	FMN-linked o
GENE BODY	Glyma.05G209500	ARID/BRIGHT
GENE BODY	Glyma.06G011200	Arabidopsis p
GENE BODY	Glyma.06G094900	transducin fa
GENE BODY	Glyma.06G096100	MSCS-like 2
GENE BODY	Glyma.06G217200	Peptidase C1
GENE BODY	Glyma.06G217700	nucleoporin-
GENE BODY (72bp); 3'UTR (128bp)	Glyma.06G222100	Protein of un
GENE BODY	Glyma.06G225200	Integrase-typ
PROMOTER	Glyma.06G233300	PHD finger fa
GENE BODY	Glyma.06G239100	Nuclear pore
GENE BODY	Glyma.06G258100	S-locus lectin
GENE BODY (47bp); 3'UTR (153bp)	Glyma.07G014300	phosphofruct
GENE BODY	Glyma.07G059800	glyoxylate re
GENE BODY	Glyma.07G098900	N/A
PROMOTER	Glyma.07G099000	N/A
GENE BODY	Glyma.07G157400	SU(VAR)3-9 h
PROMOTER	Glyma.07G181500	Chaperone D
GENE BODY	Glyma.07G201000	N/A
PROMOTER (98bp); GENE BODY (102bp)	Glyma.08G054200	HMG (high m
GENE BODY	Glyma.08G060800	receptor kina
GENE BODY	Glyma.08G071400	HXXXD-type
GENE BODY	Glyma.08G195900	ubiquitin-spe
GENE BODY	Glyma.08G253800	DNA/RNA pol
PROMOTER	Glyma.08G277400	PIF1 helicase
GENE BODY	Glyma.08G337400	Transducin/
GENE BODY	Glyma.09G084300	Outer arm dy
GENE BODY	Glyma.09G104600	SET domain p
GENE BODY	Glyma.09G106000	Nucleic acid-
3'UTR (109bp); GENE BODY (3bp)	Glyma.09G107500	N/A
GENE BODY	Glyma.09G108300	N/A
GENE BODY	Glyma.09G131700	N/A
GENE BODY	Glyma.10G053600	Pyridoxal-dep
GENE BODY	Glyma.10G104900	ARM repeat s
GENE BODY	Glyma.10G116500	Protein of un
GENE BODY	Glyma.10G118100	Protein kinas

GENE BODY	Glyma.10G124700	peroxisomal 3
PROMOTER	Glyma.10G166200	RNA-binding
GENE BODY	Glyma.10G172400	ubiquitin-spe
GENE BODY	Glyma.10G188600	TRAF-like sup
GENE BODY	Glyma.11G067000	SET domain-c
GENE BODY	Glyma.11G092100	Major facilita
GENE BODY	Glyma.11G158400	AICARFT/IMP
GENE BODY	Glyma.11G166200	N/A
PROMOTER	Glyma.11G190400	Lecithin:chole
GENE BODY	Glyma.11G230500	CRINKLY4 rela
GENE BODY	Glyma.12G044800	AAA-type AT
GENE BODY	Glyma.12G052400	protein kinas
GENE BODY	Glyma.12G139700	Uncharacteris
GENE BODY	Glyma.12G139800	Uncharacteris
GENE BODY	Glyma.12G139900	isoprenoid F
GENE BODY	Glyma.12G149800	Quinone redu
PROMOTER	Glyma.12G154900	N/A
PROMOTER	Glyma.12G155000	N/A
GENE BODY	Glyma.12G223200	Plasma-mem
PROMOTER	Glyma.13G010300	PIF1 helicase
GENE BODY	Glyma.13G024700	2-isopropylm
GENE BODY	Glyma.13G030600	P-loop contai
GENE BODY	Glyma.13G045400	phosphoglyce
PROMOTER	Glyma.13G110100	N/A
GENE BODY (29bp); 3'UTR (84bp)	Glyma.13G150800	N/A
GENE BODY	Glyma.13G167000	receptor-like
PROMOTER	Glyma.13G222200	Protein of un
PROMOTER (167bp); 5'UTR (33bp)	Glyma.13G320700	ARM repeat s
GENE BODY	Glyma.13G372100	cation excha
GENE BODY	Glyma.14G112200	TRS120
GENE BODY	Glyma.14G129900	ArfGap/RecO
3'UTR	Glyma.14G143000	ENTH/VHS/G
PROMOTER	Glyma.14G174100	copper ion bi
GENE BODY	Glyma.14G198500	exocyst subu
PROMOTER (63bp); 5'UTR (137bp)	Glyma.14G199800	WRKY DNA-bi
GENE BODY	Glyma.15G000900	P-loop contai
GENE BODY	Glyma.15G177000	Mob1/phocei
GENE BODY	Glyma.15G179700	zinc ion bindi
GENE BODY	Glyma.15G213200	cyclophilin 59
PROMOTER	Glyma.15G214600	ARM repeat s
GENE BODY	Glyma.15G236100	Major facilita
GENE BODY	Glyma.15G249000	RING/U-box s
PROMOTER	Glyma.15G274500	TTF-type zinc

GENE BODY	Glyma.15G275400	Pectin lyase-li
GENE BODY	Glyma.15G276800	magnesium io
GENE BODY	Glyma.15G276800	magnesium io
PROMOTER	Glyma.16G005000	N/A
GENE BODY	Glyma.16G101500	yeast YAK1-re
GENE BODY	Glyma.16G101500	yeast YAK1-re
5'UTR	Glyma.16G101700	N/A
GENE BODY	Glyma.16G150900	TatD related
PROMOTER	Glyma.16G181400	NAD(P)-bindi
GENE BODY	Glyma.16G184200	disease resist
GENE BODY	Glyma.16G186600	disease resist
GENE BODY	Glyma.16G192800	disease resist
GENE BODY	Glyma.17G068600	Alg9-like man
GENE BODY	Glyma.17G104100	dicer-like 4
GENE BODY	Glyma.17G104100	dicer-like 4
PROMOTER	Glyma.17G117100	early nodulin-
GENE BODY (122bp); 3'UTR (78bp)	Glyma.17G135200	Class I peptid
GENE BODY	Glyma.17G141300	protein argini
GENE BODY	Glyma.17G172700	PLC-like phos
PROMOTER (87bp); GENE BODY (113bp)	Glyma.17G198200	Mitochondria
GENE BODY	Glyma.17G204200	phytochrome
5'UTR	Glyma.17G247000	N/A
GENE BODY	Glyma.17G247100	N/A
PROMOTER	Glyma.18G047900	nodulin MtN2
GENE BODY	Glyma.18G126000	N/A
GENE BODY	Glyma.18G132200	DEA(D/H)-bo
GENE BODY	Glyma.18G137800	Radical SAM
PROMOTER	Glyma.18G137900	hAT transpos
PROMOTER (5bp); GENE BODY (195bp)	Glyma.18G163600	N/A
GENE BODY	Glyma.18G184400	Sulfite export
GENE BODY	Glyma.18G196200	mRNA cappin
GENE BODY	Glyma.18G223300	WD-40 repea
GENE BODY	Glyma.18G268000	Leucine-rich
GENE BODY	Glyma.19G064200	N/A
5'UTR	Glyma.19G064300	N/A
GENE BODY	Glyma.19G065700	Got1/Sft2-lik
GENE BODY	Glyma.19G081600	alpha/beta-H
GENE BODY	Glyma.19G081600	alpha/beta-H
3'UTR	Glyma.19G100500	N/A
GENE BODY	Glyma.19G120400	2-isopropylm
PROMOTER	Glyma.19G214900	myb domain
GENE BODY	Glyma.19G261100	pyrophospho
GENE BODY	Glyma.20G052100	N/A

GENE BODY	Glyma.20G052200	N/A
GENE BODY	Glyma.20G058500	N/A
GENE BODY	Glyma.20G058500	N/A
GENE BODY	Glyma.20G058500	N/A
GENE BODY	Glyma.20G058500	N/A
GENE BODY	Glyma.20G074000	urease access
GENE BODY	Glyma.20G106900	translation in
GENE BODY	Glyma.20G119300	Protein kinase
GENE BODY (49bp); 3'UTR (151bp)	Glyma.20G126800	Cyclase famil
GENE BODY	Glyma.20G168100	ribosomal pro
PROMOTER	Glyma.20G168300	Protein of unl
PROMOTER	Glyma.20G179900	phosphogluco
3'UTR	Glyma.20G207700	COP1-interac
GENE BODY	Glyma.20G244900	glucan syntha
GENE BODY	Glyma.U008400	carboxyl term
GENE BODY	Glyma.U028800	N/A
GENE BODY	Glyma.U036800	GroES-like zin

ATION	% Methylation Difference	q value	P value
	75.92105263	5.0649E-06	2.03203E-09
rfamily protein	79.48717949	0.00129483	2.02341E-06
-containing protein / helicase domair	72.72727273	0.00560967	1.56869E-05
e adenosine deaminase	90	0.009452	3.40217E-05
dent phosphohydrolase	56.48351648	0.00311923	6.7176E-06
of unknown function (DUF247)	62.5	0.00013589	1.07333E-07
ase P1	55.93220339	0.00309595	6.61666E-06
	65	0.00215992	4.06449E-06
mycin	29.7228895	0.00014026	1.11525E-07
ance protein (TIR-NBS-LRR class), put	49.67479675	0.00645638	1.94615E-05
idase 3	34.48275862	0.00043339	4.69811E-07
l editing factor 22	54.98502994	5.1271E-08	1.04358E-11
tion factor family protein	68.80503145	0.00123202	1.8929E-06
	60	0.00366275	8.39622E-06
uperfamily protein	67.77939042	0.00431722	1.06809E-05
	33.33333333	0.00065756	8.02622E-07
stilbene synthase family protein	68.75	1.7072E-06	5.784E-10
clease family protein	29.12280702	0.00596037	1.71725E-05
e family protein / protein phosphatas	80	0.00397247	9.44718E-06
e superfamily protein	28.03462885	0.00035602	3.65834E-07
hatase 2A-4	32.10052157	0.00013261	1.04313E-07
okinase family protein	38.91159939	6.7416E-09	1.10661E-12
e 80	26.39573071	0.00371452	8.59229E-06
ermease 3	40.53905391	0.00016466	1.37101E-07
main phosphatase-like 4	36.78215472	0.00137745	2.20316E-06
donuclease, type II-like superfamily	32.09690807	7.294E-07	2.17429E-10
tein 93	45.60606061	0.00030648	3.01246E-07
omain protein kinase 9	92.85714286	0.0027502	5.60865E-06
450, family 86, subfamily A, polypep	53.46594334	0.00255424	5.07318E-06
ng Rossmann-fold superfamily protei	34.44444444	0.00177142	3.08453E-06
ance protein (TIR-NBS-LRR class) fam	35.86956522	0.00484275	1.26584E-05
1 /EamA-like transporter family prot	29.95728155	0.00324929	7.10975E-06
e 1	46.17034314	1.2239E-05	5.76987E-09
	27.65557643	0.00016611	1.39389E-07
3	29.63015246	0.00070553	8.81092E-07
g 3	38.49486521	3.8719E-05	2.31901E-08
	100	3.6419E-07	9.73494E-11
	26.60215054	0.00097008	1.34522E-06
	37.69230769	0.00939472	3.35379E-05
se homolog 16	41.41824752	0.00288881	6.01456E-06
-transferase THETA 1	46.90635452	0.00939364	3.35279E-05

binding oxidoreductase family protei	31.57208089	0.00876582	3.02281E-05
nit of Mt ATP synthase	90	0.009452	3.40217E-05
REGION	30.52691867	0.00495282	1.30818E-05
sferase family protein	64.54545455	0.00099763	1.40074E-06
cyl-tRNA synthetase-associated dom	72.68009768	4.6825E-13	3.03809E-17
4-specific methyltransferase SET7/9 f	30.24509804	0.00676112	2.07314E-05
	54.17909575	3.6201E-23	3.56536E-28
xidoreductases superfamily protein	39.17349727	0.00174622	3.03147E-06
DNA-binding domain;ELM2 domain	28.44082036	0.00106192	1.54507E-06
rotein of unknown function (DUF241	39.68957871	0.0019817	3.62823E-06
mily protein / WD-40 repeat family p	34.02808249	0.00850822	2.89711E-05
	31.14540866	6.8399E-09	1.13174E-12
3 family	25.59348529	0.00188997	3.39864E-06
elated	30.39688925	0.00103856	1.48792E-06
known function (DUF3414)	29.41176471	0.00771569	2.5087E-05
e DNA-binding superfamily protein	27.41318891	0.00375979	8.72909E-06
mily protein / bromo-adjacent homol	62.62745098	2.0002E-06	6.93419E-10
complex protein	48.11594203	0.00196426	3.58034E-06
protein kinase family protein	58.40727595	5.9606E-08	1.24846E-11
okinase 3	60.53030303	0.00497106	1.31504E-05
uctase 1	46.94656489	0.00558662	1.55711E-05
	65.57377049	0.00218428	4.13792E-06
	65.57377049	0.00218428	4.13792E-06
omolog 9	29.35613682	0.00390898	9.21406E-06
naJ-domain superfamily protein	30.70588235	0.00626901	1.85891E-05
	38.34512023	5.569E-06	2.28167E-09
obility group) box protein with ARID/	82.35294118	0.0007888	1.02441E-06
se 3	70.33898305	0.00522065	1.40632E-05
acyl-transferase family protein	40.67085954	0.00235172	4.57212E-06
cific protease 6	41.23861566	0.00720248	2.26191E-05
ymerases superfamily protein	82.57359924	8.0372E-11	8.17955E-15
	69.75524476	0.00762124	2.46298E-05
/D40 repeat-like superfamily protein	40	0.00922614	3.26151E-05
nein light chain 1 protein	35.11705686	0.00874999	3.01448E-05
rotein 38	33.61210673	0.00029319	2.85437E-07
inding, OB-fold-like protein	74.87179487	0.00217549	4.10522E-06
	65	0.00924262	3.27037E-05
	25.89561738	0.0090487	3.17324E-05
	43.38413331	4.2986E-05	2.62769E-08
endent decarboxylase family protein	53.37209302	0.00040327	4.27893E-07
uperfamily protein	34.81481481	0.00290234	6.05423E-06
known function (DUF155)	26.36394252	0.0034899	7.89856E-06
e family protein with ARM repeat do	32.13414634	0.00153952	2.55235E-06

3-ketoacyl-CoA thiolase 3	78.81578947	0.00019181	1.66495E-07
(RRM/RBD/RNP motifs) family protei	35.88199265	0.00024484	2.28763E-07
cific protease 9	25.4854713	0.00806387	2.67181E-05
erfamily protein	42.03931204	0.00560042	1.5639E-05
ontaining protein	36.09460279	3.7402E-05	2.21755E-08
tor superfamily protein	29.7399605	0.0004227	4.535E-07
CHase bienzyme family protein	60.60606061	4.2808E-11	4.04744E-15
	31.2307261	0.00380173	8.86282E-06
esterol acyltransferase family protein	36.81006494	0.00640756	1.92434E-05
ated 3	26.5625	0.00235805	4.58753E-06
Pase family protein	38.21428571	0.00063147	7.59989E-07
e family protein	50	2.5504E-06	9.07631E-10
sed conserved protein (UCP012943)	36.23188406	1.9331E-08	3.56651E-12
sed conserved protein (UCP012943)	36.23188406	1.9331E-08	3.56651E-12
	36.23188406	1.9331E-08	3.56651E-12
ictase family protein	40.74074074	0.00199648	3.66388E-06
	50	0.00026533	2.54176E-07
	50	0.00026533	2.54176E-07
brane choline transporter family prot	29.65772433	5.2287E-05	3.37815E-08
	49.75490196	0.00236413	4.6009E-06
alate synthase 1	34.35143288	0.00756998	2.44045E-05
ning nucleoside triphosphate hydrola	27.53968254	0.00101236	1.43479E-06
erate kinase 1	38.18466354	0.00121438	1.86021E-06
	37.34939759	0.00227318	4.36869E-06
	32.35294118	0.00903918	3.16585E-05
protein kinase 1	63.39522546	3.0118E-05	1.69259E-08
known function (DUF1000)	35.48387097	0.00335014	7.42607E-06
uperfamily protein	74.63002114	0.00102548	1.46446E-06
nger 2	79.90196078	0.00755099	2.42986E-05
	41.15853659	0.00154071	2.55634E-06
-like zinc finger domain-containing pr	61.73076923	3.6775E-07	9.89981E-11
AT family protein	30.81106097	0.00569383	1.59971E-05
nding;cobalt ion binding;zinc ion binc	53.14723591	0.00134623	2.14085E-06
nit exo70 family protein B1	26.73299101	0.00189116	3.40354E-06
inding protein 4	46.66666667	0.00100689	1.42073E-06
ning nucleoside triphosphate hydrola	55.84795322	0.00420344	1.02669E-05
in family protein	31.42955024	6.5312E-05	4.44135E-08
ng;nucleic acid binding	26.63851351	0.00231869	4.49351E-06
)	35.36214242	0.006108	1.78304E-05
uperfamily protein	84.61538462	0.00211057	3.93805E-06
tor superfamily protein	34.04761905	0.00464738	1.18792E-05
uperfamily protein	41.04991394	0.00147641	2.40507E-06
finger protein with HAT dimerisation	39.39393939	0.00033545	3.40065E-07

ike superfamily protein	26.88948716	1.9012E-05	9.74922E-09
n binding;thiamin pyrophosphate bi	60.90909091	0.00745371	2.38277E-05
n binding;thiamin pyrophosphate bi	26.07551487	0.00415639	1.00756E-05
	37.9273377	0.00039841	4.21849E-07
lated gene 1	29.41306267	0.00213409	3.99348E-06
lated gene 1	37.68684146	0.00023582	2.18162E-07
	29.41306267	0.00213409	3.99348E-06
DNase	27.64804003	0.0011133	1.64909E-06
ng Rossmann-fold superfamily protei	44.68438538	1.8887E-06	6.46087E-10
ance family protein / LRR family prot	31.52856408	0.00848311	2.88744E-05
ance family protein / LRR family prot	43.96551724	0.008645	2.96312E-05
ance family protein / LRR family prot	28.98351648	0.00063614	7.67704E-07
nosyltransferase family	69.78609626	0.00302238	6.39273E-06
	26.52358691	0.00011217	8.58726E-08
	29.53384419	0.00435313	1.08326E-05
-related	55	1.5811E-07	3.78928E-11
e chain release factor	76.4516129	0.00054854	6.28491E-07
ne methyltransferase 7	90.90909091	0.009452	3.40217E-05
phodiesterases superfamily protein	28.39068826	0.00067357	8.25254E-07
l substrate carrier family protein	44.91869919	0.00747495	2.39165E-05
interacting factor 3	90.90909091	0.009452	3.40217E-05
	38.09195402	9.5509E-07	2.92228E-10
	38.09195402	9.5509E-07	2.92228E-10
1 /EamA-like transporter family prot	47.60273973	0.00787429	2.57929E-05
	76.30136986	0.00150212	2.46865E-06
RNA helicase family protein	28.50980392	0.00265997	5.36877E-06
superfamily protein	32.82940361	0.0039001	9.18033E-06
on superfamily	32.82940361	0.0039001	9.18033E-06
	80	0.00223914	4.27826E-06
er TauE/SafE family protein	27.13503838	2.704E-07	6.88859E-11
g enzyme family protein	49.24098672	0.00989921	3.66128E-05
t family protein / beige-related	75.47619048	0.0008398	1.10446E-06
epeat receptor-like protein kinase fa	30.48780488	0.00419474	1.02292E-05
	29.73402476	0.00023551	2.17264E-07
	29.73402476	0.00023551	2.17264E-07
vescicle transport protein family	76.29233512	9.8817E-05	7.38359E-08
ydrolases superfamily protein	65.90909091	0.00574888	1.6271E-05
ydrolases superfamily protein	55.51971326	2.0344E-05	1.05524E-08
	25.95070423	0.00067681	8.329E-07
alate synthase 1	40	0.00936987	3.33939E-05
protein 12	60.15037594	0.00018131	1.5571E-07
rylase 3	30.53167421	0.00042586	4.58862E-07
	29.86111111	0.00029715	2.89927E-07

	29.86111111	0.00029715	2.89927E-07
	29.75663267	0.00016835	1.41933E-07
	27.41523734	4.2188E-06	1.62875E-09
	26.71641791	0.00932889	3.31866E-05
	26.52051783	0.00014472	1.16209E-07
sory protein D	63.33333333	0.00933335	3.32147E-05
itiation factor 3 (IF-3) family protein	38.83888389	0.00346193	7.7966E-06
e superfamily protein	28.09044397	0.00545066	1.50053E-05
y protein	87.01298701	2.2302E-14	1.01038E-18
otein 1	65.30612245	0.00324597	7.09286E-06
known function (DUF1278)	65.30612245	0.00324597	7.09286E-06
osamine mutase family protein	33.45079967	0.00420225	1.02613E-05
REGION	59.04761905	0.00593636	1.70448E-05
ise-like 10	32.58444619	0.00284059	5.86574E-06
ninus of HSC70-interacting protein	54	4.20E-05	2.55E-08
	74.46808511	0.00040356	4.29E-07
nc-binding dehydrogenase family prot	37.23522854	0.00967046	3.53E-05

Supplemental Table 4: List of 120 hyper-methylated genes in

METHYLATED REGION
mytileDiff25p200.hyper_merged_CHH.Chr01.3576801-3577000
mytileDiff25p200.hyper_merged_CHH.Chr01.11564801-11565000
mytileDiff25p200.hyper_merged_CHH.Chr01.37634201-37634400
mytileDiff25p200.hyper_merged_CHH.Chr01.48025201-48025400
mytileDiff25p200.hyper_merged_CHH.Chr01.51017001-51017200
mytileDiff25p200.hyper_merged_CHH.Chr02.7246401-7246600
mytileDiff25p200.hyper_merged_CHH.Chr02.7246401-7246600
mytileDiff25p200.hyper_merged_CHH.Chr02.11742001-11742200
mytileDiff25p200.hyper_merged_CHH.Chr02.12151801-12152000
mytileDiff25p200.hyper_merged_CHH.Chr02.14365201-14365400
mytileDiff25p200.hyper_merged_CHH.Chr02.14631601-14631800
mytileDiff25p200.hyper_merged_CHH.Chr02.33475001-33475200
mytileDiff25p200.hyper_merged_CHH.Chr02.35782801-35783000
mytileDiff25p200.hyper_merged_CHH.Chr02.44605001-44605200
mytileDiff25p200.hyper_merged_CHH.Chr03.1372601-1372800
mytileDiff25p200.hyper_merged_CHH.Chr03.1440001-1440200
mytileDiff25p200.hyper_merged_CHH.Chr03.7315801-7316000
mytileDiff25p200.hyper_merged_CHH.Chr03.33605201-33605400
mytileDiff25p200.hyper_merged_CHH.Chr03.37332401-37332600
mytileDiff25p200.hyper_merged_CHH.Chr03.41763001-41763200
mytileDiff25p200.hyper_merged_CHH.Chr03.43910201-43910400
mytileDiff25p200.hyper_merged_CHH.Chr04.1509401-1509600
mytileDiff25p200.hyper_merged_CHH.Chr04.26353201-26353400
mytileDiff25p200.hyper_merged_CHH.Chr04.40387401-40387600
mytileDiff25p200.hyper_merged_CHH.Chr04.44913401-44913600
mytileDiff25p200.hyper_merged_CHH.Chr04.50068001-50068200
mytileDiff25p200.hyper_merged_CHH.Chr05.827601-827800
mytileDiff25p200.hyper_merged_CHH.Chr05.3956401-3956600
mytileDiff25p200.hyper_merged_CHH.Chr06.1538601-1538800
mytileDiff25p200.hyper_merged_CHH.Chr06.4642801-4643000
mytileDiff25p200.hyper_merged_CHH.Chr06.4644001-4644200
mytileDiff25p200.hyper_merged_CHH.Chr06.7657801-7658000
mytileDiff25p200.hyper_merged_CHH.Chr06.14400801-14401000
mytileDiff25p200.hyper_merged_CHH.Chr06.17519401-17519600
mytileDiff25p200.hyper_merged_CHH.Chr06.29811601-29811800
mytileDiff25p200.hyper_merged_CHH.Chr06.45214601-45214800
mytileDiff25p200.hyper_merged_CHH.Chr06.49391601-49391800
mytileDiff25p200.hyper_merged_CHH.Chr06.50869201-50869400
mytileDiff25p200.hyper_merged_CHH.Chr07.2389001-2389200

mytileDiff25p200.hyper_merged_CHH.Chr07.4401201-4401400
mytileDiff25p200.hyper_merged_CHH.Chr07.5072401-5072600
mytileDiff25p200.hyper_merged_CHH.Chr07.18423201-18423400
mytileDiff25p200.hyper_merged_CHH.Chr07.36876001-36876200
mytileDiff25p200.hyper_merged_CHH.Chr08.4184001-4184200
mytileDiff25p200.hyper_merged_CHH.Chr08.5477201-5477400
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mytileDiff25p200.hyper_merged_CHH.Chr08.35694401-35694600
mytileDiff25p200.hyper_merged_CHH.Chr08.43422601-43422800
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mytileDiff25p200.hyper_merged_CHH.Chr09.43413401-43413600
mytileDiff25p200.hyper_merged_CHH.Chr09.46321401-46321600
mytileDiff25p200.hyper_merged_CHH.Chr10.3980401-3980600
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mytileDiff25p200.hyper_merged_CHH.Chr10.40783601-40783800
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mytileDiff25p200.hyper_merged_CHH.Chr11.523401-523600
mytileDiff25p200.hyper_merged_CHH.Chr11.3373601-3373800
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mytileDiff25p200.hyper_merged_CHH.Chr19.44246401-44246600
mytileDiff25p200.hyper_merged_CHH.Chr19.49013201-49013400
mytileDiff25p200.hyper_merged_CHH.Chr19.50414601-50414800
mytileDiff25p200.hyper_merged_CHH.Chr20.3308801-3309000
mytileDiff25p200.hyper_merged_CHH.Chr20.9645801-9646000
mytileDiff25p200.hyper_merged_CHH.Chr20.26329001-26329200
mytileDiff25p200.hyper_merged_CHH.scaffold_21.424201-424400
mytileDiff25p200.hyper_merged_CHH.scaffold_27.230401-230600

CHH context.

REGION	GENE ID
GENE BODY (122bp); 3'UTR (78bp)	Glyma.01G034300
PROMOTER	Glyma.01G068900
GENE BODY	Glyma.01G111000
PROMOTER	Glyma.01G145400
GENE BODY	Glyma.01G172800
GENE BODY	Glyma.02G083300
PROMOTER	Glyma.02G083400
PROMOTER (139bp); 5'UTR (61bp)	Glyma.02G119200
PROMOTER	Glyma.02G122400
PROMOTER (143bp); 5'UTR (43bp); GE	Glyma.02G138700
PROMOTER	Glyma.02G141500
PROMOTER (70bp); 5'UTR (130bp)	Glyma.02G186100
GENE BODY	Glyma.02G190200
PROMOTER	Glyma.02G259000
GENE BODY	Glyma.03G013500
GENE BODY	Glyma.03G014400
GENE BODY	Glyma.03G054100
PROMOTER	Glyma.03G123200
PROMOTER	Glyma.03G157900
PROMOTER	Glyma.03G211400
GENE BODY	Glyma.03G240400
PROMOTER	Glyma.04G019200
PROMOTER	Glyma.04G144400
3'UTR	Glyma.04G162800
5'UTR	Glyma.04G182700
PROMOTER	Glyma.04G232300
PROMOTER	Glyma.05G009300
PROMOTER	Glyma.05G044200
PROMOTER	Glyma.06G020300
PROMOTER	Glyma.06G061600
GENE BODY	Glyma.06G061700
PROMOTER	Glyma.06G097000
5'UTR	Glyma.06G172000
PROMOTER (97bp); 5'UTR (103bp)	Glyma.06G195600
GENE BODY	Glyma.06G223900
PROMOTER	Glyma.06G264700
GENE BODY	Glyma.06G304900
PROMOTER	Glyma.06G320000
GENE BODY	Glyma.07G030000

GENE BODY (107bp); 3'UTR (93bp)	Glyma.07G051000
PROMOTER	Glyma.07G057000
PROMOTER	Glyma.07G151800
PROMOTER	Glyma.07G200200
PROMOTER	Glyma.08G054200
GENE BODY	Glyma.08G071400
PROMOTER	Glyma.08G081600
PROMOTER	Glyma.08G209300
PROMOTER	Glyma.08G272500
GENE BODY	Glyma.08G314100
PROMOTER	Glyma.08G345200
GENE BODY	Glyma.09G115200
GENE BODY	Glyma.09G115200
GENE BODY	Glyma.09G157300
PROMOTER (67 bp)	Glyma.09G197500
PROMOTER (19bp); 5'UTR (181bp)	Glyma.09G197600
GENE BODY	Glyma.09G209900
PROMOTER	Glyma.09G240900
PROMOTER	Glyma.10G044400
PROMOTER	Glyma.10G044600
PROMOTER (140bp); 5'UTR (60bp)	Glyma.10G174000
GENE BODY	Glyma.10G185600
PROMOTER	Glyma.11G007500
PROMOTER	Glyma.11G045500
PROMOTER	Glyma.11G096600
GENE BODY	Glyma.11G124000
PROMOTER	Glyma.11G125100
PROMOTER	Glyma.11G148800
GENE BODY	Glyma.12G174700
GENE BODY	Glyma.12G233100
GENE BODY	Glyma.13G065500
GENE BODY	Glyma.13G093300
PROMOTER (145bp); 5'UTR (55bp)	Glyma.13G139100
GENE BODY	Glyma.13G181600
PROMOTER	Glyma.13G289100
PROMOTER	Glyma.13G316600
GENE BODY	Glyma.13G319900
GENE BODY	Glyma.14G064500
PROMOTER	Glyma.14G109000
PROMOTER	Glyma.14G122600
PROMOTER	Glyma.14G131400

PROMOTER	Glyma.14G140600
GENE BODY	Glyma.14G149700
3'UTR	Glyma.15G009500
PROMOTER	Glyma.15G015100
PROMOTER	Glyma.15G020600
PROMOTER	Glyma.15G046400
PROMOTER	Glyma.15G074800
PROMOTER	Glyma.15G142800
GENE BODY	Glyma.15G145600
GENE BODY	Glyma.15G172600
GENE BODY	Glyma.16G005600
PROMOTER	Glyma.16G036900
GENE BODY	Glyma.16G082900
GENE BODY	Glyma.16G083000
PROMOTER (7bp); 5'UTR (193bp)	Glyma.16G144000
PROMOTER	Glyma.16G178100
PROMOTER	Glyma.16G178300
PROMOTER	Glyma.17G020500
PROMOTER	Glyma.17G030800
GENE BODY	Glyma.17G068600
5'UTR	Glyma.17G083300
PROMOTER	Glyma.17G108200
GENE BODY	Glyma.17G142200
GENE BODY (109bp); 3'UTR (91bp)	Glyma.17G142700
GENE BODY	Glyma.17G160600
PROMOTER	Glyma.17G170600
GENE BODY	Glyma.17G188300
PROMOTER	Glyma.18G068900
PROMOTER	Glyma.18G112700
PROMOTER (132bp); GENE BODY (68b	Glyma.18G115200
PROMOTER	Glyma.19G089900
PROMOTER	Glyma.19G110900
PROMOTER	Glyma.19G152000
PROMOTER (162bp); GENE BODY (38b	Glyma.19G184000
PROMOTER	Glyma.19G242300
PROMOTER	Glyma.19G261000
GENE BODY	Glyma.20G028300
GENE BODY	Glyma.20G049100
PROMOTER (92bp); 5'UTR (108bp)	Glyma.20G074000
PROMOTER	Glyma.U011500
PROMOTER	Glyma.U027500

GENE ANNOTATION	Methylation Differenc
TRICHOME BIREFRINGENCE-LIKE 27	31.07487923
N/A	48.25620389
Cysteine proteinases superfamily protein	33.58517719
elongation factor Ts family protein	30.35914703
NmrA-like negative transcriptional regulator family protein	46.80427607
receptor like protein 6	32.37961226
F-box family protein	32.37961226
SPIRAL1-like1	30.81589349
N/A	26.309897
Haloacid dehalogenase-like hydrolase (HAD) superfamily pro	30.50847458
DREB2A-interacting protein 2	39.90863787
autoinhibited Ca2+-ATPase 11	42.53373119
N/A	27.99797483
Aldolase-type TIM barrel family protein	38.65327381
RHO guanyl-nucleotide exchange factor 3	42.54807692
NAD(P)-binding Rossmann-fold superfamily protein	26.31641086
Disease resistance protein (TIR-NBS-LRR class)	43.88204225
Basic-leucine zipper (bZIP) transcription factor family protein	25.58922559
Cyclophilin-like peptidyl-prolyl cis-trans isomerase family pro	36.84017595
cullin 1	33.91812865
ATP binding microtubule motor family protein	34.42622951
Transmembrane amino acid transporter family protein	42.01877934
N/A	25.55555556
gamma subunit of Mt ATP synthase	42.35483871
Protein kinase superfamily protein	29.87457001
Metal-dependent protein hydrolase	30.49773756
BED zinc finger ;hAT family dimerisation domain	29.10158099
MA3 domain-containing protein	37.11340206
Pyridoxal-dependent decarboxylase family protein	45.10324484
nuclear RNA polymerase D2A	35.88383838
chorismate mutase 2	31.85823755
N/A	28.92743222
Zn-dependent exopeptidases superfamily protein	56.04288499
myb domain protein 29	29.96389892
diacylglycerol kinase 4	45.96553773
N/A	59.88323603
Ras-related small GTP-binding family protein	26.06214331
Eukaryotic protein of unknown function (DUF842)	50.45454545
fatty acid desaturase 5	30

CBL-interacting protein kinase 9	50
pentatricopeptide (PPR) repeat-containing protein	27.51241226
beta glucosidase 11	27.53567788
HSP20-like chaperones superfamily protein	41.02564103
HMG (high mobility group) box protein with ARID/BRIGHT D	33.56350701
HXXXD-type acyl-transferase family protein	25.37042903
double-stranded RNA binding protein-related / DsRBD prote	38.82166791
N/AMETHYALTED_REGION	29.06131938
Polyketide cyclase/dehydrase and lipid transport superfamil	29.52353942
Ankyrin-repeat containing protein	35.43379377
FAD/NAD(P)-binding oxidoreductase family protein	30.82417582
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	34.44055944
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	37.430283
N/A	29.14027149
N/A	25.27472527
N/A	25.27472527
extra-large GTP-binding protein 3	29.68944099
thioredoxin 2	26.05433119
N/A	44.7582205
N/A	44.7582205
N/A	49.0990991
N/A	50.95757576
ATP-dependent RNA helicase, mitochondrial (SUV3)	28.52049911
N/A	47.56097561
NAC domain containing protein 36	50
AP2/B3-like transcriptional factor family protein	25.30742459
P-loop containing nucleoside triphosphate hydrolases super	31.73884691
binding	40.98039216
Nucleotide/sugar transporter family protein	25.77436524
Leucine-rich repeat transmembrane protein kinase	44.27058257
Phosphoglycerate mutase-like family protein	26.02397602
glutamate receptor 2.5	26.51724138
Transducin/WD40 repeat-like superfamily protein	37.10462287
Tetratricopeptide repeat (TPR)-like superfamily protein	27.808136
UDP-Glycosyltransferase superfamily protein	53.37398374
Homeodomain-like superfamily protein	31.49983148
Transmembrane amino acid transporter family protein	42.83876501
Subtilisin-like serine endopeptidase family protein	30.08605621
ubiquitin-specific protease 22	27.93471438
plant glycogenin-like starch initiation protein 2	25.88614393
N/A	53.65853659

bromo-adjacent homology (BAH) domain-containing protein	26.08727255
long chain acyl-CoA synthetase 9	25.74065842
Lactoylglutathione lyase / glyoxalase I family protein	42.42424242
chitinase A	100
IQ-domain 26	25.36774316
Phosphatidylinositol-4-phosphate 5-kinase family protein	25.42982563
Protein of unknown function (DUF506)	41.70702179
N/A	48.33232262
MLP-like protein 423	30.76825598
MAP kinase kinase 2	25.34235026
transcription coactivators	25.19660271
Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-bin	29.32118165
Spc97 / Spc98 family of spindle pole body (SBP) component	46.9581749
hAT transposon superfamily	46.9581749
Protein kinase superfamily protein	33.0977918
Heavy metal transport/detoxification superfamily protein	25.46975547
Heavy metal transport/detoxification superfamily protein	43.20987654
RING/U-box superfamily protein	53.8764266
N/A	35.11047895
Alg9-like mannosyltransferase family	42.5210084
Phosphoribulokinase / Uridine kinase family	44.15584416
glucuronidase 3	68.29268293
MITOCHONDRIAL FERREDOXIN 2	26.43008475
Protein of unknown function, DUF547	25.83832335
Tetratricopeptide repeat (TPR)-like superfamily protein	45.31965561
Plant protein of unknown function (DUF869)	74.55197133
ABC1 family protein	44.42361762
Neutral/alkaline non-lysosomal ceramidase	64.19828641
Mitochondrial transcription termination factor family protei	57.33863837
pleckstrin homology (PH) domain-containing protein	33.33333333
Nucleotide-diphospho-sugar transferase family protein	27.91421653
H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 prote	37.57338552
homolog of yeast autophagy 18 (ATG18) G	41.18744699
Ribosomal protein L4/L1 family	41.63925247
O-acetylserine (thiol) lyase (OAS-TL) isoform A1	32.98980877
Protein kinase superfamily protein	28.97637795
N/A	64.45182724
N/A	26.84431609
urease accessory protein D	48.96551724
TBP-associated factor 7	34.05839274
myb domain protein 1	36.25

q value	P value
6.68106E-07	3.95286E-10
5.27234E-05	8.72624E-08
4.85284E-05	7.87667E-08
3.12975E-06	2.64803E-09
4.15523E-28	1.47718E-33
1.39808E-05	1.65863E-08
1.39808E-05	1.65863E-08
4.20563E-12	3.84453E-16
0.005247154	4.11999E-05
1.32233E-10	2.10868E-14
1.69713E-05	2.09871E-08
2.81216E-14	1.41389E-18
6.42586E-05	1.11935E-07
0.002484903	1.43562E-05
1.73353E-08	5.27349E-12
1.6306E-05	1.99491E-08
9.97353E-05	1.93721E-07
7.55432E-06	7.88784E-09
0.001911271	9.9095E-06
0.00010721	2.12289E-07
0.009560258	9.83182E-05
0.00303548	1.90357E-05
0.001339648	6.08278E-06
7.80087E-07	4.80555E-10
2.85207E-07	1.42526E-10
0.001211669	5.29462E-06
3.95209E-06	3.52243E-09
0.000283879	7.6006E-07
0.000326905	9.13278E-07
0.001191793	5.17994E-06
3.98238E-17	8.89886E-22
1.90117E-05	2.42055E-08
3.24729E-11	4.2713E-15
8.16954E-06	8.65883E-09
1.52905E-09	3.29251E-13
0.005497455	4.39949E-05
0.001281217	5.70964E-06
0.002261396	1.25228E-05
0.00443975	3.24503E-05

8.40893E-10	1.69539E-13
0.000475611	1.50939E-06
0.001825936	9.28534E-06
1.56799E-16	3.90193E-21
0.004998225	3.83776E-05
7.1236E-12	7.2355E-16
0.000812662	3.09123E-06
4.93591E-05	8.03155E-08
0.00193327	1.00666E-05
0.003229123	2.07941E-05
3.0888E-09	7.26291E-13
0.000417278	1.2662E-06
0.002877843	1.7588E-05
0.008839918	8.7868E-05
0.000211198	5.12883E-07
0.000211198	5.12883E-07
0.00815181	7.81495E-05
1.76371E-09	3.8605E-13
0.001749899	8.76315E-06
0.001749899	8.76315E-06
1.88945E-07	8.77044E-11
1.01808E-10	1.5594E-14
5.80763E-06	5.62456E-09
6.0627E-06	5.94549E-09
0.000146403	3.17082E-07
0.002396616	1.36376E-05
5.0455E-07	2.82887E-10
0.002806743	1.69439E-05
0.000222538	5.50844E-07
2.36225E-05	3.19594E-08
0.003850561	2.66239E-05
2.24554E-11	2.77119E-15
7.78441E-12	8.18344E-16
0.001882497	9.69324E-06
1.81726E-22	1.38435E-27
1.33016E-07	5.70146E-11
0.000975518	3.95416E-06
0.002995099	1.8659E-05
4.92288E-05	8.00534E-08
0.000406021	1.2193E-06
3.64162E-05	5.48608E-08

7.62582E-06	7.98185E-09
4.67186E-06	4.30172E-09
1.2525E-06	8.48539E-10
6.76189E-07	4.03022E-10
0.001967253	1.03248E-05
0.006728148	5.90102E-05
0.00981805	0.000102136
7.34145E-07	4.46288E-10
4.23642E-13	2.86147E-17
4.0229E-07	2.14112E-10
0.005465089	4.36387E-05
0.001285613	5.73838E-06
0.003518567	2.34623E-05
0.003518567	2.34623E-05
9.99893E-05	1.94386E-07
1.56763E-05	1.90354E-08
5.10723E-06	4.79322E-09
0.000828999	3.16853E-06
3.29155E-10	5.83399E-14
5.65713E-08	2.0542E-11
7.75005E-12	8.10795E-16
2.64502E-06	2.14254E-09
0.000294575	7.96627E-07
4.89083E-13	3.42768E-17
6.66504E-07	3.93999E-10
1.15653E-08	3.33615E-12
0.003539697	2.36607E-05
2.34667E-06	1.84009E-09
2.30754E-12	1.89847E-16
0.001212179	5.29952E-06
0.003051174	1.9168E-05
0.006563689	5.69406E-05
3.82949E-08	1.30791E-11
1.81726E-22	1.33179E-27
5.69784E-13	4.19582E-17
0.009900233	0.000103454
0.001191793	5.18155E-06
0.002461972	1.41456E-05
0.000643951	2.25522E-06
2.51011E-10	4.29598E-14
0.006819163	6.02096E-05

Supplemental Table 5: List of 817 hypo-methylated ge

METHYLATED REGION
mytileDiff25p200.hypo_CpG.Chr01.517401-517600
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mytileDiff25p200.hypo_CpG.Chr01.2189801-2190000
mytileDiff25p200.hypo_CpG.Chr01.2190001-2190200
mytileDiff25p200.hypo_CpG.Chr01.2399801-2400000
mytileDiff25p200.hypo_CpG.Chr01.2409601-2409800
mytileDiff25p200.hypo_CpG.Chr01.4046201-4046400
mytileDiff25p200.hypo_CpG.Chr01.4046201-4046400
mytileDiff25p200.hypo_CpG.Chr01.4158401-4158600
mytileDiff25p200.hypo_CpG.Chr01.4828401-4828600
mytileDiff25p200.hypo_CpG.Chr01.7809001-7809200
mytileDiff25p200.hypo_CpG.Chr01.9100201-9100400
mytileDiff25p200.hypo_CpG.Chr01.10100801-10101000
mytileDiff25p200.hypo_CpG.Chr01.15368201-15368400
mytileDiff25p200.hypo_CpG.Chr01.15368201-15368400
mytileDiff25p200.hypo_CpG.Chr01.26986201-26986400
mytileDiff25p200.hypo_CpG.Chr01.26996801-26997000
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mytileDiff25p200.hypo_CpG.Chr01.28636401-28636600
mytileDiff25p200.hypo_CpG.Chr01.29534201-29534400
mytileDiff25p200.hypo_CpG.Chr01.39603601-39603800
mytileDiff25p200.hypo_CpG.Chr01.39603801-39604000
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mytileDiff25p200.hypo_CpG.Chr20.38793201-38793400
mytileDiff25p200.hypo_CpG.Chr20.39251801-39252000
mytileDiff25p200.hypo_CpG.Chr20.39328401-39328600

mytileDiff25p200.hypo_CpG.Chr20.39992201-39992400
mytileDiff25p200.hypo_CpG.Chr20.40297201-40297400
mytileDiff25p200.hypo_CpG.Chr20.40365201-40365400
mytileDiff25p200.hypo_CpG.Chr20.41091001-41091200
mytileDiff25p200.hypo_CpG.Chr20.42417001-42417200
mytileDiff25p200.hypo_CpG.Chr20.42417801-42418000
mytileDiff25p200.hypo_CpG.Chr20.42441401-42441600
mytileDiff25p200.hypo_CpG.Chr20.42639601-42639800
mytileDiff25p200.hypo_CpG.Chr20.42840201-42840400
mytileDiff25p200.hypo_CpG.Chr20.43404601-43404800
mytileDiff25p200.hypo_CpG.Chr20.44505401-44505600
mytileDiff25p200.hypo_CpG.Chr20.45270801-45271000
mytileDiff25p200.hypo_CpG.Chr20.45355801-45356000
mytileDiff25p200.hypo_CpG.Chr20.45478001-45478200
mytileDiff25p200.hypo_CpG.Chr20.46646601-46646800
mytileDiff25p200.hypo_CpG.Chr20.47470601-47470800
mytileDiff25p200.hypo_CpG.scaffold_21.276801-277000
mytileDiff25p200.hypo_CpG.scaffold_21.1291801-1292000
mytileDiff25p200.hypo_CpG.scaffold_31.213601-213800
mytileDiff25p200.hypo_CpG.scaffold_31.258401-258600
mytileDiff25p200.hypo_CpG.scaffold_32.168401-168600
mytileDiff25p200.hypo_CpG.scaffold_32.247601-247800

nes in CpG context.

REGION	GENE ID
3'UTR	Glyma.01G005200
3'UTR (160bp)	Glyma.01G007300
GENE BODY	Glyma.01G007300
3'UTR	Glyma.01G021600
3'UTR	Glyma.01G021600
GENE BODY	Glyma.01G023600
GENE BODY	Glyma.01G023700
PROMOTER	Glyma.01G038200
GENE BODY	Glyma.01G038300
GENE BODY	Glyma.01G038700
GENE BODY	Glyma.01G044000
GENE BODY	Glyma.01G059100
GENE BODY	Glyma.01G063700
GENE BODY	Glyma.01G065600
GENE BODY	Glyma.01G074400
GENE BODY	Glyma.01G074500
5'UTR(60bp); GENE BODY (140 bp)	Glyma.01G089000
5'UTR(171bp); GENE BODY (29bp)	Glyma.01G089000
5'UTR(108bp); PROMOTER (92bp)	Glyma.01G089000
GENE BODY	Glyma.01G093900
GENE BODY	Glyma.01G095100
5' UTR	Glyma.01G114500
5' UTR	Glyma.01G114500
GENE BODY	Glyma.01G117500
PROMOTER	Glyma.01G120100
GENE BODY	Glyma.01G134300
GENE BODY	Glyma.01G135900
GENE BODY	Glyma.01G140200
GENE BODY	Glyma.01G141900
GENE BODY	Glyma.01G145600
GENE BODY	Glyma.01G145600
GENE BODY (117bp); PROMOTER (83bp)	Glyma.01G145700
PROMOTER	Glyma.01G145700
PROMOTER	Glyma.01G145800
PROMOTER	Glyma.01G145800
5'UTR(100bp); GENE BODY (100bp)	Glyma.01G156800
GENE BODY	Glyma.01G162200
GENE BODY	Glyma.01G166100
GENE BODY	Glyma.01G168900
GENE BODY	Glyma.01G176400
GENE BODY	Glyma.01G204900

GENE BODY	Glyma.01G209300
5'UTR (33); PROMOTER (167bp)	Glyma.01G226000
GENE BODY	Glyma.01G226800
GENE BODY	Glyma.01G234300
GENE BODY	Glyma.01G235300
GENE BODY	Glyma.01G238200
GENE BODY (169bp); 3'UTR (31bp)	Glyma.01G243200
PROMOTER (167bp); GENE BODY (33bp)	Glyma.01G245200
GENE BODY	Glyma.02G006500
GENE BODY	Glyma.02G021900
GENE BODY	Glyma.02G042000
GENE BODY	Glyma.02G048100
GENE BODY	Glyma.02G056800
GENE BODY	Glyma.02G062200
GENE BODY	Glyma.02G066700
GENE BODY	Glyma.02G067100
PROMOTER	Glyma.02G085500
GENE BODY	Glyma.02G089000
GENE BODY	Glyma.02G091300
3'UTR(3bp); GENE BODY (197bp)	Glyma.02G098100
GENE BODY	Glyma.02G099300
GENE BODY	Glyma.02G100200
GENE BODY	Glyma.02G103100
GENE BODY	Glyma.02G103100
GENE BODY	Glyma.02G106100
PROMOTER	Glyma.02G129400
PROMOTER	Glyma.02G138900
5'UTR(141bp); PROMOTER (59bp)	Glyma.02G139000
GENE BODY	Glyma.02G141600
PROMOTER	Glyma.02G141900
GENE BODY	Glyma.02G145300
GENE BODY	Glyma.02G160400
GENE BODY	Glyma.02G161100
GENE BODY	Glyma.02G162900
GENE BODY	Glyma.02G166500
PROMOTER(148bp); GENE BODY (52bp)	Glyma.02G168200
GENE BODY	Glyma.02G170500
GENE BODY	Glyma.02G172600
GENE BODY	Glyma.02G184100
GENE BODY	Glyma.02G185900
GENE BODY	Glyma.02G186300

GENE BODY	Glyma.02G189600
5' UTR	Glyma.02G197100
GENE BODY	Glyma.02G201600
PROMOTER	Glyma.02G201800
GENE BODY	Glyma.02G202300
GENE BODY	Glyma.02G215800
GENE BODY	Glyma.02G218100
GENE BODY	Glyma.02G219600
PROMOTER	Glyma.02G221500
GENE BODY	Glyma.02G251700
GENE BODY	Glyma.02G257400
GENE BODY	Glyma.02G269300
3'UTR (138bp); GENE BODY (62bp)	Glyma.02G270000
GENE BODY	Glyma.02G270300
GENE BODY	Glyma.02G274600
GENE BODY	Glyma.02G281700
3'UTR	Glyma.02G295200
GENE BODY	Glyma.02G296200
GENE BODY	Glyma.02G298500
GENE BODY	Glyma.02G305000
GENE BODY	Glyma.02G312000
GENE BODY	Glyma.03G022900
GENE BODY	Glyma.03G027600
PROMOTER	Glyma.03G031900
GENE BODY (112bp); PROMOTER (88bp)	Glyma.03G044100
GENE BODY	Glyma.03G058400
GENE BODY	Glyma.03G076800
GENE BODY	Glyma.03G076900
GENE BODY	Glyma.03G079800
GENE BODY	Glyma.03G080300
5'UTR(76bp); PROMOTER (124bp)	Glyma.03G092600
PROMOTER	Glyma.03G100100
GENE BODY	Glyma.03G116900
GENE BODY	Glyma.03G121100
GENE BODY	Glyma.03G127600
GENE BODY	Glyma.03G132000
GENE BODY	Glyma.03G132800
GENE BODY	Glyma.03G138400
5' UTR	Glyma.03G143300
GENE BODY	Glyma.03G146200
PROMOTER	Glyma.03G173600
PROMOTER	Glyma.03G179900

GENE BODY	Glyma.03G189700
PROMOTER	Glyma.03G206200
GENE BODY	Glyma.03G223300
5' UTR	Glyma.03G225700
5' UTR	Glyma.03G225700
PROMOTER	Glyma.03G225800
PROMOTER	Glyma.03G225800
GENE BODY	Glyma.03G235200
GENE BODY	Glyma.03G247300
GENE BODY	Glyma.03G256800
GENE BODY	Glyma.03G264500
GENE BODY	Glyma.04G010500
GENE BODY	Glyma.04G016300
GENE BODY	Glyma.04G017000
GENE BODY	Glyma.04G025000
GENE BODY	Glyma.04G025400
GENE BODY	Glyma.04G028300
GENE BODY	Glyma.04G034900
GENE BODY	Glyma.04G039800
GENE BODY	Glyma.04G039800
GENE BODY	Glyma.04G053800
GENE BODY	Glyma.04G064300
3'UTR(16bp); GENE BODY(184bp)	Glyma.04G075200
GENE BODY	Glyma.04G088300
GENE BODY	Glyma.04G090500
GENE BODY	Glyma.04G092200
GENE BODY	Glyma.04G096100
PROMOTER	Glyma.04G113800
GENE BODY	Glyma.04G124800
3'UTR(42bp); GENE BODY (158bp)	Glyma.04G133800
GENE BODY	Glyma.04G156500
5'UTR(95bp); GENE BODY(105bp)	Glyma.04G157200
GENE BODY	Glyma.04G176500
GENE BODY	Glyma.04G177300
PROMOTER	Glyma.04G188200
GENE BODY	Glyma.04G190500
GENE BODY	Glyma.04G193800
GENE BODY	Glyma.04G210400
GENE BODY	Glyma.04G245400
GENE BODY	Glyma.04G252700
GENE BODY	Glyma.05G000600
GENE BODY	Glyma.05G004900
GENE BODY	Glyma.05G009500

GENE BODY	Glyma.05G013500
GENE BODY	Glyma.05G020900
GENE BODY	Glyma.05G030700
GENE BODY	Glyma.05G031300
GENE BODY	Glyma.05G032600
GENE BODY	Glyma.05G032600
GENE BODY	Glyma.05G035900
GENE BODY	Glyma.05G040600
GENE BODY	Glyma.05G041600
GENE BODY	Glyma.05G047400
3'UTR	Glyma.05G049500
GENE BODY	Glyma.05G060200
GENE BODY	Glyma.05G062800
PROMOTER (92bp); 5'UTR(108bp)	Glyma.05G067200
GENE BODY	Glyma.05G068200
GENE BODY	Glyma.05G069000
GENE BODY	Glyma.05G075100
PROMOTER	Glyma.05G075200
GENE BODY	Glyma.05G080100
GENE BODY	Glyma.05G080100
PROMOTER	Glyma.05G084500
GENE BODY	Glyma.05G110200
GENE BODY	Glyma.05G118100
3'UTR(153bp); GENE BODY (47bp)	Glyma.05G118200
GENE BODY	Glyma.05G120400
GENE BODY	Glyma.05G143100
GENE BODY	Glyma.05G150300
GENE BODY	Glyma.05G151100
GENE BODY	Glyma.05G163700
GENE BODY	Glyma.05G176400
PROMOTER	Glyma.05G180000
GENE BODY	Glyma.05G186200
GENE BODY	Glyma.05G194700
GENE BODY	Glyma.05G200600
GENE BODY	Glyma.05G208100
GENE BODY	Glyma.05G221200
GENE BODY	Glyma.05G224700
GENE BODY	Glyma.06G016500
GENE BODY	Glyma.06G016500
GENE BODY	Glyma.06G016600
GENE BODY	Glyma.06G016700
GENE BODY	Glyma.06G018700
GENE BODY	Glyma.06G049000

PROMOTER	Glyma.06G090100
PROMOTER	Glyma.06G090100
GENE BODY	Glyma.06G098300
GENE BODY	Glyma.06G099100
3'UTR(32bp); GENE BODY(168bp)	Glyma.06G108900
GENE BODY	Glyma.06G111200
GENE BODY	Glyma.06G116500
GENE BODY	Glyma.06G122500
GENE BODY	Glyma.06G123000
5' UTR(73bp); GENE BODY(127bp)	Glyma.06G130800
GENE BODY	Glyma.06G137800
GENE BODY	Glyma.06G146400
GENE BODY	Glyma.06G148600
(PROMOTER 170); 5' UTR(30bp)	Glyma.06G158600
GENE BODY	Glyma.06G159900
GENE BODY	Glyma.06G163900
GENE BODY	Glyma.06G173400
GENE BODY	Glyma.06G173500
5' UTR(49bp); GENE BODY(151bp)	Glyma.06G173600
5' UTR(18bp);GENE BODY(182bp)	Glyma.06G195300
GENE BODY	Glyma.06G195300
GENE BODY	Glyma.06G199800
GENE BODY	Glyma.06G201500
GENE BODY	Glyma.06G208900
3'UTR(133bp); GENE BODY (67bp)	Glyma.06G209300
PROMOTER	Glyma.06G212600
PROMOTER(61bp); GENE BODY(139bp)	Glyma.06G212700
GENE BODY	Glyma.06G213300
GENE BODY	Glyma.06G214500
GENE BODY	Glyma.06G218500
GENE BODY	Glyma.06G220500
GENE BODY	Glyma.06G223800
GENE BODY	Glyma.06G228000
GENE BODY	Glyma.06G230100
GENE BODY	Glyma.06G237900
GENE BODY	Glyma.06G238500
GENE BODY	Glyma.06G238700
3'UTR(99bp); GENE BODY(2bp)	Glyma.06G239200
GENE BODY	Glyma.06G242800
PROMOTER	Glyma.06G247200
GENE BODY	Glyma.06G254000
5' UTR	Glyma.06G256000
5' UTR	Glyma.06G256000

GENE BODY	Glyma.06G259800
GENE BODY	Glyma.06G260100
GENE BODY	Glyma.06G260100
GENE BODY	Glyma.06G265900
GENE BODY	Glyma.06G268700
GENE BODY	Glyma.06G268800
5' UTR	Glyma.06G268900
GENE BODY	Glyma.06G269500
GENE BODY	Glyma.06G275600
PROMOTER	Glyma.06G289600
GENE BODY	Glyma.06G297300
GENE BODY	Glyma.06G308100
GENE BODY	Glyma.06G311400
GENE BODY	Glyma.06G318300
GENE BODY	Glyma.07G003600
GENE BODY	Glyma.07G004800
GENE BODY	Glyma.07G006600
GENE BODY	Glyma.07G008200
GENE BODY	Glyma.07G009000
GENE BODY	Glyma.07G026800
GENE BODY	Glyma.07G028100
GENE BODY	Glyma.07G029200
GENE BODY	Glyma.07G029500
GENE BODY	Glyma.07G034600
GENE BODY	Glyma.07G043700
GENE BODY	Glyma.07G046000
GENE BODY	Glyma.07G047300
GENE BODY	Glyma.07G069500
GENE BODY	Glyma.07G069600
GENE BODY	Glyma.07G072900
GENE BODY	Glyma.07G087700
3'UTR	Glyma.07G092600
5'UTR(100bp); GENE BODY(100bp)	Glyma.07G094000
GENE BODY	Glyma.07G103200
PROMOTER	Glyma.07G107300
GENE BODY	Glyma.07G119900
GENE BODY	Glyma.07G128300
PROMOTER	Glyma.07G136300
GENE BODY	Glyma.07G152100
PROMOTER	Glyma.07G154400
GENE BODY	Glyma.07G156500
GENE BODY	Glyma.07G169700
GENE BODY	Glyma.07G170200

GENE BODY	Glyma.07G171000
GENE BODY	Glyma.07G177100
GENE BODY	Glyma.07G184700
GENE BODY	Glyma.07G197000
GENE BODY	Glyma.07G204000
GENE BODY	Glyma.07G204700
GENE BODY	Glyma.07G205900
3'UTR	Glyma.07G218100
GENE BODY	Glyma.07G224600
GENE BODY	Glyma.07G225000
GENE BODY	Glyma.07G230600
PROMOTER	Glyma.07G232300
GENE BODY	Glyma.07G236300
GENE BODY	Glyma.07G259300
GENE BODY	Glyma.07G264000
GENE BODY	Glyma.08G004700
GENE BODY	Glyma.08G013000
GENE BODY	Glyma.08G013500
3'UTR(55bp); GENE BODY (145bp)	Glyma.08G027700
GENE BODY	Glyma.08G028200
3'UTR	Glyma.08G028400
GENE BODY	Glyma.08G041700
GENE BODY	Glyma.08G041700
GENE BODY	Glyma.08G044900
GENE BODY	Glyma.08G063500
GENE BODY	Glyma.08G065300
GENE BODY	Glyma.08G071900
GENE BODY	Glyma.08G074600
5' UTR(6bp); GENE BODY(194bp)	Glyma.08G075700
GENE BODY	Glyma.08G082500
PROMOTER (195bp); 5'UTR(5bp)	Glyma.08G083400
3'UTR(78bp); GENE BODY (122bp)	Glyma.08G092700
GENE BODY	Glyma.08G097800
GENE BODY	Glyma.08G100800
GENE BODY	Glyma.08G108500
GENE BODY	Glyma.08G111500
GENE BODY	Glyma.08G125700
GENE BODY	Glyma.08G141100
GENE BODY	Glyma.08G151600
GENE BODY	Glyma.08G170000
3'UTR(6bp); GENE BODY (194bp)	Glyma.08G171900
PROMOTER	Glyma.08G191200
GENE BODY	Glyma.08G192200

GENE BODY	Glyma.08G202800
GENE BODY	Glyma.08G209500
GENE BODY	Glyma.08G222300
GENE BODY	Glyma.08G228000
3'UTR	Glyma.08G233900
3'UTR	Glyma.08G233900
3'UTR	Glyma.08G233900
5'UTR(37bp); PROMOTER(163bp)	Glyma.08G233900
5'UTR(21bp); GENE BODY(179bp)	Glyma.08G233900
GENE BODY	Glyma.08G236700
GENE BODY	Glyma.08G237500
3'UTR(154bp); GENE BODY (46bp)	Glyma.08G238000
GENE BODY	Glyma.08G238000
GENE BODY	Glyma.08G238800
3'UTR(93bp); GENE BODY (107bp)	Glyma.08G241100
GENE BODY	Glyma.08G242700
GENE BODY	Glyma.08G249400
PROMOTER	Glyma.08G258900
GENE BODY	Glyma.08G259000
GENE BODY	Glyma.08G275100
GENE BODY(182bp); PROMOTER(18bp)	Glyma.08G275100
PROMOTER	Glyma.08G275100
GENE BODY	Glyma.08G276200
GENE BODY	Glyma.08G276200
GENE BODY	Glyma.08G279300
3'UTR	Glyma.08G282400
GENE BODY	Glyma.08G283600
PROMOTER	Glyma.08G300900
GENE BODY	Glyma.08G324900
3'UTR(20bp); GENE BODY (180bp)	Glyma.08G362400
GENE BODY	Glyma.09G002600
GENE BODY	Glyma.09G002700
GENE BODY	Glyma.09G013300
GENE BODY	Glyma.09G015100
GENE BODY	Glyma.09G016800
GENE BODY	Glyma.09G017000
GENE BODY	Glyma.09G023600
GENE BODY	Glyma.09G024400
5' UTR(75bp); GENE BODY(125bp)	Glyma.09G025000
GENE BODY	Glyma.09G025400
PROMOTER	Glyma.09G027300
PROMOTER	Glyma.09G029700
GENE BODY	Glyma.09G030300

5' UTR(67bp); GENE BODY(133bp)	Glyma.09G046700
GENE BODY	Glyma.09G056100
5' UTR(62bp); GENE BODY(138bp)	Glyma.09G057800
GENE BODY	Glyma.09G070600
PROMOTER	Glyma.09G072500
PROMOTER	Glyma.09G078600
GENE BODY	Glyma.09G089400
GENE BODY	Glyma.09G120200
GENE BODY	Glyma.09G148000
GENE BODY	Glyma.09G148500
GENE BODY	Glyma.09G170600
GENE BODY	Glyma.09G171000
5'UTR (82); PROMOTER (118bp)	Glyma.09G171400
GENE BODY	Glyma.09G188000
3'UTR(29bp); GENE BODY (171bp)	Glyma.09G190300
GENE BODY	Glyma.09G191600
GENE BODY	Glyma.09G199100
PROMOTER	Glyma.09G202900
GENE BODY(95bp); PROMOTER (105bp)	Glyma.09G219500
PROMOTER	Glyma.09G219600
GENE BODY	Glyma.09G228300
PROMOTER	Glyma.09G230600
GENE BODY	Glyma.09G234400
GENE BODY	Glyma.09G237200
GENE BODY	Glyma.09G246500
GENE BODY	Glyma.09G251200
3'UTR	Glyma.09G258900
3'UTR(11bp); GENE BODY (189bp)	Glyma.09G259200
GENE BODY	Glyma.09G271700
GENE BODY	Glyma.09G279900
GENE BODY	Glyma.10G009700
GENE BODY	Glyma.10G020700
GENE BODY	Glyma.10G023000
GENE BODY	Glyma.10G025000
GENE BODY	Glyma.10G028000
GENE BODY	Glyma.10G030000
5' UTR(6bp); GENE BODY(194bp)	Glyma.10G054400
GENE BODY	Glyma.10G083500
GENE BODY	Glyma.10G096900
PROMOTER(171bp); 5'UTR(29bp)	Glyma.10G098700
GENE BODY	Glyma.10G102200
GENE BODY	Glyma.10G102900
GENE BODY (115bp); PROMOTER(85bp)	Glyma.10G102900

GENE BODY	Glyma.10G118100
GENE BODY	Glyma.10G120900
GENE BODY	Glyma.10G143600
GENE BODY	Glyma.10G148600
GENE BODY	Glyma.10G149700
GENE BODY	Glyma.10G151500
GENE BODY	Glyma.10G151700
GENE BODY	Glyma.10G166200
3'UTR	Glyma.10G171500
GENE BODY	Glyma.10G187800
GENE BODY	Glyma.10G189200
GENE BODY	Glyma.10G191500
PROMOTER	Glyma.10G195900
GENE BODY	Glyma.10G201600
5' UTR(93bp); GENE BODY(107bp)	Glyma.10G208100
GENE BODY	Glyma.10G209400
GENE BODY	Glyma.10G209600
3'UTR(102bp)	Glyma.10G233300
GENE BODY	Glyma.10G241900
GENE BODY	Glyma.10G283000
3'UTR(47bp); GENE BODY(153bp)	Glyma.10G294300
GENE BODY	Glyma.11G002600
GENE BODY	Glyma.11G008700
GENE BODY	Glyma.11G039900
3'UTR(125bp); GENE BODY(75bp)	Glyma.11G040000
GENE BODY	Glyma.11G057000
GENE BODY	Glyma.11G065700
GENE BODY	Glyma.11G082200
PROMOTER	Glyma.11G102700
GENE BODY	Glyma.11G102800
GENE BODY	Glyma.11G108500
GENE BODY	Glyma.11G109800
GENE BODY	Glyma.11G110100
GENE BODY	Glyma.11G152600
GENE BODY	Glyma.11G188100
GENE BODY	Glyma.11G188900
3'UTR(104bp); GENE BODY (96bp)	Glyma.11G191000
GENE BODY	Glyma.11G192500
GENE BODY	Glyma.11G194700
GENE BODY	Glyma.11G222900
GENE BODY	Glyma.11G228600
PROMOTER	Glyma.11G228700
5' UTR(2bp); GENE BODY(198bp)	Glyma.11G251600

GENE BODY	Glyma.12G004100
GENE BODY	Glyma.12G004100
GENE BODY	Glyma.12G027600
GENE BODY	Glyma.12G036400
GENE BODY	Glyma.12G051000
GENE BODY	Glyma.12G051000
GENE BODY	Glyma.12G066300
5'UTR(165bp); PROMOTER (35bp)	Glyma.12G066400
GENE BODY	Glyma.12G067900
PROMOTER	Glyma.12G074700
3'UTR(84bp); GENE BODY (116bp)	Glyma.12G082100
GENE BODY	Glyma.12G084300
GENE BODY	Glyma.12G133500
GENE BODY	Glyma.12G136600
PROMOTER	Glyma.12G137100
GENE BODY(154bp); PROMOTER(46bp)	Glyma.12G140800
GENE BODY	Glyma.12G155900
GENE BODY	Glyma.12G158600
GENE BODY	Glyma.12G166100
GENE BODY	Glyma.12G180100
GENE BODY	Glyma.12G180800
GENE BODY	Glyma.12G198100
GENE BODY	Glyma.12G201100
GENE BODY	Glyma.12G203700
GENE BODY	Glyma.12G205500
GENE BODY	Glyma.12G209100
GENE BODY	Glyma.12G214200
GENE BODY	Glyma.12G219400
GENE BODY	Glyma.12G226700
GENE BODY	Glyma.12G229900
GENE BODY	Glyma.12G230600
GENE BODY	Glyma.12G241600
GENE BODY	Glyma.13G006200
GENE BODY	Glyma.13G026100
GENE BODY (158bp)	Glyma.13G030000
GENE BODY (93bp); PROMOTER (107bp)	Glyma.13G030000
PROMOTER	Glyma.13G030100
PROMOTER	Glyma.13G030100
GENE BODY	Glyma.13G036000
3'UTR	Glyma.13G036700
PROMOTER	Glyma.13G038300
GENE BODY	Glyma.13G048300
GENE BODY	Glyma.13G048300

GENE BODY	Glyma.13G048300
GENE BODY	Glyma.13G053700
GENE BODY	Glyma.13G058600
GENE BODY	Glyma.13G058800
PROMOTER	Glyma.13G062000
GENE BODY	Glyma.13G063600
PROMOTER	Glyma.13G067700
GENE BODY	Glyma.13G073900
GENE BODY	Glyma.13G078200
GENE BODY	Glyma.13G078800
GENE BODY	Glyma.13G084100
GENE BODY	Glyma.13G119100
GENE BODY	Glyma.13G127500
GENE BODY	Glyma.13G128700
GENE BODY	Glyma.13G130000
GENE BODY	Glyma.13G130700
PROMOTER	Glyma.13G130900
PROMOTER	Glyma.13G131000
GENE BODY	Glyma.13G135800
GENE BODY	Glyma.13G160000
GENE BODY	Glyma.13G174500
GENE BODY	Glyma.13G189000
5'UTR (94); PROMOTER (106bp)	Glyma.13G190500
GENE BODY	Glyma.13G194900
GENE BODY	Glyma.13G196700
GENE BODY	Glyma.13G196900
GENE BODY	Glyma.13G198700
5' UTR(97bp); GENE BODY(103bp)	Glyma.13G209200
GENE BODY	Glyma.13G221400
GENE BODY	Glyma.13G223400
PROMOTER	Glyma.13G225300
GENE BODY	Glyma.13G233400
GENE BODY	Glyma.13G235300
GENE BODY	Glyma.13G239300
GENE BODY	Glyma.13G244200
GENE BODY	Glyma.13G253600
GENE BODY	Glyma.13G259100
GENE BODY	Glyma.13G275400
GENE BODY	Glyma.13G277700
GENE BODY	Glyma.13G278800
3'UTR(129bp); GENE BODY (71bp)	Glyma.13G281900
5' UTR(111bp);GENE BODY(89bp)	Glyma.13G283900
PROMOTER	Glyma.13G289400

GENE BODY	Glyma.13G296400
3'UTR(107bp); GENE BODY (93bp)	Glyma.13G302900
PROMOTER	Glyma.13G305700
GENE BODY	Glyma.13G322000
GENE BODY	Glyma.13G326400
GENE BODY	Glyma.13G342500
GENE BODY	Glyma.13G355800
GENE BODY	Glyma.13G371300
GENE BODY	Glyma.14G018300
GENE BODY	Glyma.14G025300
GENE BODY	Glyma.14G044300
GENE BODY	Glyma.14G044900
GENE BODY	Glyma.14G066000
GENE BODY	Glyma.14G066100
GENE BODY	Glyma.14G066600
3'UTR	Glyma.14G083300
GENE BODY	Glyma.14G084400
GENE BODY	Glyma.14G092100
5'UTR (177bp); PROMOTER (23bp)	Glyma.14G095000
GENE BODY	Glyma.14G095200
GENE BODY	Glyma.14G098000
GENE BODY	Glyma.14G098100
GENE BODY	Glyma.14G099300
PROMOTER	Glyma.14G106300
PROMOTER	Glyma.14G108800
GENE BODY	Glyma.14G112200
3'UTR	Glyma.14G112600
GENE BODY	Glyma.14G112700
PROMOTER (173bp); 5'UTR (27bp)	Glyma.14G121200
GENE BODY	Glyma.14G129100
5'UTR(14bp); GENE BODY(186bp)	Glyma.14G132500
GENE BODY	Glyma.14G132500
PROMOTER	Glyma.14G137100
GENE BODY	Glyma.14G141800
PROMOTER (37bp); 5'UTR (122bp); GENE BODY (41bp)	Glyma.14G159200
GENE BODY	Glyma.14G159200
PROMOTER	Glyma.14G159200
GENE BODY	Glyma.14G160400
GENE BODY	Glyma.14G162300
GENE BODY	Glyma.14G170300
GENE BODY	Glyma.14G170300
GENE BODY	Glyma.14G179100
GENE BODY	Glyma.14G179200

GENE BODY	Glyma.14G183500
5' UTR(23bp); GENE BODY(177bp)	Glyma.14G186900
GENE BODY	Glyma.14G190200
3'UTR(72bp); GENE BODY (128bp)	Glyma.14G190400
GENE BODY	Glyma.14G190900
GENE BODY	Glyma.14G200600
GENE BODY	Glyma.14G204100
PROMOTER	Glyma.14G222200
PROMOTER	Glyma.15G015100
GENE BODY	Glyma.15G017200
GENE BODY	Glyma.15G023800
5' UTR	Glyma.15G025900
GENE BODY	Glyma.15G040100
3'UTR	Glyma.15G056300
PROMOTER	Glyma.15G056400
GENE BODY	Glyma.15G058700
GENE BODY	Glyma.15G074000
5' UTR	Glyma.15G087600
GENE BODY	Glyma.15G097000
GENE BODY	Glyma.15G098100
GENE BODY	Glyma.15G107500
GENE BODY	Glyma.15G116000
GENE BODY	Glyma.15G125700
3'UTR(67bp); GENE BODY (124bp)	Glyma.15G126100
PROMOTER (28bp); 5'UTR(161bp); GENE BODY(11bp)	Glyma.15G126100
GENE BODY	Glyma.15G154300
GENE BODY	Glyma.15G173300
5'UTR(26bp); PROMOTER (174bp)	Glyma.15G175600
PROMOTER	Glyma.15G175700
GENE BODY	Glyma.15G181200
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G194000
5' UTR	Glyma.15G197000
5' UTR	Glyma.15G197000
5' UTR	Glyma.15G197000
5'UTR(29bp); GENE BODY(171bp)	Glyma.15G198600
GENE BODY	Glyma.15G204500
3'UTR(105bp); GENE BODY (95bp)	Glyma.15G209000
GENE BODY	Glyma.15G212800
GENE BODY	Glyma.15G212800
GENE BODY	Glyma.15G215500

GENE BODY	Glyma.15G232600
GENE BODY	Glyma.15G235900
PROMOTER	Glyma.15G240300
5' UTR(107bp);GENE BODY(77bp); PROMOTER (16bp)	Glyma.15G240300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G248600
3'UTR(79bp); GENE BODY (121bp)	Glyma.15G254100
GENE BODY	Glyma.15G255900
GENE BODY	Glyma.15G271800
3'UTR(49bp); GENE BODY (151bp)	Glyma.15G273500
GENE BODY	Glyma.15G274000
GENE BODY	Glyma.16G004800
GENE BODY	Glyma.16G007000
GENE BODY	Glyma.16G009500
PROMOTER	Glyma.16G014200
GENE BODY	Glyma.16G018300
GENE BODY	Glyma.16G025500
GENE BODY	Glyma.16G039900
GENE BODY	Glyma.16G039900
GENE BODY	Glyma.16G040900
GENE BODY	Glyma.16G049600
GENE BODY	Glyma.16G052700
GENE BODY	Glyma.16G057400
GENE BODY	Glyma.16G066900
GENE BODY	Glyma.16G069300
GENE BODY	Glyma.16G071500
5'UTR (163bp); PROMOTER (37bp)	Glyma.16G077400
GENE BODY	Glyma.16G087100
GENE BODY	Glyma.16G095500
GENE BODY	Glyma.16G101800
PROMOTER	Glyma.16G112800
5'UTR(136bp); GENE BODY(64bp)	Glyma.16G128300
GENE BODY	Glyma.16G128600
GENE BODY	Glyma.16G134700
GENE BODY	Glyma.16G135000
5' UTR(22bp);GENE BODY(178bp)	Glyma.16G138300
GENE BODY	Glyma.16G138300
GENE BODY	Glyma.16G141800
GENE BODY	Glyma.16G144200
GENE BODY	Glyma.16G147000
GENE BODY	Glyma.16G153800

GENE BODY	Glyma.16G155700
GENE BODY	Glyma.16G159600
PROMOTER	Glyma.16G186000
GENE BODY	Glyma.16G189700
GENE BODY	Glyma.16G190100
GENE BODY	Glyma.17G010800
GENE BODY	Glyma.17G024000
GENE BODY	Glyma.17G024800
GENE BODY	Glyma.17G027700
GENE BODY	Glyma.17G033600
GENE BODY	Glyma.17G037600
GENE BODY	Glyma.17G039300
GENE BODY	Glyma.17G044200
GENE BODY	Glyma.17G059800
GENE BODY	Glyma.17G060300
GENE BODY	Glyma.17G062200
GENE BODY	Glyma.17G083300
GENE BODY	Glyma.17G083700
GENE BODY	Glyma.17G089100
GENE BODY	Glyma.17G094300
GENE BODY	Glyma.17G100600
GENE BODY	Glyma.17G105700
GENE BODY	Glyma.17G125500
GENE BODY	Glyma.17G129200
GENE BODY	Glyma.17G129900
GENE BODY	Glyma.17G145000
GENE BODY	Glyma.17G145500
GENE BODY	Glyma.17G158200
GENE BODY	Glyma.17G160700
GENE BODY	Glyma.17G171600
GENE BODY	Glyma.17G173300
GENE BODY	Glyma.17G173300
GENE BODY	Glyma.17G181000
GENE BODY	Glyma.17G184300
GENE BODY	Glyma.17G184300
GENE BODY(150bp); PROMOTER(50bp)	Glyma.17G184300
PROMOTER	Glyma.17G184300
PROMOTER	Glyma.17G188600
GENE BODY(107bp); PROMOTER(93bp)	Glyma.17G190200
GENE BODY	Glyma.17G191000
3'UTR	Glyma.17G191700
PROMOTER	Glyma.17G191800
GENE BODY	Glyma.17G199600

GENE BODY	Glyma.17G200200
GENE BODY	Glyma.17G201000
GENE BODY	Glyma.17G204000
GENE BODY	Glyma.17G210100
GENE BODY	Glyma.17G210100
PROMOTER	Glyma.17G213600
GENE BODY	Glyma.17G215800
3'UTR(60bp); GENE BODY (140bp)	Glyma.17G219600
GENE BODY	Glyma.17G220800
3'UTR	Glyma.17G226600
GENE BODY	Glyma.17G235400
GENE BODY	Glyma.17G244800
GENE BODY	Glyma.17G249100
3'UTR(98bp); GENE BODY (102bp)	Glyma.17G250200
GENE BODY	Glyma.17G253700
GENE BODY	Glyma.17G255500
GENE BODY	Glyma.17G257100
GENE BODY	Glyma.18G003800
GENE BODY	Glyma.18G004600
GENE BODY	Glyma.18G004600
GENE BODY	Glyma.18G011200
GENE BODY	Glyma.18G011200
PROMOTER	Glyma.18G013300
PROMOTER	Glyma.18G013300
GENE BODY	Glyma.18G016200
GENE BODY	Glyma.18G027800
5' UTR(33bp); GENE BODY(167bp)	Glyma.18G028900
GENE BODY	Glyma.18G055700
PROMOTER	Glyma.18G060800
GENE BODY	Glyma.18G064900
3'UTR(15bp); GENE BODY(185bp)	Glyma.18G068800
GENE BODY	Glyma.18G093500
GENE BODY	Glyma.18G093500
GENE BODY	Glyma.18G093600
GENE BODY	Glyma.18G107900
PROMOTER	Glyma.18G112200
GENE BODY	Glyma.18G131200
PROMOTER	Glyma.18G146700
GENE BODY	Glyma.18G154700
3'UTR	Glyma.18G159100
GENE BODY	Glyma.18G166600
PROMOTER	Glyma.18G167500
5' UTR(43bp); GENE BODY(157bp)	Glyma.18G170600

GENE BODY	Glyma.18G176400
GENE BODY(69bp); PROMOTER (131bp)	Glyma.18G178600
PROMOTER	Glyma.18G186900
GENE BODY	Glyma.18G195000
GENE BODY	Glyma.18G199800
GENE BODY	Glyma.18G209800
GENE BODY	Glyma.18G219100
GENE BODY	Glyma.18G230300
GENE BODY	Glyma.18G237100
GENE BODY	Glyma.18G237200
GENE BODY	Glyma.18G247300
GENE BODY	Glyma.18G251800
GENE BODY	Glyma.18G252800
3'UTR(75bp); GENE BODY (125bp)	Glyma.18G253400
GENE BODY	Glyma.18G280500
GENE BODY	Glyma.18G286300
GENE BODY	Glyma.18G296100
GENE BODY	Glyma.18G297900
GENE BODY	Glyma.19G001500
GENE BODY	Glyma.19G012300
GENE BODY	Glyma.19G012900
GENE BODY	Glyma.19G016300
GENE BODY	Glyma.19G023400
GENE BODY	Glyma.19G028800
GENE BODY	Glyma.19G029000
GENE BODY	Glyma.19G040200
GENE BODY	Glyma.19G040800
GENE BODY	Glyma.19G043600
GENE BODY	Glyma.19G076400
GENE BODY	Glyma.19G077100
3'UTR(5bp); GENE BODY (195bp)	Glyma.19G077200
GENE BODY	Glyma.19G082800
GENE BODY	Glyma.19G086600
GENE BODY	Glyma.19G095000
PROMOTER	Glyma.19G097300
3'UTR(44bp); GENE BODY (156bp)	Glyma.19G116000
GENE BODY	Glyma.19G117700
GENE BODY	Glyma.19G141800
GENE BODY	Glyma.19G149500
3'UTR(16bp); GENE BODY (184bp)	Glyma.19G152200
3'UTR(57bp); GENE BODY (143bp)	Glyma.19G155900
GENE BODY	Glyma.19G170700
GENE BODY	Glyma.19G175600

GENE BODY	Glyma.19G175900
GENE BODY	Glyma.19G178700
GENE BODY	Glyma.19G179300
GENE BODY	Glyma.19G180500
PROMOTER	Glyma.19G184200
3'UTR	Glyma.19G185300
GENE BODY	Glyma.19G187300
PROMOTER	Glyma.19G187400
GENE BODY	Glyma.19G208300
GENE BODY	Glyma.19G213700
5'UTR(43bp); PROMOTER (157bp)	Glyma.19G217000
GENE BODY	Glyma.19G221200
GENE BODY	Glyma.19G239400
GENE BODY	Glyma.19G239700
GENE BODY	Glyma.19G250600
3'UTR(39bp); GENE BODY (161bp)	Glyma.19G251400
GENE BODY	Glyma.19G256500
GENE BODY	Glyma.19G259200
GENE BODY	Glyma.20G013500
GENE BODY	Glyma.20G017400
GENE BODY	Glyma.20G025100
3'UTR(155bp); GENE BODY (45bp)	Glyma.20G027500
5' UTR(42bp); GENE BODY(158bp)	Glyma.20G040900
5' UTR	Glyma.20G047800
PROMOTER	Glyma.20G047900
GENE BODY	Glyma.20G054500
GENE BODY	Glyma.20G056500
GENE BODY	Glyma.20G060800
GENE BODY	Glyma.20G079600
3'UTR(43bp); GENE BODY (157bp)	Glyma.20G079800
GENE BODY	Glyma.20G086700
GENE BODY	Glyma.20G107600
GENE BODY	Glyma.20G110600
GENE BODY	Glyma.20G112200
GENE BODY	Glyma.20G116900
PROMOTER	Glyma.20G120500
GENE BODY	Glyma.20G130800
PROMOTER	Glyma.20G131200
GENE BODY	Glyma.20G146600
GENE BODY	Glyma.20G149100
GENE BODY	Glyma.20G149200
GENE BODY	Glyma.20G153600
3'UTR	Glyma.20G154300

PROMOTER	Glyma.20G162200
GENE BODY	Glyma.20G165400
GENE BODY	Glyma.20G166000
GENE BODY	Glyma.20G173200
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G185800
GENE BODY	Glyma.20G187800
GENE BODY	Glyma.20G189700
GENE BODY	Glyma.20G195700
GENE BODY	Glyma.20G208700
GENE BODY	Glyma.20G216900
GENE BODY	Glyma.20G217700
GENE BODY	Glyma.20G218900
GENE BODY	Glyma.20G233700
GENE BODY	Glyma.20G244700
GENE BODY	Glyma.U010500
PROMOTER	Glyma.U013900
GENE BODY	Glyma.U032300
GENE BODY	Glyma.U032500
GENE BODY	Glyma.U034000
PROMOTER	Glyma.U035000

GENE ANNOTATION	Methylation Differenc
gamma-glutamyl transpeptidase 4	-37.99867021
hexokinase 2	-34.41134752
hexokinase 2	-51.85185185
N/A	-58.67924528
N/A	-49.48453608
kinesin like protein for actin based chloroplast movement 1	-39.47368421
Alkaline-phosphatase-like family protein	-97.05882353
N/A	-41.93245779
SIN3-like 3	-41.93245779
N/A	-60.625
SOUL heme-binding family protein	-88.23529412
Pentatricopeptide repeat (PPR) superfamily protein	-32.60869565
Squamosa promoter-binding protein-like (SBP domain) transcripti	-100
Prolyl oligopeptidase family protein	-100
N/A	-100
Phosphoglycerate mutase family protein	-100
Nucleic acid-binding, OB-fold-like protein	-40
Nucleic acid-binding, OB-fold-like protein	-33.20087809
Nucleic acid-binding, OB-fold-like protein	-34.99128616
ARM repeat superfamily protein	-76.47058824
Zinc finger (CCCH-type) family protein	-34.36363636
glucose-6-phosphate/phosphate translocator 2	-34.26332288
glucose-6-phosphate/phosphate translocator 2	-29.71846847
TBP-associated factor 15	-40
receptor like protein 6	-74.07407407
N/A	-81.25
N/A	-91.66666667
arginase	-70.1754386
N/A	-80
N/A	-37.48902546
N/A	-52.17391304
RNA-binding (RRM/RBD/RNP motifs) family protein	-52.17391304
RNA-binding (RRM/RBD/RNP motifs) family protein	-37.48902546
protein binding	-52.17391304
protein binding	-37.48902546
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family pro	-33.46613546
RNA polymerase II large subunit	-70.83333333
calcium-dependent protein kinase 16	-56.52173913
DNA binding;zinc ion binding;nucleic acid binding;nucleic acid binc	-84.02985075
N/A	-75
SU(VAR)3-9 homolog 6	-39.47368421

RGPR-related	-47.05882353
alpha/beta-Hydrolases superfamily protein	-27.72277228
THUMP domain-containing protein	-30.97345133
RING/FYVE/PHD zinc finger superfamily protein	-90.90909091
CVP2 like 1	-63.63636364
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger	-56.03492553
somatic embryogenesis receptor-like kinase 1	-92.45283019
Tetratricopeptide repeat (TPR)-like superfamily protein	-91.66666667
ABC transporter 1	-32.11038961
N/A	-83.33333333
serine acetyltransferase 3;2	-37.39809783
TSL-kinase interacting protein 1	-96.96969697
FAD/NAD(P)-binding oxidoreductase family protein	-72.58064516
Pyridoxal phosphate (PLP)-dependent transferases superfamily pr	-44.70066519
N/A	-75
Mitochondrial substrate carrier family protein	-59.41043084
microtubule-associated proteins 70-2	-28.71590153
HEAT repeat-containing protein	-74.72527473
phenylalanyl-tRNA synthetase class IIc family protein	-79.36507937
Ribosomal protein L12/ ATP-dependent Clp protease adaptor prot	-100
methionine aminopeptidase 1B	-43.86733417
NAC (No Apical Meristem) domain transcriptional regulator super	-69.64285714
N/A	-29.76190476
N/A	-41.37931034
peroxisomal adenine nucleotide carrier 1	-46.03174603
N/A	-37.33031674
N/A	-39.52861953
N/A	-33.34991708
galacturonosyltransferase 6	-60
alpha/beta-Hydrolases superfamily protein	-77.6119403
methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-m	-95.23809524
Tetratricopeptide repeat (TPR)-like superfamily protein	-36.53846154
basic region/leucine zipper motif 60	-32.78688525
N/A	-37.93103448
Protein of unknown function, DUF593	-100
N/A	-38.8712522
P-loop containing nucleoside triphosphate hydrolases superfamily	-78.57142857
nudix hydrolase homolog 23	-57.5
Protein of unknown function (DUF288)	-73.17073171
Cyclin-like family protein	-53.84615385
MAP kinase kinase 6	-38.63636364

S-adenosyl-L-methionine-dependent methyltransferases superfam	-73.91304348
N/A	-34.28571429
chaperone protein dnaJ-related	-35.13513514
Tetratricopeptide repeat (TPR)-like superfamily protein	-70.34632035
Pseudouridine synthase family protein	-43.5483871
Golgi-body localisation protein domain ;RNA pol II promoter Fmp2	-100
indole-3-acetic acid inducible 9	-52.38095238
N/A	-25.37252056
ribosomal protein S2	-83.09659091
nucleotide binding;protein binding	-73.91304348
Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	-77.77777778
Xanthine/uracil permease family protein	-100
serine/threonine protein phosphatase 2A 55 kDa regulatory subur	-27.11864407
Protein phosphatase 2A regulatory B subunit family protein	-61.40350877
Ethylene insensitive 3 family protein	-63.15789474
auxin response factor 6	-100
hydroxyproline-rich glycoprotein family protein	-91.30434783
ENHANCED DOWNY MILDEW 2	-39.38215103
multidrug resistance-associated protein 3	-76.47058824
DNAJ heat shock N-terminal domain-containing protein	-67.14975845
Nucleotide-sugar transporter family protein	-25.92935479
SEC7-like guanine nucleotide exchange family protein	-76.92307692
RAS associated with diabetes protein 51C	-100
high mobility group	-58.72909699
Protein phosphatase 2C family protein	-29.47368421
regulatory particle AAA-ATPase 2A	-47.22222222
mRNA capping enzyme family protein	-50.90909091
defective in exine formation protein (DEX1)	-69.04761905
RHOMBOID-like 1	-50
E3 Ubiquitin ligase family protein	-63.1372549
Chloroplast Ycf2;ATPase, AAA type, core	-34.97432606
hAT dimerisation domain-containing protein	-94.28571429
alpha/beta-Hydrolases superfamily protein	-70.37037037
disproportionating enzyme 2	-83.72093023
TGACG motif-binding factor 6	-72.81553398
P-loop containing nucleoside triphosphate hydrolases superfamily	-63.88888889
N/A	-61.53846154
curculin-like (mannose-binding) lectin family protein / PAN domaiı	-90
N/A	-31.42857143
spindle pole body component 98	-75.30864198
FUS3-complementing gene 1	-30.14705882
FASCICLIN-like arabinogalactan-protein 11	-50.67126966

Pyruvate kinase family protein	-90
RHOMBOID-like protein 15	-27.77991207
Chaperone DnaJ-domain superfamily protein	-76.92307692
N/A	-29.41176471
N/A	-27.11111111
Protein phosphatase 2C family protein	-29.41176471
Protein phosphatase 2C family protein	-27.11111111
regulatory particle triple-A ATPase 5A	-47.22772277
RNA polymerase II transcription mediators	-68
Glycosyl hydrolase superfamily protein	-70.83333333
Ankyrin repeat family protein	-36.36363636
Sec14p-like phosphatidylinositol transfer family protein	-73.91304348
Galactose oxidase/kelch repeat superfamily protein	-66
Protein kinase superfamily protein	-69.13580247
glycosyl hydrolase 9B7	-66
Plant protein of unknown function (DUF869)	-48.8372093
xylem bark cysteine peptidase 3	-39.47368421
N/A	-64.28571429
RING/U-box superfamily protein	-55
RING/U-box superfamily protein	-81.81818182
homology to ABI1	-100
tyrosyl-DNA phosphodiesterase-related	-68.33333333
N/A	-100
Putative serine esterase family protein	-98
CBL-interacting protein kinase 8	-55
Rho GTPase activation protein (RhoGAP) with PH domain	-60
binding	-72.22222222
N/A	-91.66666667
zinc induced facilitator-like 1	-27.21893491
nuclear matrix protein-related	-56.71641791
Cytidine/deoxycytidylate deaminase family protein	-100
cyclic nucleotide-gated channel 17	-71.16382506
DDT domain superfamily	-74.64788732
Homeodomain-like superfamily protein	-90
Protein kinase superfamily protein	-37.5
alpha/beta-Hydrolases superfamily protein	-100
nuclear protein X1	-43.33333333
topoisomerase 3alpha	-51.72413793
histone methyltransferases(H3-K4 specific);histone methyltransfe	-53.74396135
putative protein kinase 1	-45.05882353
Transducin/WD40 repeat-like superfamily protein	-74.28571429
sirohydrochlorin ferrochelatase B	-58
Tetratricopeptide repeat (TPR)-like superfamily protein	-93.33333333

Transcription factor TFIIE, alpha subunit	-95.65217391
glycine-rich RNA-binding protein 3	-100
H(+)-ATPase 11	-68.18181818
DDT domain superfamily	-42.80661867
ARM repeat superfamily protein	-43.47826087
ARM repeat superfamily protein	-26.72998643
RNA-dependent RNA polymerase 2	-91.30434783
histone deacetylase 6	-100
ubiquitin-associated (UBA)/TS-N domain-containing protein / octi	-94.11764706
AAA-type ATPase family protein	-73.91304348
MBOAT (membrane bound O-acyl transferase) family protein	-34
O-fucosyltransferase family protein	-36.97351828
hydroxyproline-rich glycoprotein family protein	-31.41025641
Histone H3 K4-specific methyltransferase SET7/9 family protein	-28.38333107
N/A	-91.42857143
Tetratricopeptide repeat (TPR)-like superfamily protein	-59.09090909
AMP-dependent synthetase and ligase family protein	-93.33333333
AMP-dependent synthetase and ligase family protein	-93.33333333
histidine acid phosphatase family protein	-26.5625
histidine acid phosphatase family protein	-100
N/A	-27.65422859
Tubulin/FtsZ family protein	-92.85714286
Ribosomal L32p protein family	-94.44444444
pumilio 7	-68.75
P-loop containing nucleoside triphosphate hydrolases superfamily	-91.66666667
IAP-like protein 1	-47.91666667
Tic22-like family protein	-42.5
aspartate kinase-homoserine dehydrogenase ii	-71.64179104
5\'-3\' exonuclease family protein	-100
RNA-binding (RRM/RBD/RNP motifs) family protein	-57.8125
N/A	-28.93081761
essential meiotic endonuclease 1B	-44.18604651
N/A	-42.9280397
signal recognition particle-related / SRP-related	-46.08433735
P-loop nucleoside triphosphate hydrolases superfamily protein wi	-100
RNA helicase, ATP-dependent, SK12/DOB1 protein	-78.125
N/A	-74.19354839
ARM repeat superfamily protein	-100
ARM repeat superfamily protein	-44
N/A	-75
Calcium-binding EF hand family protein	-75
N/A	-100
RNA-binding protein 1	-51.16648993

RNA-binding KH domain-containing protein	-29.57746479
RNA-binding KH domain-containing protein	-36.95652174
Golgi-body localisation protein domain ;RNA pol II promoter Fmp2	-100
Tetratricopeptide repeat (TPR)-like superfamily protein	-66.07142857
MAPK/ERK kinase kinase 1	-36.36363636
YbaK/aminoacyl-tRNA synthetase-associated domain	-70.96774194
Chaperone DnaJ-domain superfamily protein	-40.625
global transcription factor group A2	-78.94736842
vacuolar protein sorting 45	-66.66666667
plastid transcriptionally active7	-81.81818182
nascent polypeptide-associated complex subunit alpha-like protei	-29.54545455
disproportionating enzyme	-51.94805195
like COV 2	-39.28571429
Nucleotidyltransferase family protein	-25.15873016
ferrochelatase 2	-73.01587302
transducin family protein / WD-40 repeat family protein	-100
glucan synthase-like 8	-100
glucan synthase-like 8	-31.66666667
N/A	-31.66666667
Protein of unknown function (DUF962)	-40
Protein of unknown function (DUF962)	-34.87394958
SNF2 domain-containing protein / helicase domain-containing pro	-67.5
N/A	-100
ATPase E1-E2 type family protein / haloacid dehalogenase-like hy	-25.58139535
homeodomain GLABROUS 2	-91.30434783
prenylated RAB acceptor 1.B4	-57.8125
Transducin/WD40 repeat-like superfamily protein	-57.8125
Stabilizer of iron transporter SufD / Polynucleotidyl transferase	-74.11764706
Protein of unknown function (DUF803)	-48.10400867
Nucleotide/sugar transporter family protein	-45.45454545
signal recognition particle receptor alpha subunit family protein	-72.30769231
cyclic nucleotide-gated channel 17	-100
DNAJ heat shock family protein	-39.13043478
N/A	-48.53603604
Ankyrin repeat family protein	-70.58823529
cytochrome P450, family 72, subfamily A, polypeptide 15	-66.66666667
phytosylfokine-alpha receptor 2	-66.66666667
ribosomal protein L6 family protein	-45
cytochrome c oxidase 17	-100
Transducin/WD40 repeat-like superfamily protein	-96.15384615
ARF-GAP domain 5	-95.12195122
Disease resistance protein (TIR-NBS-LRR class) family	-38.31831832
Disease resistance protein (TIR-NBS-LRR class) family	-30.53626543

Disease resistance protein (TIR-NBS-LRR class) family	-50.94339623
Disease resistance protein (TIR-NBS-LRR class) family	-38.7804878
Disease resistance protein (TIR-NBS-LRR class) family	-34.32835821
BED zinc finger ;hAT family dimerisation domain	-64.46808511
disease resistance protein (TIR-NBS-LRR class), putative	-41.66666667
Tetratricopeptide repeat (TPR)-like superfamily protein	-74.41860465
ortholog of human splicing factor SC35	-74.41860465
Translation initiation factor SUI1 family protein	-33.79228954
trehalose-phosphatase/synthase 7	-70.90909091
Peptidase family M48 family protein	-90.90909091
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase fam	-33.02139037
N/A	-100
nuclear factor Y, subunit C11	-54.05405405
NB-ARC domain-containing disease resistance protein	-42.85714286
exocyst complex component 84B	-50
Phox-associated domain;Phox-like;Sorting nexin, C-terminal	-56.21840243
translocon at the inner envelope membrane of chloroplasts 20	-84.84848485
N/A	-57.47303544
Metallo-hydrolase/oxidoreductase superfamily protein	-100
cation exchanger 5	-100
CemA-like proton extrusion protein-related	-28.408713
Signal recognition particle, SRP54 subunit protein	-43.14345992
Ubiquitin system component Cue protein	-52.27272727
CASC3/Barentsz eIF4AIII binding	-43.75
CCAAT-binding factor	-68
pectin methylesterase 3	-54.58669355
N/A	-64.17910448
cytochrome P450, family 86, subfamily A, polypeptide 8	-67.5
Major facilitator superfamily protein	-55.51948052
RNAhelicase-like 8	-71.96969697
MUTS homolog 7	-82.60869565
Plant protein of unknown function (DUF639)	-86.66666667
ATP-binding cassette A2	-38.89659958
Surfeit locus 1 cytochrome c oxidase biogenesis protein	-92.30769231
basic pentacysteine1	-92.30769231
Vacuolar sorting protein 39	-34.13105413
N/A	-77.50206782
N/A	-95.45454545
N/A	-100
N/A	-67.64705882
Tautomerase/MIF superfamily protein	-55.85516179
ARM repeat superfamily protein	-67.34693878
RING-finger protein for embryogenesis	-29.58579882

DYNAMIN-like 1C	-67.21311475
Pentatricopeptide repeat (PPR-like) superfamily protein	-65
Glutamyl-tRNA reductase family protein	-70.96774194
Protein of unknown function (DUF616)	-100
IQ-domain 9	-70.45454545
N/A	-39.34108527
Thioesterase/thiol ester dehydrase-isomerase superfamily protein	-97.2972973
Pentatricopeptide repeat (PPR) superfamily protein	-100
calmodulin-binding protein	-70
N/A	-60.17316017
RING/U-box superfamily protein	-50.67330211
N/A	-65.71428571
Glycosyl hydrolase superfamily protein	-41.66666667
tobamovirus multiplication 1	-100
ZCW7	-38.88719357
DDT domain-containing protein	-30.83333333
Myosin heavy chain-related protein	-62.15447154
serine racemase	-100
RNA helicase, ATP-dependent, SK12/DOB1 protein	-46.53465347
phosphorylethanolamine cytidylyltransferase 1	-93.02325581
isoamylase 1	-72.22222222
CRS1 / YhbY (CRM) domain-containing protein	-83.33333333
CRS1 / YhbY (CRM) domain-containing protein	-36.99065792
associated molecule with the SH3 domain of STAM 1	-100
Pyridoxal phosphate (PLP)-dependent transferases superfamily pr	-34.28571429
AGAMOUS-like 44	-100
Protein phosphatase 2C family protein	-100
arginine/serine-rich zinc knuckle-containing protein 33	-55.453149
RNA-binding (RRM/RBD/RNP motifs) family protein with retroviru	-49.29577465
O-acetyltransferase family protein	-35.13513514
RECQ helicase l1	-47.54098361
ZIP metal ion transporter family	-100
ornithine-delta-aminotransferase	-96.96969697
Leucine-rich repeat protein kinase family protein	-80
G10 family protein	-85.71428571
protein binding	-40
LETM1-like protein	-90
N/A	-100
Rad21/Rec8-like family protein	-71.76470588
Ribosomal protein S5/Elongation factor G/III/V family protein	-100
Trypsin family protein	-65.67164179
N/A	-53.57142857
Metallo-hydrolase/oxidoreductase superfamily protein	-100

LETM1-like protein	-100
mRNA capping enzyme family protein	-100
O-fucosyltransferase family protein	-28.57142857
EAP30/Vps36 family protein	-52.44122966
Pentatricopeptide repeat (PPR) superfamily protein	-46.15384615
Pentatricopeptide repeat (PPR) superfamily protein	-31.76470588
Pentatricopeptide repeat (PPR) superfamily protein	-28.08988764
Pentatricopeptide repeat (PPR) superfamily protein	-58.71559633
Pentatricopeptide repeat (PPR) superfamily protein	-48.88888889
Topoisomerase II-associated protein PAT1	-44.44444444
FTSH protease 12	-40.74074074
P-loop containing nucleoside triphosphate hydrolases superfamily	-55.81395349
P-loop containing nucleoside triphosphate hydrolases superfamily	-34.48275862
Phosphoinositide phosphatase family protein	-100
Tetratricopeptide repeat (TPR)-like superfamily protein	-30
calmodulin-binding protein-related	-27.53623188
Malectin/receptor-like protein kinase family protein	-27.27272727
Protein phosphatase 2C family protein	-63.88888889
NB-ARC domain-containing disease resistance protein	-63.88888889
Concanavalin A-like lectin protein kinase family protein	-43.5483871
Concanavalin A-like lectin protein kinase family protein	-43.75
Concanavalin A-like lectin protein kinase family protein	-43.90243902
N/A	-28.07268008
N/A	-25.79206701
Kinase interacting (KIP1-like) family protein	-26.08695652
cyclin-relatedMETHYLATED_REGION_CpG_HYPO	-28.94736842
Protein of Unknown Function (DUF239)	-38.83495146
open reading frame 204	-31.59003831
beta-1,2-xylosyltransferase	-66.64098613
ENTH/VHS family protein	-41.66666667
Signal transduction histidine kinase, hybrid-type, ethylene sensor	-84.12698413
indigoidine synthase A family protein	-100
pentatricopeptide (PPR) repeat-containing protein	-100
Sec14p-like phosphatidylinositol transfer family protein	-93.33333333
Transducin/WD40 repeat-like superfamily protein	-80
galacturonosyltransferase 4	-73.33333333
Homeobox-leucine zipper family protein / lipid-binding START don	-70.73170732
Calcium-dependent ARF-type GTPase activating protein family	-47.72727273
KRR1 family protein	-41.93548387
dicer-like 2	-100
FAD-binding Berberine family protein	-30.27108434
NAD(P)-binding Rossmann-fold superfamily protein	-41.26984127
NAD(P)-binding Rossmann-fold superfamily protein	-96.66666667

N/A	-30.43478261
Galactose oxidase/kelch repeat superfamily protein	-84.3373494
pumilio 5	-100
DEAD/DEAH box RNA helicase family protein	-94.73684211
protein kinase family protein / C-type lectin domain-containing pr	-46.76958262
N/A	-60.48076923
rRNA processing protein-related	-32.2290032
DNA GYRASE A	-78.94736842
zinc finger WD40 repeat protein 1	-92.30769231
hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hyd	-68.18181818
Dihydroxyacetone kinase	-69.23076923
embryo sac development arrest 7	-36.66666667
photosystem II reaction center protein M	-29.22033898
Fibronectin type III domain-containing protein	-85.71428571
N/A	-73.9088729
Tesmin/TSO1-like CXC domain-containing protein	-100
MSCS-like 2	-40
Glycosyl hydrolase family protein	-38.83784606
SAUR-like auxin-responsive protein family	-76.47058824
SAUR-like auxin-responsive protein family	-76.47058824
Uncharacterized protein	-44.11206078
N/A	-43.40909091
DNA binding;ATP binding;nucleic acid binding;binding;helicases;A	-55.55555556
Pentatricopeptide repeat (PPR-like) superfamily protein	-76.69902913
DNA-directed RNA polymerases	-69.6969697
zinc finger protein 1	-60
SKP1-like 21	-70.90909091
Protein of unknown function (DUF3741)	-81.25
RNA-binding KH domain-containing protein	-100
SCAR homolog 2	-52.27272727
Polyketide cyclase/dehydrase and lipid transport superfamily prot	-37.83783784
Zinc finger C-x8-C-x5-C-x3-H type family protein	-90.90909091
transducin family protein / WD-40 repeat family protein	-83.33333333
N/A	-28.94557823
Galactose oxidase/kelch repeat superfamily protein	-67.56756757
Beige/BEACH domain ;WD domain, G-beta repeat protein	-60.86956522
Mitochondrial transcription termination factor family protein	-35.02739467
N/A	-95
kinesin 1	-32.53333333
N/A	-33.51032448
N/A	-34.53199365
Arginyl-tRNA synthetase, class Ic	-57.20238095
Arginyl-tRNA synthetase, class Ic	-92.72727273

Protein kinase family protein with ARM repeat domain	-57.33333333
ubiquitin-specific protease 13	-100
Protein of unknown function (DUF3411)	-40.1744186
Polynucleotidyl transferase, ribonuclease H-like superfamily prote	-49.15254237
mitochondrially targeted single-stranded DNA binding protein	-38.28551913
RING/U-box superfamily protein	-100
N/A	-100
RNA-binding (RRM/RBD/RNP motifs) family protein	-48.57142857
RNA binding (RRM/RBD/RNP motifs) family protein	-95.23809524
Uncharacterised protein family (UPF0497)	-38.70967742
Protein of unknown function (DUF810)	-25.75138009
N/A	-100
nudix hydrolase homolog 26	-36.43697019
Transmembrane amino acid transporter family protein	-100
Sec1/munc18-like (SM) proteins superfamily	-76.47058824
Zim17-type zinc finger protein	-47.02380952
Zinc finger (C2H2 type) family protein / transcription factor jumon	-55
N/A	-37.5
DEAD box RNA helicase (PRH75)	-39.02439024
Protein of unknown function (DUF630 and DUF632)	-26.2987013
tonneau 1b (TON1b)	-98.61111111
target of rapamycin	-37.04274162
N/A	-100
pleckstrin homology (PH) domain-containing protein	-81.81818182
N/A	-44.44444444
P-loop containing nucleoside triphosphate hydrolases superfamily	-81.31868132
Pentatricopeptide repeat (PPR) superfamily protein	-100
ACT-like protein tyrosine kinase family protein	-34.64912281
Ubiquitin-like superfamily protein	-40
N/A	-40
Plant protein of unknown function (DUF827)	-47.27272727
RING/FYVE/PHD zinc finger superfamily protein	-100
ATPase, F0/V0 complex, subunit C protein	-100
Ribosomal RNA processing Brix domain protein	-100
tRNAisopentenyltransferase 2	-72.5
Ribosomal protein L24e family protein	-41.77927928
vacuolar protein sorting 41	-31.48148148
ribosomal protein L9	-100
ABC transporter family protein	-90.90909091
BTB/POZ/MATH-domains containing protein	-100
Yippee family putative zinc-binding protein	-100
N/A	-100
Galactose oxidase/kelch repeat superfamily protein	-100

AGC (cAMP-dependent, cGMP-dependent and protein kinase C) ki	-72.22222222
AGC (cAMP-dependent, cGMP-dependent and protein kinase C) ki	-53.84615385
mitogen-activated protein kinase kinase kinase 7	-90.47619048
Basic-leucine zipper (bZIP) transcription factor family protein	-100
RNA binding	-37.5
RNA binding	-42.3661509
N/A	-90
N/A	-90
DHBP synthase RibB-like alpha/beta domain	-100
NOT2 / NOT3 / NOT5 family	-43.83561644
Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] do	-42.64705882
PHD finger family protein	-31.22015915
Protein kinase superfamily protein	-100
kinesin 3	-51.84275184
Protein kinase superfamily protein	-25.36509176
S-locus lectin protein kinase family protein	-83.33333333
Leucine-rich repeat transmembrane protein kinase	-61.9047619
homogentisate 1,2-dioxygenase	-100
shaggy-like protein kinase 41	-91.66666667
ARM repeat superfamily protein	-100
DNA/RNA helicase protein	-100
S-locus lectin protein kinase family protein	-45
zinc ion binding	-36.73245614
N/A	-100
RING 1A	-59.36853002
global transcription factor group E4	-90.90909091
Tetratricopeptide repeat (TPR)-like superfamily protein	-60.86956522
myosin 2	-65.43209877
Yippee family putative zinc-binding protein	-72.89719626
N/A	-74.50980392
RAB GTPase homolog A1B	-63.15789474
eukaryotic translation initiation factor SUI1 family protein	-59.64285714
homolog of yeast ADA2 2A	-62.5
Endomembrane protein 70 protein family	-54.05405405
N/A	-28.19875776
N/A	-49.33333333
high mobility group B2	-28.19875776
high mobility group B2	-49.33333333
Target of Myb protein 1	-96.15384615
DNAJ heat shock N-terminal domain-containing protein	-51.28205128
Auxin efflux carrier family protein	-38.46153846
N/A	-29.18192918
N/A	-27.817005

N/A	-42.62295082
Malectin/receptor-like protein kinase family protein	-27.00743049
casein lytic proteinase B3	-64.86486486
EID1-like 2	-67.85714286
NAC domain containing protein 100	-35.93073593
cullin 3	-100
hydroxyproline-rich glycoprotein family protein	-59.26370548
protein kinase 2A	-62.85714286
Disease resistance protein (TIR-NBS-LRR class) family	-28.57142857
3\'-5\' exonuclease domain-containing protein	-75
MAPK/ERK kinase kinase 1	-76.78571429
HAD-superfamily hydrolase, subfamily IG, 5\'-nucleotidase	-100
multidrug resistance-associated protein 5	-100
myosin 2	-100
CLIP-associated protein	-98.14814815
HSP20-like chaperones superfamily protein	-73.45238095
heat shock cognate protein 70-1	-29.2334248
PIF1 helicase	-29.2334248
Protein kinase superfamily protein	-76.66666667
BED zinc finger ;hAT family dimerisation domain	-91.66666667
Protein of unknown function (DUF1162)	-76.15384615
cysteine-rich RLK (RECEPTOR-like protein kinase) 10	-70
Peptidase S24/S26A/S26B/S26C family protein	-50.02462448
Disease resistance protein (TIR-NBS-LRR class) family	-68.08510638
Phosphatidylinositol-4-phosphate 5-kinase family protein	-100
nuclear RNA polymerase D1B	-57.57575758
uridine 5\'-monophosphate synthase / UMP synthase (PYRE-F) (UI	-54.76190476
CBS domain-containing protein with a domain of unknown functio	-100
auxin response factor 8	-48.17391304
Integrin-linked protein kinase family	-32.64051522
N/A	-27.63918252
glutamate receptor 2.7	-51.35746606
Homeodomain-like transcriptional regulator	-28.62318841
callose synthase 5	-74.46808511
STRUBBELIG-receptor family 3	-88.37209302
pyrophosphorylase 6	-100
RING/U-box superfamily protein	-89.76190476
MATE efflux family protein	-28.47144457
Nucleotidyltransferase family protein	-65.85365854
Leucine-rich repeat (LRR) family protein	-63.07692308
myosin 2	-52.56099832
BURP domain-containing protein	-30.27912621
WRKY DNA-binding protein 69	-90

Protein kinase superfamily protein	-100
photosynthetic electron transfer C	-76.05633803
Receptor-like protein kinase-related family protein	-49.93257417
N/A	-91.17647059
4-hydroxy-3-methylbut-2-enyl diphosphate synthase	-77.22222222
ETHYLENE-INSENSITIVE3-like 3	-53.03571429
ENTH/VHS family protein	-68.125
N/A	-100
microtubule-associated proteins 65-1	-43.24561404
polymerase gamma 2	-34.61538462
F-box protein 2	-80
Structural maintenance of chromosomes (SMC) family protein	-95.45454545
Regulator of chromosome condensation (RCC1) family protein	-72.5
Pentatricopeptide repeat (PPR-like) superfamily protein	-87.5
sec7 domain-containing protein	-71.23287671
THO complex, subunit 5	-96
N/A	-46.529723
Transketolase family protein	-75
nucleotide binding protein 35	-34.11764706
Small nuclear ribonucleoprotein family protein	-38.25161887
G protein alpha subunit 1	-100
Chalcone-flavanone isomerase family protein	-37.14285714
ACT-like protein tyrosine kinase family protein	-55.78378378
N/A	-43.24324324
N/A	-43.36170213
TRS120	-100
N/A	-63.89578164
SET domain group 29	-63.89578164
alcohol dehydrogenase 1	-62.73465957
RING/U-box superfamily protein	-52.08333333
ubiquitin-specific protease 26	-36.80555556
ubiquitin-specific protease 26	-100
DNA topoisomerase, type IA, core	-34.16208791
Tetratricopeptide repeat (TPR)-like superfamily protein	-100
Tetratricopeptide repeat (TPR)-like superfamily protein	-40.06159015
Tetratricopeptide repeat (TPR)-like superfamily protein	-36.02150538
Tetratricopeptide repeat (TPR)-like superfamily protein	-76.92307692
N/A	-33.68159204
NADH-dependent glutamate synthase 1	-35.18156121
O-fucosyltransferase family protein	-29.13806255
O-fucosyltransferase family protein	-37.96061723
Target SNARE coiled-coil domain protein	-100
N/A	-54.88721805

TRAF-type zinc finger-related	-75
Transketolase family protein	-47.54221388
RNAse E/G-like	-83.63636364
B-box type zinc finger protein with CCT domain	-27.94117647
phosphate transporter 4;3	-50.79365079
Protein of unknown function (DUF567)	-52.13600697
Basic-leucine zipper (bZIP) transcription factor family protein	-55.83982202
LYR family of Fe/S cluster biogenesis protein	-44.8630137
chitinase A	-30.15151515
Poly (ADP-ribose) glycohydrolase (PARG)	-30.80882353
beta galactosidase 1	-100
casein kinase 1-like protein 2	-38.63636364
ACT domain-containing protein	-62.98003072
Tetratricopeptide repeat (TPR)-like superfamily protein	-30.55555556
pyruvate decarboxylase-2	-30.55555556
dynamin-related protein 3A	-100
glucan synthase-like 1	-75.71428571
Ankyrin repeat family protein	-40.29888551
chromatin remodeling factor17	-35.06979063
beta-amylase 3	-74.19354839
N/A	-37.81609195
Thymidine kinase	-55.31400966
Galactose oxidase/kelch repeat superfamily protein	-100
PSAJ	-95.85492228
PSAJ	-78.37465565
homolog of yeast sucrose nonfermenting 4	-100
nuclear factor Y, subunit A5	-30.82251082
XS domain-containing protein / XS zinc finger domain-containing	-34.06593407
XS domain-containing protein / XS zinc finger domain-containing	-34.06593407
P-loop containing nucleoside triphosphate hydrolases superfamily	-27.53623188
Riboflavin synthase-like superfamily protein	-38.23529412
Riboflavin synthase-like superfamily protein	-31.81818182
Riboflavin synthase-like superfamily protein	-25.97402597
binding;RNA binding	-54.16666667
Pentatricopeptide repeat (PPR) superfamily protein	-30.30165913
Pentatricopeptide repeat (PPR) superfamily protein	-35.71428571
Pentatricopeptide repeat (PPR) superfamily protein	-28.57142857
Major facilitator superfamily protein	-38.82896764
XH/XS domain-containing protein	-41.07142857
Ribosomal protein L13 family protein	-94.44444444
guanyl-nucleotide exchange factors;GTPase binding;GTP binding	-100
guanyl-nucleotide exchange factors;GTPase binding;GTP binding	-54.13533835
cycling DOF factor 1	-50

Disease resistance protein (TIR-NBS-LRR class) family	-32.84406141
nuclear RNA polymerase D1B	-96.77419355
N/A	-40
N/A	-48.53560931
cytochrome P450, family 72, subfamily A, polypeptide 15	-52.11267606
cytochrome P450, family 72, subfamily A, polypeptide 15	-48.24561404
cytochrome P450, family 72, subfamily A, polypeptide 15	-34.42622951
photosystem II reaction center protein K precursor	-46.38709981
Ribosomal protein L1p/L10e family	-31.62393162
eukaryotic translation initiation factor 2 gamma subunit	-33.1443299
tetratricopeptide repeat (TPR)-containing protein	-58.33333333
N/A	-33.78378378
telomerase reverse transcriptase	-26.96629213
ATPases;nucleotide binding;ATP binding;nucleoside-triphosphatas	-100
Transcription initiation factor TFIID subunit A	-100
Small nuclear ribonucleoprotein family protein	-71.83673469
exocyst complex component sec10	-52.5
pyruvate dehydrogenase E1 alpha	-84.72222222
Plant protein 1589 of unknown function	-40.12195122
ARM repeat superfamily protein	-85.48387097
ARM repeat superfamily protein	-49.73488865
adenosine-5\'-phosphosulfate (APS) kinase 3	-100
ARM repeat superfamily protein	-100
ENTH/VHS family protein	-63.26530612
regulatory particle triple-A 1A	-42.56542997
GDSL-motif lipase 5	-92.85714286
NAC domain containing protein 85	-89.47368421
N/A	-81.48148148
N/A	-44.52347084
Disease resistance protein (TIR-NBS-LRR class) family	-80.64516129
RNA recognition motif (RRM)-containing protein	-100
Leucine-rich repeat protein kinase family protein	-100
RNA polymerase I specific transcription initiation factor RRN3 prot	-33.20261438
TSL-kinase interacting protein 1	-54.20899855
calcium-dependent protein kinase 28	-100
S-adenosyl-L-methionine-dependent methyltransferases superfam	-37.14285714
N/A	-56.25
ARM repeat superfamily protein	-43.47826087
ARM repeat superfamily protein	-95.23809524
Protein of unknown function (DUF677)	-55.73770492
Protein of unknown function (DUF1162)	-71.66666667
Disease resistance protein (TIR-NBS-LRR class) family	-38.46153846
novel cap-binding protein	-100

glutathione-disulfide reductase	-61.29032258
disease resistance protein (TIR-NBS-LRR class), putative	-33.33333333
Arabidopsis thaliana protein of unknown function (DUF821)	-78.125
Myosin heavy chain-related protein	-57.67195767
CAP160 protein	-38.85714286
tRNA synthetase class I (I, L, M and V) family protein	-90.90909091
Galactose oxidase/kelch repeat superfamily protein	-98.46153846
CW-type Zinc Finger	-100
multifunctional protein 2	-100
ATP-citrate lyase B-1	-58.33333333
ubiquitin protein ligase 6	-52.38095238
pleiotropic drug resistance 9	-61.84210526
Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	-91.66666667
PA-domain containing subtilase family protein	-35.33204384
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase fam	-54.20168067
Transducin/WD40 repeat-like superfamily protein	-62.5
Phosphoribulokinase / Uridine kinase family	-78.125
tRNA synthetase beta subunit family protein	-93.75
Transducin family protein / WD-40 repeat family protein	-100
plastid transcriptionally active 2	-58.82352941
malate dehydrogenase	-68.75
Ribosomal protein S5/Elongation factor G/III/V family protein	-59.72222222
FUS3-complementing gene 2	-29.22374429
AAA-type ATPase family protein	-76.19047619
N/A	-37.78284363
PPPDE putative thiol peptidase family protein	-80
ubiquitin C-terminal hydrolase 3	-100
N/A	-80
Arabinanase/levansucrase/invertase	-50
phytochrome and flowering time regulatory protein (PFT1)	-28.53670886
N/A	-48.90510949
N/A	-27.05902638
Ribosomal protein S21 family protein	-83.60655738
N/A	-50.64935065
N/A	-39.77272727
N/A	-43.47826087
N/A	-35.8974359
non-ATPase subunit 9	-88.23529412
Tetratricopeptide repeat (TPR)-like superfamily protein	-40.54054054
ENTH/VHS/GAT family protein	-40.96385542
N/A	-39.57960644
N/A	-29.01234568
RNA 2\'-phosphotransferase, Tpt1 / KptA family	-36.11111111

Zinc finger protein 622	-61.66666667
ubiquitin-specific protease 26	-27.69230769
embryo defective 2410	-40.54054054
N/A	-26.88172043
N/A	-28.26412138
calcium-binding EF hand family protein	-39.43502825
aberrant lateral root formation 4	-100
CTC-interacting domain 7	-60
histidine kinase 5	-74.3902439
Chalcone-flavanone isomerase family protein	-28.35820896
Protein of unknown function (DUF1218)	-62
RNA-binding protein 47C	-77.5
Protein phosphatase 2C family protein	-73.7704918
Erythronate-4-phosphate dehydrogenase family protein	-100
UDP-Glycosyltransferase superfamily protein	-100
LSD1-like 3	-100
5\'-3\' exoribonuclease 3	-70.58823529
phragmoplast-associated kinesin-related protein, putative	-27.83505155
ferritin 4	-31.81818182
ferritin 4	-30.8083177
N/A	-73.61111111
N/A	-90.90909091
sphere organelles protein-related	-36.95652174
sphere organelles protein-related	-60
DNAJ heat shock family protein	-67.64705882
SGNH hydrolase-type esterase superfamily protein	-73.52941176
anthranilate synthase alpha subunit 1	-33.33333333
translocon at the inner envelope membrane of chloroplasts 110	-100
potassium transporter 1	-37.8968254
peptide transporter 1	-100
Neutral/alkaline non-lysosomal ceramidase	-72.22222222
NB-ARC domain-containing disease resistance protein	-31.50684932
NB-ARC domain-containing disease resistance protein	-47.82608696
NB-ARC domain-containing disease resistance protein	-45.26315789
glucan synthase-like 7	-96.96969697
N/A	-42.72727273
N/A	-32.29376258
kinesin like protein for actin based chloroplast movement 1	-65.95744681
Phototropic-responsive NPH3 family protein	-47.05882353
Nuclear transport factor 2 (NTF2) family protein with RNA binding	-27.87787788
GPI transamidase component PIG-S-related	-33.05785124
dolichol-phosphate mannosyltransferase-related	-32.00147984
N/A	-78.84615385

plant U-box 13	-30.6122449
N/A	-27.38828968
AAA-type ATPase family protein	-36.02614124
Protein of unknown function (DUF674)	-27.20462329
Yippee family putative zinc-binding protein	-32.59504132
Protein of unknown function (DUF567)	-50.84745763
Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	-70.59961315
Serine/threonine-protein kinase Rio1	-56.25
Protein kinase superfamily protein	-72.22222222
binding	-100
ATPase, V1 complex, subunit B protein	-90
Protein kinase superfamily protein	-97.14285714
Pentatricopeptide repeat (PPR-like) superfamily protein	-38.8185654
ARABIDILLO-1	-47.61904762
little nuclei1	-32.72727273
mitogen-activated protein kinase phosphatase 1	-27.03801945
RNA-binding (RRM/RBD/RNP motifs) family protein	-100
HEAT repeat-containing protein	-100
REF4-related 1	-92.30769231
BAH domain ;TFIIS helical bundle-like domain	-75
Heavy metal transport/detoxification superfamily protein	-53.94957983
SIN3-like 2	-80.55555556
Pentatricopeptide repeat (PPR) superfamily protein	-41.57608696
biotin carboxyl carrier protein 2	-96.66666667
PHD finger family protein	-47.10144928
cell division protein ftsH, putative	-63.69047619
Proline-rich spliceosome-associated (PSP) family protein / zinc kn	-77.35849057
RAB GTPase homolog A1D	-65.38835324
Cytochrome C1 family	-79.41176471
Mitochondrial ribosomal protein L37	-47.36842105
Ribonuclease inhibitor	-100
DEAD-box protein abstrakt, putative	-90
ARM repeat superfamily protein	-83.33333333
N/A	-41.93548387
N/A	-80.95238095
Peptidase M50 family protein	-76.31578947
Cyclin/Brf1-like TBP-binding protein	-43.61702128
mitochondrial RNAediting factor 1	-32.75862069
spindle pole body component 98	-70.14925373
receptor-like kinase in in flowers 3	-25.3968254
N/A	-70.83333333
myosin 2	-77.08333333
Lipin family protein	-100

endomembrane-type CA-ATPase 4	-60.86956522
N/A	-84.61538462
P-loop containing nucleoside triphosphate hydrolases superfamily	-44
Ribosomal protein L13 family protein	-76.47058824
Nucleotide-diphospho-sugar transferases superfamily protein	-44.68085106
ACT-like superfamily protein	-59.3220339
N/A	-26.54462243
UDP-glucosyl transferase 73C2	-26.54462243
peroxin 6	-86.36363636
NAD+ transporter 1	-100
WRKY DNA-binding protein 35	-100
N/A	-100
DHHC-type zinc finger family protein	-65.51724138
DNAJ heat shock N-terminal domain-containing protein	-55.31914894
transcription activators	-50
MuDR family transposase	-47.5
zinc knuckle (CCHC-type) family protein	-51.73745174
RNA-binding (RRM/RBD/RNP motifs) family protein	-76.38888889
FORMS APLOID AND BINUCLEATE CELLS 1C	-97.14285714
O-fucosyltransferase family protein	-49.50146628
purin-rich alpha 1	-85.71428571
Plant protein of unknown function (DUF863)	-100
Got1/Sft2-like vescicle transport protein family	-96.2962963
RINT-1 / TIP-1 family	-66.9924812
hAT dimerisation domain-containing protein / transposase-relatec	-66.9924812
chitin elicitor receptor kinase 1	-100
N/A	-85.8974359
N/A	-28.24899026
BLISTER	-67.59259259
N/A	-67.59259259
TRAF-like superfamily protein	-48.88888889
Arabidopsis phospholipase-like protein (PEARLI 4) family	-90.90909091
ARM repeat superfamily protein	-36.36363636
N/A	-44.44444444
MBOAT (membrane bound O-acyl transferase) family protein	-65.54487179
N/A	-25.24959368
Homeodomain-like protein with RING/FYVE/PHD-type zinc finger	-40.8445577
transducin family protein / WD-40 repeat family protein	-72.22222222
N/A	-80.90909091
Tesmin/TSO1-like CXC domain-containing protein	-55.88235294
Kinase interacting (KIP1-like) family protein	-31.05010661
phosphoglucomutase	-63.15789474
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily	-25.32440019

N/A	-34.82772935
Regulator of chromosome condensation (RCC1) family with FYVE z	-42.57164404
Pyridoxal phosphate (PLP)-dependent transferases superfamily pr	-36.42089094
FORMS APLOID AND BINUCLEATE CELLS 1A	-100
Transmembrane Fragile-X-F-associated protein	-72.16117216
Transmembrane Fragile-X-F-associated protein	-40.47619048
NAC (No Apical Meristem) domain transcriptional regulator super	-59.28853755
N/A	-68.75
mRNA splicing factor, thioredoxin-like U5 snRNP	-96.15384615
phosphofructokinase 4	-60.81081081
N/A	-32.76315789
UBX domain-containing protein	-51.85185185
RING/FYVE/PHD zinc finger superfamily protein	-84.14634146
Eukaryotic aspartyl protease family protein	-100
MIRO-related GTP-ase 1	-93.33333333
PRLI-interacting factor, putative	-62.05741627
BRI1 suppressor 1 (BSU1)-like 2	-82.8125
N/A	-51.05359217
exocyst subunit exo70 family protein A1	-100
uricase / urate oxidase / nodulin 35, putative	-52.93040293
nuclear RNA polymerase C1	-44.42724458
N/A	-83.33333333

q value	P value
0.00540647	1.10102E-05
0.00510403	1.00911E-05
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2.14544E-06	6.16749E-10
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1.25008E-06	3.34099E-10
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0.000277356	2.24346E-07
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0.005825239	1.21236E-05
0.002338548	3.63227E-06
0.001884159	2.6543E-06
0.000204663	1.55191E-07
0.005639884	1.16344E-05
1.4686E-13	5.92341E-18
0.001659154	2.25824E-06

0.005368098	1.08927E-05
1.07017E-05	4.13588E-09
0.006637079	1.44167E-05
8.17472E-06	3.00942E-09
2.96636E-07	6.4608E-11
3.04177E-08	4.7736E-12
2.98325E-07	6.51947E-11
0.005553767	1.13916E-05
0.000319764	2.65918E-07
0.006488141	1.39743E-05
1.25154E-06	3.35917E-10
0.006603368	1.4286E-05
0.000646723	6.48445E-07
0.001933999	2.83514E-06
0.005353107	1.08251E-05
1.83775E-06	5.21557E-10
0.002394843	3.74781E-06
0.000195624	1.47619E-07
2.15676E-08	3.16328E-12
0.000926295	1.06022E-06
0.004847211	9.36297E-06
0.00327541	5.60865E-06
0.005426294	1.10705E-05
0.007151411	1.59483E-05
0.005381589	1.09359E-05
7.77224E-05	4.73075E-08
0.002800712	4.56988E-06
2.76356E-05	1.28935E-08
0.000243157	1.9169E-07
0.001933999	2.83514E-06
0.005009981	9.83638E-06
0.002942538	4.86309E-06
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1.04662E-06	2.73239E-10
1.61356E-06	4.52016E-10
1.70743E-05	7.11209E-09
0.009976212	2.47938E-05
0.000910494	1.03814E-06
5.98645E-05	3.45062E-08
0.007337824	1.64985E-05
6.33332E-07	1.56055E-10
0.007322684	1.6443E-05
0.002157919	3.2805E-06

0.003545459	6.21927E-06
0.000107531	6.9867E-08
1.81671E-22	1.78575E-27
0.004434307	8.30525E-06
6.45494E-06	2.28163E-09
1.00554E-09	1.04438E-13
0.000703795	7.33411E-07
0.001627191	2.20161E-06
0.008546843	2.02511E-05
0.0002397	1.88262E-07
0.00295471	4.89482E-06
1.92469E-07	4.00852E-11
0.009486365	2.32324E-05
0.006746728	1.47391E-05
0.009894751	2.45405E-05
0.001768776	2.44766E-06
0.001933999	2.83514E-06
0.001933999	2.83514E-06
0.001904087	2.69215E-06
0.004932456	9.64338E-06
0.000598497	5.87251E-07
0.000823006	9.16783E-07
2.43309E-06	7.31558E-10
1.38812E-06	3.82756E-10
0.001437431	1.87529E-06
0.00010836	7.05647E-08
1.78787E-08	2.54358E-12
1.89176E-41	2.77461E-47
0.000523011	4.93239E-07
0.001735936	2.38948E-06
0.000440203	4.00618E-07
0.005869408	1.22371E-05
0.000240795	1.89475E-07
0.000308141	2.5444E-07
7.73161E-05	4.70035E-08
5.29223E-05	2.92629E-08
0.00284178	4.65641E-06
0.000649383	6.53373E-07
0.005368098	1.08852E-05
0.00909331	2.19393E-05
3.35904E-08	5.51784E-12
0.003785477	6.75967E-06
3.68175E-05	1.83059E-08

0.006922846	1.52339E-05
0.008526819	2.01911E-05
0.009296876	2.26282E-05
0.003960437	7.17084E-06
0.000833382	9.32619E-07
5.08666E-05	2.7865E-08
0.001496817	1.97911E-06
0.001496817	1.97911E-06
2.43736E-05	1.1082E-08
0.000796198	8.74075E-07
2.29387E-06	6.79605E-10
0.000703795	7.39602E-07
0.000944887	1.0865E-06
0.000799921	8.79922E-07
0.000554647	5.3487E-07
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9.28656E-05	5.84316E-08
9.21935E-06	3.44807E-09
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0.001933999	2.82117E-06
0.000796198	8.74075E-07
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0.000512793	4.81722E-07
0.000512793	4.81722E-07
0.000440203	4.00618E-07
1.23273E-05	4.93644E-09
0.004622879	8.76014E-06
0.002982454	4.95609E-06
0.002982454	4.95609E-06
0.003702328	6.57318E-06
0.004921546	9.61483E-06
0.00635582	1.35821E-05
0.007447034	1.67823E-05
0.005068597	9.99132E-06
0.007733475	1.75809E-05
0.001017712	1.19114E-06
0.008968817	2.15798E-05
0.000144904	1.01057E-07
4.67456E-06	1.56567E-09
0.002393079	3.74329E-06
0.002793865	4.55665E-06
0.000463193	4.24259E-07

0.000979829	1.13459E-06
0.00047655	4.39637E-07
2.75723E-08	4.22596E-12
2.64011E-11	1.98005E-15
5.42254E-09	6.87946E-13
4.92908E-05	2.65406E-08
0.009486365	2.32425E-05
0.000620945	6.15197E-07
1.03113E-09	1.08889E-13
3.20131E-08	5.14321E-12
1.47339E-05	6.03996E-09
0.009192263	2.2259E-05
2.40672E-05	1.08897E-08
0.000703795	7.39602E-07
0.002195562	3.36519E-06
2.55693E-17	5.4378E-22
1.12951E-07	2.13706E-11
4.84E-44	3.54937E-50
0.000440203	4.00618E-07
0.001240448	1.53019E-06
0.004503487	8.47115E-06
2.14878E-12	1.1976E-16

Supplemental Table 6: List of 350 hypo-methylated genes in C

METHYLATED REGION
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mytileDiff25p200.hypo_merged_CHG.Chr01.15362201-15362400
mytileDiff25p200.hypo_merged_CHG.Chr01.16544001-16544200
mytileDiff25p200.hypo_merged_CHG.Chr01.26997001-26997200
mytileDiff25p200.hypo_merged_CHG.Chr01.26996801-26997000
mytileDiff25p200.hypo_merged_CHG.Chr01.28298001-28298200
mytileDiff25p200.hypo_merged_CHG.Chr01.33985201-33985400
mytileDiff25p200.hypo_merged_CHG.Chr01.34325801-34326000
mytileDiff25p200.hypo_merged_CHG.Chr01.39603801-39604000
mytileDiff25p200.hypo_merged_CHG.Chr01.40579801-40580000
mytileDiff25p200.hypo_merged_CHG.Chr01.40582201-40582400
mytileDiff25p200.hypo_merged_CHG.Chr01.41289801-41290000
mytileDiff25p200.hypo_merged_CHG.Chr01.41290201-41290400
mytileDiff25p200.hypo_merged_CHG.Chr01.41290001-41290200
mytileDiff25p200.hypo_merged_CHG.Chr01.48062001-48062200
mytileDiff25p200.hypo_merged_CHG.Chr01.48068801-48069000
mytileDiff25p200.hypo_merged_CHG.Chr01.48068801-48069000
mytileDiff25p200.hypo_merged_CHG.Chr01.49102001-49102200
mytileDiff25p200.hypo_merged_CHG.Chr01.53574201-53574400
mytileDiff25p200.hypo_merged_CHG.Chr01.56617801-56618000
mytileDiff25p200.hypo_merged_CHG.Chr01.56739601-56739800
mytileDiff25p200.hypo_merged_CHG.Chr02.1125601-1125800
mytileDiff25p200.hypo_merged_CHG.Chr02.8965401-8965600
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mytileDiff25p200.hypo_merged_CHG.Chr02.14391201-14391400
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G context.

REGION	GENE ID
3'UTR(38bp)	Glyma.01G006800
3'UTR	Glyma.01G021600
GENE BODY	Glyma.01G074400
GENE BODY	Glyma.01G074400
GENE BODY	Glyma.01G074700
PROMOTER (92bp); 5'UTR (108bp)	Glyma.01G089000
5'UTR(171bp); GENE BODY (29bp)	Glyma.01G089000
GENE BODY	Glyma.01G093200
GENE BODY	Glyma.01G102100
GENE BODY	Glyma.01G102800
5'UTR	Glyma.01G114500
PROMOTER(60bp), 5'UTR(39bp); GENE BODY(	Glyma.01G117400
GENE BODY	Glyma.01G117500
PROMOTER	Glyma.01G120100
PROMOTER	Glyma.01G120100
PROMOTER	Glyma.01G120100
5'UTR(148bp); GENE BODY(52bp)	Glyma.01G145600
PROMOTER	Glyma.01G145700
PROMOTER	Glyma.01G145800
PROMOTER	Glyma.01G153600
GENE BODY	Glyma.01G203000
GENE BODY (169bp); 3'UTR(31bp)	Glyma.01G243200
3'UTR(65bp)	Glyma.01G245100
3'UTR(58bp)	Glyma.02G012600
GENE BODY	Glyma.02G098200
GENE BODY	Glyma.02G112500
PROMOTER	Glyma.02G129400
PROMOTER	Glyma.02G129400
PROMOTER	Glyma.02G138900
PROMOTER	Glyma.02G138900
5'UTR(141bp); PROMOTER (59bp)	Glyma.02G139000
5'UTR(110bp); GENE BODY (90bp)	Glyma.02G139000
3'UTR	Glyma.02G140700
PROMOTER	Glyma.02G141900
GENE BODY	Glyma.02G163200
GENE BODY	Glyma.02G177900
PROMOTER(100bp); GENE BODY(100bp)	Glyma.02G180800
PROMOTER	Glyma.02G190300
5'UTR(135bp); GENE BODY (65bp)	Glyma.02G192300
PROMOTER	Glyma.02G258100
GENE BODY (78bp); 3'UTR(122bp)	Glyma.02G277700

GENE BODY	Glyma.02G287400
3'UTR	Glyma.03G027100
PROMOTER	Glyma.03G034100
GENE BODY (119bp); 3'UTR(81bp)	Glyma.03G047800
GENE BODY	Glyma.03G051700
GENE BODY	Glyma.03G057800
GENE BODY	Glyma.03G060900
3'UTR(79bp)	Glyma.03G085700
5'UTR(76bp); PROMOTER(124bp)	Glyma.03G092600
GENE BODY	Glyma.03G105000
PROMOTER	Glyma.03G114000
GENE BODY	Glyma.03G133200
3'UTR(188bp)	Glyma.03G159000
5'UTR	Glyma.03G225700
PROMOTER	Glyma.03G225800
GENE BODY	Glyma.04G079800
GENE BODY	Glyma.04G096100
GENE BODY	Glyma.04G096100
GENE BODY	Glyma.04G096900
GENE BODY	Glyma.04G096900
GENE BODY	Glyma.04G101100
GENE BODY	Glyma.04G114800
PROMOTER	Glyma.04G115000
PROMOTER	Glyma.04G115800
PROMOTER	Glyma.04G115800
GENE BODY	Glyma.04G116200
GENE BODY	Glyma.04G116700
GENE BODY	Glyma.04G121500
GENE BODY	Glyma.04G124800
GENE BODY	Glyma.04G128600
GENE BODY (34bp); 3'UTR(166bp)	Glyma.04G139200
GENE BODY	Glyma.04G146900
GENE BODY	Glyma.04G155000
GENE BODY	Glyma.04G158400
GENE BODY (24bp); 3'UTR(176bp)	Glyma.04G162400
GENE BODY	Glyma.04G182900
GENE BODY	Glyma.04G182900
GENE BODY	Glyma.05G031900
GENE BODY	Glyma.05G032600
GENE BODY	Glyma.05G044500
GENE BODY	Glyma.05G060200
PROMOTER	Glyma.05G060700
PROMOTER(92bp); GENE BODY(108bp)	Glyma.05G067200

GENE BODY	Glyma.05G075400
PROMOTER	Glyma.05G078500
GENE BODY	Glyma.05G078600
GENE BODY	Glyma.05G100500
GENE BODY	Glyma.05G100500
GENE BODY	Glyma.05G100500
GENE BODY	Glyma.05G115200
GENE BODY	Glyma.05G136600
PROMOTER(26bp); 5'UTR(174bp)	Glyma.05G236500
GENE BODY	Glyma.05G236500
GENE BODY	Glyma.05G236500
GENE BODY	Glyma.05G236500
GENE BODY	Glyma.05G236500
GENE BODY	Glyma.06G067100
PROMOTER	Glyma.06G090100
5'UTR(41bp); GENE BODY (159bp)	Glyma.06G090100
GENE BODY	Glyma.06G108200
GENE BODY	Glyma.06G115100
GENE BODY	Glyma.06G173500
GENE BODY	Glyma.06G185000
GENE BODY	Glyma.06G195300
5'UTR(18bp); GENE BODY (182bp)	Glyma.06G195300
3'UTR	Glyma.06G197600
GENE BODY	Glyma.06G202500
GENE BODY	Glyma.06G205200
GENE BODY	Glyma.06G214500
GENE BODY	Glyma.06G214500
GENE BODY	Glyma.06G218500
GENE BODY	Glyma.06G218500
GENE BODY	Glyma.06G228000
GENE BODY	Glyma.06G228000
GENE BODY	Glyma.06G238900
PROMOTER	Glyma.06G243400
GENE BODY	Glyma.06G243700
GENE BODY	Glyma.06G261400
GENE BODY	Glyma.06G271800
PROMOTER	Glyma.06G289500
PROMOTER(183bp); 5'UTR(17bp)	Glyma.06G296500
GENE BODY	Glyma.06G309800
GENE BODY	Glyma.07G028100
GENE BODY	Glyma.07G069500
GENE BODY	Glyma.07G079000
3'UTR	Glyma.07G079100

PROMOTER(87bp); GENE BODY(113bp)	Glyma.07G079200
PROMOTER	Glyma.07G079300
GENE BODY	Glyma.07G101200
GENE BODY	Glyma.07G113100
GENE BODY (122bp); 3'UTR(78bp)	Glyma.07G124500
GENE BODY	Glyma.07G125300
GENE BODY	Glyma.07G125300
GENE BODY	Glyma.07G149900
PROMOTER	Glyma.07G190600
GENE BODY	Glyma.07G264000
GENE BODY	Glyma.08G127200
GENE BODY	Glyma.08G139300
GENE BODY	Glyma.08G140100
GENE BODY	Glyma.08G194600
GENE BODY	Glyma.08G213900
5'UTR(37bp); PROMOTER(163bp)	Glyma.08G233900
3'UTR (178bp); GENE BODY (22bp)	Glyma.08G233900
3'UTR	Glyma.08G233900
GENE BODY	Glyma.08G236400
GENE BODY	Glyma.08G236700
GENE BODY	Glyma.08G236700
GENE BODY	Glyma.08G236700
5'UTR(156bp); GENE BODY (44bp)	Glyma.08G238500
GENE BODY	Glyma.08G253800
GENE BODY	Glyma.08G264900
GENE BODY	Glyma.08G265300
GENE BODY (151bp); 3'UTR(49bp)	Glyma.08G273000
GENE BODY	Glyma.08G273000
PROMOTER	Glyma.08G275100
GENE BODY	Glyma.08G275100
GENE BODY	Glyma.08G276200
GENE BODY	Glyma.08G279100
GENE BODY	Glyma.08G279800
GENE BODY	Glyma.08G288100
GENE BODY	Glyma.08G291800
GENE BODY	Glyma.08G344800
PROMOTER(191bp); 5'UTR(9bp)	Glyma.08G357000
5'UTR(67bp); GENE BODY (133bp)	Glyma.09G046700
GENE BODY	Glyma.09G057400
GENE BODY	Glyma.09G065300
GENE BODY	Glyma.09G065300
GENE BODY	Glyma.09G083800
GENE BODY	Glyma.09G084300

GENE BODY	Glyma.09G095400
PROMOTER	Glyma.09G110200
GENE BODY	Glyma.09G110300
GENE BODY	Glyma.09G116800
GENE BODY	Glyma.09G121300
GENE BODY	Glyma.09G124400
PROMOTER	Glyma.09G129600
GENE BODY	Glyma.09G130900
PROMOTER	Glyma.09G144900
3'UTR	Glyma.09G148100
GENE BODY	Glyma.09G194400
PROMOTER	Glyma.09G202900
GENE BODY	Glyma.10G008300
GENE BODY	Glyma.10G023300
GENE BODY	Glyma.10G065800
GENE BODY	Glyma.10G065900
GENE BODY	Glyma.10G075900
GENE BODY	Glyma.10G078900
GENE BODY	Glyma.10G095200
GENE BODY	Glyma.10G095200
GENE BODY	Glyma.10G095200
GENE BODY	Glyma.10G095200
GENE BODY	Glyma.10G095200
PROMOTER(171bp); 5'UTR(29bp)	Glyma.10G098700
GENE BODY	Glyma.10G104300
GENE BODY	Glyma.10G108500
GENE BODY	Glyma.10G111500
GENE BODY	Glyma.10G118800
GENE BODY	Glyma.10G123400
GENE BODY	Glyma.10G123400
GENE BODY	Glyma.10G159500
GENE BODY	Glyma.10G202600
PROMOTER	Glyma.10G229600
3'UTR(102bp)	Glyma.10G233300
3'UTR(8bp)	Glyma.10G246000
5'UTR(81bp); GENE BODY (119bp)	Glyma.10G294000
GENE BODY	Glyma.10G298900
GENE BODY	Glyma.11G037300
GENE BODY	Glyma.11G256800
GENE BODY	Glyma.12G051000
GENE BODY	Glyma.12G096900
PROMOTER	Glyma.12G117500
GENE BODY	Glyma.12G133500

GENE BODY	Glyma.12G152300
GENE BODY	Glyma.12G152700
GENE BODY	Glyma.12G156200
GENE BODY	Glyma.12G157800
GENE BODY	Glyma.12G205500
GENE BODY	Glyma.13G003500
GENE BODY	Glyma.13G027100
PROMOTER(107bp); GENE BODY(93bp)	Glyma.13G030000
PROMOTER	Glyma.13G030000
PROMOTER	Glyma.13G030100
PROMOTER	Glyma.13G030100
GENE BODY	Glyma.13G030600
GENE BODY	Glyma.13G035200
GENE BODY	Glyma.13G048300
GENE BODY (166bp); 3'UTR (34bp)	Glyma.13G059000
PROMOTER	Glyma.13G062000
GENE BODY	Glyma.13G078200
GENE BODY	Glyma.13G156600
PROMOTER	Glyma.13G156900
GENE BODY	Glyma.13G166100
GENE BODY	Glyma.13G174900
GENE BODY	Glyma.13G184600
GENE BODY	Glyma.13G233400
5'UTR(111bp); GENE BODY (89bp)	Glyma.13G283900
PROMOTER	Glyma.13G305700
GENE BODY	Glyma.13G372400
GENE BODY	Glyma.14G031300
GENE BODY	Glyma.14G045600
GENE BODY	Glyma.14G091400
GENE BODY	Glyma.14G104400
GENE BODY	Glyma.14G105100
GENE BODY	Glyma.14G105100
PROMOTER	Glyma.14G106300
PROMOTER	Glyma.14G108800
5'UTR	Glyma.14G110800
GENE BODY	Glyma.14G119200
GENE BODY	Glyma.14G119200
PROMOTER	Glyma.14G120000
GENE BODY	Glyma.14G128300
GENE BODY	Glyma.14G138900
GENE BODY (130bp); 3'UTR (70bp)	Glyma.14G140600
GENE BODY	Glyma.14G142100
GENE BODY	Glyma.14G145000

5'UTR	Glyma.14G150500
PROMOTER (37bp); 5'UTR(122bp); GENE BOD	Glyma.14G159200
GENE BODY	Glyma.14G160400
3'UTR(17bp)	Glyma.14G160400
GENE BODY	Glyma.14G161200
GENE BODY	Glyma.14G162300
GENE BODY	Glyma.14G162300
GENE BODY	Glyma.14G162300
GENE BODY	Glyma.14G163000
GENE BODY	Glyma.14G163000
5'UTR(117bp); GENE BODY (83bp)	Glyma.14G163100
GENE BODY	Glyma.14G164000
GENE BODY	Glyma.14G164000
3'UTR	Glyma.14G166700
GENE BODY	Glyma.14G192900
PROMOTER	Glyma.14G200800
GENE BODY	Glyma.14G211800
GENE BODY	Glyma.15G006900
GENE BODY	Glyma.15G030400
PROMOTER	Glyma.15G046800
GENE BODY	Glyma.15G076300
PROMOTER	Glyma.15G126100
3'UTR(67bp); GENE BODY (124bp)	Glyma.15G126100
GENE BODY	Glyma.15G127200
PROMOTER(156bp); GENE BODY(44bp)	Glyma.15G135300
GENE BODY	Glyma.15G161200
GENE BODY	Glyma.15G163200
GENE BODY	Glyma.15G173900
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G192300
GENE BODY	Glyma.15G192300
5'UTR	Glyma.15G197000
GENE BODY	Glyma.15G204600
GENE BODY	Glyma.15G204600
GENE BODY	Glyma.15G204600
GENE BODY	Glyma.15G204600
GENE BODY	Glyma.15G204700
GENE BODY	Glyma.15G212200
GENE BODY	Glyma.15G213000
GENE BODY	Glyma.15G213000

GENE BODY	Glyma.15G213200
3'UTR	Glyma.15G219300
GENE BODY	Glyma.15G220900
GENE BODY	Glyma.15G226200
PROMOTER(16bp); 5'UTR(107bp); GENE BOD	Glyma.15G240300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G245300
PROMOTER	Glyma.15G245400
GENE BODY	Glyma.15G248600
GENE BODY (173bp); 3'UTR(13bp)	Glyma.15G252500
GENE BODY	Glyma.16G053100
PROMOTER	Glyma.16G056800
5'UTR(101bp); GENE BODY (99bp)	Glyma.16G058000
GENE BODY	Glyma.16G066900
GENE BODY	Glyma.16G073700
GENE BODY (145bp); 3'UTR(55bp)	Glyma.16G088100
GENE BODY	Glyma.16G091400
GENE BODY (3bp); 3'UTR(197bp)	Glyma.16G092800
PROMOTER	Glyma.16G112800
PROMOTER	Glyma.16G113800
GENE BODY	Glyma.16G114200
GENE BODY	Glyma.16G115200
PROMOTER	Glyma.16G115300
GENE BODY	Glyma.16G115700
GENE BODY	Glyma.16G115700
GENE BODY	Glyma.16G131100
5'UTR(54bp); GENE BODY (146bp)	Glyma.16G136400
GENE BODY	Glyma.16G148600
PROMOTER	Glyma.16G159900
5'UTR	Glyma.16G164700
GENE BODY	Glyma.16G172300
GENE BODY	Glyma.16G172400
GENE BODY	Glyma.16G182700
PROMOTER	Glyma.16G183300
GENE BODY	Glyma.17G001100
GENE BODY	Glyma.17G041900
GENE BODY	Glyma.17G094300
GENE BODY	Glyma.17G129900
PROMOTER	Glyma.17G150300
PROMOTER	Glyma.17G169200
PROMOTER	Glyma.17G171400
PROMOTER	Glyma.17G171400

GENE BODY	Glyma.17G171400
GENE BODY	Glyma.17G171400
GENE BODY	Glyma.17G171400
GENE BODY	Glyma.17G171400
GENE BODY	Glyma.17G173200
GENE BODY	Glyma.17G183400
PROMOTER(93bp); GENE BODY(107bp)	Glyma.17G190200
PROMOTER(172bp); GENE BODY(28bp)	Glyma.17G191800
GENE BODY	Glyma.17G204000
PROMOTER	Glyma.17G205900
PROMOTER(187bp); GENE BODY(13bp)	Glyma.17G206000
GENE BODY	Glyma.17G206400
PROMOTER	Glyma.17G207600
GENE BODY	Glyma.17G212600
GENE BODY	Glyma.17G222100
GENE BODY	Glyma.17G222200
PROMOTER	Glyma.17G235400
GENE BODY	Glyma.17G235400
GENE BODY	Glyma.18G000100
GENE BODY	Glyma.18G000100
GENE BODY	Glyma.18G004600
GENE BODY	Glyma.18G019600
GENE BODY	Glyma.18G087700
GENE BODY	Glyma.18G093600
GENE BODY	Glyma.18G109100
GENE BODY	Glyma.18G109100
3'UTR	Glyma.18G119200
GENE BODY (173bp); 3'UTR(27bp)	Glyma.18G127700
GENE BODY	Glyma.18G128900
GENE BODY	Glyma.18G137700
GENE BODY	Glyma.18G140800
GENE BODY	Glyma.18G140800
PROMOTER	Glyma.18G142600
GENE BODY	Glyma.18G149700
GENE BODY	Glyma.18G149700
GENE BODY	Glyma.18G156300
PROMOTER (127bp); 5'UTR(73bp)	Glyma.18G157300
GENE BODY	Glyma.18G162500
GENE BODY	Glyma.18G166600
GENE BODY	Glyma.18G166600
PROMOTER	Glyma.18G171700
GENE BODY	Glyma.18G195000
GENE BODY	Glyma.18G199800

GENE BODY	Glyma.18G241400
GENE BODY	Glyma.18G241400
GENE BODY	Glyma.18G279600
GENE BODY	Glyma.18G297900
PROMOTER	Glyma.19G003900
PROMOTER	Glyma.19G024600
PROMOTER	Glyma.19G031100
PROMOTER(3bp); GENE BODY(197bp)	Glyma.19G043600
GENE BODY	Glyma.19G043600
GENE BODY	Glyma.19G043600
GENE BODY	Glyma.19G056700
3'UTR(44bp); GENE BODY(9bp)	Glyma.19G059600
GENE BODY	Glyma.19G060900
GENE BODY	Glyma.19G060900
GENE BODY	Glyma.19G061900
GENE BODY	Glyma.19G066800
GENE BODY	Glyma.19G067100
GENE BODY	Glyma.19G102500
GENE BODY	Glyma.19G104300
3'UTR	Glyma.19G124000
3'UTR	Glyma.19G124000
GENE BODY	Glyma.19G247000
GENE BODY	Glyma.19G251400
GENE BODY	Glyma.20G000700
PROMOTER	Glyma.20G008000
GENE BODY	Glyma.20G032200
PROMOTER	Glyma.20G046500
GENE BODY	Glyma.20G058500
3'UTR	Glyma.20G058600
GENE BODY	Glyma.20G064100
GENE BODY	Glyma.20G070800
GENE BODY	Glyma.20G071200
3'UTR	Glyma.20G135900
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G199500
GENE BODY	Glyma.20G248000
GENE BODY	Glyma.U010800

GENE ANNOTATION	% Methylation Differences	q value
Pectin lyase-like superfamily protein	-40.53030303	2.77707E-05
N/A	-37.25490196	0.000219161
N/A	-37.52631579	0.000734571
N/A	-39.40813073	8.69842E-08
Nucleoporin autopeptidase	-34.84341382	0.00106169
Nucleic acid-binding, OB-fold-like protein	-28.57142857	0.001233443
Nucleic acid-binding, OB-fold-like protein	-27.27272727	9.31835E-09
Metal-dependent phosphohydrolase	-38.18272095	0.001021096
Protein of unknown function (DUF604)	-61.33587786	0.000212198
N/A	-84.65909091	0.000157021
glucose-6-phosphate/phosphate translocato	-33.24863884	0.000422084
STAS domain / Sulfate transporter family	-28.35820896	0.005104314
TBP-associated factor 15	-27.77777778	0.006638408
receptor like protein 6	-60.28514589	9.08552E-22
receptor like protein 6	-73.07692308	0.00012701
receptor like protein 6	-32.25806452	2.10036E-06
N/A	-25.33960293	0.004282959
RNA-binding (RRM/RBD/RNP motifs) family p	-27.53623188	0.000213257
protein binding	-27.53623188	0.000213257
xyloglucanase 113	-51.94424065	0.003368248
N/A	-35.10278428	0.000804136
somatic embryogenesis receptor-like kinase	-67.89772727	0.000395776
histone deacetylase 1	-71.21212121	0.006813334
Concanavalin A-like lectin protein kinase fam	-28.09237583	0.004623602
Transmembrane amino acid transporter fami	-26.86567164	0.002172447
Transducin/WD40 repeat-like superfamily pr	-30.14090259	0.007160035
N/A	-37.66039029	8.71878E-13
N/A	-28.21081358	1.4755E-05
N/A	-37.26133076	0.002967841
N/A	-25.89996814	6.28127E-07
N/A	-37.26133076	0.002967841
N/A	-25.89996814	6.28127E-07
N/A	-92.30769231	0.004021801
alpha/beta-Hydrolases superfamily protein	-64.17910448	1.39619E-13
P-loop containing nucleoside triphosphate hy	-26.67390125	0.001742711
NIMA-related kinase 2	-55.44715447	2.5401E-05
homeobox protein 22	-43.81377551	0.004526603
Nucleic acid-binding, OB-fold-like protein	-90.69767442	7.37599E-05
RING-H2 group F2A	-38.23529412	5.94643E-06
E3 ubiquitin ligase, putative	-85.65217391	0.001513714
early nodulin-like protein 18	-76.92307692	1.5835E-06

protodermal factor 1	-33.63095238	0.009357303
N/A	-38.7755102	0.003689797
Preprotein translocase Sec, Sec61-beta subu	-27.04100677	0.00032695
P-loop containing nucleoside triphosphate h	-30.64516129	1.29933E-08
N/A	-45.11241447	0.00938922
Rhodanese/Cell cycle control phosphatase s	-72.72727273	0.008355196
BCL-2-associated athanogene 6	-46.66666667	0.00495282
Protein kinase superfamily protein	-46.2962963	0.003213284
Chloroplast Ycf2;ATPase, AAA type, coreMET	-38.07950192	1.23977E-10
basic helix-loop-helix (bHLH) DNA-binding su	-67.9791546	0.003976657
N/A	-27.47092057	0.003932664
Transmembrane proteins 14C	-31.66410601	0.000111168
alpha/beta-Hydrolases superfamily protein	-66.95116169	5.19212E-05
N/A	-39.04761905	5.12743E-08
Protein phosphatase 2C family protein	-39.04761905	5.12743E-08
Ribosomal protein S5 family protein	-28.40153195	3.81865E-05
binding	-39.00069396	0.001134112
binding	-29.67687075	2.53661E-09
ubiquitin-protein ligase 1	-33.9569161	3.89002E-07
ubiquitin-protein ligase 1	-31.55011655	0.000144838
APR-like 4	-31.41928494	0.001524982
chloride channel F	-25.90340208	0.009080022
N/A	-25.90340208	0.009080022
Ribosomal L32p protein family	-52.50982104	1.46832E-06
Ribosomal L32p protein family	-28.125	6.85703E-07
N/A	-38.26815642	3.14448E-08
peroxin 5	-37.35930736	0.004282959
Phosphoinositide phosphatase family protei	-47.64079148	1.69031E-05
zinc induced facilitator-like 1	-31.75501801	1.34583E-07
alpha/beta-Hydrolases superfamily protein	-57.44047619	0.000510142
ribosomal protein large subunit 27	-67.72727273	0.003020605
nucleoporin-related	-41.66666667	0.005157159
Family of unknown function (DUF566)	-48.40654608	0.009401203
transducin family protein / WD-40 repeat fa	-72.72727273	0.008355196
exocyst subunit exo70 family protein E2	-38.7477314	0.003825746
ataxia-telangiectasia mutated	-39.3258427	6.2256E-05
ataxia-telangiectasia mutated	-64.61038961	0.002251172
ARM repeat superfamily protein	-30.99415205	0.004700162
ARM repeat superfamily protein	-27.83018868	3.76748E-13
26S proteasome, regulatory subunit Rpn7;Pr	-36.86046512	0.003350142
O-fucosyltransferase family protein	-44.29123001	0.008480288
plant glycogenin-like starch initiation protein	-33.19284802	0.004921377
Histone H3 K4-specific methyltransferase SE	-39.09905426	0.008616815

Proteasome component (PCI) domain protei	-30.47504026	0.003248343
PIF1 helicase	-70.625	0.001759016
N/A	-70.625	0.001759016
WD-40 repeat family protein	-31.43079662	0.00015733
WD-40 repeat family protein	-27.53211629	0.000429667
WD-40 repeat family protein	-37.54813864	0.004517985
Pentatricopeptide repeat (PPR) superfamily	-30.07493644	0.000112224
N/A	-38.95877009	0.000971663
RNA-binding CRS1 / YhbY (CRM) domain prot	-29.36425339	2.45546E-15
RNA-binding CRS1 / YhbY (CRM) domain prot	-37.54696726	2.99552E-14
RNA-binding CRS1 / YhbY (CRM) domain prot	-35.69601754	0.005428867
RNA-binding CRS1 / YhbY (CRM) domain prot	-38.21656051	9.62756E-14
RNA-binding CRS1 / YhbY (CRM) domain prot	-42.23602484	6.51509E-18
Phox (PX) domain-containing protein	-79.6347032	8.97856E-06
RNA-binding KH domain-containing protein	-25.19900498	0.009582246
RNA-binding KH domain-containing protein	-28.33333333	0.000548443
Vacuolar sorting protein 9 (VPS9) domain	-25.83900227	8.24282E-07
IAA-leucine resistant (ILR)-like gene 6	-50.25031289	0.000491077
glucan synthase-like 8	-54.08163265	6.45425E-05
GATA type zinc finger transcription factor fa	-58.90410959	0.000675074
Protein of unknown function (DUF962)	-27.84810127	5.06925E-19
Protein of unknown function (DUF962)	-43.24324324	0.000311801
Leucine-rich repeat protein kinase family pro	-25.44489093	0.000741281
U5 small nuclear ribonucleoprotein helicase	-33.76344086	0.004529719
P-loop containing nucleoside triphosphate h	-44.68085106	0.000962609
Protein of unknown function (DUF803)	-28.29226848	0.002182126
Protein of unknown function (DUF803)	-31.12582781	4.65625E-06
Nucleotide/sugar transporter family protein	-52.94117647	0.001082744
Nucleotide/sugar transporter family protein	-47.31182796	3.20327E-06
DNAJ heat shock family protein	-36.80981595	2.99385E-06
DNAJ heat shock family protein	-26.41134557	4.65395E-05
3-hydroxyacyl-CoA dehydrogenase family pro	-41.69398907	0.000591822
pleiotropic drug resistance 12	-31.68119099	0.005614165
Galactose oxidase/kelch repeat superfamily	-31.1789905	0.002371301
disease resistance protein (TIR-NBS-LRR clas	-51.26705653	0.000192914
N/A	-39.09294155	0.009285204
N/A	-44.44444444	0.004415854
Auxin-responsive GH3 family protein	-48.47094801	2.71881E-07
TBP-associated factor 7	-73.51916376	0.000788288
CemA-like proton extrusion protein-related	-28.38350377	0.002603975
cytochrome P450, family 86, subfamily A, po	-62.5	8.96604E-08
response regulator 2	-26.20155039	0.005708866
N/A	-26.20155039	0.005708866

N/A	-26.20155039	0.005708866
N/A	-26.20155039	0.005708866
BED zinc finger ;hAT family dimerisation dom	-38.56008055	3.75717E-09
Auxin efflux carrier family protein	-74.28571429	0.001547796
hexokinase 1	-28.7012987	0.009138996
nuclear RNA polymerase C2	-34.12277378	0.001057295
nuclear RNA polymerase C2	-27.14449601	1.17287E-08
LMBR1-like membrane protein	-28.92466935	0.001049893
Transducin/WD40 repeat-like superfamily pr	-40	0.001455577
ZCW7	-31.72774869	0.001509362
UDP-glucose:glycoprotein glucosyltransferas	-27.41779497	0.002902342
binding	-41.3372093	0.008379863
bZIP transcription factor family protein	-34.48275862	0.004920032
multidrug resistance-associated protein 6	-76.81818182	0.007707273
alpha/beta-Hydrolases superfamily protein	-59.83333333	9.62541E-05
Pentatricopeptide repeat (PPR) superfamily p	-41.22807018	8.19788E-11
Pentatricopeptide repeat (PPR) superfamily p	-38.88888889	9.90426E-06
Pentatricopeptide repeat (PPR) superfamily p	-36.92307692	5.94833E-05
GTP-binding protein-related	-72.36842105	0.004811332
Topoisomerase II-associated protein PAT1	-44.0885265	2.39163E-10
Topoisomerase II-associated protein PAT1	-41.94444444	0.000314104
Topoisomerase II-associated protein PAT1	-54.28571429	1.09852E-07
SPla/RYanodine receptor (SPRY) domain-con	-38.13559322	0.002997114
DNA/RNA polymerases superfamily protein	-26.84620344	0.002697389
phototropin 2	-73.70689655	0.001134112
RNA recognition motif (RRM)-containing prot	-39.73888209	6.70594E-06
N/A	-49.82275218	2.87662E-08
N/A	-42.55319149	0.000916451
Concanavalin A-like lectin protein kinase fam	-32.43243243	0.008862698
Concanavalin A-like lectin protein kinase fam	-44.44444444	0.000222668
N/A	-33.95061728	3.28415E-14
Xanthine/uracil permease family protein	-25.41193182	0.007072412
kinesin like protein for actin based chloroplas	-26.28332232	0.000917646
spermidine synthase 1	-47.53623188	0.000354228
pentatricopeptide (PPR) repeat-containing pr	-57.26273726	4.1663E-08
N/A	-28.20048309	0.000167035
RINT-1 / TIP-1 family	-64.23537703	5.03038E-08
N/A	-29.54545455	0.000135885
villin 4	-36.42512077	0.004992772
membrane bound O-acyl transferase (MBOA	-31.22129989	1.6685E-05
membrane bound O-acyl transferase (MBOA	-27.91871766	0.000160042
VPS54	-31.74369542	0.001876515
Outer arm dynein light chain 1 protein	-45.35857299	0.003115914

Cyclophilin-like peptidyl-prolyl cis-trans isom	-26.93346842	0.000586742
PYRIMIDINE B	-46.04166667	0.003441086
P-loop containing nucleoside triphosphate hy	-46.04166667	0.003441086
Chaperone DnaJ-domain superfamily protein	-93.33333333	0.001063149
Protein kinase superfamily protein	-36.15384615	0.00572838
Caleosin-related family protein	-43.47670251	0.003425268
DNA primases	-50.78039927	0.00034223
Heavy metal transport/detoxification superfa	-39.61916462	6.46745E-07
2-oxoglutarate (2OG) and Fe(II)-dependent o	-76.19047619	0.000297757
GroES-like zinc-binding alcohol dehydrogena:	-27.08616011	1.52214E-05
sugar transporter 14	-37.35909823	0.000920785
Glycosyl hydrolase family protein	-31.47239086	2.69086E-06
Target SNARE coiled-coil domain protein	-33.95566922	0.001277483
Protein kinase family protein	-34.84617728	0.002748854
Folylpolyglutamate synthetase family protein	-40.875	0.006649015
demeter-like 1	-26.81218851	0.005410003
LETM1-like protein	-28.125	0.005116276
ribosomal protein L2	-29.20458787	2.64846E-13
nuclear RNA polymerase A1	-35.78646934	7.35679E-14
nuclear RNA polymerase A1	-29.05525847	0.004191551
nuclear RNA polymerase A1	-34.44770563	4.07335E-12
nuclear RNA polymerase A1	-28.44001897	0.00016537
nuclear RNA polymerase A1	-39.69639932	4.62287E-14
N/A	-36.32607705	4.36783E-19
SERINE CARBOXYPEPTIDASE-LIKE 49	-29.50208706	0.001832074
Ran BP2/NZF zinc finger-like superfamily prot	-58.33333333	7.37312E-34
Leucine-rich repeat protein kinase family pro	-78.4591195	0.000362188
VEFS-Box of polycomb protein	-26.87598116	0.007958909
P-loop containing nucleoside triphosphate hy	-53.31991952	0.008189209
P-loop containing nucleoside triphosphate hy	-28.59459459	0.002241335
ARM repeat superfamily protein	-44.12818471	0.001741729
N/A	-100	0.001061922
VIRB2-interacting protein 1	-50.71895425	0.004230545
N/A	-38.59649123	8.94899E-07
CVP2 like 1	-45.8781362	0.003782564
HMG (high mobility group) box protein with /	-59.84848485	0.003294694
hydroxyproline-rich glycoprotein family prote	-27.43589744	0.004578929
N/A	-45	0.001968856
RNA polymerase II transcription mediators	-28.8003663	0.005714746
RNA binding	-33.88648389	4.42115E-06
cellulose synthase-like B3	-76	0.004139529
N/A	-44.83333333	0.006177282
Protein kinase superfamily protein	-33.33333333	0.000800279

cyclic nucleotide gated channel 5	-29.16121801	0.005269453
Domain of unknown function (DUF3598)	-34.46691176	0.008463618
Uncharacterised BCR, YbaB family COG0718	-32.99284985	0.000136801
N/A	-26.19047619	0.005289772
RING 1A	-27.56699755	3.10227E-05
disease resistance family protein / LRR family	-25.92592593	0.003959094
N/A	-47.50957854	0.005208049
N/A	-45.3125	1.15695E-08
N/A	-55.93220339	1.16646E-06
high mobility group B2	-55.93220339	1.16646E-06
high mobility group B2	-45.3125	1.15695E-08
P-loop containing nucleoside triphosphate hy	-86.36363636	0.000920785
alcohol dehydrogenase 1	-27.64204545	9.8674E-06
N/A	-29	1.63281E-08
N/A	-64.19753086	3.18591E-09
NAC domain containing protein 100	-33.26367119	0.001049893
Disease resistance protein (TIR-NBS-LRR class	-36.28318584	2.24047E-09
Protein of unknown function (DUF1336)	-40.39316975	0.00032109
D111/G-patch domain-containing protein	-39.57875458	0.000160123
Protein kinase superfamily protein	-29.95126706	0.000577716
HAESA-like 1	-30.15777309	0.000246278
N/A	-57.44444444	0.003594702
glutamate receptor 2.7	-34.50292398	0.004743378
BURP domain-containing protein	-80.71428571	0.001273263
Receptor-like protein kinase-related family p	-44.68085106	3.66052E-05
autoinhibited Ca(2+)-ATPase 9	-53.48837209	4.74737E-05
NPR1-like protein 3	-32.05808081	0.003347015
RNA-binding KH domain-containing protein	-41.51747656	0.005278573
Pseudouridine synthase family protein	-36.88311688	0.009989518
Peroxidase superfamily protein	-28.23335021	3.627E-12
ARF-GAP domain 15	-41.81818182	6.42181E-10
ARF-GAP domain 15	-48.55072464	5.47955E-05
N/A	-31.12033195	2.59439E-15
N/A	-47.5	0.000950387
delta1-pyrroline-5-carboxylate synthase 1	-38.46153846	0.005037736
Polynucleotidyl transferase, ribonuclease H-l	-31.93582649	3.16895E-06
Polynucleotidyl transferase, ribonuclease H-l	-27.12943275	1.27598E-07
Protein of unknown function, DUF593	-25.33125	0.00559587
LisH dimerisation motif;WD40/YVTN repeat-l	-66.66666667	0.000865438
Ribosomal protein L14	-40.93406593	0.001023852
bromo-adjacent homology (BAH) domain-cor	-33.67256637	0.004803448
signal peptide peptidase	-55.53359684	0.006171873
appr-1-p processing enzyme family protein	-72.70114943	0.001833685

N/A	-58.01838611	0.005049871
Tetratricopeptide repeat (TPR)-like superfam	-46.31578947	3.05399E-12
N/A	-37.28813559	3.41544E-10
N/A	-53.84615385	0.000498983
DNAJ heat shock N-terminal domain-containi	-77.71929825	0.000281029
NADH-dependent glutamate synthase 1	-34.93150685	5.21247E-07
NADH-dependent glutamate synthase 1	-63.63636364	2.02431E-10
NADH-dependent glutamate synthase 1	-34.48275862	0.009612209
Ribonuclease II/R family protein	-28.82675439	1.87289E-08
Ribonuclease II/R family protein	-31.01265823	9.38846E-13
N/A	-33.63248967	0.000114373
N/A	-33.36627141	3.55252E-11
N/A	-32.74336283	1.12545E-09
N/AMETHYLATED_REGION	-46.35897436	0.005869797
RNA recognition motif (RRM)-containing prot	-28.70286576	0.005958211
O-methyltransferase family protein	-47.22222222	0.003166326
N/A	-49.74025974	0.000107393
Molecular chaperone Hsp40/DnaJ family pro	-29.75743936	0.000404024
ARM repeat superfamily protein	-26.02739726	0.003444049
emp24/gp25L/p24 family/GOLD family prote	-34.30499325	0.005547905
protease-related	-25.10712894	0.001119278
PSAJ	-37.86163522	2.68576E-11
PSAJ	-81.77777778	2.8487E-23
NPR1-like protein 3	-44.96551724	0.009341857
Ubiquitin carboxyl-terminal hydrolase family	-66.15384615	5.61302E-05
Protein kinase superfamily protein	-35.87301587	0.003911856
N/A	-27.08333333	0.004710357
N/A	-35.67176871	0.003042672
Riboflavin synthase-like superfamily protein	-42.52960443	2.2436E-13
Riboflavin synthase-like superfamily protein	-36.14457831	3.64193E-07
Riboflavin synthase-like superfamily protein	-28.49162011	1.01598E-09
Riboflavin synthase-like superfamily protein	-29.92989452	1.10901E-16
VPS54	-57.28669846	8.48188E-05
VPS54	-69.56521739	0.000453169
Pentatricopeptide repeat (PPR) superfamily p	-33.33333333	0.000329424
XH/XS domain-containing protein	-28.57603612	0.000566192
XH/XS domain-containing protein	-27.10341144	9.17156E-06
XH/XS domain-containing protein	-27.22359532	3.5589E-09
XH/XS domain-containing protein	-42.28221788	3.5242E-08
XH/XS domain-containing protein	-30.92497869	6.32629E-06
N/A	-48.33333333	6.53496E-05
myosin 2	-33.49078885	4.2188E-06
myosin 2	-35.48412144	2.53041E-06

cyclophilin 59	-27.96296296	0.007251536
Ca(2)-dependent phospholipid-binding prote	-62.78801843	0.001061922
long-chain acyl-CoA synthetase 7	-31.89655172	0.004169739
beta galactosidase 9	-29.52586207	0.001981666
N/A	-33.33333333	1.00118E-05
cytochrome P450, family 72, subfamily A, po	-28.16901408	0.006782381
cytochrome P450, family 72, subfamily A, po	-46.66877838	9.92563E-11
cytochrome P450, family 72, subfamily A, po	-35.9375	0.006953375
Ribosomal protein L18ae family	-27.55102041	0.000917646
photosystem II reaction center protein K pre	-29.04692082	0.004195621
glutathione S-transferase TAU 20	-41.74962293	0.000583123
N/A	-39.40985246	0.004639193
N/A	-41.74174174	3.0417E-05
Alpha-L RNA-binding motif/Ribosomal protei	-88.46153846	0.00085171
GDSL-motif lipase 5	-50	0.009924873
Uncharacterised protein family (UPF0497)	-35.56231003	0.009235795
N/A	-30.6981982	0.000398413
male gametophyte defective 3	-62.82051282	0.008480288
Ribosomal protein L13 family protein	-53.11594203	0.00839767
RNA polymerase I specific transcription initia	-28.0377735	5.82596E-09
Glucose-6-phosphate/phosphate translocato	-40.95238095	0.001045479
Subtilase family protein	-48.71794872	0.009904325
ATPase, F0 complex, subunit B/B\', bacterial/	-49.24242424	0.009083579
ATP synthase subunit alpha	-49.24242424	0.009083579
diacylglycerol acyltransferase family	-26.4203985	0.003476223
diacylglycerol acyltransferase family	-28.4376672	0.00164362
Protein of unknown function (DUF1640)	-52.59259259	0.008333981
N/A	-50	0.009301166
nudix hydrolase homolog 12	-31.89908683	0.003007079
HSP20-like chaperones superfamily protein	-42.15180545	0.000143484
Protein Transporter, Pam16	-56.15989515	1.16384E-12
disease resistance family protein / LRR family	-36.87641723	0.000330287
multidrug resistance-associated protein 14	-52.50965251	0.004811332
disease resistance family protein / LRR family	-45.69892473	0.003522876
disease resistance family protein / LRR family	-28.73176207	0.008465582
RNA helicase family protein	-25.56536866	0.003871064
N/A	-75.65217391	0.008144325
plastid transcriptionally active 2	-29.71264368	0.000459098
N/A	-33.51648352	2.63621E-10
nicotinate/nicotinamide mononucleotide ade	-25.20325203	5.1489E-05
Protein of unknown function (DUF579)	-50.5952381	0.009051124
kinase interacting (KIP1-like) family protein	-27.95698925	0.004582646
kinase interacting (KIP1-like) family protein	-45.04504505	0.005209895

kinase interacting (KIP1-like) family protein	-48.60022396	8.54617E-09
kinase interacting (KIP1-like) family protein	-27.43362832	3.66749E-07
kinase interacting (KIP1-like) family protein	-29.14107918	2.29193E-11
kinase interacting (KIP1-like) family protein	-31.68316832	2.4918E-14
dihydroflavonol 4-reductase	-25.46583851	1.48802E-06
nuclear RNA polymerase A2	-41.88311688	0.00866945
Tetratricopeptide repeat (TPR)-like superfam	-31.05126269	3.89002E-07
N/A	-27.63157895	7.61226E-05
embryo defective 2410	-77.64705882	0.000691311
CBS domain-containing protein with a domai	-60.74766355	0.009828008
ankyrin repeat protein	-60.74766355	0.009828008
HXXXD-type acyl-transferase family protein	-37.93103448	0.002590829
N/A	-32.81509121	0.003397932
IQ-domain 19	-25.12820513	1.26675E-05
N/A	-52.60869565	0.006301595
TBP-associated factor 5	-33.67412828	0.000148109
Protein of unknown function (DUF1218)	-26.78014865	0.006430787
Protein of unknown function (DUF1218)	-54.65116279	3.93644E-10
RNA polymerase II transcription mediators	-32.50547345	0.000538326
RNA polymerase II transcription mediators	-28.15100579	0.002276985
ferritin 4	-37.33333333	4.57306E-06
binding	-25.24312896	0.001956084
NB-ARC domain-containing disease resistanc	-25.98690409	6.2445E-05
NB-ARC domain-containing disease resistanc	-32.46753247	0.000811469
glucan synthase-like 7	-35.84507042	9.72511E-05
glucan synthase-like 7	-46.96969697	5.90648E-05
N/A	-61.29411765	0.00161732
alpha/beta-Hydrolases superfamily protein	-33.30827068	3.13055E-05
aminophospholipid ATPase 3	-29.48606272	0.000713932
UB-like protease 1D	-85.71428571	0.000743599
Plant protein of unknown function (DUF828)	-31.05128205	0.005967596
Plant protein of unknown function (DUF828)	-28.96212525	2.82727E-05
SOUL heme-binding family protein	-29.87711214	0.000553287
UDP-Glycosyltransferase superfamily protein	-45.19632414	0.001732018
UDP-Glycosyltransferase superfamily protein	-44.375	2.88148E-05
Signal recognition particle, SRP9/SRP14 subu	-26.95926872	0.000564005
Ribosomal protein S8e family protein	-30.30450908	2.5857E-06
F-box family protein	-35.89256647	0.001854191
GPI transamidase component PIG-S-related	-33.00970874	9.77754E-06
GPI transamidase component PIG-S-related	-43.24324324	7.15679E-05
Protein kinase superfamily protein	-41.29554656	3.39505E-07
Protein of unknown function (DUF674)	-27.43902439	1.72039E-10
Yippee family putative zinc-binding protein	-26.32010354	1.46832E-06

Uncharacterized protein family (UPF0016)	-40.87265231	4.77489E-07
Uncharacterized protein family (UPF0016)	-25.69007264	0.001114632
N/A	-29.56567242	0.008817792
HEAT repeat-containing protein	-25.81578416	1.59077E-05
RNA-binding (RRM/RBD/RNP motifs) family p	-70	0.009734505
HVA22-like protein K	-33.95983936	0.000330978
N/A	-27.91255665	0.003708649
RAB GTPase homolog A1D	-47.23415682	6.7166E-12
RAB GTPase homolog A1D	-50.79772995	7.78881E-31
RAB GTPase homolog A1D	-29.44175971	1.2481E-13
golgin candidate 6	-34.92747253	0.000472038
auxin response factor 8	-60	0.005453457
CLIP-associated protein	-28.35820896	2.47181E-05
CLIP-associated protein	-28.84615385	0.006424062
peptide deformylase 1B	-25.47172588	0.000939253
SET domain group 29	-39.84848485	3.34188E-05
TLC ATP/ADP transporter	-34.98217469	0.006817451
MALE GAMETOPHYTE DEFECTIVE 2	-34.54829471	0.001051588
Protein of unknown function (DUF3754)	-53.04347826	0.004918235
DHHC-type zinc finger family protein	-35.95505618	5.17298E-07
DHHC-type zinc finger family protein	-57.89473684	4.30994E-10
plant glycogenin-like starch initiation protein	-78.26086957	0.003349409
MuDR family transposase	-25.04862462	0.004100339
P-loop containing nucleoside triphosphate hy	-53.64238411	4.0498E-10
extra-large G-protein 1	-80.64516129	0.003261074
EXS (ERD1/XPR1/SYG1) family protein	-36.84210526	5.11057E-05
zinc ion binding;nucleic acid binding	-75.71428571	0.002789447
N/A	-50.79113924	0.004912718
ortholog of human splicing factor SC35	-50.79113924	0.004912718
N/A	-27.74864025	0.001834553
GRAM domain family protein	-45.20833333	6.07347E-08
ubiquitin-specific protease 13	-25.31282051	4.60196E-14
F-box family protein	-44.54545455	4.18748E-05
Transmembrane Fragile-X-F-associated prote	-32.96296296	1.66982E-08
Transmembrane Fragile-X-F-associated prote	-38.41269841	0.000454697
Transmembrane Fragile-X-F-associated prote	-54.05128205	1.72039E-10
N/A	-62.16216216	0.004306119
lipase class 3 family protein	-30.12350265	0.004310897
Protein of unknown function (DUF2296)	-28.30572508	0.002165398

P value
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2.94858E-05

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3.05715E-06
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1.35124E-06
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1.43578E-18
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5.1835E-18
1.8822E-22
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3.47697E-05
6.27749E-07
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3.0849E-07
9.36585E-07
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4.12778E-06
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1.59388E-06
1.19043E-09
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3.93294E-08
1.25257E-05
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1.69533E-06
2.86198E-09
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1.67882E-05
1.71565E-05
6.8523E-06
8.15837E-08
4.2975E-07
7.74229E-06
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6.34577E-06
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8.17656E-17
3.32884E-07
1.25256E-05
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7.57662E-06
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1.87514E-05
1.20002E-07
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6.52574E-07
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1.51487E-06
1.29396E-05
1.47749E-10
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9.88589E-06
4.94583E-14
7.14299E-06
3.26159E-08
5.73815E-06
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1.29135E-05
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1.28406E-11
2.2662E-18
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4.07765E-06

Supplemental Table 7: List of 282 hypo-methylated genes in C

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mytileDiff25p200.hypo_merged_CHH.Chr01.45569801-45570000
mytileDiff25p200.hypo_merged_CHH.Chr01.45752201-45752400
mytileDiff25p200.hypo_merged_CHH.Chr01.49102001-49102200
mytileDiff25p200.hypo_merged_CHH.Chr01.49437001-49437200
mytileDiff25p200.hypo_merged_CHH.Chr01.50436601-50436800
mytileDiff25p200.hypo_merged_CHH.Chr01.50606401-50606600
mytileDiff25p200.hypo_merged_CHH.Chr01.50606201-50606400
mytileDiff25p200.hypo_merged_CHH.Chr01.51982201-51982400
mytileDiff25p200.hypo_merged_CHH.Chr01.52517201-52517400
mytileDiff25p200.hypo_merged_CHH.Chr01.53463601-53463800
mytileDiff25p200.hypo_merged_CHH.Chr01.56617801-56618000
mytileDiff25p200.hypo_merged_CHH.Chr02.408001-408200
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mytileDiff25p200.hypo_merged_CHH.Chr02.11529601-11529800
mytileDiff25p200.hypo_merged_CHH.Chr02.14091001-14091200
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mytileDiff25p200.hypo_merged_CHH.Chr03.25563601-25563800
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mytileDiff25p200.hypo_merged_CHH.Chr13.2724601-2724800
mytileDiff25p200.hypo_merged_CHH.Chr13.13560801-13561000
mytileDiff25p200.hypo_merged_CHH.Chr13.14950801-14951000
mytileDiff25p200.hypo_merged_CHH.Chr13.15700801-15701000
mytileDiff25p200.hypo_merged_CHH.Chr13.20379601-20379800
mytileDiff25p200.hypo_merged_CHH.Chr13.22914001-22914200
mytileDiff25p200.hypo_merged_CHH.Chr13.24272201-24272400
mytileDiff25p200.hypo_merged_CHH.Chr13.24327201-24327400
mytileDiff25p200.hypo_merged_CHH.Chr13.24687601-24687800
mytileDiff25p200.hypo_merged_CHH.Chr13.27213201-27213400
mytileDiff25p200.hypo_merged_CHH.Chr13.27588801-27589000
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mytileDiff25p200.hypo_merged_CHH.Chr13.36357601-36357800
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mytileDiff25p200.hypo_merged_CHH.Chr13.45372801-45373000
mytileDiff25p200.hypo_merged_CHH.Chr13.45755601-45755800
mytileDiff25p200.hypo_merged_CHH.Chr14.3356801-3357000
mytileDiff25p200.hypo_merged_CHH.Chr14.4442001-4442200
mytileDiff25p200.hypo_merged_CHH.Chr14.8867601-8867800
mytileDiff25p200.hypo_merged_CHH.Chr14.10752601-10752800
mytileDiff25p200.hypo_merged_CHH.Chr14.22556201-22556400
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mytileDiff25p200.hypo_merged_CHH.Chr14.32615401-32615600
mytileDiff25p200.hypo_merged_CHH.Chr14.42387001-42387200
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mytileDiff25p200.hypo_merged_CHH.Chr14.46480401-46480600
mytileDiff25p200.hypo_merged_CHH.Chr14.46583201-46583400
mytileDiff25p200.hypo_merged_CHH.Chr15.109201-109400
mytileDiff25p200.hypo_merged_CHH.Chr15.2098401-2098600
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mytileDiff25p200.hypo_merged_CHH.Chr15.2823601-2823800
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mytileDiff25p200.hypo_merged_CHH.Chr16.3874801-3875000
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mytileDiff25p200.hypo_merged_CHH.Chr18.14110401-14110600
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mytileDiff25p200.hypo_merged_CHH.Chr18.19036001-19036200
mytileDiff25p200.hypo_merged_CHH.Chr18.25241801-25242000
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mytileDiff25p200.hypo_merged_CHH.Chr20.3140601-3140800
mytileDiff25p200.hypo_merged_CHH.Chr20.3753601-3753800
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mytileDiff25p200.hypo_merged_CHH.scaffold_223.13001-13200
mytileDiff25p200.hypo_merged_CHH.scaffold_31.263201-263400
mytileDiff25p200.hypo_merged_CHH.scaffold_32.247601-247800
mytileDiff25p200.hypo_merged_CHH.scaffold_361.3401-3600

HH context.

REGION	GENE ID
PROMOTER	Glyma.01G022300
PROMOTER	Glyma.01G038600
3'UTR	Glyma.01G076200
PROMOTER(72bp); 5'UTR(128bp)	Glyma.01G089600
GENE BODY	Glyma.01G134300
GENE BODY (102bp); 3'UTR(98bp)	Glyma.01G135400
PROMOTER	Glyma.01G153600
PROMOTER	Glyma.01G156800
PROMOTER	Glyma.01G166400
GENE BODY	Glyma.01G168400
GENE BODY	Glyma.01G168400
GENE BODY	Glyma.01G184500
PROMOTER	Glyma.01G190400
PROMOTER	Glyma.01G201000
GENE BODY (169bp); 3'UTR(31bp)	Glyma.01G243200
GENE BODY	Glyma.02G003600
GENE BODY	Glyma.02G027500
GENE BODY	Glyma.02G090400
PROMOTER	Glyma.02G102900
PROMOTER	Glyma.02G116700
PROMOTER	Glyma.02G117700
GENE BODY	Glyma.02G135900
GENE BODY	Glyma.02G159400
GENE BODY	Glyma.02G170200
GENE BODY	Glyma.02G228000
PROMOTER	Glyma.02G233500
3'UTR	Glyma.02G273400
3'UTR	Glyma.02G277700
PROMOTER	Glyma.02G307400
PROMOTER	Glyma.03G028200
PROMOTER	Glyma.03G028200
GENE BODY	Glyma.03G068100
PROMOTER(145bp); 5'UTR(55bp)	Glyma.03G086600
PROMOTER(174bp); GENE BODY(26bp)	Glyma.03G097200
PROMOTER	Glyma.03G102800
GENE BODY	Glyma.03G114700
GENE BODY	Glyma.03G118200
PROMOTER	Glyma.03G121600
PROMOTER	Glyma.03G147700
PROMOTER	Glyma.03G179900
PROMOTER(6bp); 5'UTR(194bp)	Glyma.03G232300

PROMOTER	Glyma.03G252500
PROMOTER	Glyma.04G007400
PROMOTER	Glyma.04G007500
GENE BODY (57bp); 3'UTR(143bp)	Glyma.04G011500
PROMOTER	Glyma.04G018200
PROMOTER	Glyma.04G064100
PROMOTER	Glyma.04G065700
GENE BODY	Glyma.04G113100
PROMOTER	Glyma.04G122800
GENE BODY	Glyma.04G123500
PROMOTER	Glyma.04G191100
PROMOTER	Glyma.04G193500
PROMOTER (164bp); 5'UTR(36bp)	Glyma.04G194600
GENE BODY	Glyma.04G205000
PROMOTER	Glyma.04G218200
PROMOTER	Glyma.04G234000
PROMOTER	Glyma.05G044900
PROMOTER	Glyma.05G053000
PROMOTER	Glyma.05G083300
PROMOTER	Glyma.05G125000
GENE BODY	Glyma.05G154700
GENE BODY	Glyma.05G161000
GENE BODY	Glyma.05G248000
PROMOTER	Glyma.06G032800
3'UTR	Glyma.06G033700
GENE BODY	Glyma.06G056300
GENE BODY	Glyma.06G061900
GENE BODY	Glyma.06G073100
GENE BODY	Glyma.06G114500
PROMOTER	Glyma.06G126000
GENE BODY	Glyma.06G179300
GENE BODY	Glyma.06G211100
GENE BODY	Glyma.06G223300
PROMOTER	Glyma.06G247200
PROMOTER	Glyma.06G276200
PROMOTER	Glyma.06G285000
GENE BODY	Glyma.06G286700
PROMOTER	Glyma.06G305100
PROMOTER	Glyma.06G315300
GENE BODY	Glyma.07G035100
GENE BODY	Glyma.07G051000
GENE BODY	Glyma.07G077400
PROMOTER	Glyma.07G087000

GENE BODY	Glyma.07G114200
3'UTR	Glyma.07G116900
GENE BODY (122bp); 3'UTR(78bp)	Glyma.07G124500
PROMOTER	Glyma.07G129700
GENE BODY	Glyma.07G136200
PROMOTER	Glyma.07G157400
PROMOTER	Glyma.07G165700
PROMOTER	Glyma.07G209100
PROMOTER	Glyma.07G212700
PROMOTER	Glyma.07G236900
PROMOTER	Glyma.07G268700
PROMOTER	Glyma.07G274200
PROMOTER	Glyma.07G274300
GENE BODY	Glyma.08G036600
PROMOTER	Glyma.08G039800
PROMOTER	Glyma.08G115800
PROMOTER	Glyma.08G140400
GENE BODY	Glyma.08G197700
GENE BODY	Glyma.08G219200
PROMOTER	Glyma.08G220700
GENE BODY (11bp); 3'UTR(189bp)	Glyma.08G239000
GENE BODY	Glyma.08G240400
PROMOTER	Glyma.08G241900
GENE BODY	Glyma.08G264900
PROMOTER	Glyma.08G268800
PROMOTER	Glyma.08G271700
PROMOTER	Glyma.08G279800
GENE BODY	Glyma.08G328500
PROMOTER	Glyma.08G349000
PROMOTER (191bp); 5'UTR (9bp)	Glyma.08G357000
PROMOTER	Glyma.09G042800
PROMOTER	Glyma.09G049100
PROMOTER	Glyma.09G055900
PROMOTER	Glyma.09G068500
GENE BODY	Glyma.09G073100
PROMOTER	Glyma.09G109200
PROMOTER	Glyma.09G111900
PROMOTER (167bp); GENE BODY(33bp)	Glyma.09G112800
PROMOTER	Glyma.09G124900
3'UTR (85bp)	Glyma.09G126300
GENE BODY	Glyma.09G153500
PROMOTER	Glyma.09G154200
GENE BODY	Glyma.09G180800

PROMOTER	Glyma.09G183100
PROMOTER	Glyma.09G193200
PROMOTER	Glyma.09G259300
PROMOTER	Glyma.09G286200
GENE BODY (191bp); 3'UTR(9bp)	Glyma.10G034900
5'UTR(110bp); GENE BODY (90bp)	Glyma.10G043400
GENE BODY	Glyma.10G060000
GENE BODY	Glyma.10G078700
GENE BODY(64bp); 3'UTR(136bp)	Glyma.10G152500
GENE BODY	Glyma.10G159300
PROMOTER	Glyma.10G164400
PROMOTER	Glyma.10G174000
GENE BODY	Glyma.10G183000
PROMOTER	Glyma.10G197100
PROMOTER	Glyma.10G235100
PROMOTER	Glyma.10G243300
PROMOTER	Glyma.10G281900
PROMOTER	Glyma.11G020100
PROMOTER	Glyma.11G020100
PROMOTER	Glyma.11G055200
PROMOTER	Glyma.11G096200
PROMOTER	Glyma.11G129700
PROMOTER	Glyma.11G141100
PROMOTER(198bp); GENE BODY(2bp)	Glyma.11G170700
GENE BODY	Glyma.11G184900
GENE BODY	Glyma.11G193100
PROMOTER	Glyma.11G200200
PROMOTER	Glyma.11G206200
PROMOTER	Glyma.11G252300
GENE BODY	Glyma.12G016700
PROMOTER	Glyma.12G041100
PROMOTER	Glyma.12G051800
PROMOTER	Glyma.12G060800
GENE BODY	Glyma.12G119500
PROMOTER(46bp); GENE BODY(154bp)	Glyma.12G140800
PROMOTER	Glyma.12G147400
GENE BODY	Glyma.12G192300
GENE BODY	Glyma.12G198100
GENE BODY	Glyma.12G216200
PROMOTER	Glyma.12G223100
GENE BODY	Glyma.12G231800
GENE BODY	Glyma.12G235100
GENE BODY	Glyma.13G010000

GENE BODY	Glyma.13G010000
3'UTR	Glyma.13G042400
PROMOTER	Glyma.13G052600
3'UTR	Glyma.13G059600
GENE BODY	Glyma.13G089300
GENE BODY	Glyma.13G115500
GENE BODY	Glyma.13G129900
3'UTR	Glyma.13G130500
GENE BODY	Glyma.13G134400
PROMOTER	Glyma.13G156900
PROMOTER	Glyma.13G160300
PROMOTER	Glyma.13G235300
PROMOTER	Glyma.13G259200
PROMOTER	Glyma.13G277200
5'UTR (111bp); GENE BODY (89bp)	Glyma.13G283900
PROMOTER	Glyma.13G328200
PROMOTER	Glyma.13G345000
PROMOTER	Glyma.13G345100
PROMOTER	Glyma.13G352500
GENE BODY	Glyma.13G367200
PROMOTER	Glyma.13G368100
GENE BODY	Glyma.13G372400
GENE BODY	Glyma.14G044300
PROMOTER	Glyma.14G056000
PROMOTER (151bp); 5'UTR(49bp)	Glyma.14G095300
PROMOTER	Glyma.14G104800
GENE BODY	Glyma.14G131700
PROMOTER	Glyma.14G137400
GENE BODY	Glyma.14G151100
PROMOTER	Glyma.14G171200
PROMOTER	Glyma.14G179000
PROMOTER	Glyma.14G199800
PROMOTER (111bp); GENE BODY(89bp)	Glyma.14G200800
PROMOTER	Glyma.15G000900
5'UTR	Glyma.15G025900
5'UTR(71bp); GENE BODY (129bp)	Glyma.15G030500
PROMOTER	Glyma.15G035400
PROMOTER	Glyma.15G046800
GENE BODY	Glyma.15G057900
GENE BODY	Glyma.15G058900
PROMOTER	Glyma.15G071300
PROMOTER	Glyma.15G138400
PROMOTER	Glyma.15G145400

PROMOTER	Glyma.15G165300
GENE BODY	Glyma.15G172700
PROMOTER	Glyma.15G192800
GENE BODY	Glyma.15G193400
GENE BODY	Glyma.15G214400
PROMOTER	Glyma.15G234900
GENE BODY	Glyma.15G246800
PROMOTER (160bp); 5'UTR(40bp)	Glyma.15G248800
PROMOTER	Glyma.15G255100
PROMOTER	Glyma.15G255800
GENE BODY	Glyma.16G041300
PROMOTER	Glyma.16G067500
PROMOTER	Glyma.16G078500
PROMOTER	Glyma.16G088500
PROMOTER	Glyma.16G088600
PROMOTER	Glyma.16G111800
3'UTR	Glyma.16G127900
GENE BODY	Glyma.16G202300
GENE BODY	Glyma.17G017700
GENE BODY	Glyma.17G027700
PROMOTER	Glyma.17G044800
GENE BODY	Glyma.17G057300
GENE BODY	Glyma.17G060300
PROMOTER	Glyma.17G093700
PROMOTER	Glyma.17G093700
GENE BODY	Glyma.17G114400
PROMOTER	Glyma.17G118400
GENE BODY	Glyma.17G145700
GENE BODY	Glyma.17G212300
PROMOTER	Glyma.17G245500
GENE BODY	Glyma.17G258800
PROMOTER	Glyma.18G009100
PROMOTER	Glyma.18G012700
GENE BODY (37bp), 3'UTR(163bp)	Glyma.18G082200
GENE BODY	Glyma.18G099600
GENE BODY	Glyma.18G115800
PROMOTER	Glyma.18G124900
PROMOTER	Glyma.18G133400
GENE BODY	Glyma.18G147700
PROMOTER	Glyma.18G179500
PROMOTER (40bp), 5'UTR(110bp); GENE B	Glyma.18G216900
GENE BODY	Glyma.18G299200
GENE BODY	Glyma.19G006200

PROMOTER	Glyma.19G011000
GENE BODY	Glyma.19G117600
GENE BODY	Glyma.19G124700
PROMOTER	Glyma.19G156500
GENE BODY (92bp); 3'UTR(108bp)	Glyma.19G185900
3'UTR (49bp)	Glyma.19G192300
PROMOTER	Glyma.19G224000
GENE BODY	Glyma.19G226000
GENE BODY	Glyma.19G230000
GENE BODY	Glyma.19G251700
GENE BODY	Glyma.19G251800
3'UTR (164bp)	Glyma.19G252900
5'UTR(39bp); GENE BODY (161bp)	Glyma.20G005000
PROMOTER	Glyma.20G010700
5'UTR	Glyma.20G024300
PROMOTER	Glyma.20G027600
PROMOTER	Glyma.20G030800
PROMOTER	Glyma.20G094700
GENE BODY	Glyma.20G104000
3'UTR	Glyma.20G104100
PROMOTER	Glyma.20G118000
PROMOTER	Glyma.20G140100
GENE BODY	Glyma.20G178600
5'UTR	Glyma.20G182900
GENE BODY	Glyma.20G198700
PROMOTER	Glyma.20G235400
PROMOTER	Glyma.20G241600
PROMOTER	Glyma.U024600
PROMOTER	Glyma.U032500
PROMOTER	Glyma.U035000
GENE BODY	Glyma.U036800

GENE ANNOTATION	1ethylation Differer
UDP-glucosyl transferase 85A3	-49.47368421
myb-like transcription factor family protein	-42.30769231
N/A	-26.9620391
N/A	-28.07766677
N/A	-53.75722543
Nucleotidyltransferase family protein	-31.66666667
xyloglucanase 113	-83.83380205
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family proteir	-30.26819923
Phosphatidylinositol 3- and 4-kinase family protein with FAT domain	-25.69892473
Lactoylglutathione lyase / glyoxalase I family protein	-28.07129094
Lactoylglutathione lyase / glyoxalase I family protein	-27.89048866
Transducin/WD40 repeat-like superfamily protein	-25.52700415
cytochrome P450, family 81, subfamily D, polypeptide 4	-32.12264151
plastid ribosomal protein l11	-31.11367719
somatic embryogenesis receptor-like kinase 1	-38.11398575
RNA-binding (RRM/RBD/RNP motifs) family protein	-25.24565382
zinc ion binding	-40
DNA LIGASE 6	-67.35632184
plant U-box 26	-25.5089717
Pentatricopeptide repeat (PPR) superfamily protein	-31.63265306
phosphoenolpyruvate carboxylase 4	-42.00971984
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily prc	-25.34246575
Zinc knuckle (CCHC-type) family protein	-30.89393939
Thioesterase superfamily protein	-80.625
Plant protein of unknown function (DUF828)	-39.03372646
Pseudouridine synthase family protein	-30.95085568
UDP-Glycosyltransferase superfamily proteinMETHYLATED_REGION	-50.15698587
early nodulin-like protein 18	-46.26370625
N/A	-32.52608048
Protein of unknown function (DUF565)	-44.9376947
Protein of unknown function (DUF565)	-38.80034773
rubisco activase	-30.23255814
Cellulose-synthase-like C6	-100
N/A	-41.14583333
DYNAMIN-like 1E	-34.95297806
Plant protein of unknown function (DUF247)	-36.90360273
transcription regulators	-39.840842
lupeol synthase 2	-26.02678571
Disease resistance-responsive (dirigent-like protein) family protein	-26.01455698
FASCICLIN-like arabinogalactan-protein 11	-44.93557087
Protein of unknown function (DUF3511)	-27.62414511

Li-tolerant lipase 1	-43.52501169
FMN-linked oxidoreductases superfamily protein	-27.30141309
ATPase, F0/V0 complex, subunit C protein	-27.30141309
Arabidopsis protein of unknown function (DUF241)	-27.40925886
N/A	-28.63636364
KNOTTED1-like homeobox gene 3	-37.82230806
Phox (PX) domain-containing protein	-31.73935891
alpha/beta-Hydrolases superfamily protein	-25.3968254
N/A	-30.01808318
HAC13 protein (HAC13)	-80.13157895
Pectin lyase-like superfamily protein	-28.87657058
glyceraldehyde-3-phosphate dehydrogenase C subunit 1	-44.3175853
RNA-metabolising metallo-beta-lactamase family protein	-28.41234291
Protein kinase superfamily protein	-29.04233171
Nucleotide-sugar transporter family protein	-71.53310105
plastid transcriptionally active7	-30.40229885
26S proteasome, regulatory subunit Rpn7;Proteasome component (P	-36.28909809
glycine-rich protein	-40.54580897
Transcription initiation factor IIF, beta subunit	-29.80769231
FAD-binding Berberine family protein	-36.08654076
Protein of unknown function, DUF538	-37.96440489
NAD(P)-binding Rossmann-fold superfamily protein	-28.87307458
annexin 5	-25.99302201
BED zinc finger ;hAT family dimerisation domain	-30.14853648
Chaperone DnaJ-domain superfamily protein	-80
P-type ATPase of Arabidopsis 2	-69.44136145
WRKY DNA-binding protein 40	-26.76767677
RING/U-box superfamily protein	-37.58865248
N/A	-26.20844564
FTSH protease 11	-35.77694236
D111/G-patch domain-containing protein	-40.87504071
PIF1 helicase	-32.1291866
SET domain group 4	-38.38709677
Transducin/WD40 repeat-like superfamily protein	-43.56435644
multiprotein bridging factor 1B	-29.72659486
protein kinase C substrate, heavy chain-related	-25.64102564
O-methyltransferase family protein	-29.0805417
N/A	-25.98357596
N/A	-31.06796117
aminopeptidase M1	-25.98484848
CBL-interacting protein kinase 9	-38.42105263
S-adenosyl-L-methionine-dependent methyltransferases superfamily	-36.86868687
Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein	-27.47252747

Fatty acid hydroxylase superfamily	-31.18762475
endoplasmic reticulum oxidoreductins 2	-30
hexokinase 1	-25.43847385
Alkaline-phosphatase-like family protein	-37.84652471
NAD(P)-binding Rossmann-fold superfamily protein	-26.92307692
SU(VAR)3-9 homolog 9	-33.66503368
N/A	-35.62172594
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily pro	-47.72727273
cytochrome P450, family 707, subfamily A, polypeptide 4	-26.60347985
N/A	-27.46443409
Sec14p-like phosphatidylinositol transfer family protein	-30.45751634
phosphate transporter 4;6	-44.93251243
Smg-4/UPF3 family protein	-44.93251243
BURP domain-containing protein	-27.13235294
Fibronectin type III domain-containing protein	-27.45257453
general regulatory factor 9	-30.93407873
cytochrome P450, family 71, subfamily B, polypeptide 34	-26.19937695
Leucine-rich repeat transmembrane protein kinase protein	-39.86842105
Low PSII Accumulation 3	-25.73336826
cyclin-dependent kinase B1;2	-27.20238095
N/A	-35.3125
SNF1 kinase homolog 10	-27.8592545
PIF1 helicase	-30.14824798
phototropin 2	-28.90271493
Nucleic acid-binding, OB-fold-like protein	-27.89983538
ARF-GAP domain 8	-37.81773782
kinesin like protein for actin based chloroplast movement 1	-32.79722485
Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	-28.49878935
dolichol-phosphate mannosyltransferase-related	-38.59649123
RINT-1 / TIP-1 family	-35.11689417
LYR family of Fe/S cluster biogenesis protein	-35.44180885
cytochrome P450, family 81, subfamily D, polypeptide 3	-36.56923405
lectin protein kinase family protein	-28.65693584
alfin-like 5	-59.15254237
N/A	-33.28379224
Aha1 domain-containing protein	-25.95238095
fatty acid desaturase 2	-36.70833333
N/A	-70
N/A	-25.92342342
plastidic pyruvate kinase beta subunit 1	-25.36873156
Microtubule associated protein (MAP65/ASE1) family protein	-33.02459763
Tetratricopeptide repeat (TPR)-like superfamily protein	-46.8627451
Reticulon family protein	-41.03899573

associated molecule with the SH3 domain of STAM 1	-37.47987118
S-adenosyl-L-methionine-dependent methyltransferases superfamily	-26.86433528
Protein of unknown function (DUF3245)	-25.5036208
N/A	-26.6226138
Outer membrane OMP85 family protein	-27.07143361
N/A	-30.4964539
phosphatidyl inositol monophosphate 5 kinase	-26.4957265
N/A	-28.18766393
Transducin/WD40 repeat-like superfamily protein	-26.77433694
Nucleolar histone methyltransferase-related protein	-28.77894737
N/A	-29.62992889
N/A	-41.66666667
fatty alcohol oxidase 3	-28.86102403
ribosomal protein L6 family protein	-32.6899456
tubulin beta 8	-43.98335583
Aluminium induced protein with YGL and LRDR motifs	-27.59076531
Cupredoxin superfamily protein	-54.24528302
Ribosomal protein S5 family protein	-26.52412281
Ribosomal protein S5 family protein	-27.44488412
ralf-like 34	-35.76923077
Pyridoxal phosphate (PLP)-dependent transferases superfamily protei	-32.49249249
beta glucosidase 13	-26.49859944
SEC14 cytosolic factor family protein / phosphoglyceride transfer fami	-28.45827961
cleavage and polyadenylation specificity factor 100	-33.67521368
homolog of histone chaperone HIRA	-32.45415207
DNA ligase 1	-28.8814751
Phototropic-responsive NPH3 family protein	-28.91772735
receptor kinase 3	-28.71496563
K-box region and MADS-box transcription factor family protein	-37.45045188
N/A	-28.10522811
cytochrome BC1 synthesis	-34.86756106
pfkB-like carbohydrate kinase family protein	-50.58201058
RING/U-box superfamily protein	-40.8496732
PIF1 helicase	-25.77186964
S-locus lectin protein kinase family protein	-41.50943396
ARF-GAP domain 5	-29.09132007
Exostosin family protein	-40.1299505
S-locus lectin protein kinase family protein	-34.04862317
terpene synthase 21	-33.75764994
Seven transmembrane MLO family protein	-46.66666667
Leucine-rich repeat transmembrane protein kinase	-30.77211394
senescence-related gene 1	-28.06172322
N/A	-25.89222615

N/A	-25.27718802
N/A	-37.75946276
BTB/POZ domain-containing protein	-25.09070449
PIF1 helicase	-25.8382832
NOD26-like intrinsic protein 1;2	-40.77109897
lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctic	-37.40653863
GDSL-like Lipase/Acylhydrolase superfamily protein	-35.12817125
N/A	-37.78901855
N/A	-29.76506252
D111/G-patch domain-containing protein	-27.91664294
Tetratricopeptide repeat (TPR)-like superfamily protein	-39.44444444
Homeodomain-like transcriptional regulator	-51.51515152
interactor of constitutive active rops 1	-31.88932981
P-loop containing nucleoside triphosphate hydrolases superfamily pro	-43.33333333
BURP domain-containing protein	-45.95393253
N/A	-47.87878788
Tetratricopeptide repeat (TPR)-like superfamily protein	-48.29956156
Calcium-dependent phosphotriesterase superfamily protein	-48.29956156
RNA methyltransferase family protein	-38.88888889
Leucine-rich repeat family protein	-29.30094386
GPI transamidase component Gpi16 subunit family protein	-25.12768131
autoinhibited Ca(2+)-ATPase 9	-75.75757576
F-box protein 2	-33.33333333
sorting nexin 2B	-26.84556696
N/A	-35.71428571
cullin 1	-30.84571852
Protein of unknown function (DUF1218)	-31.02275538
N/A	-28.28455458
disease resistance protein (TIR-NBS-LRR class), putative	-42.37762238
ER lumen protein retaining receptor family protein	-37.61276374
phosphoenolpyruvate carboxylase-related kinase 2	-27.20848057
WRKY DNA-binding protein 4	-38.10786914
O-methyltransferase family protein	-29.6875
P-loop containing nucleoside triphosphate hydrolases superfamily pro	-31.71101017
casein kinase 1-like protein 2	-32.07920792
N/A	-25.60825377
N/A	-28.15934066
emp24/gp25L/p24 family/GOLD family protein	-27.69024817
K-box region and MADS-box transcription factor family protein	-41.0130719
aldehyde dehydrogenase 6B2	-46.04519774
Aluminium induced protein with YGL and LRDR motifs	-27.56201129
Plant invertase/pectin methylesterase inhibitor superfamily protein	-38.4496124
Drought-responsive family protein	-29.07779791

DNA binding;DNA-directed RNA polymerases	-26.12179487
homolog of CFIM-25	-37.44377811
Outer arm dynein light chain 1 protein	-26.70977011
cation-chloride co-transporter 1	-27.63377926
S-locus lectin protein kinase family protein	-43.64295125
N/A	-41.76319176
NB-ARC domain-containing disease resistance protein	-25.96153846
Family of unknown function (DUF572)	-56.15079365
N/A	-26.75
Lojap-related protein	-31.05921089
BED zinc finger ;hAT family dimerisation domain	-43.66197183
alpha/beta-Hydrolases superfamily protein	-25.24938829
translocase inner membrane subunit 17-2	-43.77300408
N/A	-27.83411807
Protein of unknown function (DUF674)	-27.83411807
Endoribonuclease/protein kinase IRE1-like	-35.21380345
Disease resistance protein (TIR-NBS-LRR class) family	-31.02380952
HXXXD-type acyl-transferase family protein	-25.62230335
CBS domain-containing protein with a domain of unknown function (D	-31.47514105
multifunctional protein 2	-27.40046838
F-box family protein	-29.87109137
Auxin efflux carrier family protein	-26.63776114
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family p	-28.18181818
N/A	-29.11681371
N/A	-44.48346503
Ypt/Rab-GAP domain of gyp1p superfamily protein	-30.34429099
RING/FYVE/PHD zinc finger superfamily protein	-42.57567105
N/A	-30.70265166
Exostosin family protein	-36.4673913
ADR1-like 1	-35.68438003
N/A	-51.09489051
Lojap-related protein	-31.5362841
P-glycoprotein 18	-70.41420118
NB-ARC domain-containing disease resistance protein	-25.35211268
EAP30/Vps36 family protein	-26.49350649
N/A	-31.11111111
Major facilitator superfamily protein	-25.75276445
eukaryotic translation initiation factor 3G1	-42.54716981
Xanthine/uracil permease family protein	-64.86318408
DIE2/ALG10 family	-31.99974395
nuclear shuttle interacting	-32.73167358
Major facilitator superfamily protein	-30.85585586
Pectin lyase-like superfamily protein	-26.5445801

NHL domain-containing protein	-27.84008046
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family p	-29.57844251
alpha-L-arabinofuranosidase 1	-54.54545455
N/A	-30.76443155
alpha carbonic anhydrase 7	-31.89840723
Duplicated homeodomain-like superfamily protein	-35.32163743
Translation initiation factor 2, small GTP-binding protein	-53.22580645
Protein kinase superfamily protein	-31.05413105
Polynucleotidyl transferase, ribonuclease H-like superfamily protein	-30.06993007
PIN domain-like family protein	-60
N/A	-60
N/A	-46.68067227
N/AMETHYLATED_REGION	-36.36875123
N/A	-45.92397275
DNAJ heat shock N-terminal domain-containing protein	-30.96660031
N/A	-37.23076923
N/A	-33.03240741
pentatricopeptide (PPR) repeat-containing protein	-37.77777778
thioredoxin X	-42.29607251
N/A	-42.29607251
Metallo-hydrolase/oxidoreductase superfamily protein	-51.25
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	-26.35332435
serine carboxypeptidase-like 27	-40.60606061
N/A	-33.15942029
N/A	-25.0113413
P-loop containing nucleoside triphosphate hydrolases superfamily pro	-33.60215892
Chalcone-flavanone isomerase family protein	-66.00498487
Carbohydrate-binding-like fold	-36.07769424
uricase / urate oxidase / nodulin 35, putative	-42.5990676
N/A	-72.91157441
GroES-like zinc-binding dehydrogenase family protein	-80.95238095

q value	P value
0.000214557	5.23789E-07
0.00867934	8.55033E-05
0.004126839	2.93584E-05
1.90E-06	1.40716E-09
2.43E-11	3.05611E-15
0.000521764	1.70647E-06
4.27E-48	2.17042E-54
0.005036561	3.88024E-05
0.007356445	6.72406E-05
3.78E-12	3.33967E-16
0.00183603	9.35492E-06
5.31329E-05	8.81033E-08
6.59E-08	2.4484E-11
6.62E-12	6.51884E-16
0.000376343	1.10204E-06
6.0915E-05	1.04223E-07
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0.002992509	1.86277E-05
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7.49481E-05	1.35694E-07
8.26E-07	5.12771E-10
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3.46E-09	8.2963E-13
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6.31017E-05	1.09279E-07
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9.94E-07	6.4095E-10
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0.001104377	4.66705E-06
6.47E-07	3.78981E-10
0.001448062	6.79174E-06
1.37E-07	5.91722E-11
0.008774511	8.68731E-05
1.12E-06	7.35589E-10
2.29779E-05	3.08073E-08
1.46572E-06	1.03319E-09
0.000209491	5.07566E-07
2.29E-07	1.10348E-10
9.15E-08	3.64649E-11
0.009386163	9.58036E-05
0.009386163	9.58036E-05
0.002058826	1.10079E-05
1.16155E-05	1.31833E-08
0.000306799	8.36889E-07
1.34359E-05	1.57827E-08
2.26E-08	7.11949E-12
1.70661E-05	2.11217E-08
6.56E-09	1.71198E-12
0.003315973	2.15522E-05
2.40E-10	4.08646E-14
5.64E-06	5.44338E-09
0.000112111	2.24898E-07
0.003017536	1.888E-05
2.01837E-05	2.60873E-08
3.48577E-05	5.17095E-08
0.000448077	1.39175E-06
1.13E-11	1.24256E-15
6.51E-08	2.41075E-11
0.001984978	1.04649E-05
0.004528533	3.33725E-05
0.000414166	1.25234E-06
0.003980985	2.78746E-05
0.00013003	2.73192E-07
0.003301486	2.14128E-05
1.70E-06	1.23044E-09
3.03E-08	9.96807E-12
0.000386208	1.14054E-06
6.60E-07	3.8869E-10
4.25E-13	2.89179E-17

0.000534963	1.76322E-06
2.22E-07	1.06075E-10
0.004932584	3.76482E-05
1.96E-08	6.07591E-12
2.26E-06	1.7561E-09
0.001012789	4.14977E-06
7.40109E-07	4.51417E-10
5.34E-06	5.07192E-09
1.67E-06	1.2086E-09
0.000877666	3.41605E-06
0.000877666	3.41605E-06
1.43E-14	6.62673E-19
4.02E-16	1.22356E-20
2.58549E-05	3.57413E-08
4.35097E-05	6.81901E-08
0.000261045	6.79967E-07
7.86E-09	2.12228E-12
0.002427585	1.38818E-05
2.26154E-05	3.01146E-08
2.26154E-05	3.01146E-08
0.008757372	8.6617E-05
0.000255436	6.59259E-07
0.00046218	1.45194E-06
0.000359561	1.03683E-06
4.94954E-05	8.0688E-08
2.33E-11	2.9228E-15
1.13E-13	6.43181E-18
1.79E-07	8.21974E-11
3.99E-07	2.1117E-10
7.19E-22	6.94041E-27
0.003422193	2.25694E-05

Supplemental Table 8: List of 703 unique hyper-methylated genes

METHYLATED REGIONS
mytileDiff25p200.hyper_CpG.Chr01.422401-422600
mytileDiff25p200.hyper_CpG.Chr01.2841001-2841200
mytileDiff25p200.hyper_CpG.Chr01.3016201-3016400
mytileDiff25p200.hyper_merged_CHG.Chr01.3247801-3248000
mytileDiff25p200.hyper_merged_CHH.Chr01.3576801-3577000
mytileDiff25p200.hyper_merged_CHG.Chr01.3809801-3810000
mytileDiff25p200.hyper_CpG.Chr01.4030601-4030800
mytileDiff25p200.hyper_CpG.Chr01.5279201-5279400
mytileDiff25p200.hyper_merged_CHH.Chr01.11564801-11565000
mytileDiff25p200.hyper_CpG.Chr01.14063401-14063600
mytileDiff25p200.hyper_merged_CHG.Chr01.14059801-14060000
mytileDiff25p200.hyper_CpG.Chr01.16538001-16538200
mytileDiff25p200.hyper_CpG.Chr01.27007401-27007600
mytileDiff25p200.hyper_merged_CHG.Chr01.27947801-27948000
mytileDiff25p200.hyper_merged_CHG.Chr01.28296001-28296200
mytileDiff25p200.hyper_merged_CHH.Chr01.37634201-37634400
mytileDiff25p200.hyper_CpG.Chr01.38062001-38062200
mytileDiff25p200.hyper_merged_CHG.Chr01.39914801-39915000
mytileDiff25p200.hyper_CpG.Chr01.46839601-46839800
mytileDiff25p200.hyper_CpG.Chr01.46839601-46839800
mytileDiff25p200.hyper_merged_CHH.Chr01.48025201-48025400
mytileDiff25p200.hyper_CpG.Chr01.49566001-49566200
mytileDiff25p200.hyper_CpG.Chr01.50644001-50644200
mytileDiff25p200.hyper_CpG.Chr01.50750201-50750400
mytileDiff25p200.hyper_CpG.Chr01.51017001-51017200
mytileDiff25p200.hyper_merged_CHH.Chr01.51017001-51017200
mytileDiff25p200.hyper_merged_CHG.Chr01.51419601-51419800
mytileDiff25p200.hyper_CpG.Chr01.51872001-51872200
mytileDiff25p200.hyper_CpG.Chr01.52398001-52398200
mytileDiff25p200.hyper_merged_CHG.Chr01.54098201-54098400
mytileDiff25p200.hyper_CpG.Chr01.54133801-54134000
mytileDiff25p200.hyper_merged_CHG.Chr01.56514201-56514400
mytileDiff25p200.hyper_CpG.Chr01.56740801-56741000
mytileDiff25p200.hyper_CpG.Chr02.816801-817000
mytileDiff25p200.hyper_CpG.Chr02.826801-827000
mytileDiff25p200.hyper_CpG.Chr02.1085201-1085400
mytileDiff25p200.hyper_CpG.Chr02.1285001-1285200
mytileDiff25p200.hyper_merged_CHG.Chr02.3944201-3944400
mytileDiff25p200.hyper_CpG.Chr02.3988001-3988200
mytileDiff25p200.hyper_merged_CHG.Chr02.4705401-4705600
mytileDiff25p200.hyper_CpG.Chr02.4982601-4982800
mytileDiff25p200.hyper_CpG.Chr02.6778801-6779000
mytileDiff25p200.hyper_CpG.Chr02.6899401-6899600
mytileDiff25p200.hyper_merged_CHH.Chr02.7246401-7246600

mytileDiff25p200.hyper_merged_CHH.Chr02.7246401-7246600
mytileDiff25p200.hyper_merged_CHG.Chr02.8446601-8446800
mytileDiff25p200.hyper_CpG.Chr02.8524601-8524800
mytileDiff25p200.hyper_CpG.Chr02.8735001-8735200
mytileDiff25p200.hyper_merged_CHG.Chr02.8836201-8836400
mytileDiff25p200.hyper_CpG.Chr02.9714001-9714200
mytileDiff25p200.hyper_CpG.Chr02.10252601-10252800
mytileDiff25p200.hyper_CpG.Chr02.11023001-11023200
mytileDiff25p200.hyper_merged_CHH.Chr02.11742001-11742200
mytileDiff25p200.hyper_merged_CHG.Chr02.11813801-11814000
mytileDiff25p200.hyper_merged_CHH.Chr02.12151801-12152000
mytileDiff25p200.hyper_CpG.Chr02.12959201-12959400
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mytileDiff25p200.hyper_merged_CHG.Chr02.14173401-14173600
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mytileDiff25p200.hyper_merged_CHH.Chr02.14631601-14631800
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mytileDiff25p200.hyper_merged_CHG.Chr02.24762401-24762600
mytileDiff25p200.hyper_merged_CHG.Chr02.26134801-26135000
mytileDiff25p200.hyper_merged_CHG.Chr02.26356201-26356400
mytileDiff25p200.hyper_CpG.Chr02.31200201-31200400
mytileDiff25p200.hyper_CpG.Chr02.31238201-31238400
mytileDiff25p200.hyper_merged_CHH.Chr02.33475001-33475200
mytileDiff25p200.hyper_merged_CHG.Chr02.35290201-35290400
mytileDiff25p200.hyper_merged_CHG.Chr02.35678401-35678600
mytileDiff25p200.hyper_merged_CHH.Chr02.35782801-35783000
mytileDiff25p200.hyper_merged_CHG.Chr02.38833001-38833200
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mytileDiff25p200.hyper_CpG.Chr02.40121801-40122000
mytileDiff25p200.hyper_merged_CHG.Chr02.40121801-40122000
mytileDiff25p200.hyper_CpG.Chr02.41137001-41137200
mytileDiff25p200.hyper_CpG.Chr02.42040001-42040200
mytileDiff25p200.hyper_CpG.Chr02.43332201-43332400
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mytileDiff25p200.hyper_merged_CHH.Chr02.44605001-44605200
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mytileDiff25p200.hyper_CpG.Chr03.439401-439600

mytileDiff25p200.hyper_merged_CHG.Chr03.791401-791600
mytileDiff25p200.hyper_CpG.Chr03.1328201-1328400
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mytileDiff25p200.hyper_merged_CHG.Chr04.52278001-52278200
mytileDiff25p200.hyper_CpG.Chr04.52320401-52320600
mytileDiff25p200.hyper_CpG.Chr05.528401-528600
mytileDiff25p200.hyper_merged_CHH.Chr05.827601-827800
mytileDiff25p200.hyper_CpG.Chr05.2534401-2534600
mytileDiff25p200.hyper_merged_CHH.Chr05.3956401-3956600
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mytileDiff25p200.hyper_CpG.Chr19.26564401-26564600
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mytileDiff25p200.hyper_CpG.Chr19.38418201-38418400
mytileDiff25p200.hyper_merged_CHH.Chr19.41253201-41253400
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mytileDiff25p200.hyper_merged_CHG.Chr20.47540201-47540400
mytileDiff25p200.hyper_merged_CHG.scaffold_197.12001-12200
mytileDiff25p200.hyper_merged_CHH.scaffold_21.424201-424400
mytileDiff25p200.hyper_merged_CHH.scaffold_27.230401-230600
mytileDiff25p200.hyper_merged_CHG.scaffold_28.78801-79000
mytileDiff25p200.hyper_merged_CHG.scaffold_361.7201-7400

in all sequence contexts.

REGION	GENE ID
GENE BODY	Glyma.01G004100
PROMOTER	Glyma.01G027100
GENE BODY	Glyma.01G028700
PROMOTER	Glyma.01G031200
GENE BODY (122bp); 3'UTR (78bp)	Glyma.01G034300
GENE BODY	Glyma.01G036200
GENE BODY	Glyma.01G038000
GENE BODY	Glyma.01G045800
PROMOTER	Glyma.01G068900
GENE BODY	Glyma.01G073400
GENE BODY	Glyma.01G073400
GENE BODY	Glyma.01G074700
GENE BODY	Glyma.01G089100
GENE BODY	Glyma.01G092400
GENE BODY	Glyma.01G093200
GENE BODY	Glyma.01G111000
3'UTR	Glyma.01G112200
GENE BODY	Glyma.01G115300
GENE BODY	Glyma.01G140200
PROMOTER	Glyma.01G140300
PROMOTER	Glyma.01G145400
GENE BODY	Glyma.01G157600
GENE BODY	Glyma.01G168900
3'UTR	Glyma.01G170000
GENE BODY	Glyma.01G172800
GENE BODY	Glyma.01G172800
GENE BODY	Glyma.01G177700
GENE BODY	Glyma.01G183500
GENE BODY	Glyma.01G188700
GENE BODY	Glyma.01G209300
GENE BODY	Glyma.01G209800
GENE BODY	Glyma.01G241300
GENE BODY	Glyma.01G245100
GENE BODY	Glyma.02G007900
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GENE BODY	Glyma.02G011800
GENE BODY	Glyma.02G014200
GENE BODY	Glyma.02G041800
GENE BODY	Glyma.02G042400
GENE BODY	Glyma.02G051700
GENE BODY	Glyma.02G055100
GENE BODY	Glyma.02G078600
PROMOTER	Glyma.02G080100
GENE BODY	Glyma.02G083300

PROMOTER	Glyma.02G083400
GENE BODY	Glyma.02G094200
PROMOTER	Glyma.02G095000
GENE BODY	Glyma.02G097200
GENE BODY	Glyma.02G097900
GENE BODY	Glyma.02G102600
GENE BODY	Glyma.02G107500
GENE BODY	Glyma.02G113300
PROMOTER (139bp); 5'UTR (61bp)	Glyma.02G119200
PROMOTER	Glyma.02G119900
PROMOTER	Glyma.02G122400
PROMOTER	Glyma.02G127500
GENE BODY	Glyma.02G129000
PROMOTER	Glyma.02G129000
GENE BODY	Glyma.02G129400
GENE BODY	Glyma.02G130400
PROMOTER	Glyma.02G131900
GENE BODY	Glyma.02G136800
GENE BODY	Glyma.02G137000
PROMOTER (143bp); 5'UTR (43bp); GENI	Glyma.02G138700
PROMOTER	Glyma.02G141500
GENE BODY	Glyma.02G162300
GENE BODY	Glyma.02G165800
GENE BODY	Glyma.02G169200
GENE BODY	Glyma.02G170100
GENE BODY	Glyma.02G182200
GENE BODY	Glyma.02G182400
PROMOTER (70bp); 5'UTR (130bp)	Glyma.02G186100
GENE BODY	Glyma.02G188900
PROMOTER	Glyma.02G190100
GENE BODY	Glyma.02G190200
PROMOTER	Glyma.02G203000
GENE BODY	Glyma.02G211800
PROMOTER	Glyma.02G215200
PROMOTER	Glyma.02G215200
GENE BODY	Glyma.02G223600
GENE BODY	Glyma.02G232900
GENE BODY	Glyma.02G245200
PROMOTER(3bp) ; GENE BODY (197bp)	Glyma.02G252400
GENE BODY	Glyma.02G258100
PROMOTER	Glyma.02G259000
PROMOTER	Glyma.02G291300
GENE BODY	Glyma.02G301500
GENE BODY	Glyma.03G002700
GENE BODY	Glyma.03G004900

GENE BODY	Glyma.03G008100
GENE BODY	Glyma.03G013000
GENE BODY	Glyma.03G013500
GENE BODY	Glyma.03G014400
GENE BODY	Glyma.03G014400
GENE BODY	Glyma.03G021900
PROMOTER	Glyma.03G023000
GENE BODY	Glyma.03G052800
GENE BODY	Glyma.03G054100
GENE BODY	Glyma.03G059100
GENE BODY	Glyma.03G061000
3'UTR	Glyma.03G064400
PROMOTER	Glyma.03G101500
GENE BODY	Glyma.03G102100
GENE BODY	Glyma.03G103900
PROMOTER	Glyma.03G123200
GENE BODY	Glyma.03G132000
GENE BODY	Glyma.03G133000
5'UTR	Glyma.03G133900
GENE BODY	Glyma.03G140100
PROMOTER (102bp); 5'UTR (98bp)	Glyma.03G141100
GENE BODY	Glyma.03G151200
PROMOTER	Glyma.03G157900
GENE BODY	Glyma.03G168700
GENE BODY	Glyma.03G193300
PROMOTER	Glyma.03G211400
GENE BODY	Glyma.03G219500
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GENE BODY	Glyma.03G240400
GENE BODY	Glyma.03G243400
GENE BODY	Glyma.03G243700
GENE BODY	Glyma.03G250400
GENE BODY	Glyma.03G256300
GENE BODY	Glyma.04G005800
GENE BODY	Glyma.04G014400
PROMOTER	Glyma.04G019200
GENE BODY	Glyma.04G031600
GENE BODY	Glyma.04G041900
GENE BODY	Glyma.04G044200
GENE BODY	Glyma.04G057200
PROMOTER	Glyma.04G062100
GENE BODY	Glyma.04G075900
GENE BODY	Glyma.04G089400
5'UTR (104bp); GENE BODY (96bp)	Glyma.04G092900
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GENE BODY	Glyma.04G094100

GENE BODY	Glyma.04G094400
PROMOTER	Glyma.04G129400
PROMOTER (187bp); 5'UTR (13bp)	Glyma.04G132900
GENE BODY	Glyma.04G135000
GENE BODY	Glyma.04G135300
GENE BODY	Glyma.04G138200
PROMOTER	Glyma.04G144400
GENE BODY	Glyma.04G155100
3'UTR	Glyma.04G162800
3'UTR	Glyma.04G162800
5'UTR	Glyma.04G182700
GENE BODY	Glyma.04G192600
GENE BODY	Glyma.04G201400
GENE BODY	Glyma.04G207200
GENE BODY	Glyma.04G211000
GENE BODY	Glyma.04G221900
GENE BODY	Glyma.04G221900
PROMOTER	Glyma.04G232100
PROMOTER	Glyma.04G232300
GENE BODY	Glyma.04G236900
GENE BODY	Glyma.04G237100
GENE BODY	Glyma.04G253400
GENE BODY	Glyma.04G256700
GENE BODY	Glyma.04G257000
GENE BODY	Glyma.05G006000
PROMOTER	Glyma.05G009300
PROMOTER	Glyma.05G029500
PROMOTER	Glyma.05G044200
PROMOTER	Glyma.05G046400
PROMOTER	Glyma.05G058200
GENE BODY	Glyma.05G060200
GENE BODY	Glyma.05G062300
3'UTR (138bp)	Glyma.05G067200
GENE BODY	Glyma.05G073400
GENE BODY	Glyma.05G084600
GENE BODY	Glyma.05G084600
GENE BODY	Glyma.05G084600
3'UTR	Glyma.05G096300
GENE BODY	Glyma.05G105000
GENE BODY	Glyma.05G111000
GENE BODY	Glyma.05G117000
GENE BODY	Glyma.05G131500
GENE BODY	Glyma.05G197500
GENE BODY	Glyma.05G209500
GENE BODY	Glyma.05G215400
GENE BODY	Glyma.05G219000

GENE BODY	Glyma.05G223100
PROMOTER	Glyma.05G223100
GENE BODY	Glyma.06G001600
GENE BODY	Glyma.06G011200
PROMOTER	Glyma.06G020300
GENE BODY	Glyma.06G046000
PROMOTER	Glyma.06G046100
PROMOTER	Glyma.06G061600
GENE BODY	Glyma.06G061700
GENE BODY	Glyma.06G072200
GENE BODY	Glyma.06G094900
GENE BODY	Glyma.06G096100
PROMOTER	Glyma.06G097000
GENE BODY	Glyma.06G097900
GENE BODY	Glyma.06G098900
GENE BODY	Glyma.06G140200
GENE BODY (147bp); 3'UTR (53bp)	Glyma.06G141300
5'UTR	Glyma.06G172000
GENE BODY	Glyma.06G174400
GENE BODY	Glyma.06G192000
PROMOTER (97bp); 5'UTR (103bp)	Glyma.06G195600
GENE BODY	Glyma.06G214100
GENE BODY	Glyma.06G216700
GENE BODY	Glyma.06G217200
GENE BODY	Glyma.06G217700
GENE BODY (72bp); 3'UTR (128bp)	Glyma.06G222100
GENE BODY	Glyma.06G223900
GENE BODY	Glyma.06G225200
PROMOTER	Glyma.06G233300
GENE BODY	Glyma.06G239100
GENE BODY	Glyma.06G258100
GENE BODY	Glyma.06G258100
GENE BODY	Glyma.06G262600
PROMOTER	Glyma.06G264700
GENE BODY	Glyma.06G286700
GENE BODY	Glyma.06G292200
GENE BODY	Glyma.06G304900
GENE BODY	Glyma.06G305000
PROMOTER	Glyma.06G320000
GENE BODY	Glyma.06G321400
GENE BODY	Glyma.06G322700
GENE BODY	Glyma.06G324800
GENE BODY	Glyma.07G004000
GENE BODY	Glyma.07G013800
GENE BODY	Glyma.07G014200
GENE BODY (47bp); 3'UTR (153bp)	Glyma.07G014300

GENE BODY	Glyma.07G026300
GENE BODY	Glyma.07G030000
GENE BODY	Glyma.07G047100
GENE BODY (107bp); 3'UTR (93bp)	Glyma.07G051000
PROMOTER	Glyma.07G057000
GENE BODY	Glyma.07G059800
GENE BODY	Glyma.07G059900
PROMOTER	Glyma.07G098200
GENE BODY	Glyma.07G098900
PROMOTER	Glyma.07G099000
GENE BODY	Glyma.07G104700
GENE BODY	Glyma.07G114400
GENE BODY	Glyma.07G122000
GENE BODY	Glyma.07G137300
GENE BODY	Glyma.07G150700
PROMOTER	Glyma.07G151800
GENE BODY	Glyma.07G157400
GENE BODY	Glyma.07G157400
GENE BODY	Glyma.07G171600
GENE BODY	Glyma.07G172400
PROMOTER	Glyma.07G181500
5'UTR (101bp); GENE BODY (99bp)	Glyma.07G188600
PROMOTER	Glyma.07G200200
GENE BODY	Glyma.07G201000
GENE BODY	Glyma.07G245900
GENE BODY	Glyma.07G256500
GENE BODY	Glyma.07G259500
3'UTR	Glyma.08G022100
GENE BODY	Glyma.08G033500
PROMOTER	Glyma.08G054200
PROMOTER (98bp); GENE BODY (102bp)	Glyma.08G054200
GENE BODY	Glyma.08G060800
GENE BODY	Glyma.08G071400
GENE BODY	Glyma.08G071400
GENE BODY	Glyma.08G077800
PROMOTER	Glyma.08G081600
GENE BODY	Glyma.08G082600
GENE BODY	Glyma.08G084400
GENE BODY	Glyma.08G096300
GENE BODY	Glyma.08G109400
GENE BODY	Glyma.08G114600
GENE BODY	Glyma.08G126200
GENE BODY	Glyma.08G134600
GENE BODY	Glyma.08G138800
GENE BODY	Glyma.08G162300
GENE BODY	Glyma.08G176800

GENE BODY	Glyma.08G193600
GENE BODY	Glyma.08G193700
GENE BODY	Glyma.08G195900
PROMOTER	Glyma.08G209300
GENE BODY	Glyma.08G248800
GENE BODY	Glyma.08G252600
GENE BODY	Glyma.08G253800
GENE BODY	Glyma.08G263100
PROMOTER	Glyma.08G272500
PROMOTER	Glyma.08G277400
GENE BODY	Glyma.08G279300
GENE BODY	Glyma.08G285000
GENE BODY	Glyma.08G314100
GENE BODY	Glyma.08G322700
GENE BODY	Glyma.08G337400
PROMOTER	Glyma.08G345200
GENE BODY (155bp); 3'UTR (45bp)	Glyma.08G356300
GENE BODY	Glyma.09G013400
GENE BODY	Glyma.09G021200
GENE BODY	Glyma.09G023300
GENE BODY	Glyma.09G024700
GENE BODY	Glyma.09G024800
GENE BODY	Glyma.09G028600
GENE BODY	Glyma.09G063400
GENE BODY (158bp); 3'UTR (42bp)	Glyma.09G081800
GENE BODY	Glyma.09G084300
GENE BODY	Glyma.09G086600
GENE BODY	Glyma.09G104600
GENE BODY	Glyma.09G106000
3'UTR (109bp); GENE BODY (3bp)	Glyma.09G107500
GENE BODY	Glyma.09G108300
GENE BODY	Glyma.09G115200
GENE BODY	Glyma.09G115200
GENE BODY	Glyma.09G131700
GENE BODY	Glyma.09G131700
GENE BODY	Glyma.09G154100
GENE BODY	Glyma.09G155200
GENE BODY	Glyma.09G157300
GENE BODY	Glyma.09G177600
GENE BODY	Glyma.09G182600
GENE BODY	Glyma.09G188100
GENE BODY	Glyma.09G188300
GENE BODY	Glyma.09G194400
PROMOTER (67 bp)	Glyma.09G197500
PROMOTER (19bp); 5'UTR (181bp)	Glyma.09G197600
GENE BODY	Glyma.09G209900

PROMOTER	Glyma.09G217700
PROMOTER	Glyma.09G240900
GENE BODY	Glyma.09G247600
GENE BODY	Glyma.09G248800
GENE BODY	Glyma.09G253700
GENE BODY	Glyma.09G267400
GENE BODY	Glyma.09G282500
GENE BODY	Glyma.09G286500
GENE BODY	Glyma.10G028000
GENE BODY	Glyma.10G029000
PROMOTER	Glyma.10G044400
PROMOTER	Glyma.10G044600
GENE BODY	Glyma.10G053600
GENE BODY	Glyma.10G058500
GENE BODY	Glyma.10G067400
GENE BODY	Glyma.10G104300
GENE BODY	Glyma.10G104900
GENE BODY	Glyma.10G106500
PROMOTER	Glyma.10G112600
PROMOTER	Glyma.10G112700
GENE BODY	Glyma.10G116500
GENE BODY	Glyma.10G117200
GENE BODY	Glyma.10G118100
GENE BODY	Glyma.10G124700
GENE BODY	Glyma.10G132600
GENE BODY	Glyma.10G142800
GENE BODY	Glyma.10G150000
GENE BODY	Glyma.10G155100
GENE BODY	Glyma.10G155800
GENE BODY	Glyma.10G160500
PROMOTER	Glyma.10G166200
GENE BODY	Glyma.10G172400
PROMOTER (140bp); 5'UTR (60bp)	Glyma.10G174000
PROMOTER	Glyma.10G180400
GENE BODY	Glyma.10G181400
GENE BODY	Glyma.10G182000
GENE BODY	Glyma.10G185600
GENE BODY	Glyma.10G188600
GENE BODY	Glyma.10G205500
GENE BODY	Glyma.10G214100
GENE BODY	Glyma.10G222900
GENE BODY	Glyma.10G250500
GENE BODY	Glyma.10G250800
5'UTR	Glyma.10G266600
GENE BODY (174bp); 3'UTR (26bp)	Glyma.10G266600
5'UTR (19bp); GENEBODY (181bp)	Glyma.10G266800

GENE BODY (68bp); 3'UTR (26 bp)	Glyma.10G266800
GENE BODY	Glyma.10G270800
GENE BODY	Glyma.10G274500
GENE BODY	Glyma.11G007200
PROMOTER	Glyma.11G007500
GENE BODY	Glyma.11G013900
GENE BODY	Glyma.11G024700
GENE BODY	Glyma.11G027000
GENE BODY (44bp); 3'UTR (156bp)	Glyma.11G038500
PROMOTER	Glyma.11G045500
GENE BODY	Glyma.11G046100
GENE BODY	Glyma.11G047800
GENE BODY	Glyma.11G059600
GENE BODY	Glyma.11G067000
GENE BODY	Glyma.11G075600
GENE BODY	Glyma.11G077000
GENE BODY	Glyma.11G081200
GENE BODY	Glyma.11G092100
PROMOTER	Glyma.11G096600
PROMOTER (170bp); GENE BODY (30bp)	Glyma.11G115900
GENE BODY	Glyma.11G124000
GENE BODY	Glyma.11G125100
PROMOTER	Glyma.11G125100
GENE BODY	Glyma.11G131600
GENE BODY	Glyma.11G135300
PROMOTER	Glyma.11G148800
GENE BODY	Glyma.11G158400
PROMOTER (134bp); GENE BODY (66bp)	Glyma.11G160300
PROMOTER	Glyma.11G162300
GENE BODY	Glyma.11G166200
GENE BODY	Glyma.11G170700
PROMOTER	Glyma.11G190400
GENE BODY	Glyma.11G211200
GENE BODY	Glyma.11G218000
GENE BODY	Glyma.11G230500
3'UTR	Glyma.11G234200
GENE BODY	Glyma.12G001100
GENE BODY	Glyma.12G001400
5'UTR (95bp); GENE BODY (105bp)	Glyma.12G022400
GENE BODY	Glyma.12G027400
PROMOTER	Glyma.12G028200
GENE BODY	Glyma.12G044800
GENE BODY	Glyma.12G052000
GENE BODY	Glyma.12G052400
GENE BODY	Glyma.12G052700
GENE BODY	Glyma.12G052800

GENE BODY	Glyma.12G072900
GENE BODY	Glyma.12G095300
GENE BODY	Glyma.12G101500
GENE BODY	Glyma.12G107000
GENE BODY	Glyma.12G139700
GENE BODY	Glyma.12G139800
GENE BODY	Glyma.12G139900
GENE BODY	Glyma.12G149800
GENE BODY	Glyma.12G151500
PROMOTER	Glyma.12G152500
PROMOTER	Glyma.12G154900
PROMOTER	Glyma.12G155000
GENE BODY	Glyma.12G157700
GENE BODY	Glyma.12G174700
GENE BODY	Glyma.12G180800
GENE BODY	Glyma.12G188100
GENE BODY	Glyma.12G189100
GENE BODY	Glyma.12G223200
GENE BODY	Glyma.12G233100
PROMOTER	Glyma.13G010300
GENE BODY	Glyma.13G024700
GENE BODY	Glyma.13G030600
GENE BODY	Glyma.13G040300
GENE BODY	Glyma.13G045400
GENE BODY	Glyma.13G048900
GENE BODY	Glyma.13G051300
GENE BODY (76bp); 3'UTR (124bp)	Glyma.13G054500
GENE BODY	Glyma.13G065500
GENE BODY	Glyma.13G073900
GENE BODY	Glyma.13G080100
GENE BODY	Glyma.13G093300
GENE BODY	Glyma.13G107100
PROMOTER	Glyma.13G110100
GENE BODY	Glyma.13G120800
GENE BODY	Glyma.13G124000
GENE BODY (145bp); 3'UTR (55bp)	Glyma.13G127100
PROMOTER (145bp); 5'UTR (55bp)	Glyma.13G139100
PROMOTER (145bp); 5'UTR (55bp)	Glyma.13G139100
GENE BODY (166bp); 3'UTR (34bp)	Glyma.13G145400
GENE BODY	Glyma.13G149200
GENE BODY (29bp); 3'UTR (84bp)	Glyma.13G150800
GENE BODY	Glyma.13G154200
GENE BODY	Glyma.13G163500
GENE BODY	Glyma.13G167000
GENE BODY	Glyma.13G181600
GENE BODY	Glyma.13G207200

GENE BODY	Glyma.13G221200
PROMOTER	Glyma.13G222200
PROMOTER	Glyma.13G222200
GENE BODY	Glyma.13G238000
5'UTR (14bp); GENE BODY (186bp)	Glyma.13G250900
PROMOTER	Glyma.13G289100
GENE BODY	Glyma.13G297200
PROMOTER	Glyma.13G316600
GENE BODY	Glyma.13G319900
PROMOTER (167bp); 5'UTR (33bp)	Glyma.13G320700
PROMOTER (167bp); GENE BODY (33bp)	Glyma.13G320700
GENE BODY	Glyma.13G336200
GENE BODY	Glyma.13G341000
GENE BODY	Glyma.13G342900
GENE BODY (155bp); 3'UTR (45bp)	Glyma.13G344400
GENE BODY	Glyma.13G346900
GENE BODY	Glyma.13G351800
GENE BODY	Glyma.13G362000
GENE BODY	Glyma.13G366100
GENE BODY	Glyma.13G372100
GENE BODY	Glyma.14G007700
GENE BODY	Glyma.14G012200
GENE BODY	Glyma.14G064500
GENE BODY	Glyma.14G068900
GENE BODY	Glyma.14G097800
PROMOTER	Glyma.14G109000
GENE BODY	Glyma.14G112200
PROMOTER	Glyma.14G122600
GENE BODY	Glyma.14G123700
GENE BODY (44bp); 3'UTR (156bp)	Glyma.14G127700
GENE BODY	Glyma.14G129900
PROMOTER	Glyma.14G131400
5'UTR (89bp); GENE BODY (111bp)	Glyma.14G135900
PROMOTER	Glyma.14G140600
GENE BODY	Glyma.14G142300
3'UTR	Glyma.14G143000
GENE BODY	Glyma.14G146200
GENE BODY	Glyma.14G149700
GENE BODY	Glyma.14G149700
3'UTR	Glyma.14G149800
PROMOTER	Glyma.14G174100
GENE BODY	Glyma.14G182400
GENE BODY	Glyma.14G182500
GENE BODY	Glyma.14G198500
PROMOTER (63bp); 5'UTR (137bp)	Glyma.14G199800
GENE BODY (153bp); 3'UTR (47bp)	Glyma.14G210200

GENE BODY	Glyma.15G000900
3'UTR	Glyma.15G009500
GENE BODY	Glyma.15G013500
PROMOTER	Glyma.15G015100
PROMOTER	Glyma.15G020600
PROMOTER	Glyma.15G046400
GENE BODY	Glyma.15G047100
GENE BODY	Glyma.15G068100
PROMOTER	Glyma.15G074800
GENE BODY (177bp); 3'UTR (23bp)	Glyma.15G084700
GENE BODY	Glyma.15G086200
GENE BODY	Glyma.15G091000
GENE BODY	Glyma.15G093600
GENE BODY (189bp); 3'UTR (11bp)	Glyma.15G094500
3'UTR	Glyma.15G094600
GENE BODY	Glyma.15G115500
GENE BODY	Glyma.15G134800
GENE BODY (181bp); 5'UTR (19bp)	Glyma.15G140300
PROMOTER	Glyma.15G142000
PROMOTER	Glyma.15G142800
GENE BODY	Glyma.15G145600
GENE BODY	Glyma.15G171400
GENE BODY	Glyma.15G172600
GENE BODY	Glyma.15G177000
GENE BODY	Glyma.15G177000
GENE BODY	Glyma.15G179700
GENE BODY	Glyma.15G195700
GENE BODY	Glyma.15G213200
PROMOTER	Glyma.15G214600
GENE BODY	Glyma.15G230500
GENE BODY	Glyma.15G235500
GENE BODY	Glyma.15G236100
GENE BODY	Glyma.15G249000
GENE BODY	Glyma.15G255300
PROMOTER	Glyma.15G274500
GENE BODY	Glyma.15G275000
GENE BODY	Glyma.15G275400
GENE BODY	Glyma.15G276800
GENE BODY	Glyma.15G276800
GENE BODY	Glyma.16G004800
PROMOTER	Glyma.16G005000
GENE BODY	Glyma.16G005600
GENE BODY	Glyma.16G018400
GENE BODY	Glyma.16G022600
GENE BODY	Glyma.16G026000

PROMOTER	Glyma.16G036900
GENE BODY	Glyma.16G043300
5'UTR (145bp); GENE BODY (55bp)	Glyma.16G069400
GENE BODY	Glyma.16G070900
GENE BODY	Glyma.16G077500
GENE BODY	Glyma.16G082400
GENE BODY	Glyma.16G082900
GENE BODY	Glyma.16G083000
GENE BODY	Glyma.16G092500
GENE BODY	Glyma.16G101500
GENE BODY	Glyma.16G101500
5'UTR	Glyma.16G101700
GENE BODY	Glyma.16G131900
GENE BODY	Glyma.16G131900
PROMOTER (7bp); 5'UTR (193 bp)	Glyma.16G144000
PROMOTER (7bp); 5'UTR (193bp)	Glyma.16G144000
GENE BODY	Glyma.16G150900
GENE BODY	Glyma.16G174700
PROMOTER	Glyma.16G178100
PROMOTER	Glyma.16G178300
PROMOTER	Glyma.16G181400
GENE BODY	Glyma.16G184200
GENE BODY	Glyma.16G186600
GENE BODY	Glyma.16G192800
GENE BODY	Glyma.16G193200
3'UTR	Glyma.16G195300
GENE BODY	Glyma.16G210200
GENE BODY	Glyma.17G006600
GENE BODY	Glyma.17G011500
GENE BODY	Glyma.17G015000
GENE BODY	Glyma.17G015200
PROMOTER	Glyma.17G020500
GENE BODY (140bp); 3'UTR (60bp)	Glyma.17G022900
PROMOTER	Glyma.17G030800
GENE BODY	Glyma.17G031900
GENE BODY (190bp); 3'UTR (10bp)	Glyma.17G033700
GENE BODY	Glyma.17G046900
GENE BODY	Glyma.17G052100
GENE BODY	Glyma.17G068600
GENE BODY	Glyma.17G068600
5'UTR	Glyma.17G083300
GENE BODY	Glyma.17G104100
GENE BODY	Glyma.17G104100
GENE BODY	Glyma.17G107600
PROMOTER	Glyma.17G108200

PROMOTER	Glyma.17G117100
5'UTR (6bp); GENE BODY (194bp)	Glyma.17G120400
GENE BODY	Glyma.17G120900
GENE BODY	Glyma.17G121700
GENE BODY	Glyma.17G122300
GENE BODY (122bp); 3'UTR (78bp)	Glyma.17G135200
GENE BODY	Glyma.17G139100
GENE BODY	Glyma.17G141300
GENE BODY	Glyma.17G142200
GENE BODY (109bp); 3'UTR (91bp)	Glyma.17G142700
GENE BODY	Glyma.17G145000
GENE BODY	Glyma.17G146400
GENE BODY	Glyma.17G157100
GENE BODY	Glyma.17G160600
GENE BODY	Glyma.17G163700
5'UTR (58bp); GENE BODY (142bp)	Glyma.17G166700
PROMOTER	Glyma.17G170600
GENE BODY	Glyma.17G172700
GENE BODY	Glyma.17G188300
PROMOTER (87bp); GENE BODY (113bp)	Glyma.17G198200
GENE BODY	Glyma.17G204200
3'UTR	Glyma.17G204900
GENE BODY	Glyma.17G220800
PROMOTER	Glyma.17G221300
GENE BODY	Glyma.17G245800
5'UTR	Glyma.17G247000
GENE BODY	Glyma.17G247100
GENE BODY	Glyma.17G249900
GENE BODY	Glyma.18G002400
5'UTR	Glyma.18G016800
GENE BODY	Glyma.18G018300
GENE BODY	Glyma.18G021500
GENE BODY	Glyma.18G039000
GENE BODY	Glyma.18G040400
GENE BODY	Glyma.18G044200
PROMOTER	Glyma.18G047900
PROMOTER	Glyma.18G047900
GENE BODY	Glyma.18G063000
GENE BODY	Glyma.18G067400
PROMOTER	Glyma.18G068900
GENE BODY	Glyma.18G085100
GENE BODY	Glyma.18G085200
GENE BODY (52bp); 5'UTR (148bp)	Glyma.18G087100
GENE BODY	Glyma.18G106800
PROMOTER	Glyma.18G112700
PROMOTER (132bp); GENE BODY (68bp)	Glyma.18G115200

GENE BODY	Glyma.18G126000
GENE BODY	Glyma.18G132200
GENE BODY	Glyma.18G136200
GENE BODY	Glyma.18G137800
PROMOTER	Glyma.18G137900
GENE BODY	Glyma.18G154700
GENE BODY	Glyma.18G155200
PROMOTER (5bp); GENE BODY (195bp)	Glyma.18G163600
GENE BODY	Glyma.18G181300
PROMOTER	Glyma.18G181400
GENE BODY	Glyma.18G181500
GENE BODY	Glyma.18G184400
GENE BODY	Glyma.18G184400
GENE BODY	Glyma.18G196200
GENE BODY (173bp); 3'UTR (27bp)	Glyma.18G197600
GENE BODY	Glyma.18G222100
GENE BODY	Glyma.18G223300
GENE BODY	Glyma.18G224000
GENE BODY	Glyma.18G228000
GENE BODY	Glyma.18G232900
GENE BODY	Glyma.18G251900
GENE BODY	Glyma.18G268000
GENE BODY	Glyma.18G298100
GENE BODY	Glyma.19G020200
GENE BODY	Glyma.19G021700
GENE BODY	Glyma.19G026600
GENE BODY	Glyma.19G029100
GENE BODY	Glyma.19G033500
GENE BODY	Glyma.19G039100
GENE BODY	Glyma.19G040800
GENE BODY	Glyma.19G053500
GENE BODY	Glyma.19G064200
5'UTR	Glyma.19G064300
GENE BODY	Glyma.19G065700
GENE BODY	Glyma.19G073600
GENE BODY	Glyma.19G081600
GENE BODY	Glyma.19G081600
PROMOTER	Glyma.19G089900
PROMOTER	Glyma.19G091700
3'UTR	Glyma.19G100500
GENE BODY	Glyma.19G103200
PROMOTER	Glyma.19G110900
GENE BODY	Glyma.19G120400
GENE BODY	Glyma.19G125800
PROMOTER	Glyma.19G152000
PROMOTER	Glyma.19G169700

PROMOTER (51bp); GENE BODY (149bp)	Glyma.19G169800
GENE BODY	Glyma.19G170200
GENE BODY	Glyma.19G175400
PROMOTER (162bp); GENE BODY (38bp)	Glyma.19G184000
PROMOTER (162bp); GENE BODY (38bp)	Glyma.19G184000
GENE BODY	Glyma.19G186900
GENE BODY	Glyma.19G191800
GENE BODY	Glyma.19G191900
3'UTR	Glyma.19G204200
PROMOTER	Glyma.19G214900
5'UTR	Glyma.19G217200
GENE BODY	Glyma.19G229200
GENE BODY	Glyma.19G237000
GENE BODY	Glyma.19G239700
PROMOTER	Glyma.19G242300
GENE BODY	Glyma.19G256500
PROMOTER	Glyma.19G261000
GENE BODY	Glyma.19G261100
GENE BODY	Glyma.20G005400
GENE BODY	Glyma.20G005400
GENE BODY	Glyma.20G028300
GENE BODY	Glyma.20G036600
GENE BODY	Glyma.20G049100
GENE BODY	Glyma.20G052100
GENE BODY	Glyma.20G052200
GENE BODY	Glyma.20G058500
GENE BODY	Glyma.20G058500
GENE BODY	Glyma.20G058500
GENE BODY	Glyma.20G058500
GENE BODY	Glyma.20G074000
PROMOTER (92bp); 5'UTR (108bp)	Glyma.20G074000
GENE BODY	Glyma.20G087700
GENE BODY	Glyma.20G093200
GENE BODY	Glyma.20G102800
GENE BODY	Glyma.20G106900
GENE BODY	Glyma.20G111200
GENE BODY	Glyma.20G119300
GENE BODY	Glyma.20G121600
3'UTR (151bp); GENE BODY (49bp)	Glyma.20G126800
GENE BODY (49bp); 3'UTR (151bp)	Glyma.20G126800
GENE BODY	Glyma.20G130800
PROMOTER	Glyma.20G131200
GENE BODY	Glyma.20G138600
GENE BODY	Glyma.20G161800
GENE BODY	Glyma.20G168100

PROMOTER	Glyma.20G168300
GENE BODY	Glyma.20G170500
PROMOTER	Glyma.20G179900
GENE BODY	Glyma.20G192200
3'UTR	Glyma.20G207700
GENE BODY	Glyma.20G239100
GENE BODY	Glyma.20G242400
GENE BODY	Glyma.20G244900
GENE BODY	Glyma.U008400
PROMOTER	Glyma.U011500
PROMOTER	Glyma.U027500
GENE BODY	Glyma.U028800
GENE BODY	Glyma.U036800

GENE ANNOTATION	% Methylation Difference
Regulator of Vps4 activity in the MVB pathway protein	59.97067449
protein kinase family protein / peptidoglycan-binding LysM domain-con	100
NSP-interacting kinase 3	100
N/A	75.92105263
TRICHOME BIREFRINGENCE-LIKE 27	31.07487923
RNI-like superfamily protein	79.48717949
pyruvate dehydrogenase complex E1 alpha subunit	100
peroxisomal adenine nucleotide carrier 1	53.65853659
N/A	48.25620389
SNF2 domain-containing protein / helicase domain-containing protein	50.71428571
SNF2 domain-containing protein / helicase domain-containing pro	72.72727273
Nucleoporin autopeptidase	100
Family of unknown function (DUF572)	86.66666667
tRNA arginine adenosine deaminase	90
Metal-dependent phosphohydrolase	56.48351648
Cysteine proteinases superfamily protein	33.58517719
Disease resistance protein (TIR-NBS-LRR class) family	25.70010973
Plant protein of unknown function (DUF247)	62.5
arginase	100
SLOW GROWTH 1	100
elongation factor Ts family protein	30.35914703
N/A	46.2962963
DNA binding;zinc ion binding;nucleic acid binding;nucleic acid binding	75.91836735
Cytochrome P450 superfamily protein	30.5785124
NmrA-like negative transcriptional regulator family protein	67.79661017
NmrA-like negative transcriptional regulator family protein	46.80427607
aminopeptidase P1	55.93220339
Protein kinase superfamily protein	69.57328386
RNA-binding (RRM/RBD/RNP motifs) family protein	44.44444444
RGPR-related	65
DNAJ heat shock N-terminal domain-containing protein	90.90909091
target of rapamycin	29.7228895
histone deacetylase 1	100
germin-like protein 10	37.25490196
ATP binding cassette subfamily B4	81.81818182
nuclear encoded CLP protease 5	63.26530612
CTP synthase family protein	100
disease resistance protein (TIR-NBS-LRR class), putative	49.67479675
Calcium-dependent phosphotriesterase superfamily protein	33.33333333
beta-galactosidase 3	34.48275862
Chaperone DnaJ-domain superfamily protein	57.44680851
NAD(P)-binding Rossmann-fold superfamily protein	50
Protein Transporter, Pam16	27.97131148
receptor like protein 6	32.37961226

F-box family protein	32.37961226
mitochondrial editing factor 22	54.98502994
ribosomal protein L23AB	90
dihydrosphingosine phosphate lyase	85.71428571
bZIP transcription factor family protein	68.80503145
Protein kinase superfamily protein	51.2195122
RING/FYVE/PHD zinc finger superfamily protein	27.53623188
Plant protein of unknown function (DUF863)	94.73684211
SPIRAL1-like1	30.81589349
N/A	60
N/A	26.309897
glutamine synthetase 1;4	55.74712644
ARM repeat superfamily protein	76
ARM repeat superfamily protein	67.77939042
N/A	33.33333333
Chalcone and stilbene synthase family protein	68.75
fucosyltransferase 11	37.70177839
Phox-associated domain;Phox-like;Sorting nexin, C-terminal	29.10605847
5\'-3\' exonuclease family protein	29.12280702
Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	30.50847458
DREB2A-interacting protein 2	39.90863787
protein kinase family protein / protein phosphatase 2C (PP2C) fa	80
Protein kinase superfamily protein	28.03462885
protein phosphatase 2A-4	32.10052157
Phosphofructokinase family protein	38.91159939
curculin-like (mannose-binding) lectin family protein / PAN domain-con	48.38709677
guanylate kinase	44.28571429
autoinhibited Ca2+-ATPase 11	42.53373119
AGAMOUS-like 80	26.39573071
amino acid permease 3	40.53905391
N/A	27.99797483
C-terminal domain phosphatase-like 4	36.78215472
auxin F-box protein 5	100
Restriction endonuclease, type II-like superfamily protein	41.91561845
Restriction endonuclease, type II-like superfamily protein	32.09690807
RING/U-box superfamily protein	67.3951049
HEAT/U-box domain-containing protein	97.77777778
Protein of unknown function, DUF593	36.81427627
beta HLH protein 93	45.60606061
E3 ubiquitin ligase, putative	88.88888889
Aldolase-type TIM barrel family protein	38.65327381
calmodulin-domain protein kinase 9	92.85714286
Sucrase/ferredoxin-like family protein	36.92307692
S-locus lectin protein kinase family protein	46.96969697
ENTH/VHS family protein	54.16666667

cytochrome P450, family 86, subfamily A, polypeptide 8	53.46594334
RNAhelicase-like 8	100
RHO guanyl-nucleotide exchange factor 3	42.54807692
NAD(P)-binding Rossmann-fold superfamily protein	34.44444444
NAD(P)-binding Rossmann-fold superfamily protein	26.31641086
growth-regulating factor 9	70.90909091
LOB domain-containing protein 18	47.45762712
Disease resistance protein (TIR-NBS-LRR class) family	35.86956522
Disease resistance protein (TIR-NBS-LRR class)	43.88204225
nodulin MtN21 /EamA-like transporter family protein	29.95728155
glycoprotease 1	46.17034314
GPI transamidase component Gpi16 subunit family protein	86.20689655
N/A	27.65557643
IQ-domain 18	29.63015246
Vacuolar sorting protein 39	100
Basic-leucine zipper (bZIP) transcription factor family protein	25.58922559
P-loop containing nucleoside triphosphate hydrolases superfamily prot	70
RECA homolog 3	38.49486521
N/A	100
NIMA-related kinase 5	55.3030303
N/A	100
debranching enzyme 1	64.70588235
Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	36.84017595
GroES-like zinc-binding dehydrogenase family protein	100
Basic-leucine zipper (bZIP) transcription factor family protein	47.22222222
cullin 1	33.91812865
Prolyl oligopeptidase family protein	100
glucose-6-phosphate dehydrogenase 4	100
ATP binding microtubule motor family protein	34.42622951
ARM repeat superfamily protein	39.05187835
Esterase/lipase/thioesterase family protein	86.66666667
Ankyrin repeat family protein	88.75
Protein of unknown function (DUF3133)	73.33333333
ER lumen protein retaining receptor family protein	30.43478261
switch subunit 3	41.61573213
Transmembrane amino acid transporter family protein	42.01877934
DNA glycosylase superfamily protein	38.33333333
Protein of unknown function (DUF3223)	61.11111111
glycine-rich protein	39.3764063
CTC-interacting domain 7	97.14285714
Pentatricopeptide repeat (PPR) superfamily protein	51.31578947
Peptidyl-tRNA hydrolase II (PTH2) family protein	90.90909091
N/A	26.60215054
sequence-specific DNA binding transcription factors;transcription regul	52.10803689
conserved peptide upstream open reading frame 37	52.10803689
O-fucosyltransferase family protein	95.65217391

P-loop containing nucleoside triphosphate hydrolases superfamily prot	100
N/A	37.69230769
Ribosomal protein S19e family protein	100
nudix hydrolase homolog 16	41.41824752
Thioredoxin z	67.56756757
glutathione S-transferase THETA 1	46.90635452
N/A	25.55555556
FAD/NAD(P)-binding oxidoreductase family protein	31.57208089
gamma subunit of Mt ATP synthase	90
gamma subunit of Mt ATP synthase	42.35483871
Protein kinase superfamily protein	29.87457001
Galactose oxidase/kelch repeat superfamily protein	77.14285714
DCD (Development and Cell Death) domain protein	100
N/A	100
Copine (Calcium-dependent phospholipid-binding protein) family	30.52691867
ribonuclease II family protein	90
ribonuclease II family protein	36.0673847
P-loop containing nucleoside triphosphate hydrolases superfamily prot	26.46587061
Metal-dependent protein hydrolase	30.49773756
NADH-dependent glutamate synthase 1	44.23076923
Protein of unknown function (DUF668)	80.90909091
Protein of unknown function (DUF1644)	25.95866256
O-fucosyltransferase family protein	64.54545455
Smg-4/UPF3 family protein	59.46428571
ADP-ribosylation factor A1B	34.14634146
BED zinc finger ;hAT family dimerisation domain	29.10158099
HSP20-like chaperones superfamily protein	100
MA3 domain-containing protein	37.11340206
homolog of nucleolar protein NOP56	28.191246
YbaK/aminoacyl-tRNA synthetase-associated domain	72.68009768
O-fucosyltransferase family protein	100
myb-like transcription factor family protein	91.66666667
Histone H3 K4-specific methyltransferase SET7/9 family protein	30.24509804
N/A	86.36363636
N/A	41.17406487
N/A	36.91548692
N/A	54.17909575
FMN-linked oxidoreductases superfamily protein	39.17349727
Phototropic-responsive NPH3 family protein	42.64705882
N/A	85.71428571
Calmodulin-binding transcription activator protein with CG-1 and Anky	93.33333333
chromatin remodeling 4	64.2962963
ENTH/VHS/GAT family protein	95.45454545
ARID/BRIGHT DNA-binding domain;ELM2 domain protein	28.44082036
TRICHOME BIREFRINGENCE-LIKE 23Methylated_Region_promoter	100
Tetratricopeptide repeat (TPR)-like superfamily protein	52.94117647

Mitochondrial ATP synthase subunit G protein	86.66666667
Mitochondrial ATP synthase subunit G protein	90
RNApolymerase sigma subunit 2	64.58333333
Arabidopsis protein of unknown function (DUF241)	39.68957871
Pyridoxal-dependent decarboxylase family protein	45.10324484
autoinhibited Ca2+-ATPase 1	66.66666667
N/A	66.66666667
nuclear RNA polymerase D2A	35.88383838
chorismate mutase 2	31.85823755
LisH dimerisation motif;WD40/YVTN repeat-like-containing domain	93.10344828
transducin family protein / WD-40 repeat family protein	34.02808249
MSCS-like 2	31.14540866
N/A	28.92743222
GATA-type zinc finger protein with TIFY domain	28.52408308
phosphoenolpyruvate carboxylase-related kinase 2	25.32994428
alpha/beta-Hydrolases superfamily protein	87.5
N/A	54.16666667
Zn-dependent exopeptidases superfamily protein	56.04288499
Peptidase C78, ubiquitin fold modifier-specific peptidase 1/ 2	100
Protein Transporter, Pam16	58
myb domain protein 29	29.96389892
N/A	100
nudix hydrolase homolog 19	64.28571429
Peptidase C13 family	25.59348529
nucleoporin-related	30.39688925
Protein of unknown function (DUF3414)	29.41176471
diacylglycerol kinase 4	45.96553773
Integrase-type DNA-binding superfamily protein	27.41318891
PHD finger family protein / bromo-adjacent homology (BAH) dom	62.62745098
Nuclear pore complex protein	48.11594203
S-locus lectin protein kinase family protein	54.05405405
S-locus lectin protein kinase family protein	58.40727595
S-locus lectin protein kinase family protein	48.03921569
N/A	59.88323603
O-methyltransferase family protein	28.7049732
Protein kinase superfamily protein	62.16216216
Ras-related small GTP-binding family protein	26.06214331
glutamate receptor 3.4	90
Eukaryotic protein of unknown function (DUF842)	50.45454545
WPP domain interacting protein 1	32.88299935
SNARE-like superfamily protein	46.55172414
O-fucosyltransferase family protein	92.30769231
exocyst subunit exo70 family protein G1	42.37891738
glucose-6-phosphate dehydrogenase 1	100
actin binding protein family	90
phosphofructokinase 3	60.53030303

NAD(P)-binding Rossmann-fold superfamily protein	40.15151515
fatty acid desaturase 5	30
Calcineurin-like metallo-phosphoesterase superfamily protein	78.66666667
CBL-interacting protein kinase 9	50
pentatricopeptide (PPR) repeat-containing protein	27.51241226
glyoxylate reductase 1	46.94656489
ribosomal protein L5 B	100
Copper transport protein family	30
N/A	65.57377049
N/A	65.57377049
NF-X-like 1	66.46766169
Protein kinase superfamily protein	77.01149425
Phosphoribosyltransferase family protein	54.54545455
delta 1-pyrroline-5-carboxylate synthase 2	65.43478261
DNAJ heat shock family protein	100
beta glucosidase 11	27.53567788
SU(VAR)3-9 homolog 9	49.89316239
SU(VAR)3-9 homolog 9	29.35613682
basic helix-loop-helix (bHLH) DNA-binding superfamily protein	46.66666667
SERINE CARBOXYPEPTIDASE-LIKE 49	25.34040518
Chaperone DnaJ-domain superfamily protein	30.70588235
receptor kinase 1	30.74176104
HSP20-like chaperones superfamily protein	41.02564103
N/A	38.34512023
Fumarylacetoacetate (FAA) hydrolase family	44.68267581
CBS domain-containing protein with a domain of unknown function (DU	39.53488372
RNA-binding (RRM/RBD/RNP motifs) family protein	45.90163934
alpha/beta-Hydrolases superfamily protein	52.82258065
tRNA/rRNA methyltransferase (SpoU) family protein	100
HMG (high mobility group) box protein with ARID/BRIGHT DNA-bi	33.56350701
HMG (high mobility group) box protein with ARID/BRIGHT DNA-bi	82.35294118
receptor kinase 3	70.33898305
HXXXD-type acyl-transferase family protein	40.67085954
HXXXD-type acyl-transferase family protein	25.37042903
Sec1/munc18-like (SM) proteins superfamily	73.21428571
double-stranded RNA binding protein-related / DsRBD protein-rel	38.82166791
starch synthase 4	71.23287671
Minichromosome maintenance (MCM2/3/5) family protein	100
Transketolase family protein	76.66666667
Chalcone and stilbene synthase family protein	28.18035427
Protein of unknown function (DUF1644)	92.59259259
RAB GDP dissociation inhibitor 2	66.66666667
leucine-rich repeat transmembrane protein kinase family protein	60.95571096
aspartate aminotransferase	72.22222222
nuclear pore anchor	91.66666667
ubiquinol-cytochrome C chaperone family protein	88.23529412

N/A	100
DEA(D/H)-box RNA helicase family protein	100
ubiquitin-specific protease 6	41.23861566
N/A	29.06131938
ATP-dependent peptidases;nucleotide binding;serine-type endopeptida	27.16384739
auxin transport protein (BIG)	45.45454545
DNA/RNA polymerases superfamily protein	82.57359924
male gametophyte defective 3	38.85714286
Polyketide cyclase/dehydrase and lipid transport superfamily pro	29.52353942
PIF1 helicase	69.75524476
Kinase interacting (KIP1-like) family protein	36.40254341
RNA-binding CRS1 / YhbY (CRM) domain-containing protein	67.85714286
Ankyrin-repeat containing protein	35.43379377
TATA BOX ASSOCIATED FACTOR II 59	100
Transducin/WD40 repeat-like superfamily protein	40
FAD/NAD(P)-binding oxidoreductase family protein	30.82417582
Protein of unknown function (DUF1644)	95.55555556
pentatricopeptide (PPR) repeat-containing protein	90.90909091
tubulin folding cofactor E / Pfifferling (PFI)	90
Intron maturase, type II family protein	91.89189189
hercules receptor kinase 2	83.33333333
GTP binding	54.54545455
toprim domain-containing protein	92.30769231
Translation initiation factor SUI1 family protein	44.92753623
Protein kinase superfamily protein	33.65732369
Outer arm dynein light chain 1 protein	35.11705686
Pentatricopeptide repeat (PPR-like) superfamily protein	61.8556701
SET domain protein 38	33.61210673
Nucleic acid-binding, OB-fold-like protein	74.87179487
N/A	65
N/A	25.89561738
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase fam	34.44055944
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase fam	37.430283
N/A	62.87878788
N/A	43.38413331
N/A	72.95238095
ATP-dependent Clp protease	84.59459459
N/A	29.14027149
protein tyrosine kinase family protein	60.60606061
zinc finger protein-related	56.66666667
Protein of unknown function, DUF538	100
NSP (nuclear shuttle protein)-interacting GTPase	50
sugar transporter 14	49.31677019
N/A	25.27472527
N/A	25.27472527
extra-large GTP-binding protein 3	29.68944099

N/A	65.46610169
thioredoxin 2	26.05433119
sister chromatid cohesion 1 protein 4	100
LUC7 related protein	81.81818182
GRIP-related ARF-binding domain-containing protein 1	68.75
titan9	82.22222222
myosin XI D	100
ribonuclease Ps	50
Galactose oxidase/kelch repeat superfamily protein	72.36842105
NIMA-related kinase 4	90.90909091
N/A	44.7582205
N/A	44.7582205
Pyridoxal-dependent decarboxylase family protein	53.37209302
chloroplast RNA-binding protein 29	77.27272727
KCBP-interacting protein kinase	81.81818182
SERINE CARBOXYPEPTIDASE-LIKE 49	100
ARM repeat superfamily protein	34.81481481
INO80 ortholog	84.61538462
N/A	31
10-formyltetrahydrofolate synthetase	31
Protein of unknown function (DUF155)	26.36394252
Transcriptional coactivator/pterin dehydratase	35.38461538
Protein kinase family protein with ARM repeat domain	32.13414634
peroxisomal 3-ketoacyl-CoA thiolase 3	78.81578947
S-adenosyl-L-methionine-dependent methyltransferases superfamily pı	91.30434783
anaphase-promoting complex/cyclosome 11	92.85714286
TOPLESS-related 3	78.65497076
N/A	100
HSP20-like chaperones superfamily protein	72.72727273
zeta-carotene desaturase	57.14285714
RNA-binding (RRM/RBD/RNP motifs) family protein	35.88199265
ubiquitin-specific protease 9	25.4854713
N/A	49.0990991
CAMV movement protein interacting protein 7	30.76761525
S-adenosyl-L-methionine-dependent methyltransferases superfamily pı	72.15189873
N/A	56
N/A	50.95757576
TRAF-like superfamily protein	42.03931204
phosphoenolpyruvate carboxylase 4	68.11594203
N/A	58.65102639
DHHC-type zinc finger family protein	82.5
Homeotic gene regulator	40.55258467
NPK1-related protein kinase 3	84.61538462
Endosomal targeting BRO1-like domain-containing protein	80
Endosomal targeting BRO1-like domain-containing protein	77.5862069
N/A	80

N/A	77.5862069
trehalose phosphatase/synthase 5	96
N/A	34.11329137
N/A	78
ATP-dependent RNA helicase, mitochondrial (SUV3)	28.52049911
KH domain-containing protein	80
Leucine-rich repeat protein kinase family protein	90.90909091
hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-	100
Restriction endonuclease, type II-like superfamily protein	32.67973856
N/A	47.56097561
Carbohydrate-binding protein	40.38461538
plant U-box 49	62.71186441
Pentatricopeptide repeat (PPR) superfamily protein	90
SET domain-containing protein	36.09460279
N/A	75.51020408
Phosphatidylinositol 3- and 4-kinase family protein with FAT domain	67.85714286
RNA polymerase II large subunit	33.79120879
Major facilitator superfamily protein	29.7399605
NAC domain containing protein 36	50
Chloroplast Ycf2;ATPase, AAA type, core	40.24435394
AP2/B3-like transcriptional factor family protein	25.30742459
P-loop containing nucleoside triphosphate hydrolases superfamily prot	72.72727273
P-loop containing nucleoside triphosphate hydrolases superfamil	31.73884691
Putative glycosyl hydrolase of unknown function (DUF1680)	100
Tetratricopeptide repeat (TPR)-like superfamily protein	76.92307692
binding	40.98039216
AICARFT/IMPCHase bienzyme family protein	60.60606061
Insulinase (Peptidase family M16) family protein	60.38647343
homolog of histone chaperone HIRA	35.48387097
N/A	31.2307261
cleavage and polyadenylation specificity factor 100	100
Lecithin:cholesterol acyltransferase family protein	36.81006494
transcription factor-related	25.05145798
DegP protease 7	47.43961353
CRINKLY4 related 3	26.5625
N/A	58.20895522
Pentatricopeptide repeat (PPR) superfamily protein	90
Methylthiotransferase	80
N/A	29.6875
nucleolin like 2	51.45424837
Calcium-dependent lipid-binding (CaLB domain) family protein	33.01127214
AAA-type ATPase family protein	38.21428571
Far-red impaired responsive (FAR1) family protein	76
protein kinase family protein	50
ARM repeat superfamily protein	100
cell division cycle protein 48-related / CDC48-related	100

N/A	100
BRI1 suppressor 1 (BSU1)-like 2	100
Protein of unknown function (DUF604)	100
NAD(P)H dehydrogenase B1	100
Uncharacterised conserved protein (UCP012943)	36.23188406
Uncharacterised conserved protein (UCP012943)	36.23188406
isoprenoid F	36.23188406
Quinone reductase family protein	40.74074074
Nucleotide-diphospho-sugar transferases superfamily protein	58.33333333
purine permease 5	43.65576284
N/A	50
N/A	50
phosphoesterase	100
Nucleotide/sugar transporter family protein	25.77436524
DNA/RNA helicase protein	61.52829191
Leucine-rich repeat protein kinase family protein	71.42857143
mitochondrial editing factor 20	51.12299465
Plasma-membrane choline transporter family protein	29.65772433
Leucine-rich repeat transmembrane protein kinase	44.27058257
PIF1 helicase	49.75490196
2-isopropylmalate synthase 1	34.35143288
P-loop containing nucleoside triphosphate hydrolases superfamily	27.53968254
plastid division1	100
phosphoglycerate kinase 1	38.18466354
glycosyl hydrolase family 81 protein	67.27272727
N/A	57.26227795
ARM repeat superfamily protein	100
Phosphoglycerate mutase-like family protein	26.02397602
protein kinase 2A	36.1025641
Tetratricopeptide repeat (TPR)-like superfamily protein	71.02272727
glutamate receptor 2.5	26.51724138
Ribosomal protein L18ae family	71.875
N/A	37.34939759
P-loop containing nucleoside triphosphate hydrolases superfamily prot	43.63636364
Rho termination factor	70.50092764
Leucine-rich repeat transmembrane protein kinase family protein	52.10803689
Transducin/WD40 repeat-like superfamily protein	37.10462287
Transducin/WD40 repeat-like superfamily protein	68.88888889
ACT-like superfamily protein	42.22222222
ser/arg-rich protein kinase 4	81.03448276
N/A	32.35294118
Ubiquitin C-terminal hydrolases superfamily protein	71.42857143
Leucine-rich repeat family protein	64
receptor-like protein kinase 1	63.39522546
Tetratricopeptide repeat (TPR)-like superfamily protein	27.808136
NAD(P)-binding Rossmann-fold superfamily protein	51.46871009

Phototropic-responsive NPH3 family protein	90.90909091
Protein of unknown function (DUF1000)	48.14814815
Protein of unknown function (DUF1000)	35.48387097
Telomerase activating protein Est1	100
Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferas	85.71428571
UDP-Glycosyltransferase superfamily protein	53.37398374
Protein of unknown function (DUF1421)	94.44444444
Homeodomain-like superfamily protein	31.49983148
Transmembrane amino acid transporter family protein	42.83876501
ARM repeat superfamily protein	74.63002114
ARM repeat superfamily protein	80.85106383
triosephosphate isomerase	56.41025641
A20/AN1-like zinc finger family protein	86.36363636
topoisomerase 6 subunit B	66.66666667
crinkly4	29.78723404
CTC-interacting domain 4	100
Protein phosphatase 2A, regulatory subunit PR55	94.44444444
pleiotropic drug resistance 12	48.93617021
Pre-mRNA-processing-splicing factor	90
cation exchanger 2	79.90196078
HEAT SHOCK PROTEIN 89.1	70.76923077
Kinase-related protein of unknown function (DUF1296)	100
Subtilisin-like serine endopeptidase family protein	30.08605621
ARM repeat superfamily protein	65.83333333
S-adenosyl-L-methionine-dependent methyltransferases superfamily p	37.14285714
ubiquitin-specific protease 22	27.93471438
TRS120	41.15853659
plant glycogenin-like starch initiation protein 2	25.88614393
plastid division1	40.90909091
Ribosomal protein L33 family protein	87.5
ArfGap/RecO-like zinc finger domain-containing protein	61.73076923
N/A	53.65853659
N/A	42.36641221
bromo-adjacent homology (BAH) domain-containing protein	26.08727255
Sulfite exporter TauE/SafE family protein	100
ENTH/VHS/GAT family protein	30.81106097
N/A	77.36842105
long chain acyl-CoA synthetase 9	28.74006453
long chain acyl-CoA synthetase 9	25.74065842
N/A	28.74006453
copper ion binding;cobalt ion binding;zinc ion binding	53.14723591
hydroxyproline-rich glycoprotein family protein	90.90909091
Restriction endonuclease, type II-like superfamily protein	90.90909091
exocyst subunit exo70 family protein B1	26.73299101
WRKY DNA-binding protein 4	46.66666667
autophagy protein Apg5 family	91.30434783

P-loop containing nucleoside triphosphate hydrolases superfamily	55.84795322
Lactoylglutathione lyase / glyoxalase I family protein	42.42424242
CASC3/Barentsz eIF4AIII binding	36.69172932
chitinase A	100
IQ-domain 26	25.36774316
Phosphatidylinositol-4-phosphate 5-kinase family protein	25.42982563
Plant protein of unknown function (DUF639)	95.65217391
Tetratricopeptide repeat (TPR)-like superfamily protein	58.97435897
Protein of unknown function (DUF506)	41.70702179
Pentatricopeptide repeat (PPR) superfamily protein	47.61904762
plant U-box 17	65.625
auxin response factor 8	76.19047619
cullin4	31.27548049
alpha-mannosidase 3	93.33333333
potassium channel in Arabidopsis thaliana 1	93.33333333
Inositol monophosphatase family protein	68.29268293
Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein C	100
ATP-citrate lyase B-1	25.49019608
N/A	92.30769231
N/A	48.33232262
MLP-like protein 423	30.76825598
N/A	88.23529412
MAP kinase kinase 2	25.34235026
Mob1/phocein family protein	53.84615385
Mob1/phocein family protein	31.42955024
zinc ion binding;nucleic acid binding	26.63851351
N/A	53.08641975
cyclophilin 59	35.36214242
ARM repeat superfamily protein	84.61538462
Polynucleotidyl transferase, ribonuclease H-like superfamily protein	60.41666667
PREFOLDIN 1	52.17391304
Major facilitator superfamily protein	34.04761905
RING/U-box superfamily protein	41.04991394
Trypsin family protein	53.03030303
TTF-type zinc finger protein with HAT dimerisation domain	39.39393939
Cellulose synthase family protein	80
Pectin lyase-like superfamily protein	26.88948716
magnesium ion binding;thiamin pyrophosphate binding;hydro-lya	60.90909091
magnesium ion binding;thiamin pyrophosphate binding;hydro-lya	26.07551487
ATPases;nucleotide binding;ATP binding;nucleoside-triphosphatases;tr	26.66666667
N/A	37.9273377
transcription coactivators	25.19660271
transducin family protein / WD-40 repeat family protein	100
Protein kinase superfamily protein	54.54545455
pentatricopeptide (PPR) repeat-containing protein	86.14718615

Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding	29.32118165
apyrase 2	74.46428571
S-adenosyl-L-methionine-dependent methyltransferases superfamily p	71.52777778
RNA-binding (RRM/RBD/RNP motifs) family protein	76.59574468
golgin candidate 1	88.57142857
Sec23/Sec24 protein transport family protein	100
Spc97 / Spc98 family of spindle pole body (SBP) component	46.9581749
hAT transposon superfamily	46.9581749
N/A	100
yeast YAK1-related gene 1	29.41306267
yeast YAK1-related gene 1	37.68684146
N/A	29.41306267
compromised recognition of TCV 1	61.53846154
compromised recognition of TCV 1	100
Protein kinase superfamily protein	51.2195122
Protein kinase superfamily protein	33.0977918
TatD related DNase	27.64804003
disease resistance family protein / LRR family protein	35.75989783
Heavy metal transport/detoxification superfamily protein	25.46975547
Heavy metal transport/detoxification superfamily protein	43.20987654
NAD(P)-binding Rossmann-fold superfamily protein	44.68438538
disease resistance family protein / LRR family protein	31.52856408
disease resistance family protein / LRR family protein	43.96551724
disease resistance family protein / LRR family protein	28.98351648
CAP160 protein	52.38095238
F-box/RNI-like superfamily protein	44.11764706
hydroxyproline-rich glycoprotein family protein	72.80701754
microtubule-associated proteins 70-5	28.57699805
Saposin-like aspartyl protease family protein	100
tobamovirus multiplication 1	52.38095238
phospholipases;galactolipases	30.80467919
RING/U-box superfamily protein	53.8764266
N/A	45.65217391
N/A	35.11047895
calmodulin binding;transcription regulators	64.28571429
PAS domain-containing protein tyrosine kinase family protein	100
ARM repeat superfamily protein	71.42857143
Transducin/WD40 repeat-like superfamily protein	54.23728814
Alg9-like mannosyltransferase family	69.78609626
Alg9-like mannosyltransferase family	42.5210084
Phosphoribulokinase / Uridine kinase family	44.15584416
dicer-like 4	26.52358691
dicer-like 4	29.53384419
N/A	33.30395829
glucuronidase 3	68.29268293

early nodulin-related	55
fatty acyl-ACP thioesterases B	28.38612368
histone deacetylase 15	47.54299754
Transcription factor TFIIE, alpha subunit	57.89473684
arogenate dehydrogenase	29.15662651
Class I peptide chain release factor	76.4516129
Phosphatidic acid phosphatase (PAP2) family protein	68.75
protein arginine methyltransferase 7	90.90909091
MITOCHONDRIAL FERREDOXIN 2	26.43008475
Protein of unknown function, DUF547	25.83832335
PPPDE putative thiol peptidase family protein	91.66666667
Plant VAMP (vesicle-associated membrane protein) family protein	75
N/A	37.67292127
Tetratricopeptide repeat (TPR)-like superfamily protein	45.31965561
casein kinase alpha 1	69.49152542
MRG family protein	63.08243728
Plant protein of unknown function (DUF869)	74.55197133
PLC-like phosphodiesterases superfamily protein	28.39068826
ABC1 family protein	44.42361762
Mitochondrial substrate carrier family protein	44.91869919
phytochrome interacting factor 3	90.90909091
mitotic-like cyclin 3B from Arabidopsis	100
histidine kinase 5	25.83476027
Protein of unknown function (DUF1336)	38.98305085
N/A	86.42857143
N/A	38.09195402
N/A	38.09195402
GYF domain-containing protein	56
DNA repair-recombination protein (RAD50)	43.44086022
ubiquitin-specific protease 4	52
Protein of unknown function (DUF630 and DUF632)	45.27272727
Uroporphyrinogen decarboxylase	55.69620253
DegP protease 7	92.30769231
ALWAYS EARLY 4	40.47354791
Homeodomain-like superfamily protein	37.89431384
nodulin MtN21 /EamA-like transporter family protein	29.69866418
nodulin MtN21 /EamA-like transporter family protein	47.60273973
smr (Small MutS Related) domain-containing protein	95.23809524
RNA helicase, ATP-dependent, SK12/DOB1 protein	60
Neutral/alkaline non-lysosomal ceramidase	64.19828641
beta-1,2-xylosyltransferase	51.66666667
beta-1,2-xylosyltransferase	51.66666667
N/A	52.07017544
MAP kinase 20	29.78723404
Mitochondrial transcription termination factor family protein	57.33863837
pleckstrin homology (PH) domain-containing protein	33.33333333

N/A	76.30136986
DEA(D/H)-box RNA helicase family protein	28.50980392
trehalose phosphate synthase	100
Radical SAM superfamily protein	32.82940361
hAT transposon superfamily	32.82940361
Phototropic-responsive NPH3 family protein	40.36697248
plant U-box 9	100
N/A	80
myb-like HTH transcriptional regulator family protein	45.47088426
N/A	45.47088426
protein kinase 1B	92.85714286
Sulfite exporter TauE/SafE family protein	27.42470296
Sulfite exporter TauE/SafE family protein	27.13503838
mRNA capping enzyme family protein	49.24098672
sulfoquinovosyldiacylglycerol 2	41.19743407
zinc finger protein-related	54.28571429
WD-40 repeat family protein / beige-related	75.47619048
Calcium-dependent lipid-binding (CaLB domain) family protein	100
5\'-3\' exonuclease family protein	75
RNA polymerase II transcription mediators	56
Protein of unknown function (DUF630 and DUF632)	100
Leucine-rich repeat receptor-like protein kinase family protein	30.48780488
TCP-1/cpn60 chaperonin family protein	39.0625
Pectate lyase family protein	55
N/A	78.33333333
purple acid phosphatase 23	61.11111111
PHD finger family protein	100
COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protei	78.57142857
NSP-interacting kinase 1	75.97402597
Proline-rich spliceosome-associated (PSP) family protein / zinc knuckle	77.27272727
NAD-dependent glycerol-3-phosphate dehydrogenase family protein	54.16666667
N/A	29.73402476
N/A	29.73402476
Got1/Sft2-like vescicle transport protein family	76.29233512
NAD+ transporter 2	73.21428571
alpha/beta-Hydrolases superfamily protein	65.90909091
alpha/beta-Hydrolases superfamily protein	55.51971326
Nucleotide-diphospho-sugar transferase family protein	27.91421653
zinc ion binding;nucleic acid binding;zinc ion binding	88.46153846
N/A	25.95070423
Glycosyl hydrolase family 38 protein	76.47058824
H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein	37.57338552
2-isopropylmalate synthase 1	40
disproportionating enzyme 2	100
homolog of yeast autophagy 18 (ATG18) G	41.18744699
response regulator 24	25.33151059

ENTH/VHS/GAT family protein	25.33151059
plus-3 domain-containing protein	84.84848485
ankyrin repeat family protein	63.0952381
Ribosomal protein L4/L1 family	49.14021164
Ribosomal protein L4/L1 family	41.63925247
ARM repeat superfamily protein	54.54545455
ENTH/VHS family protein	38.55421687
ENTH/VHS family protein	100
Cleavage and polyadenylation specificity factor (CPSF) A subunit protei	42.82296651
myb domain protein 12	60.15037594
HIT zinc finger ;PAPA-1-like conserved region	30.6122449
N/A	32.14101904
D-aminoacid aminotransferase-like PLP-dependent enzymes superfami	65.78947368
DNAJ heat shock N-terminal domain-containing protein	92.85714286
O-acetylserine (thiol) lyase (OAS-TL) isoform A1	32.98980877
zinc knuckle (CCHC-type) family protein	100
Protein kinase superfamily protein	28.97637795
pyrophosphorylase 3	30.53167421
SU(VAR)3-9 homolog 9	39.9897855
SU(VAR)3-9 homolog 9	75.58441558
N/A	64.45182724
Protein of unknown function (DUF1666)	100
N/A	26.84431609
N/A	29.86111111
N/A	29.86111111
N/A	29.75663267
N/A	27.41523734
N/A	26.71641791
N/A	26.52051783
urease accessory protein D	63.33333333
urease accessory protein D	48.96551724
Protein of unknown function (DUF668)	92.30769231
Protein kinase superfamily protein	57.77777778
Nucleotidylyl transferase superfamily protein	100
translation initiation factor 3 (IF-3) family protein	38.83888389
clathrin adaptor complexes medium subunit family protein	90.47619048
Protein kinase superfamily protein	28.09044397
Ubiquitin-like superfamily protein	45.90301003
Cyclase family protein	92
Cyclase family protein	87.01298701
Homeodomain-like protein with RING/FYVE/PHD-type zinc finger doma	70
transducin family protein / WD-40 repeat family protein	36.71096346
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	25.71022727
Methyltransferase MT-A70 family protein	35.17412698
ribosomal protein 1	65.30612245

Protein of unknown function (DUF1278)	65.30612245
DNAse I-like superfamily protein	27.99422799
phosphoglucosamine mutase family protein	33.45079967
lactate/malate dehydrogenase family protein	100
COP1-interacting protein-relatedMETHYLATED_REGIONS	59.04761905
syntaxin of plants 43	68.88888889
N/A	100
glucan synthase-like 10	32.58444619
carboxyl terminus of HSC70-interacting protein	54
TBP-associated factor 7	34.05839274
myb domain protein 1	36.25
N/A	74.46808511
GroES-like zinc-binding dehydrogenase family protein	37.23522854

q value	P value
0.00460124	8.70901E-06
2.6925E-08	4.08726E-12
3.38582E-06	1.07761E-09
5.06491E-06	2.03203E-09
6.68106E-07	3.95286E-10
0.001294834	2.02341E-06
0.000703795	7.39602E-07
0.002540759	4.03019E-06
5.27234E-05	8.72624E-08
0.001320947	1.68651E-06
0.005609672	1.56869E-05
0.000115391	7.66995E-08
0.008526819	2.01911E-05
0.009452001	3.40217E-05
0.003119226	6.7176E-06
4.85284E-05	7.87667E-08
7.82947E-08	1.39522E-11
0.000135885	1.07333E-07
0.005353107	1.08251E-05
0.005353107	1.08251E-05
3.12975E-06	2.64803E-09
0.005823103	1.21106E-05
2.4749E-05	1.12889E-08
0.002048788	3.05751E-06
2.79341E-06	8.48089E-10
4.15523E-28	1.47718E-33
0.003095952	6.61666E-06
0.006793816	1.48569E-05
0.004287198	7.92597E-06
0.002159916	4.06449E-06
1.40706E-05	5.73713E-09
0.00014026	1.11525E-07
1.13095E-05	4.42884E-09
8.05292E-08	1.44686E-11
0.001920592	2.72816E-06
0.001455847	1.90893E-06
0.001240448	1.54644E-06
0.006456384	1.94615E-05
0.001021467	1.19629E-06
0.000433394	4.69811E-07
0.001337013	1.70997E-06
0.009463526	2.31518E-05
0.008193419	1.91181E-05
1.39808E-05	1.65863E-08

1.39808E-05	1.65863E-08
5.12709E-08	1.04358E-11
5.18275E-05	2.85434E-08
0.004907369	9.52608E-06
0.001232024	1.8929E-06
0.000310115	2.56757E-07
0.002670807	4.29593E-06
0.000566467	5.49176E-07
4.20563E-12	3.84453E-16
0.003662749	8.39622E-06
0.005247154	4.11999E-05
0.004907369	9.53081E-06
0.004550831	8.57689E-06
0.004317217	1.06809E-05
0.000657565	8.02622E-07
1.7072E-06	5.784E-10
5.09444E-06	1.73768E-09
3.23379E-05	1.56517E-08
0.005960371	1.71725E-05
1.32233E-10	2.10868E-14
1.69713E-05	2.09871E-08
0.003972467	9.44718E-06
0.000356021	3.65834E-07
0.000132613	1.04313E-07
6.74157E-09	1.10661E-12
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2.81216E-14	1.41389E-18
0.003714523	8.59229E-06
0.000164662	1.37101E-07
6.42586E-05	1.11935E-07
0.001377452	2.20316E-06
0.001933999	2.83514E-06
2.53603E-13	1.06007E-17
7.29404E-07	2.17429E-10
0.00422635	7.77938E-06
2.56349E-09	3.00785E-13
0.00139898	1.80373E-06
0.000306483	3.01246E-07
0.000299513	2.45563E-07
0.002484903	1.43562E-05
0.002750196	5.60865E-06
0.005115318	1.01284E-05
1.14187E-08	1.55753E-12
0.000424206	3.80149E-07

0.002554241	5.07318E-06
1.41839E-07	2.80843E-11
1.73353E-08	5.27349E-12
0.00177142	3.08453E-06
1.6306E-05	1.99491E-08
0.004876312	9.42644E-06
0.000581895	5.66904E-07
0.004842753	1.26584E-05
9.97353E-05	1.93721E-07
0.003249293	7.10975E-06
1.22391E-05	5.76987E-09
7.97829E-06	2.9254E-09
0.000166113	1.39389E-07
0.000705533	8.81092E-07
3.22217E-05	1.55009E-08
7.55432E-06	7.88784E-09
0.005646129	1.16556E-05
3.87195E-05	2.31901E-08
0.001240448	1.54644E-06
3.94734E-05	2.00027E-08
3.64193E-07	9.73494E-11
0.000501408	4.69924E-07
0.001911271	9.9095E-06
2.39209E-05	1.08037E-08
0.004284865	7.91851E-06
0.00010721	2.12289E-07
0.001933999	2.83514E-06
0.005353107	1.08251E-05
0.009560258	9.83182E-05
0.00460124	8.70536E-06
0.003440723	5.98256E-06
7.33139E-05	4.39252E-08
0.005282421	1.05794E-05
0.00319357	5.4287E-06
0.002243341	3.45642E-06
0.00303548	1.90357E-05
0.00112567	1.35052E-06
0.000713436	7.53919E-07
0.003161348	5.35538E-06
2.92739E-06	8.99497E-10
0.003175057	5.39257E-06
0.004921546	9.61483E-06
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0.002888808	6.01456E-06
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7.80087E-07	4.80555E-10
2.85207E-07	1.42526E-10
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0.001933999	2.83514E-06
6.22335E-07	1.52888E-10
0.00495282	1.30818E-05
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0.001211669	5.29462E-06
0.00286027	4.70062E-06
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1.72831E-07	3.48546E-11
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3.93888E-06	1.28829E-09
0.006270513	1.33244E-05
3.95209E-06	3.52243E-09
0.000534009	5.09877E-07
0.000283879	7.6006E-07
6.41886E-05	3.77185E-08
4.68247E-13	3.03809E-17
0.000534009	5.09877E-07
9.72954E-05	6.20037E-08
0.006761117	2.07314E-05
0.001058832	1.25558E-06
6.64903E-17	1.4628E-21
5.906E-10	5.71707E-14
3.62009E-23	3.56536E-28
0.001746216	3.03147E-06
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2.45968E-10	2.18258E-14
0.000753828	8.05448E-07
2.14973E-05	9.48292E-09
0.001061922	1.54507E-06
1.85987E-10	1.58215E-14
0.006971016	1.53878E-05

0.008526819	2.01911E-05
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0.001981703	3.62823E-06
0.000326905	9.13278E-07
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0.001191793	5.17994E-06
3.98238E-17	8.89886E-22
0.000147771	1.03815E-07
0.008508216	2.89711E-05
6.83992E-09	1.13174E-12
1.90117E-05	2.42055E-08
0.00256575	4.09053E-06
0.001563456	2.0913E-06
0.005934657	1.24253E-05
7.19661E-05	4.29594E-08
3.24729E-11	4.2713E-15
0.001933999	2.83514E-06
0.001418149	1.84286E-06
8.16954E-06	8.65883E-09
0.000163436	1.18536E-07
0.00397489	7.20284E-06
0.001889972	3.39864E-06
0.001038557	1.48792E-06
0.007715694	2.5087E-05
1.52905E-09	3.29251E-13
0.00375979	8.72909E-06
2.00018E-06	6.93419E-10
0.001964261	3.58034E-06
9.65375E-05	6.13792E-08
5.96063E-08	1.24846E-11
4.40126E-05	2.31098E-08
0.005497455	4.39949E-05
4.50083E-07	1.05951E-10
2.58813E-05	1.19193E-08
0.001281217	5.70964E-06
0.004165018	7.64816E-06
0.002261396	1.25228E-05
5.92326E-06	2.06763E-09
0.003404756	5.88812E-06
0.001904087	2.69215E-06
0.000137185	9.3863E-08
0.000277356	2.24346E-07
4.31948E-05	2.2427E-08
0.004971065	1.31504E-05

0.001323216	1.69135E-06
0.00443975	3.24503E-05
3.79056E-05	1.90528E-08
8.40893E-10	1.69539E-13
0.000475611	1.50939E-06
0.005586621	1.55711E-05
0.001933999	2.83514E-06
1.88168E-05	8.11773E-09
0.002184277	4.13792E-06
0.002184277	4.13792E-06
0.001753712	2.42167E-06
0.001735936	2.38899E-06
0.005925316	1.23804E-05
0.000740742	7.89836E-07
0.000796198	8.74075E-07
0.001825936	9.28534E-06
0.00837369	1.96873E-05
0.003908976	9.21406E-06
0.007949013	1.82925E-05
8.32659E-06	3.07143E-09
0.006269008	1.85891E-05
0.0089048	2.13605E-05
1.56799E-16	3.90193E-21
5.56897E-06	2.28167E-09
0.001749681	2.41225E-06
0.005008332	9.82772E-06
0.003910739	7.04931E-06
0.001574405	2.11518E-06
0.000703795	7.39602E-07
0.004998225	3.83776E-05
0.000788803	1.02441E-06
0.005220646	1.40632E-05
0.00235172	4.57212E-06
7.1236E-12	7.2355E-16
0.003456358	6.01228E-06
0.000812662	3.09123E-06
0.003865571	6.94645E-06
9.19326E-05	5.75246E-08
0.002979043	4.94387E-06
0.000254749	2.03258E-07
1.99309E-05	8.72584E-09
0.000107792	7.01159E-08
0.001687678	2.31143E-06
0.008968817	2.15798E-05
0.000531226	5.03324E-07
0.000181199	1.34475E-07

4.77422E-10	4.48144E-14
4.77422E-10	4.48144E-14
0.007202482	2.26191E-05
4.93591E-05	8.03155E-08
0.005579319	1.14563E-05
0.000389249	3.44255E-07
8.03719E-11	8.17955E-15
4.70906E-06	1.58163E-09
0.00193327	1.00666E-05
0.007621244	2.46298E-05
5.94932E-05	3.4205E-08
0.003062832	5.13743E-06
0.003229123	2.07941E-05
9.291E-06	3.49531E-09
0.00922614	3.26151E-05
3.0888E-09	7.26291E-13
1.65597E-07	3.32744E-11
0.002195562	3.36519E-06
0.000150272	1.06221E-07
8.92381E-05	5.5233E-08
0.002153108	3.27161E-06
0.001442614	1.88523E-06
0.004921546	9.61483E-06
4.56951E-05	2.41273E-08
0.000760638	8.14956E-07
0.008749987	3.01448E-05
2.22958E-06	6.49987E-10
0.000293193	2.85437E-07
0.002175488	4.10522E-06
0.009242621	3.27037E-05
0.009048705	3.17324E-05
0.000417278	1.2662E-06
0.002877843	1.7588E-05
2.19395E-05	9.75002E-09
4.29864E-05	2.62769E-08
9.0706E-06	3.38578E-09
0.000427669	3.84506E-07
0.008839918	8.7868E-05
0.005062639	9.97215E-06
0.000128408	8.68221E-08
0.000175386	1.2943E-07
0.003675254	6.51198E-06
0.000229292	1.78238E-07
0.000211198	5.12883E-07
0.000211198	5.12883E-07
0.00815181	7.81495E-05

5.63119E-06	1.94654E-09
1.76371E-09	3.8605E-13
9.19326E-05	5.75246E-08
0.007012912	1.55164E-05
0.000299513	2.45156E-07
0.000229292	1.78103E-07
0.000534009	5.09877E-07
0.005183954	1.03252E-05
7.96564E-06	2.91492E-09
0.00016351	1.1884E-07
0.001749899	8.76315E-06
0.001749899	8.76315E-06
0.000403274	4.27893E-07
0.000499771	4.67291E-07
0.001485491	1.96087E-06
6.21853E-10	6.20201E-14
0.002902342	6.05423E-06
0.00023892	1.86949E-07
3.16655E-05	1.50593E-08
3.16655E-05	1.50593E-08
0.003489905	7.89856E-06
0.005353107	1.07557E-05
0.001539522	2.55235E-06
0.000191812	1.66495E-07
0.000152866	1.09054E-07
0.00327541	5.60865E-06
1.104E-05	4.27989E-09
0.000534009	5.09877E-07
8.96769E-05	5.56361E-08
0.005146361	1.02201E-05
0.000244843	2.28763E-07
0.00806387	2.67181E-05
1.88945E-07	8.77044E-11
0.009714209	2.39574E-05
0.006029944	1.26867E-05
0.008180794	1.90667E-05
1.01808E-10	1.5594E-14
0.005600423	1.5639E-05
0.008002959	1.84582E-05
0.00170456	2.33629E-06
1.43495E-12	7.57662E-17
0.006311455	1.34549E-05
0.0016582	2.25451E-06
0.008552	2.02696E-05
0.002492172	3.93485E-06
0.008552	2.03E-05

0.002492172	3.93485E-06
3.94723E-05	1.99732E-08
2.29387E-06	6.78122E-10
0.000292927	2.38445E-07
5.80763E-06	5.62456E-09
0.007299149	1.6358E-05
0.002195562	3.36519E-06
0.000796198	8.74075E-07
0.008596793	2.0401E-05
6.0627E-06	5.94549E-09
0.001806186	2.51532E-06
0.005164617	1.02677E-05
0.000120058	8.03835E-08
3.74018E-05	2.21755E-08
0.005173153	1.02923E-05
5.74583E-05	3.25294E-08
0.000664113	6.7405E-07
0.0004227	4.535E-07
0.000146403	3.17082E-07
0.000837685	9.39278E-07
0.002396616	1.36376E-05
0.003077442	5.17793E-06
5.0455E-07	2.82887E-10
0.000175386	1.2943E-07
0.004905666	9.51905E-06
0.002806743	1.69439E-05
4.2808E-11	4.04744E-15
0.000776284	8.3912E-07
0.001920592	2.72598E-06
0.003801734	8.86282E-06
0.001240448	1.54644E-06
0.00640756	1.92434E-05
2.23026E-05	9.92772E-09
0.000227945	1.76856E-07
0.002358053	4.58753E-06
0.002774689	4.51724E-06
0.000150272	1.06221E-07
0.001078742	1.28235E-06
0.005960506	1.24838E-05
1.35949E-07	2.68185E-11
0.002262668	3.49782E-06
0.000631468	7.59989E-07
0.001056985	1.25184E-06
2.55045E-06	9.07631E-10
0.000356554	3.05926E-07
1.79916E-05	7.62613E-09

1.80662E-05	7.75047E-09
0.005353107	1.08251E-05
0.000534009	5.09877E-07
2.76356E-05	1.28935E-08
1.93306E-08	3.56651E-12
1.93306E-08	3.56651E-12
1.93306E-08	3.56651E-12
0.001996483	3.66388E-06
0.004382042	8.1463E-06
4.8246E-08	8.06682E-12
0.00026533	2.54176E-07
0.00026533	2.54176E-07
0.000175386	1.2943E-07
0.000222538	5.50844E-07
6.15235E-07	1.49791E-10
0.000954694	1.09988E-06
5.77753E-08	9.95672E-12
5.22867E-05	3.37815E-08
2.36225E-05	3.19594E-08
0.002364131	4.6009E-06
0.007569984	2.44045E-05
0.001012355	1.43479E-06
7.77969E-06	2.81835E-09
0.001214375	1.86021E-06
0.006637634	1.44228E-05
0.003828761	6.86223E-06
0.000703795	7.39602E-07
0.003850561	2.66239E-05
0.005131118	1.01758E-05
0.006329252	1.35068E-05
2.24554E-11	2.77119E-15
0.003804626	6.81339E-06
0.002273185	4.36869E-06
0.000340295	2.87235E-07
0.009132855	2.20549E-05
0.008172975	1.90416E-05
7.78441E-12	8.18344E-16
2.29387E-06	6.75522E-10
2.62633E-05	1.21723E-08
0.000429508	3.8679E-07
0.009039179	3.16585E-05
0.005353107	1.08145E-05
0.000343098	2.90355E-07
3.01183E-05	1.69259E-08
0.001882497	9.69324E-06
0.009468768	2.31716E-05

0.004921546	9.61483E-06
7.79233E-06	2.82864E-09
0.003350142	7.42607E-06
0.001240448	1.54644E-06
0.003645592	6.44839E-06
1.81726E-22	1.38435E-27
0.000775974	8.38216E-07
1.33016E-07	5.70146E-11
0.000975518	3.95416E-06
0.001025477	1.46446E-06
2.49223E-05	1.13863E-08
0.007970342	1.83649E-05
0.001440019	1.88078E-06
3.08821E-05	1.46074E-08
7.14707E-05	4.26113E-08
1.65617E-05	6.87651E-09
5.62741E-05	3.18177E-08
0.00195593	2.8759E-06
0.000312342	2.59288E-07
0.007550987	2.42986E-05
0.00244009	3.84009E-06
0.005353107	1.08251E-05
0.002995099	1.8659E-05
0.000664113	6.74524E-07
0.008730732	2.08206E-05
4.92288E-05	8.00534E-08
0.001540706	2.55634E-06
0.000406021	1.2193E-06
0.000785474	8.51358E-07
0.00077132	8.32057E-07
3.67747E-07	9.89981E-11
3.64162E-05	5.48608E-08
0.000406439	3.61843E-07
7.62582E-06	7.98185E-09
0.005353107	1.08251E-05
0.00569383	1.59971E-05
0.000903423	1.02558E-06
2.20084E-06	6.35903E-10
4.67186E-06	4.30172E-09
2.20084E-06	6.35903E-10
0.001346231	2.14085E-06
0.000566467	5.49176E-07
0.000566467	5.49176E-07
0.001891161	3.40354E-06
0.001006889	1.42073E-06
0.000325828	2.72634E-07

0.004203443	1.02669E-05
1.2525E-06	8.48539E-10
0.003705057	6.58346E-06
6.76189E-07	4.03022E-10
0.001967253	1.03248E-05
0.006728148	5.90102E-05
1.61342E-06	4.50794E-10
0.00412992	7.55645E-06
0.00981805	0.000102136
0.001314704	1.67179E-06
0.000464513	4.2683E-07
0.002126331	3.21845E-06
0.000375798	3.27398E-07
0.000116803	7.78614E-08
0.000116803	7.78614E-08
2.16506E-05	9.60573E-09
0.000115391	7.66995E-08
0.001933999	2.78943E-06
5.87593E-05	3.36107E-08
7.34145E-07	4.46288E-10
4.23642E-13	2.86147E-17
0.004244872	7.82335E-06
4.0229E-07	2.14112E-10
0.008698249	2.06864E-05
6.53124E-05	4.44135E-08
0.002318693	4.49351E-06
2.39209E-05	1.0806E-08
0.006107997	1.78304E-05
0.002110574	3.93805E-06
0.008827127	2.11353E-05
0.003546663	6.23179E-06
0.004647382	1.18792E-05
0.001476412	2.40507E-06
0.002618347	4.19359E-06
0.000335445	3.40065E-07
0.00218781	3.34038E-06
1.90119E-05	9.74922E-09
0.007453707	2.38277E-05
0.004156391	1.00756E-05
0.005771093	1.1973E-05
0.000398413	4.21849E-07
0.005465089	4.36387E-05
0.000796198	8.74075E-07
3.56531E-05	1.75962E-08
0.00139578	1.79811E-06

0.001285613	5.73838E-06
7.49529E-05	4.51821E-08
1.80691E-11	1.28533E-15
0.004387699	8.16793E-06
1.04662E-06	2.7272E-10
0.001933999	2.83514E-06
0.003518567	2.34623E-05
0.003518567	2.34623E-05
0.001933999	2.83514E-06
0.002134094	3.99348E-06
0.000235817	2.18162E-07
0.002134094	3.99348E-06
0.002461367	3.88079E-06
1.15987E-09	1.26737E-13
0.001098386	1.31234E-06
9.99893E-05	1.94386E-07
0.001113299	1.64909E-06
0.005071096	9.99996E-06
1.56763E-05	1.90354E-08
5.10723E-06	4.79322E-09
1.88869E-06	6.46087E-10
0.008483108	2.88744E-05
0.008645	2.96312E-05
0.000636143	7.67704E-07
0.002365643	3.68476E-06
0.00432082	8.01981E-06
0.001484791	1.95779E-06
0.007765513	1.76766E-05
0.000115391	7.66995E-08
0.001724632	2.36878E-06
0.005009981	9.83903E-06
0.000828999	3.16853E-06
0.008725044	2.07821E-05
3.29155E-10	5.83399E-14
2.84235E-06	8.65029E-10
0.001933999	2.83514E-06
0.006163469	1.30067E-05
0.000379699	3.33581E-07
0.00302238	6.39273E-06
5.65713E-08	2.0542E-11
7.75005E-12	8.10795E-16
0.000112166	8.58726E-08
0.004353135	1.08326E-05
0.00037888	3.324E-07
2.64502E-06	2.14254E-09

1.58114E-07	3.78928E-11
0.007118315	1.5864E-05
0.008669534	2.05972E-05
0.001262576	1.58699E-06
0.002726993	4.40959E-06
0.000548542	6.28491E-07
0.007623546	1.72863E-05
0.009452001	3.40217E-05
0.000294575	7.96627E-07
4.89083E-13	3.42768E-17
0.000531226	5.03324E-07
0.001377202	1.76844E-06
1.67271E-13	6.86935E-18
6.66504E-07	3.93999E-10
0.00716723	1.59888E-05
0.0002397	1.87884E-07
1.15653E-08	3.33615E-12
0.00067357	8.25254E-07
0.003539697	2.36607E-05
0.007474952	2.39165E-05
0.009452001	3.40217E-05
0.000703795	7.39602E-07
0.00795685	1.83222E-05
0.000788107	8.55946E-07
0.000603677	5.94415E-07
9.55087E-07	2.92228E-10
9.55087E-07	2.92228E-10
0.004902405	9.50562E-06
0.000813972	9.03138E-07
0.002856708	4.69267E-06
4.18656E-05	2.15109E-08
0.000102596	6.59081E-08
0.001904087	2.69215E-06
0.001643595	2.22863E-06
0.000137899	9.47969E-08
0.002513721	3.97809E-06
0.007874286	2.57929E-05
2.50298E-08	3.74449E-12
0.005907747	1.2333E-05
2.34667E-06	1.84009E-09
0.000105925	6.86686E-08
0.000105925	6.86686E-08
0.009832971	2.43585E-05
0.004711596	8.99044E-06
2.30754E-12	1.89847E-16
0.001212179	5.29952E-06

0.001502121	2.46865E-06
0.002659973	5.36877E-06
2.29387E-06	6.77352E-10
0.003900102	9.18033E-06
0.003900102	9.18033E-06
0.001244221	1.55571E-06
0.000534009	5.09877E-07
0.002239137	4.27826E-06
0.008806789	2.10672E-05
0.008806789	2.10672E-05
0.001904087	2.69215E-06
0.000407564	3.63144E-07
2.70399E-07	6.88859E-11
0.009899206	3.66128E-05
3.16655E-05	1.50702E-08
0.007693472	1.74787E-05
0.000839799	1.10446E-06
0.000703795	7.39602E-07
0.000244744	1.9366E-07
0.006489924	1.39829E-05
1.15987E-09	1.26737E-13
0.004194739	1.02292E-05
0.009395572	2.29579E-05
0.000441067	4.01728E-07
0.001959434	2.88392E-06
0.001369449	1.75748E-06
5.68891E-07	1.36839E-10
0.00338527	5.83931E-06
2.47622E-10	2.21541E-14
0.006226358	1.31913E-05
0.005138627	1.0201E-05
0.000235514	2.17264E-07
0.000235514	2.17264E-07
9.88171E-05	7.38359E-08
0.005836783	1.21562E-05
0.005748875	1.6271E-05
2.03437E-05	1.05524E-08
0.003051174	1.9168E-05
0.000464062	4.25735E-07
0.000676813	8.329E-07
0.000150717	1.06659E-07
0.006563689	5.69406E-05
0.009369875	3.33939E-05
0.00014754	1.03544E-07
3.82949E-08	1.30791E-11
0.009895324	2.45492E-05

0.009895324	2.45492E-05
0.001249711	1.56624E-06
0.006619382	1.43394E-05
6.03721E-06	2.12069E-09
1.81726E-22	1.33179E-27
0.009312357	2.26932E-05
0.001574215	2.11146E-06
5.45404E-07	1.30389E-10
0.00197301	2.91114E-06
0.000181307	1.5571E-07
0.003545459	6.21927E-06
0.005228525	1.04484E-05
0.002174657	3.31392E-06
0.000709141	7.4782E-07
5.69784E-13	4.19582E-17
0.000534009	5.09877E-07
0.009900233	0.000103454
0.000425857	4.58862E-07
0.000586613	5.72673E-07
5.35014E-05	2.98129E-08
0.001191793	5.18155E-06
8.63345E-08	1.57648E-11
0.002461972	1.41456E-05
0.000297151	2.89927E-07
0.000297151	2.89927E-07
0.000168355	1.41933E-07
4.2188E-06	1.62875E-09
0.009328889	3.31866E-05
0.000144717	1.16209E-07
0.009333353	3.32147E-05
0.000643951	2.25522E-06
0.000709141	7.4782E-07
0.001304542	1.65313E-06
0.001240448	1.54644E-06
0.003461927	7.7966E-06
0.000310043	2.5647E-07
0.00545066	1.50053E-05
0.001927119	2.74309E-06
8.79837E-06	3.26481E-09
2.23019E-14	1.01038E-18
0.006629474	1.43753E-05
0.006801176	1.4878E-05
0.005353107	1.07817E-05
2.46415E-09	2.85516E-13
0.003245971	7.09286E-06

0.003245971	7.09286E-06
0.00674261	1.47182E-05
0.004202254	1.02613E-05
0.000356554	3.05926E-07
0.005936358	1.70448E-05
0.006458536	1.38654E-05
0.001933999	2.83514E-06
0.002840594	5.86574E-06
4.20E-05	2.55E-08
2.51011E-10	4.29598E-14
0.006819163	6.02096E-05
0.000403557	4.29E-07
0.009670462	3.53E-05

Supplemental Table 9: List of 1346 unique hypo-methylated gen

METHYLATED REGION
mytileDiff25p200.hypo_CpG.Chr01.517401-517600
mytileDiff25p200.hypo_merged_CHG.Chr01.668801-669000
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mytileDiff25p200.hypo_CpG.Chr19.104001-104200
mytileDiff25p200.hypo_merged_CHG.Chr19.300001-300200
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mytileDiff25p200.hypo_CpG.Chr20.35283001-35283200

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mytileDiff25p200.hypo_merged_CHG.scaffold_21.349201-349400
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mytileDiff25p200.hypo_merged_CHH.scaffold_223.13001-13200
mytileDiff25p200.hypo_CpG.scaffold_31.213601-213800

mytileDiff25p200.hypo_CpG.scaffold_31.258401-258600
mytileDiff25p200.hypo_merged_CHH.scaffold_31.263201-263400
mytileDiff25p200.hypo_CpG.scaffold_32.168401-168600
mytileDiff25p200.hypo_merged_CHH.scaffold_32.247601-247800
mytileDiff25p200.hypo_CpG.scaffold_32.247601-247800
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es in all sequence contexts.

REGION	GENE ID
3'UTR	Glyma.01G005200
3'UTR (38bp)	Glyma.01G006800
3'UTR (160bp)	Glyma.01G007300
GENE BODY	Glyma.01G007300
3'UTR	Glyma.01G021600
3'UTR	Glyma.01G021600
3'UTR	Glyma.01G021600
PROMOTER	Glyma.01G022300
GENE BODY	Glyma.01G023600
GENE BODY	Glyma.01G023700
PROMOTER	Glyma.01G038200
GENE BODY	Glyma.01G038300
PROMOTER	Glyma.01G038600
GENE BODY	Glyma.01G038700
GENE BODY	Glyma.01G044000
GENE BODY	Glyma.01G059100
GENE BODY	Glyma.01G063700
GENE BODY	Glyma.01G065600
GENE BODY	Glyma.01G074400
GENE BODY	Glyma.01G074400
GENE BODY	Glyma.01G074400
GENE BODY	Glyma.01G074500
GENE BODY	Glyma.01G074700
3'UTR	Glyma.01G076200
5'UTR(108bp); PROMOTER (92bp)	Glyma.01G089000
5'UTR(108bp); PROMOTER(92bp)	Glyma.01G089000
5'UTR(171bp); GENE BODY (29bp)	Glyma.01G089000
5'UTR(171bp); GENE BODY(29bp)	Glyma.01G089000
5'UTR(60bp); GENE BODY(140 bp)	Glyma.01G089000
5'UTR(128bp); PROMOTER(72bp)	Glyma.01G089600
GENE BODY	Glyma.01G093200
GENE BODY	Glyma.01G093900
GENE BODY	Glyma.01G095100
GENE BODY	Glyma.01G102100
GENE BODY	Glyma.01G102800
5' UTR	Glyma.01G114500
5' UTR	Glyma.01G114500
5'UTR	Glyma.01G114500
PROMOTER(60bp); 5'UTR(39bp); GENE BODY	Glyma.01G117400
GENE BODY	Glyma.01G117500
GENE BODY	Glyma.01G117500
PROMOTER	Glyma.01G120100

PROMOTER	Glyma.01G120100
PROMOTER	Glyma.01G120100
PROMOTER	Glyma.01G120100
GENE BODY	Glyma.01G134300
GENE BODY	Glyma.01G134300
GENE BODY (102bp); 3'UTR(98bp)	Glyma.01G135400
GENE BODY	Glyma.01G135900
GENE BODY	Glyma.01G140200
GENE BODY	Glyma.01G141900
5'UTR(148bp); GENE BODY(52bp)	Glyma.01G145600
GENE BODY	Glyma.01G145600
GENE BODY	Glyma.01G145600
GENE BODY (117bp); PROMOTER (83bp)	Glyma.01G145700
PROMOTER	Glyma.01G145700
PROMOTER	Glyma.01G145700
PROMOTER	Glyma.01G145800
PROMOTER	Glyma.01G145800
PROMOTER	Glyma.01G145800
PROMOTER	Glyma.01G153600
PROMOTER	Glyma.01G153600
5'UTR(100bp); GENE BODY(100bp)	Glyma.01G156800
PROMOTER	Glyma.01G156800
GENE BODY	Glyma.01G162200
GENE BODY	Glyma.01G166100
PROMOTER	Glyma.01G166400
GENE BODY	Glyma.01G168400
GENE BODY	Glyma.01G168400
GENE BODY	Glyma.01G168900
GENE BODY	Glyma.01G176400
GENE BODY	Glyma.01G184500
PROMOTER	Glyma.01G190400
PROMOTER	Glyma.01G201000
GENE BODY	Glyma.01G203000
GENE BODY	Glyma.01G204900
GENE BODY	Glyma.01G209300
5'UTR (33bp); PROMOTER (167bp)	Glyma.01G226000
GENE BODY	Glyma.01G226800
GENE BODY	Glyma.01G234300
GENE BODY	Glyma.01G235300
GENE BODY	Glyma.01G238200
3'UTR(31bp); GENE BODY (169bp)	Glyma.01G243200
GENE BODY (169bp); 3'UTR (31bp)	Glyma.01G243200
GENE BODY (169bp); 3'UTR(31bp)	Glyma.01G243200
3'UTR(65bp)	Glyma.01G245100

PROMOTER (167bp); GENE BODY (33bp)	Glyma.01G245200
GENE BODY	Glyma.02G003600
GENE BODY	Glyma.02G006500
3'UTR(58bp)	Glyma.02G012600
GENE BODY	Glyma.02G021900
GENE BODY	Glyma.02G027500
GENE BODY	Glyma.02G042000
GENE BODY	Glyma.02G048100
GENE BODY	Glyma.02G056800
GENE BODY	Glyma.02G062200
GENE BODY	Glyma.02G066700
GENE BODY	Glyma.02G067100
PROMOTER	Glyma.02G085500
GENE BODY	Glyma.02G089000
GENE BODY	Glyma.02G090400
GENE BODY	Glyma.02G091300
3'UTR(3bp); GENE BODY (197bp)	Glyma.02G098100
GENE BODY	Glyma.02G098200
GENE BODY	Glyma.02G099300
GENE BODY	Glyma.02G100200
PROMOTER	Glyma.02G102900
GENE BODY	Glyma.02G103100
GENE BODY	Glyma.02G103100
GENE BODY	Glyma.02G106100
GENE BODY	Glyma.02G112500
PROMOTER	Glyma.02G116700
PROMOTER	Glyma.02G117700
PROMOTER	Glyma.02G129400
PROMOTER	Glyma.02G129400
PROMOTER	Glyma.02G129400
GENE BODY	Glyma.02G135900
PROMOTER	Glyma.02G138900
PROMOTER	Glyma.02G138900
PROMOTER	Glyma.02G138900
5'UTR(110bp); GENE BODY (90bp)	Glyma.02G139000
5'UTR(141bp); PROMOTER (59bp)	Glyma.02G139000
5'UTR(141bp); PROMOTER (59bp)	Glyma.02G139000
3'UTR	Glyma.02G140700
GENE BODY	Glyma.02G141600
PROMOTER	Glyma.02G141900
PROMOTER	Glyma.02G141900
GENE BODY	Glyma.02G145300
GENE BODY	Glyma.02G159400
GENE BODY	Glyma.02G160400

GENE BODY	Glyma.02G161100
GENE BODY	Glyma.02G162900
GENE BODY	Glyma.02G163200
GENE BODY	Glyma.02G166500
PROMOTER(148bp); GENE BODY(52bp)	Glyma.02G168200
GENE BODY	Glyma.02G170200
GENE BODY	Glyma.02G170500
GENE BODY	Glyma.02G172600
GENE BODY	Glyma.02G177900
GENE BODY(100bp); PROMOTER(100bp)	Glyma.02G180800
GENE BODY	Glyma.02G184100
GENE BODY	Glyma.02G185900
GENE BODY	Glyma.02G186300
GENE BODY	Glyma.02G189600
PROMOTER	Glyma.02G190300
5'UTR(135bp); GENE BODY (65bp)	Glyma.02G192300
5' UTR	Glyma.02G197100
GENE BODY	Glyma.02G201600
PROMOTER	Glyma.02G201800
GENE BODY	Glyma.02G202300
GENE BODY	Glyma.02G215800
GENE BODY	Glyma.02G218100
GENE BODY	Glyma.02G219600
PROMOTER	Glyma.02G221500
GENE BODY	Glyma.02G228000
PROMOTER	Glyma.02G233500
GENE BODY	Glyma.02G251700
GENE BODY	Glyma.02G257400
PROMOTER	Glyma.02G258100
GENE BODY	Glyma.02G269300
3'UTR(138bp); GENE BODY (62bp)	Glyma.02G270000
GENE BODY	Glyma.02G270300
3'UTR	Glyma.02G273400
GENE BODY	Glyma.02G274600
3'UTR	Glyma.02G277700
3'UTR(122bp); GENE BODY (78bp)	Glyma.02G277700
GENE BODY	Glyma.02G281700
GENE BODY	Glyma.02G287400
3'UTR	Glyma.02G295200
GENE BODY	Glyma.02G296200
GENE BODY	Glyma.02G298500
GENE BODY	Glyma.02G305000
PROMOTER	Glyma.02G307400
GENE BODY	Glyma.02G312000

GENE BODY	Glyma.03G022900
3'UTR	Glyma.03G027100
GENE BODY	Glyma.03G027600
PROMOTER	Glyma.03G028200
PROMOTER	Glyma.03G028200
PROMOTER	Glyma.03G031900
PROMOTER	Glyma.03G034100
GENE BODY(112bp); PROMOTER(88bp)	Glyma.03G044100
3'UTR(81bp); GENE BODY (119bp)	Glyma.03G047800
GENE BODY	Glyma.03G051700
GENE BODY	Glyma.03G057800
GENE BODY	Glyma.03G058400
GENE BODY	Glyma.03G060900
GENE BODY	Glyma.03G068100
GENE BODY	Glyma.03G076800
GENE BODY	Glyma.03G076900
GENE BODY	Glyma.03G079800
GENE BODY	Glyma.03G080300
3'UTR(79bp)	Glyma.03G085700
5'UTR(55bp); PROMOTER(145bp)	Glyma.03G086600
5'UTR(76bp); PROMOTER(124bp)	Glyma.03G092600
5'UTR(76bp); PROMOTER(124bp)	Glyma.03G092600
GENE BODY(26bp); PROMOTER(174bp)	Glyma.03G097200
PROMOTER	Glyma.03G100100
PROMOTER	Glyma.03G102800
GENE BODY	Glyma.03G105000
PROMOTER	Glyma.03G114000
GENE BODY	Glyma.03G114700
GENE BODY	Glyma.03G116900
GENE BODY	Glyma.03G118200
GENE BODY	Glyma.03G121100
PROMOTER	Glyma.03G121600
GENE BODY	Glyma.03G127600
GENE BODY	Glyma.03G132000
GENE BODY	Glyma.03G132800
GENE BODY	Glyma.03G133200
GENE BODY	Glyma.03G138400
5' UTR	Glyma.03G143300
GENE BODY	Glyma.03G146200
PROMOTER	Glyma.03G147700
3'UTR(188bp)	Glyma.03G159000
PROMOTER	Glyma.03G173600
PROMOTER	Glyma.03G179900
PROMOTER	Glyma.03G179900

GENE BODY	Glyma.03G189700
PROMOTER	Glyma.03G206200
GENE BODY	Glyma.03G223300
5' UTR	Glyma.03G225700
5' UTR	Glyma.03G225700
5'UTR	Glyma.03G225700
PROMOTER	Glyma.03G225800
PROMOTER	Glyma.03G225800
PROMOTER	Glyma.03G225800
5'UTR(194bp); PROMOTER(6bp)	Glyma.03G232300
GENE BODY	Glyma.03G235200
GENE BODY	Glyma.03G247300
PROMOTER	Glyma.03G252500
GENE BODY	Glyma.03G256800
GENE BODY	Glyma.03G264500
PROMOTER	Glyma.04G007400
PROMOTER	Glyma.04G007500
GENE BODY	Glyma.04G010500
GENE BODY (57bp); 3'UTR(143bp)	Glyma.04G011500
GENE BODY	Glyma.04G016300
GENE BODY	Glyma.04G017000
PROMOTER	Glyma.04G018200
GENE BODY	Glyma.04G025000
GENE BODY	Glyma.04G025400
GENE BODY	Glyma.04G028300
GENE BODY	Glyma.04G034900
GENE BODY	Glyma.04G039800
GENE BODY	Glyma.04G039800
GENE BODY	Glyma.04G053800
PROMOTER	Glyma.04G064100
GENE BODY	Glyma.04G064300
PROMOTER	Glyma.04G065700
3'UTR(16bp); GENE BODY(184bp)	Glyma.04G075200
GENE BODY	Glyma.04G079800
GENE BODY	Glyma.04G088300
GENE BODY	Glyma.04G090500
GENE BODY	Glyma.04G092200
GENE BODY	Glyma.04G096100
GENE BODY	Glyma.04G096100
GENE BODY	Glyma.04G096100
GENE BODY	Glyma.04G096900
GENE BODY	Glyma.04G096900
GENE BODY	Glyma.04G101100
GENE BODY	Glyma.04G113100

PROMOTER	Glyma.04G113800
GENE BODY	Glyma.04G114800
PROMOTER	Glyma.04G115000
PROMOTER	Glyma.04G115800
PROMOTER	Glyma.04G115800
GENE BODY	Glyma.04G116200
GENE BODY	Glyma.04G116700
GENE BODY	Glyma.04G121500
PROMOTER	Glyma.04G122800
GENE BODY	Glyma.04G123500
GENE BODY	Glyma.04G124800
GENE BODY	Glyma.04G124800
GENE BODY	Glyma.04G128600
3'UTR(42bp); GENE BODY (158bp)	Glyma.04G133800
3'UTR(166bp); GENE BODY (34bp)	Glyma.04G139200
GENE BODY	Glyma.04G146900
GENE BODY	Glyma.04G155000
GENE BODY	Glyma.04G156500
5'UTR(95bp); PROMOTER (105bp)	Glyma.04G157200
GENE BODY	Glyma.04G158400
3'UTR(176bp); GENE BODY (24bp)	Glyma.04G162400
GENE BODY	Glyma.04G176500
GENE BODY	Glyma.04G177300
GENE BODY	Glyma.04G182900
GENE BODY	Glyma.04G182900
PROMOTER	Glyma.04G188200
GENE BODY	Glyma.04G190500
PROMOTER	Glyma.04G191100
PROMOTER	Glyma.04G193500
GENE BODY	Glyma.04G193800
5'UTR(36bp); PROMOTER(164bp)	Glyma.04G194600
GENE BODY	Glyma.04G205000
GENE BODY	Glyma.04G210400
PROMOTER	Glyma.04G218200
PROMOTER	Glyma.04G234000
GENE BODY	Glyma.04G245400
GENE BODY	Glyma.04G252700
GENE BODY	Glyma.05G000600
GENE BODY	Glyma.05G004900
GENE BODY	Glyma.05G009500
GENE BODY	Glyma.05G013500
GENE BODY	Glyma.05G020900
GENE BODY	Glyma.05G030700
GENE BODY	Glyma.05G031300

GENE BODY	Glyma.05G031900
GENE BODY	Glyma.05G032600
GENE BODY	Glyma.05G032600
GENE BODY	Glyma.05G032600
GENE BODY	Glyma.05G035900
GENE BODY	Glyma.05G040600
GENE BODY	Glyma.05G041600
GENE BODY	Glyma.05G044500
PROMOTER	Glyma.05G044900
GENE BODY	Glyma.05G047400
3'UTR	Glyma.05G049500
PROMOTER	Glyma.05G053000
GENE BODY	Glyma.05G060200
GENE BODY	Glyma.05G060200
PROMOTER	Glyma.05G060700
GENE BODY	Glyma.05G062800
PROMOTER (92bp); 5'UTR(108bp)	Glyma.05G067200
PROMOTER (92bp); 5'UTR(108bp)	Glyma.05G067200
GENE BODY	Glyma.05G068200
GENE BODY	Glyma.05G069000
GENE BODY	Glyma.05G075100
PROMOTER	Glyma.05G075200
GENE BODY	Glyma.05G075400
PROMOTER	Glyma.05G078500
GENE BODY	Glyma.05G078600
GENE BODY	Glyma.05G080100
GENE BODY	Glyma.05G080100
PROMOTER	Glyma.05G083300
PROMOTER	Glyma.05G084500
GENE BODY	Glyma.05G100500
GENE BODY	Glyma.05G100500
GENE BODY	Glyma.05G100500
GENE BODY	Glyma.05G110200
GENE BODY	Glyma.05G115200
GENE BODY	Glyma.05G118100
3'UTR(153bp); GENE BODY (47bp)	Glyma.05G118200
GENE BODY	Glyma.05G120400
PROMOTER	Glyma.05G125000
GENE BODY	Glyma.05G136600
GENE BODY	Glyma.05G143100
GENE BODY	Glyma.05G150300
GENE BODY	Glyma.05G151100
GENE BODY	Glyma.05G154700
GENE BODY	Glyma.05G161000

GENE BODY	Glyma.05G163700
GENE BODY	Glyma.05G176400
PROMOTER	Glyma.05G180000
GENE BODY	Glyma.05G186200
GENE BODY	Glyma.05G194700
GENE BODY	Glyma.05G200600
GENE BODY	Glyma.05G208100
GENE BODY	Glyma.05G221200
GENE BODY	Glyma.05G224700
5'UTR(174bp); PROMOTER(26bp)	Glyma.05G236500
GENE BODY	Glyma.05G236500
GENE BODY	Glyma.05G236500
GENE BODY	Glyma.05G236500
GENE BODY	Glyma.05G236500
GENE BODY	Glyma.05G248000
GENE BODY	Glyma.06G016500
GENE BODY	Glyma.06G016500
GENE BODY	Glyma.06G016600
GENE BODY	Glyma.06G016700
GENE BODY	Glyma.06G018700
PROMOTER	Glyma.06G032800
3'UTR	Glyma.06G033700
GENE BODY	Glyma.06G049000
GENE BODY	Glyma.06G056300
GENE BODY	Glyma.06G061900
GENE BODY	Glyma.06G067100
GENE BODY	Glyma.06G073100
5'UTR(41bp); GENE BODY (159bp)	Glyma.06G090100
PROMOTER	Glyma.06G090100
PROMOTER	Glyma.06G090100
PROMOTER	Glyma.06G090100
GENE BODY	Glyma.06G098300
GENE BODY	Glyma.06G099100
GENE BODY	Glyma.06G108200
3'UTR(32bp); GENE BODY(168bp)	Glyma.06G108900
GENE BODY	Glyma.06G111200
GENE BODY	Glyma.06G114500
GENE BODY	Glyma.06G115100
GENE BODY	Glyma.06G116500
GENE BODY	Glyma.06G122500
GENE BODY	Glyma.06G123000
PROMOTER	Glyma.06G126000
5'UTR(73bp); GENE BODY(127bp)	Glyma.06G130800
GENE BODY	Glyma.06G137800

GENE BODY	Glyma.06G146400
GENE BODY	Glyma.06G148600
PROMOTER (170bp); 5' UTR (30bp)	Glyma.06G158600
GENE BODY	Glyma.06G159900
GENE BODY	Glyma.06G163900
GENE BODY	Glyma.06G173400
GENE BODY	Glyma.06G173500
GENE BODY	Glyma.06G173500
5'UTR(49bp); GENE BODY(151bp)	Glyma.06G173600
GENE BODY	Glyma.06G179300
GENE BODY	Glyma.06G185000
5'UTR(18bp); GENE BODY (182bp)	Glyma.06G195300
5'UTR(18bp); GENE BODY(182bp)	Glyma.06G195300
GENE BODY	Glyma.06G195300
GENE BODY	Glyma.06G195300
3'UTR	Glyma.06G197600
GENE BODY	Glyma.06G199800
GENE BODY	Glyma.06G201500
GENE BODY	Glyma.06G202500
GENE BODY	Glyma.06G205200
GENE BODY	Glyma.06G208900
3'UTR(133bp); GENE BODY (67bp)	Glyma.06G209300
GENE BODY	Glyma.06G211100
PROMOTER	Glyma.06G212600
PROMOTER(61bp); GENE BODY(139bp)	Glyma.06G212700
GENE BODY	Glyma.06G213300
GENE BODY	Glyma.06G214500
GENE BODY	Glyma.06G214500
GENE BODY	Glyma.06G214500
GENE BODY	Glyma.06G218500
GENE BODY	Glyma.06G218500
GENE BODY	Glyma.06G218500
GENE BODY	Glyma.06G220500
GENE BODY	Glyma.06G223300
GENE BODY	Glyma.06G223800
GENE BODY	Glyma.06G228000
GENE BODY	Glyma.06G228000
GENE BODY	Glyma.06G228000
GENE BODY	Glyma.06G230100
GENE BODY	Glyma.06G237900
GENE BODY	Glyma.06G238500
GENE BODY	Glyma.06G238700
GENE BODY	Glyma.06G238900
3'UTR(99bp); GENE BODY(2bp)	Glyma.06G239200

GENE BODY	Glyma.06G242800
PROMOTER	Glyma.06G243400
GENE BODY	Glyma.06G243700
PROMOTER	Glyma.06G247200
PROMOTER	Glyma.06G247200
GENE BODY	Glyma.06G254000
5' UTR	Glyma.06G256000
5' UTR	Glyma.06G256000
GENE BODY	Glyma.06G259800
GENE BODY	Glyma.06G260100
GENE BODY	Glyma.06G260100
GENE BODY	Glyma.06G261400
GENE BODY	Glyma.06G265900
GENE BODY	Glyma.06G268700
GENE BODY	Glyma.06G268800
5' UTR	Glyma.06G268900
GENE BODY	Glyma.06G269500
GENE BODY	Glyma.06G271800
GENE BODY	Glyma.06G275600
PROMOTER	Glyma.06G276200
PROMOTER	Glyma.06G285000
GENE BODY	Glyma.06G286700
PROMOTER	Glyma.06G289500
PROMOTER	Glyma.06G289600
PROMOTER(183bp); 5'UTR(17bp)	Glyma.06G296500
GENE BODY	Glyma.06G297300
PROMOTER	Glyma.06G305100
GENE BODY	Glyma.06G308100
GENE BODY	Glyma.06G309800
GENE BODY	Glyma.06G311400
PROMOTER	Glyma.06G315300
GENE BODY	Glyma.06G318300
GENE BODY	Glyma.07G003600
GENE BODY	Glyma.07G004800
GENE BODY	Glyma.07G006600
GENE BODY	Glyma.07G008200
GENE BODY	Glyma.07G009000
GENE BODY	Glyma.07G026800
GENE BODY	Glyma.07G028100
GENE BODY	Glyma.07G028100
GENE BODY	Glyma.07G029200
GENE BODY	Glyma.07G029500
GENE BODY	Glyma.07G034600
GENE BODY	Glyma.07G035100

GENE BODY	Glyma.07G043700
GENE BODY	Glyma.07G046000
GENE BODY	Glyma.07G047300
GENE BODY	Glyma.07G051000
GENE BODY	Glyma.07G069500
GENE BODY	Glyma.07G069500
GENE BODY	Glyma.07G069600
GENE BODY	Glyma.07G072900
GENE BODY	Glyma.07G077400
GENE BODY	Glyma.07G079000
3'UTR	Glyma.07G079100
GENE BODY(113bp); PROMOTER(87bp)	Glyma.07G079200
PROMOTER	Glyma.07G079300
PROMOTER	Glyma.07G087000
GENE BODY	Glyma.07G087700
3'UTR	Glyma.07G092600
5'UTR(100bp); GENE BODY(100bp)	Glyma.07G094000
GENE BODY	Glyma.07G101200
GENE BODY	Glyma.07G103200
PROMOTER	Glyma.07G107300
GENE BODY	Glyma.07G113100
GENE BODY	Glyma.07G114200
3'UTR	Glyma.07G116900
GENE BODY	Glyma.07G119900
GENE BODY (122bp); 3'UTR(78bp)	Glyma.07G124500
GENE BODY (122bp); 3'UTR(78bp)	Glyma.07G124500
GENE BODY	Glyma.07G125300
GENE BODY	Glyma.07G125300
GENE BODY	Glyma.07G128300
PROMOTER	Glyma.07G129700
GENE BODY	Glyma.07G136200
PROMOTER	Glyma.07G136300
GENE BODY	Glyma.07G149900
GENE BODY	Glyma.07G152100
PROMOTER	Glyma.07G154400
GENE BODY	Glyma.07G156500
PROMOTER	Glyma.07G157400
PROMOTER	Glyma.07G165700
GENE BODY	Glyma.07G169700
GENE BODY	Glyma.07G170200
GENE BODY	Glyma.07G171000
GENE BODY	Glyma.07G177100
GENE BODY	Glyma.07G184700
PROMOTER	Glyma.07G190600

GENE BODY	Glyma.07G197000
GENE BODY	Glyma.07G204000
GENE BODY	Glyma.07G204700
GENE BODY	Glyma.07G205900
PROMOTER	Glyma.07G209100
PROMOTER	Glyma.07G212700
3'UTR	Glyma.07G218100
GENE BODY	Glyma.07G224600
GENE BODY	Glyma.07G225000
GENE BODY	Glyma.07G230600
PROMOTER	Glyma.07G232300
GENE BODY	Glyma.07G236300
PROMOTER	Glyma.07G236900
GENE BODY	Glyma.07G259300
GENE BODY	Glyma.07G264000
GENE BODY	Glyma.07G264000
PROMOTER	Glyma.07G268700
PROMOTER	Glyma.07G274200
PROMOTER	Glyma.07G274300
GENE BODY	Glyma.08G004700
GENE BODY	Glyma.08G013000
GENE BODY	Glyma.08G013500
3'UTR(55bp); GENE BODY (145bp)	Glyma.08G027700
GENE BODY	Glyma.08G028200
3'UTR	Glyma.08G028400
GENE BODY	Glyma.08G036600
PROMOTER	Glyma.08G039800
GENE BODY	Glyma.08G041700
GENE BODY	Glyma.08G041700
GENE BODY	Glyma.08G044900
GENE BODY	Glyma.08G063500
GENE BODY	Glyma.08G065300
GENE BODY	Glyma.08G071900
GENE BODY	Glyma.08G074600
5'UTR(6bp); GENE BODY(194bp)	Glyma.08G075700
GENE BODY	Glyma.08G082500
PROMOTER (195bp); 5'UTR(5bp)	Glyma.08G083400
3'UTR(78bp); GENE BODY (122bp)	Glyma.08G092700
GENE BODY	Glyma.08G097800
GENE BODY	Glyma.08G100800
GENE BODY	Glyma.08G108500
GENE BODY	Glyma.08G111500
PROMOTER	Glyma.08G115800
GENE BODY	Glyma.08G125700

GENE BODY	Glyma.08G127200
GENE BODY	Glyma.08G139300
GENE BODY	Glyma.08G140100
PROMOTER	Glyma.08G140400
GENE BODY	Glyma.08G141100
GENE BODY	Glyma.08G151600
GENE BODY	Glyma.08G170000
3'UTR(6bp); GENE BODY (194bp)	Glyma.08G171900
PROMOTER	Glyma.08G191200
GENE BODY	Glyma.08G192200
GENE BODY	Glyma.08G194600
GENE BODY	Glyma.08G197700
GENE BODY	Glyma.08G202800
GENE BODY	Glyma.08G209500
GENE BODY	Glyma.08G213900
GENE BODY	Glyma.08G219200
PROMOTER	Glyma.08G220700
GENE BODY	Glyma.08G222300
GENE BODY	Glyma.08G228000
3'UTR	Glyma.08G233900
3'UTR	Glyma.08G233900
3'UTR	Glyma.08G233900
3'UTR	Glyma.08G233900
3'UTR (178bp); GENE BODY (22bp)	Glyma.08G233900
5'UTR(21bp); GENE BODY(179bp)	Glyma.08G233900
5'UTR(37bp); PROMOTER(163bp)	Glyma.08G233900
5'UTR(37bp); PROMOTER(163bp)	Glyma.08G233900
GENE BODY	Glyma.08G236400
GENE BODY	Glyma.08G236700
GENE BODY	Glyma.08G236700
GENE BODY	Glyma.08G236700
GENE BODY	Glyma.08G236700
GENE BODY	Glyma.08G237500
3'UTR(154bp); GENE BODY (46bp)	Glyma.08G238000
GENE BODY	Glyma.08G238000
5'UTR(156bp); GENE BODY (44bp)	Glyma.08G238500
GENE BODY	Glyma.08G238800
3'UTR(189bp); GENE BODY (11bp)	Glyma.08G239000
GENE BODY	Glyma.08G240400
3'UTR(93bp); GENE BODY (107bp)	Glyma.08G241100
PROMOTER	Glyma.08G241900
GENE BODY	Glyma.08G242700
GENE BODY	Glyma.08G249400
GENE BODY	Glyma.08G253800

PROMOTER	Glyma.08G258900
GENE BODY	Glyma.08G259000
GENE BODY	Glyma.08G264900
GENE BODY	Glyma.08G264900
GENE BODY	Glyma.08G265300
PROMOTER	Glyma.08G268800
PROMOTER	Glyma.08G271700
3'UTR(49bp); GENE BODY (151bp)	Glyma.08G273000
GENE BODY	Glyma.08G273000
GENE BODY	Glyma.08G275100
GENE BODY	Glyma.08G275100
GENE BODY(182bp); PROMOTER(18bp)	Glyma.08G275100
PROMOTER	Glyma.08G275100
PROMOTER	Glyma.08G275100
GENE BODY	Glyma.08G276200
GENE BODY	Glyma.08G276200
GENE BODY	Glyma.08G276200
GENE BODY	Glyma.08G279100
GENE BODY	Glyma.08G279300
GENE BODY	Glyma.08G279800
PROMOTER	Glyma.08G279800
3'UTR	Glyma.08G282400
GENE BODY	Glyma.08G283600
GENE BODY	Glyma.08G288100
GENE BODY	Glyma.08G291800
PROMOTER	Glyma.08G300900
GENE BODY	Glyma.08G324900
GENE BODY	Glyma.08G328500
GENE BODY	Glyma.08G344800
PROMOTER	Glyma.08G349000
PROMOTER(191bp); 5'UTR(9bp)	Glyma.08G357000
PROMOTER(191bp); 5'UTR(9bp)	Glyma.08G357000
3'UTR(20bp); GENE BODY (180bp)	Glyma.08G362400
GENE BODY	Glyma.09G002600
GENE BODY	Glyma.09G002700
GENE BODY	Glyma.09G013300
GENE BODY	Glyma.09G015100
GENE BODY	Glyma.09G016800
GENE BODY	Glyma.09G017000
GENE BODY	Glyma.09G023600
GENE BODY	Glyma.09G024400
5'UTR(75bp); GENE BODY(125bp)	Glyma.09G025000
GENE BODY	Glyma.09G025400
PROMOTER	Glyma.09G027300

PROMOTER	Glyma.09G029700
GENE BODY	Glyma.09G030300
PROMOTER	Glyma.09G042800
5'UTR(67bp); GENE BODY (133bp)	Glyma.09G046700
5'UTR(67bp); GENE BODY(133bp)	Glyma.09G046700
PROMOTER	Glyma.09G049100
PROMOTER	Glyma.09G055900
GENE BODY	Glyma.09G056100
GENE BODY	Glyma.09G057400
5'UTR(62bp); GENE BODY(138bp)	Glyma.09G057800
GENE BODY	Glyma.09G065300
GENE BODY	Glyma.09G065300
PROMOTER	Glyma.09G068500
GENE BODY	Glyma.09G070600
PROMOTER	Glyma.09G072500
GENE BODY	Glyma.09G073100
PROMOTER	Glyma.09G078600
GENE BODY	Glyma.09G083800
GENE BODY	Glyma.09G084300
GENE BODY	Glyma.09G089400
GENE BODY	Glyma.09G095400
PROMOTER	Glyma.09G109200
PROMOTER	Glyma.09G110200
GENE BODY	Glyma.09G110300
PROMOTER	Glyma.09G111900
PROMOTER(167bp); GENE BODY(33bp)	Glyma.09G112800
GENE BODY	Glyma.09G116800
GENE BODY	Glyma.09G120200
GENE BODY	Glyma.09G121300
GENE BODY	Glyma.09G124400
PROMOTER	Glyma.09G124900
3'UTR(85bp)	Glyma.09G126300
PROMOTER	Glyma.09G129600
GENE BODY	Glyma.09G130900
PROMOTER	Glyma.09G144900
GENE BODY	Glyma.09G148000
3'UTR	Glyma.09G148100
GENE BODY	Glyma.09G148500
GENE BODY	Glyma.09G153500
PROMOTER	Glyma.09G154200
GENE BODY	Glyma.09G170600
GENE BODY	Glyma.09G171000
5'UTR (82bp); PROMOTER (118bp)	Glyma.09G171400
GENE BODY	Glyma.09G180800

PROMOTER	Glyma.09G183100
GENE BODY	Glyma.09G188000
3'UTR(29bp); GENE BODY (171bp)	Glyma.09G190300
GENE BODY	Glyma.09G191600
PROMOTER	Glyma.09G193200
GENE BODY	Glyma.09G194400
GENE BODY	Glyma.09G199100
PROMOTER	Glyma.09G202900
PROMOTER	Glyma.09G202900
GENE BODY(95bp); PROMOTER (105bp)	Glyma.09G219500
PROMOTER	Glyma.09G219600
GENE BODY	Glyma.09G228300
PROMOTER	Glyma.09G230600
GENE BODY	Glyma.09G234400
GENE BODY	Glyma.09G237200
GENE BODY	Glyma.09G246500
GENE BODY	Glyma.09G251200
3'UTR	Glyma.09G258900
3'UTR(11bp); GENE BODY (189bp)	Glyma.09G259200
PROMOTER	Glyma.09G259300
GENE BODY	Glyma.09G271700
GENE BODY	Glyma.09G279900
PROMOTER	Glyma.09G286200
GENE BODY	Glyma.10G008300
GENE BODY	Glyma.10G009700
GENE BODY	Glyma.10G020700
GENE BODY	Glyma.10G023000
GENE BODY	Glyma.10G023300
GENE BODY	Glyma.10G025000
GENE BODY	Glyma.10G028000
GENE BODY	Glyma.10G030000
GENE BODY (191bp); 3'UTR(9bp)	Glyma.10G034900
5'UTR(110bp); GENE BODY (90bp)	Glyma.10G043400
5'UTR(6bp); GENE BODY(194bp)	Glyma.10G054400
GENE BODY	Glyma.10G060000
GENE BODY	Glyma.10G065800
GENE BODY	Glyma.10G065900
GENE BODY	Glyma.10G075900
GENE BODY	Glyma.10G078700
GENE BODY	Glyma.10G078900
GENE BODY	Glyma.10G083500
GENE BODY	Glyma.10G095200
GENE BODY	Glyma.10G095200
GENE BODY	Glyma.10G095200

GENE BODY	Glyma.10G095200
GENE BODY	Glyma.10G095200
GENE BODY	Glyma.10G096900
PROMOTER(171bp); 5'UTR(29bp)	Glyma.10G098700
PROMOTER(171bp); 5'UTR(29bp)	Glyma.10G098700
GENE BODY	Glyma.10G102200
GENE BODY	Glyma.10G102900
GENE BODY (115bp); PROMOTER(85bp)	Glyma.10G102900
GENE BODY	Glyma.10G104300
GENE BODY	Glyma.10G108500
GENE BODY	Glyma.10G111500
GENE BODY	Glyma.10G118100
GENE BODY	Glyma.10G118800
GENE BODY	Glyma.10G120900
GENE BODY	Glyma.10G123400
GENE BODY	Glyma.10G123400
GENE BODY	Glyma.10G143600
GENE BODY	Glyma.10G148600
GENE BODY	Glyma.10G149700
GENE BODY	Glyma.10G151500
GENE BODY	Glyma.10G151700
3'UTR(136bp); GENE BODY (64bp)	Glyma.10G152500
GENE BODY	Glyma.10G159300
GENE BODY	Glyma.10G159500
PROMOTER	Glyma.10G164400
GENE BODY	Glyma.10G166200
3'UTR	Glyma.10G171500
PROMOTER	Glyma.10G174000
GENE BODY	Glyma.10G183000
GENE BODY	Glyma.10G187800
GENE BODY	Glyma.10G189200
GENE BODY	Glyma.10G191500
PROMOTER	Glyma.10G195900
PROMOTER	Glyma.10G197100
GENE BODY	Glyma.10G201600
GENE BODY	Glyma.10G202600
5'UTR(93bp); GENE BODY(107bp)	Glyma.10G208100
GENE BODY	Glyma.10G209400
GENE BODY	Glyma.10G209600
PROMOTER	Glyma.10G229600
3'UTR(102bp)	Glyma.10G233300
3'UTR(102bp)	Glyma.10G233300
PROMOTER	Glyma.10G235100
GENE BODY	Glyma.10G241900

PROMOTER	Glyma.10G243300
3'UTR(8bp)	Glyma.10G246000
PROMOTER	Glyma.10G281900
GENE BODY	Glyma.10G283000
5'UTR(81bp); GENE BODY (119bp)	Glyma.10G294000
3'UTR(47bp); GENE BODY(153bp)	Glyma.10G294300
GENE BODY	Glyma.10G298900
GENE BODY	Glyma.11G002600
GENE BODY	Glyma.11G008700
PROMOTER	Glyma.11G020100
PROMOTER	Glyma.11G020100
GENE BODY	Glyma.11G037300
GENE BODY	Glyma.11G039900
3'UTR(125bp); GENE BODY(75bp)	Glyma.11G040000
PROMOTER	Glyma.11G055200
GENE BODY	Glyma.11G057000
GENE BODY	Glyma.11G065700
GENE BODY	Glyma.11G082200
PROMOTER	Glyma.11G096200
PROMOTER	Glyma.11G102700
GENE BODY	Glyma.11G102800
GENE BODY	Glyma.11G108500
GENE BODY	Glyma.11G109800
GENE BODY	Glyma.11G110100
PROMOTER	Glyma.11G129700
PROMOTER	Glyma.11G141100
GENE BODY	Glyma.11G152600
PROMOTER(198bp); GENE BODY(2bp)	Glyma.11G170700
GENE BODY	Glyma.11G184900
GENE BODY	Glyma.11G188100
GENE BODY	Glyma.11G188900
3'UTR(104bp); GENE BODY (96bp)	Glyma.11G191000
GENE BODY	Glyma.11G192500
GENE BODY	Glyma.11G193100
GENE BODY	Glyma.11G194700
PROMOTER	Glyma.11G200200
PROMOTER	Glyma.11G206200
GENE BODY	Glyma.11G222900
GENE BODY	Glyma.11G228600
PROMOTER	Glyma.11G228700
5'UTR(2bp); GENE BODY(198bp)	Glyma.11G251600
PROMOTER	Glyma.11G252300
GENE BODY	Glyma.11G256800
GENE BODY	Glyma.12G004100

GENE BODY	Glyma.12G004100
GENE BODY	Glyma.12G016700
GENE BODY	Glyma.12G027600
GENE BODY	Glyma.12G036400
PROMOTER	Glyma.12G041100
GENE BODY	Glyma.12G051000
GENE BODY	Glyma.12G051000
GENE BODY	Glyma.12G051000
PROMOTER	Glyma.12G051800
PROMOTER	Glyma.12G060800
GENE BODY	Glyma.12G066300
5'UTR(165bp); PROMOTER (35bp)	Glyma.12G066400
GENE BODY	Glyma.12G067900
PROMOTER	Glyma.12G074700
3'UTR(84bp); GENE BODY (116bp)	Glyma.12G082100
GENE BODY	Glyma.12G084300
GENE BODY	Glyma.12G096900
PROMOTER	Glyma.12G117500
GENE BODY	Glyma.12G119500
GENE BODY	Glyma.12G133500
GENE BODY	Glyma.12G133500
GENE BODY	Glyma.12G136600
PROMOTER	Glyma.12G137100
GENE BODY(154bp); PROMOTER(46bp)	Glyma.12G140800
GENE BODY(154bp); PROMOTER(46bp)	Glyma.12G140800
PROMOTER	Glyma.12G147400
GENE BODY	Glyma.12G152300
GENE BODY	Glyma.12G152700
GENE BODY	Glyma.12G155900
GENE BODY	Glyma.12G156200
GENE BODY	Glyma.12G157800
GENE BODY	Glyma.12G158600
GENE BODY	Glyma.12G166100
GENE BODY	Glyma.12G180100
GENE BODY	Glyma.12G180800
GENE BODY	Glyma.12G192300
GENE BODY	Glyma.12G198100
GENE BODY	Glyma.12G198100
GENE BODY	Glyma.12G201100
GENE BODY	Glyma.12G203700
GENE BODY	Glyma.12G205500
GENE BODY	Glyma.12G205500
GENE BODY	Glyma.12G209100
GENE BODY	Glyma.12G214200

GENE BODY	Glyma.12G216200
GENE BODY	Glyma.12G219400
PROMOTER	Glyma.12G223100
GENE BODY	Glyma.12G226700
GENE BODY	Glyma.12G229900
GENE BODY	Glyma.12G230600
GENE BODY	Glyma.12G231800
GENE BODY	Glyma.12G235100
GENE BODY	Glyma.12G241600
GENE BODY	Glyma.13G003500
GENE BODY	Glyma.13G006200
GENE BODY	Glyma.13G010000
GENE BODY	Glyma.13G010000
GENE BODY	Glyma.13G026100
GENE BODY	Glyma.13G027100
GENE BODY (158bp)	Glyma.13G030000
GENE BODY (93bp); PROMOTER (107bp)	Glyma.13G030000
PROMOTER	Glyma.13G030000
PROMOTER(107bp); GENE BODY(93bp)	Glyma.13G030000
PROMOTER	Glyma.13G030100
PROMOTER	Glyma.13G030100
PROMOTER	Glyma.13G030100
PROMOTER	Glyma.13G030100
GENE BODY	Glyma.13G030600
GENE BODY	Glyma.13G035200
GENE BODY	Glyma.13G036000
3'UTR	Glyma.13G036700
PROMOTER	Glyma.13G038300
3'UTR	Glyma.13G042400
GENE BODY	Glyma.13G048300
GENE BODY	Glyma.13G048300
GENE BODY	Glyma.13G048300
GENE BODY	Glyma.13G048300
PROMOTER	Glyma.13G052600
GENE BODY	Glyma.13G053700
GENE BODY	Glyma.13G058600
GENE BODY	Glyma.13G058800
3'UTR(34bp); GENE BODY (166bp)	Glyma.13G059000
3'UTR	Glyma.13G059600
PROMOTER	Glyma.13G062000
PROMOTER	Glyma.13G062000
GENE BODY	Glyma.13G063600
PROMOTER	Glyma.13G067700
GENE BODY	Glyma.13G073900

GENE BODY	Glyma.13G078200
GENE BODY	Glyma.13G078200
GENE BODY	Glyma.13G078800
GENE BODY	Glyma.13G084100
GENE BODY	Glyma.13G089300
GENE BODY	Glyma.13G115500
GENE BODY	Glyma.13G119100
GENE BODY	Glyma.13G127500
GENE BODY	Glyma.13G128700
GENE BODY	Glyma.13G129900
GENE BODY	Glyma.13G130000
3'UTR	Glyma.13G130500
GENE BODY	Glyma.13G130700
PROMOTER	Glyma.13G130900
PROMOTER	Glyma.13G131000
GENE BODY	Glyma.13G134400
GENE BODY	Glyma.13G135800
GENE BODY	Glyma.13G156600
PROMOTER	Glyma.13G156900
PROMOTER	Glyma.13G156900
GENE BODY	Glyma.13G160000
PROMOTER	Glyma.13G160300
GENE BODY	Glyma.13G166100
GENE BODY	Glyma.13G174500
GENE BODY	Glyma.13G174900
GENE BODY	Glyma.13G184600
GENE BODY	Glyma.13G189000
5'UTR (94bp); PROMOTER (106bp)	Glyma.13G190500
GENE BODY	Glyma.13G194900
GENE BODY	Glyma.13G196700
GENE BODY	Glyma.13G196900
GENE BODY	Glyma.13G198700
5'UTR(97bp); GENE BODY(103bp)	Glyma.13G209200
GENE BODY	Glyma.13G221400
GENE BODY	Glyma.13G223400
PROMOTER	Glyma.13G225300
GENE BODY	Glyma.13G233400
GENE BODY	Glyma.13G233400
GENE BODY	Glyma.13G235300
PROMOTER	Glyma.13G235300
GENE BODY	Glyma.13G239300
GENE BODY	Glyma.13G244200
GENE BODY	Glyma.13G253600
GENE BODY	Glyma.13G259100

PROMOTER	Glyma.13G259200
GENE BODY	Glyma.13G275400
PROMOTER	Glyma.13G277200
GENE BODY	Glyma.13G277700
GENE BODY	Glyma.13G278800
3'UTR(129bp); GENE BODY (71bp)	Glyma.13G281900
5'UTR(111bp); GENE BODY (89bp)	Glyma.13G283900
5'UTR(111bp); GENE BODY (89bp)	Glyma.13G283900
5'UTR(111bp); GENE BODY (89bp)	Glyma.13G283900
PROMOTER	Glyma.13G289400
GENE BODY	Glyma.13G296400
3'UTR(107bp); GENE BODY (93bp)	Glyma.13G302900
PROMOTER	Glyma.13G305700
PROMOTER	Glyma.13G305700
GENE BODY	Glyma.13G322000
GENE BODY	Glyma.13G326400
PROMOTER	Glyma.13G328200
GENE BODY	Glyma.13G342500
PROMOTER	Glyma.13G345000
PROMOTER	Glyma.13G345100
PROMOTER	Glyma.13G352500
GENE BODY	Glyma.13G355800
GENE BODY	Glyma.13G367200
PROMOTER	Glyma.13G368100
GENE BODY	Glyma.13G371300
GENE BODY	Glyma.13G372400
GENE BODY	Glyma.13G372400
GENE BODY	Glyma.14G018300
GENE BODY	Glyma.14G025300
GENE BODY	Glyma.14G031300
GENE BODY	Glyma.14G044300
GENE BODY	Glyma.14G044300
GENE BODY	Glyma.14G044900
GENE BODY	Glyma.14G045600
PROMOTER	Glyma.14G056000
GENE BODY	Glyma.14G066000
GENE BODY	Glyma.14G066100
GENE BODY	Glyma.14G066600
3'UTR	Glyma.14G083300
GENE BODY	Glyma.14G084400
GENE BODY	Glyma.14G091400
GENE BODY	Glyma.14G092100
5'UTR (177bp); PROMOTER (23bp)	Glyma.14G095000
GENE BODY	Glyma.14G095200

5'UTR(49bp); PROMOTER(151bp)	Glyma.14G095300
GENE BODY	Glyma.14G098000
GENE BODY	Glyma.14G098100
GENE BODY	Glyma.14G099300
GENE BODY	Glyma.14G104400
PROMOTER	Glyma.14G104800
GENE BODY	Glyma.14G105100
GENE BODY	Glyma.14G105100
PROMOTER	Glyma.14G106300
PROMOTER	Glyma.14G106300
PROMOTER	Glyma.14G108800
PROMOTER	Glyma.14G108800
5'UTR	Glyma.14G110800
GENE BODY	Glyma.14G112200
3'UTR	Glyma.14G112600
GENE BODY	Glyma.14G112700
GENE BODY	Glyma.14G119200
GENE BODY	Glyma.14G119200
PROMOTER	Glyma.14G120000
PROMOTER (173bp); 5' UTR (27bp)	Glyma.14G121200
GENE BODY	Glyma.14G128300
GENE BODY	Glyma.14G129100
GENE BODY	Glyma.14G131700
5'UTR(14bp); GENE BODY(186bp)	Glyma.14G132500
GENE BODY	Glyma.14G132500
PROMOTER	Glyma.14G137100
PROMOTER	Glyma.14G137400
GENE BODY	Glyma.14G138900
3'UTR(70bp); GENE BODY (130bp)	Glyma.14G140600
GENE BODY	Glyma.14G141800
GENE BODY	Glyma.14G142100
GENE BODY	Glyma.14G145000
5'UTR	Glyma.14G150500
GENE BODY	Glyma.14G151100
PROMOTER (37bp); 5' UTR(122bp); GENE BO	Glyma.14G159200
GENE BODY	Glyma.14G159200
PROMOTER	Glyma.14G159200
PROMOTER(37bp); 5'UTR(122bp); GENE BOD	Glyma.14G159200
3'UTR(17bp)	Glyma.14G160400
GENE BODY	Glyma.14G160400
GENE BODY	Glyma.14G160400
GENE BODY	Glyma.14G161200
GENE BODY	Glyma.14G162300
GENE BODY	Glyma.14G162300

GENE BODY	Glyma.14G162300
GENE BODY	Glyma.14G162300
GENE BODY	Glyma.14G163000
GENE BODY	Glyma.14G163000
5'UTR(117bp); GENE BODY (83bp)	Glyma.14G163100
GENE BODY	Glyma.14G164000
GENE BODY	Glyma.14G164000
3'UTR	Glyma.14G166700
GENE BODY	Glyma.14G170300
GENE BODY	Glyma.14G170300
PROMOTER	Glyma.14G171200
PROMOTER	Glyma.14G179000
GENE BODY	Glyma.14G179100
GENE BODY	Glyma.14G179200
GENE BODY	Glyma.14G183500
5'UTR(23bp); GENE BODY(177bp)	Glyma.14G186900
GENE BODY	Glyma.14G190200
3'UTR(72bp); GENE BODY (128bp)	Glyma.14G190400
GENE BODY	Glyma.14G190900
GENE BODY	Glyma.14G192900
PROMOTER	Glyma.14G199800
GENE BODY	Glyma.14G200600
GENE BODY(89bp); PROMOTER(111bp)	Glyma.14G200800
PROMOTER	Glyma.14G200800
GENE BODY	Glyma.14G204100
GENE BODY	Glyma.14G211800
PROMOTER	Glyma.14G222200
PROMOTER	Glyma.15G000900
GENE BODY	Glyma.15G006900
PROMOTER	Glyma.15G015100
GENE BODY	Glyma.15G017200
GENE BODY	Glyma.15G023800
5' UTR	Glyma.15G025900
5'UTR	Glyma.15G025900
GENE BODY	Glyma.15G030400
5'UTR(71bp); GENE BODY (129bp)	Glyma.15G030500
PROMOTER	Glyma.15G035400
GENE BODY	Glyma.15G040100
PROMOTER	Glyma.15G046800
PROMOTER	Glyma.15G046800
3'UTR	Glyma.15G056300
PROMOTER	Glyma.15G056400
GENE BODY	Glyma.15G057900
GENE BODY	Glyma.15G058700

GENE BODY	Glyma.15G058900
PROMOTER	Glyma.15G071300
GENE BODY	Glyma.15G074000
GENE BODY	Glyma.15G076300
5' UTR	Glyma.15G087600
GENE BODY	Glyma.15G097000
GENE BODY	Glyma.15G098100
GENE BODY	Glyma.15G107500
GENE BODY	Glyma.15G116000
GENE BODY	Glyma.15G125700
3'UTR(67bp); GENE BODY (124bp)	Glyma.15G126100
3'UTR(67bp); GENE BODY (124bp)	Glyma.15G126100
PROMOTER	Glyma.15G126100
PROMOTER (28bp); 5'UTR(161bp); GENE BOD	Glyma.15G126100
GENE BODY	Glyma.15G127200
PROMOTER(156bp); GENE BODY(44bp)	Glyma.15G135300
PROMOTER	Glyma.15G138400
PROMOTER	Glyma.15G145400
GENE BODY	Glyma.15G154300
GENE BODY	Glyma.15G161200
GENE BODY	Glyma.15G163200
PROMOTER	Glyma.15G165300
GENE BODY	Glyma.15G172700
GENE BODY	Glyma.15G173300
GENE BODY	Glyma.15G173900
5'UTR(26bp); PROMOTER (174bp)	Glyma.15G175600
PROMOTER	Glyma.15G175700
GENE BODY	Glyma.15G181200
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G182000
GENE BODY	Glyma.15G192300
GENE BODY	Glyma.15G192300
PROMOTER	Glyma.15G192800
GENE BODY	Glyma.15G193400
GENE BODY	Glyma.15G194000
5' UTR	Glyma.15G197000
5' UTR	Glyma.15G197000
5' UTR	Glyma.15G197000
5'UTR	Glyma.15G197000

5'UTR(29bp); GENE BODY(171bp)	Glyma.15G198600
GENE BODY	Glyma.15G204500
GENE BODY	Glyma.15G204600
GENE BODY	Glyma.15G204600
GENE BODY	Glyma.15G204600
GENE BODY	Glyma.15G204600
GENE BODY	Glyma.15G204700
3'UTR(105bp); GENE BODY (95bp)	Glyma.15G209000
GENE BODY	Glyma.15G212200
GENE BODY	Glyma.15G212800
GENE BODY	Glyma.15G212800
GENE BODY	Glyma.15G213000
GENE BODY	Glyma.15G213000
GENE BODY	Glyma.15G213200
GENE BODY	Glyma.15G214400
GENE BODY	Glyma.15G215500
3'UTR	Glyma.15G219300
GENE BODY	Glyma.15G220900
GENE BODY	Glyma.15G226200
GENE BODY	Glyma.15G232600
PROMOTER	Glyma.15G234900
GENE BODY	Glyma.15G235900
PROMOTER	Glyma.15G240300
PROMOTER(16bp); 5'UTR(107bp); GENE BOD	Glyma.15G240300
PROMOTER(16bp); 5'UTR(107bp); GENE BOD	Glyma.15G240300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G245300
GENE BODY	Glyma.15G245300
PROMOTER	Glyma.15G245400
GENE BODY	Glyma.15G246800
GENE BODY	Glyma.15G248600
GENE BODY	Glyma.15G248600
5'UTR(40bp); PROMOTER(160bp)	Glyma.15G248800
3'UTR(13bp); GENE BODY(173bp)	Glyma.15G252500
3'UTR(79bp); GENE BODY (121bp)	Glyma.15G254100
PROMOTER	Glyma.15G255100
PROMOTER	Glyma.15G255800
GENE BODY	Glyma.15G255900
GENE BODY	Glyma.15G271800
3'UTR(49bp); GENE BODY (151bp)	Glyma.15G273500
GENE BODY	Glyma.15G274000

GENE BODY	Glyma.16G004800
GENE BODY	Glyma.16G007000
GENE BODY	Glyma.16G009500
PROMOTER	Glyma.16G014200
GENE BODY	Glyma.16G018300
GENE BODY	Glyma.16G025500
GENE BODY	Glyma.16G039900
GENE BODY	Glyma.16G039900
GENE BODY	Glyma.16G040900
GENE BODY	Glyma.16G041300
GENE BODY	Glyma.16G049600
GENE BODY	Glyma.16G052700
GENE BODY	Glyma.16G053100
PROMOTER	Glyma.16G056800
GENE BODY	Glyma.16G057400
5'UTR(101bp); GENE BODY (99bp)	Glyma.16G058000
GENE BODY	Glyma.16G066900
GENE BODY	Glyma.16G066900
PROMOTER	Glyma.16G067500
GENE BODY	Glyma.16G069300
GENE BODY	Glyma.16G071500
GENE BODY	Glyma.16G073700
5'UTR (163bp); PROMOTER (37bp)	Glyma.16G077400
PROMOTER	Glyma.16G078500
GENE BODY	Glyma.16G087100
3'UTR(55bp); GENE BODY (145bp)	Glyma.16G088100
PROMOTER	Glyma.16G088500
PROMOTER	Glyma.16G088600
GENE BODY	Glyma.16G091400
3'UTR(197bp); GENE BODY (3bp)	Glyma.16G092800
GENE BODY	Glyma.16G095500
GENE BODY	Glyma.16G101800
PROMOTER	Glyma.16G111800
PROMOTER	Glyma.16G112800
PROMOTER	Glyma.16G112800
PROMOTER	Glyma.16G113800
GENE BODY	Glyma.16G114200
GENE BODY	Glyma.16G115200
PROMOTER	Glyma.16G115300
GENE BODY	Glyma.16G115700
GENE BODY	Glyma.16G115700
3'UTR	Glyma.16G127900
5'UTR(136bp); GENE BODY(64bp)	Glyma.16G128300
GENE BODY	Glyma.16G128600

GENE BODY	Glyma.16G131100
GENE BODY	Glyma.16G134700
GENE BODY	Glyma.16G135000
5'UTR(54bp); GENE BODY (146bp)	Glyma.16G136400
5'UTR(22bp); GENE BODY(178bp)	Glyma.16G138300
GENE BODY	Glyma.16G138300
GENE BODY	Glyma.16G141800
GENE BODY	Glyma.16G144200
GENE BODY	Glyma.16G147000
GENE BODY	Glyma.16G148600
GENE BODY	Glyma.16G153800
GENE BODY	Glyma.16G155700
GENE BODY	Glyma.16G159600
PROMOTER	Glyma.16G159900
5'UTR	Glyma.16G164700
GENE BODY	Glyma.16G172300
GENE BODY	Glyma.16G172400
GENE BODY	Glyma.16G182700
PROMOTER	Glyma.16G183300
PROMOTER	Glyma.16G186000
GENE BODY	Glyma.16G189700
GENE BODY	Glyma.16G190100
GENE BODY	Glyma.16G202300
GENE BODY	Glyma.17G001100
GENE BODY	Glyma.17G010800
GENE BODY	Glyma.17G017700
GENE BODY	Glyma.17G024000
GENE BODY	Glyma.17G024800
GENE BODY	Glyma.17G027700
GENE BODY	Glyma.17G027700
GENE BODY	Glyma.17G033600
GENE BODY	Glyma.17G037600
GENE BODY	Glyma.17G039300
GENE BODY	Glyma.17G041900
GENE BODY	Glyma.17G044200
PROMOTER	Glyma.17G044800
GENE BODY	Glyma.17G057300
GENE BODY	Glyma.17G059800
GENE BODY	Glyma.17G060300
GENE BODY	Glyma.17G060300
GENE BODY	Glyma.17G062200
GENE BODY	Glyma.17G083300
GENE BODY	Glyma.17G083700
GENE BODY	Glyma.17G089100

PROMOTER	Glyma.17G093700
PROMOTER	Glyma.17G093700
GENE BODY	Glyma.17G094300
GENE BODY	Glyma.17G094300
GENE BODY	Glyma.17G100600
GENE BODY	Glyma.17G105700
GENE BODY	Glyma.17G114400
PROMOTER	Glyma.17G118400
GENE BODY	Glyma.17G125500
GENE BODY	Glyma.17G129200
GENE BODY	Glyma.17G129900
GENE BODY	Glyma.17G129900
GENE BODY	Glyma.17G145000
GENE BODY	Glyma.17G145500
GENE BODY	Glyma.17G145700
PROMOTER	Glyma.17G150300
GENE BODY	Glyma.17G158200
GENE BODY	Glyma.17G160700
PROMOTER	Glyma.17G169200
GENE BODY	Glyma.17G171400
GENE BODY	Glyma.17G171400
GENE BODY	Glyma.17G171400
GENE BODY	Glyma.17G171400
PROMOTER	Glyma.17G171400
PROMOTER	Glyma.17G171400
GENE BODY	Glyma.17G171600
GENE BODY	Glyma.17G173200
GENE BODY	Glyma.17G173300
GENE BODY	Glyma.17G173300
GENE BODY	Glyma.17G181000
GENE BODY	Glyma.17G183400
GENE BODY	Glyma.17G184300
GENE BODY	Glyma.17G184300
GENE BODY(150bp); PROMOTER(50bp)	Glyma.17G184300
PROMOTER	Glyma.17G184300
PROMOTER	Glyma.17G188600
PROMOTER(93bp); GENE BODY(107bp)	Glyma.17G190200
PROMOTER(93bp); GENE BODY(107bp)	Glyma.17G190200
GENE BODY	Glyma.17G191000
3'UTR	Glyma.17G191700
PROMOTER	Glyma.17G191800
PROMOTER(172bp); GENE BODY(28bp)	Glyma.17G191800
GENE BODY	Glyma.17G199600
GENE BODY	Glyma.17G200200

GENE BODY	Glyma.17G201000
GENE BODY	Glyma.17G204000
GENE BODY	Glyma.17G204000
PROMOTER	Glyma.17G205900
PROMOTER(187bp); GENE BODY(13bp)	Glyma.17G206000
GENE BODY	Glyma.17G206400
PROMOTER	Glyma.17G207600
GENE BODY	Glyma.17G210100
GENE BODY	Glyma.17G210100
GENE BODY	Glyma.17G212300
GENE BODY	Glyma.17G212600
PROMOTER	Glyma.17G213600
GENE BODY	Glyma.17G215800
3'UTR(60bp); GENE BODY (140bp)	Glyma.17G219600
GENE BODY	Glyma.17G220800
GENE BODY	Glyma.17G222100
GENE BODY	Glyma.17G222200
3'UTR	Glyma.17G226600
GENE BODY	Glyma.17G235400
GENE BODY	Glyma.17G235400
PROMOTER	Glyma.17G235400
GENE BODY	Glyma.17G244800
PROMOTER	Glyma.17G245500
GENE BODY	Glyma.17G249100
3'UTR(98bp); GENE BODY (102bp)	Glyma.17G250200
GENE BODY	Glyma.17G253700
GENE BODY	Glyma.17G255500
GENE BODY	Glyma.17G257100
GENE BODY	Glyma.17G258800
GENE BODY	Glyma.18G000100
GENE BODY	Glyma.18G000100
GENE BODY	Glyma.18G003800
GENE BODY	Glyma.18G004600
GENE BODY	Glyma.18G004600
GENE BODY	Glyma.18G004600
PROMOTER	Glyma.18G009100
GENE BODY	Glyma.18G011200
GENE BODY	Glyma.18G011200
PROMOTER	Glyma.18G012700
PROMOTER	Glyma.18G013300
PROMOTER	Glyma.18G013300
GENE BODY	Glyma.18G016200
GENE BODY	Glyma.18G019600
GENE BODY	Glyma.18G027800

5'UTR(33bp); GENE BODY(167bp)	Glyma.18G028900
GENE BODY	Glyma.18G055700
PROMOTER	Glyma.18G060800
GENE BODY	Glyma.18G064900
3'UTR(15bp); GENE BODY(185bp)	Glyma.18G068800
3'UTR(163bp); GENE BODY (37bp)	Glyma.18G082200
GENE BODY	Glyma.18G087700
GENE BODY	Glyma.18G093500
GENE BODY	Glyma.18G093500
GENE BODY	Glyma.18G093600
GENE BODY	Glyma.18G093600
GENE BODY	Glyma.18G099600
GENE BODY	Glyma.18G107900
GENE BODY	Glyma.18G109100
GENE BODY	Glyma.18G109100
PROMOTER	Glyma.18G112200
GENE BODY	Glyma.18G115800
3'UTR	Glyma.18G119200
PROMOTER	Glyma.18G124900
3'UTR(27bp); GENE BODY (173bp)	Glyma.18G127700
GENE BODY	Glyma.18G128900
GENE BODY	Glyma.18G131200
PROMOTER	Glyma.18G133400
GENE BODY	Glyma.18G137700
GENE BODY	Glyma.18G140800
GENE BODY	Glyma.18G140800
PROMOTER	Glyma.18G142600
PROMOTER	Glyma.18G146700
GENE BODY	Glyma.18G147700
GENE BODY	Glyma.18G149700
GENE BODY	Glyma.18G149700
GENE BODY	Glyma.18G154700
GENE BODY	Glyma.18G156300
5'UTR(73bp); PROMOTER(127bp)	Glyma.18G157300
3'UTR	Glyma.18G159100
GENE BODY	Glyma.18G162500
GENE BODY	Glyma.18G166600
GENE BODY	Glyma.18G166600
GENE BODY	Glyma.18G166600
PROMOTER	Glyma.18G167500
5'UTR(43bp); GENE BODY(157bp)	Glyma.18G170600
PROMOTER	Glyma.18G171700
GENE BODY	Glyma.18G176400
GENE BODY(69bp); PROMOTER (131bp)	Glyma.18G178600

PROMOTER	Glyma.18G179500
PROMOTER	Glyma.18G186900
GENE BODY	Glyma.18G195000
GENE BODY	Glyma.18G195000
GENE BODY	Glyma.18G199800
GENE BODY	Glyma.18G199800
GENE BODY	Glyma.18G209800
PROMOTER (40bp), 5'UTR(110bp); GENE BO	Glyma.18G216900
GENE BODY	Glyma.18G219100
GENE BODY	Glyma.18G230300
GENE BODY	Glyma.18G237100
GENE BODY	Glyma.18G237200
GENE BODY	Glyma.18G241400
GENE BODY	Glyma.18G241400
GENE BODY	Glyma.18G247300
GENE BODY	Glyma.18G251800
GENE BODY	Glyma.18G252800
3'UTR(75bp); GENE BODY (125bp)	Glyma.18G253400
GENE BODY	Glyma.18G279600
GENE BODY	Glyma.18G280500
GENE BODY	Glyma.18G286300
GENE BODY	Glyma.18G296100
GENE BODY	Glyma.18G297900
GENE BODY	Glyma.18G297900
GENE BODY	Glyma.18G299200
GENE BODY	Glyma.19G001500
PROMOTER	Glyma.19G003900
GENE BODY	Glyma.19G006200
PROMOTER	Glyma.19G011000
GENE BODY	Glyma.19G012300
GENE BODY	Glyma.19G012900
GENE BODY	Glyma.19G016300
GENE BODY	Glyma.19G023400
PROMOTER	Glyma.19G024600
GENE BODY	Glyma.19G028800
GENE BODY	Glyma.19G029000
PROMOTER	Glyma.19G031100
GENE BODY	Glyma.19G040200
GENE BODY	Glyma.19G040800
GENE BODY	Glyma.19G043600
GENE BODY	Glyma.19G043600
GENE BODY	Glyma.19G043600
PROMOTER(3bp); GENE BODY(197bp)	Glyma.19G043600
GENE BODY	Glyma.19G056700

3'UTR(44bp); GENE BODY(9bp)	Glyma.19G059600
GENE BODY	Glyma.19G060900
GENE BODY	Glyma.19G060900
GENE BODY	Glyma.19G061900
GENE BODY	Glyma.19G066800
GENE BODY	Glyma.19G067100
GENE BODY	Glyma.19G076400
GENE BODY	Glyma.19G077100
3'UTR(5bp); GENE BODY (195bp)	Glyma.19G077200
GENE BODY	Glyma.19G082800
GENE BODY	Glyma.19G086600
GENE BODY	Glyma.19G095000
PROMOTER	Glyma.19G097300
GENE BODY	Glyma.19G102500
GENE BODY	Glyma.19G104300
3'UTR(44bp); GENE BODY (156bp)	Glyma.19G116000
GENE BODY	Glyma.19G117600
GENE BODY	Glyma.19G117700
3'UTR	Glyma.19G124000
3'UTR	Glyma.19G124000
GENE BODY	Glyma.19G124700
GENE BODY	Glyma.19G141800
GENE BODY	Glyma.19G149500
3'UTR(16bp); GENE BODY (184bp)	Glyma.19G152200
3'UTR(57bp); GENE BODY (143bp)	Glyma.19G155900
PROMOTER	Glyma.19G156500
GENE BODY	Glyma.19G170700
GENE BODY	Glyma.19G175600
GENE BODY	Glyma.19G175900
GENE BODY	Glyma.19G178700
GENE BODY	Glyma.19G179300
GENE BODY	Glyma.19G180500
PROMOTER	Glyma.19G184200
3'UTR	Glyma.19G185300
3'UTR(108bp); GENE BODY (92bp)	Glyma.19G185900
GENE BODY	Glyma.19G187300
PROMOTER	Glyma.19G187400
3'UTR(49bp)	Glyma.19G192300
GENE BODY	Glyma.19G208300
GENE BODY	Glyma.19G213700
5'UTR(43bp); PROMOTER (157bp)	Glyma.19G217000
GENE BODY	Glyma.19G221200
PROMOTER	Glyma.19G224000
GENE BODY	Glyma.19G226000

GENE BODY	Glyma.19G230000
GENE BODY	Glyma.19G239400
GENE BODY	Glyma.19G239700
GENE BODY	Glyma.19G247000
GENE BODY	Glyma.19G250600
3'UTR(39bp); GENE BODY (161bp)	Glyma.19G251400
GENE BODY	Glyma.19G251400
GENE BODY	Glyma.19G251700
GENE BODY	Glyma.19G251800
3'UTR(164bp)	Glyma.19G252900
GENE BODY	Glyma.19G256500
GENE BODY	Glyma.19G259200
GENE BODY	Glyma.20G000700
5'UTR(39bp); GENE BODY (161bp)	Glyma.20G005000
PROMOTER	Glyma.20G008000
PROMOTER	Glyma.20G010700
GENE BODY	Glyma.20G013500
GENE BODY	Glyma.20G017400
5'UTR	Glyma.20G024300
GENE BODY	Glyma.20G025100
3'UTR(155bp); GENE BODY (45bp)	Glyma.20G027500
PROMOTER	Glyma.20G027600
PROMOTER	Glyma.20G030800
GENE BODY	Glyma.20G032200
5'UTR(42bp); GENE BODY(158bp)	Glyma.20G040900
PROMOTER	Glyma.20G046500
5' UTR	Glyma.20G047800
PROMOTER	Glyma.20G047900
GENE BODY	Glyma.20G054500
GENE BODY	Glyma.20G056500
GENE BODY	Glyma.20G058500
3'UTR	Glyma.20G058600
GENE BODY	Glyma.20G060800
GENE BODY	Glyma.20G064100
GENE BODY	Glyma.20G070800
GENE BODY	Glyma.20G071200
GENE BODY	Glyma.20G079600
3'UTR(43bp); GENE BODY (157bp)	Glyma.20G079800
GENE BODY	Glyma.20G086700
PROMOTER	Glyma.20G094700
GENE BODY	Glyma.20G104000
3'UTR	Glyma.20G104100
GENE BODY	Glyma.20G107600
GENE BODY	Glyma.20G110600

GENE BODY	Glyma.20G112200
GENE BODY	Glyma.20G116900
PROMOTER	Glyma.20G118000
PROMOTER	Glyma.20G120500
GENE BODY	Glyma.20G130800
PROMOTER	Glyma.20G131200
3'UTR	Glyma.20G135900
PROMOTER	Glyma.20G140100
GENE BODY	Glyma.20G146600
GENE BODY	Glyma.20G149100
GENE BODY	Glyma.20G149200
GENE BODY	Glyma.20G153600
3'UTR	Glyma.20G154300
PROMOTER	Glyma.20G162200
GENE BODY	Glyma.20G165400
GENE BODY	Glyma.20G166000
GENE BODY	Glyma.20G173200
GENE BODY	Glyma.20G178600
5'UTR	Glyma.20G182900
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G185600
GENE BODY	Glyma.20G185800
GENE BODY	Glyma.20G187800
GENE BODY	Glyma.20G189700
GENE BODY	Glyma.20G195700
GENE BODY	Glyma.20G198700
GENE BODY	Glyma.20G199500
GENE BODY	Glyma.20G208700
GENE BODY	Glyma.20G216900
GENE BODY	Glyma.20G217700
GENE BODY	Glyma.20G218900
GENE BODY	Glyma.20G233700
PROMOTER	Glyma.20G235400
PROMOTER	Glyma.20G241600
GENE BODY	Glyma.20G244700
GENE BODY	Glyma.20G248000
GENE BODY	Glyma.U010500
GENE BODY	Glyma.U010800
PROMOTER	Glyma.U013900
PROMOTER	Glyma.U024600
GENE BODY	Glyma.U032300

GENE BODY	Glyma.U032500
PROMOTER	Glyma.U032500
GENE BODY	Glyma.U034000
PROMOTER	Glyma.U035000
PROMOTER	Glyma.U035000
GENE BODY	Glyma.U036800

GENE ANNOTATION	Methylation Differen	q value	P value
gamma-glutamyl transpeptidase 4	-37.99867021	0.00540647	1.10102E-05
Pectin lyase-like superfamily protein	-40.53030303	2.77707E-05	1.53347E-08
hexokinase 2	-34.41134752	0.00510403	1.00911E-05
hexokinase 2	-51.85185185	0.009566348	2.35016E-05
N/A	-49.48453608	3.19341E-14	1.05384E-18
N/A	-37.25490196	0.000219161	1.97285E-07
N/A	-58.67924528	2.14544E-06	6.16749E-10
UDP-glucosyl transferase 85A3	-49.47368421	0.000214557	5.23789E-07
kinesin like protein for actin based chloroplas	-39.47368421	0.005368098	1.08927E-05
Alkaline-phosphatase-like family protein	-97.05882353	1.25008E-06	3.34099E-10
N/A	-41.93245779	0.000889943	1.00636E-06
SIN3-like 3	-41.93245779	0.000889943	1.00636E-06
myb-like transcription factor family protein	-42.30769231	0.00867934	8.55033E-05
N/A	-60.625	0.005314371	1.06512E-05
SOUL heme-binding family protein	-88.23529412	1.54212E-05	6.34433E-09
Pentatricopeptide repeat (PPR) superfamily p	-32.60869565	0.003464669	6.03944E-06
Squamosa promoter-binding protein-like (SBI	-100	0.005353107	1.08251E-05
Prolyl oligopeptidase family protein	-100	0.001933999	2.83514E-06
N/A	-37.52631579	0.000734571	9.25555E-07
N/A	-39.40813073	8.69842E-08	1.91899E-11
N/A	-100	0.000277356	2.24346E-07
Phosphoglycerate mutase family protein	-100	0.000277356	2.24346E-07
Nucleoporin autopeptidase	-34.84341382	0.00106169	1.5405E-06
N/A	-26.9620391	0.004126839	2.93584E-05
Nucleic acid-binding, OB-fold-like protein	-28.57142857	0.001233443	1.89696E-06
Nucleic acid-binding, OB-fold-like protein	-34.99128616	7.52347E-14	2.81381E-18
Nucleic acid-binding, OB-fold-like protein	-27.27272727	9.31835E-09	1.603E-12
Nucleic acid-binding, OB-fold-like protein	-33.20087809	1.541E-19	1.92113E-24
Nucleic acid-binding, OB-fold-like protein	-40	0.000703599	7.25482E-07
N/A	-28.07766677	1.90E-06	1.40716E-09
Metal-dependent phosphohydrolase	-38.18272095	0.001021096	1.45485E-06
ARM repeat superfamily protein	-76.47058824	0.000181646	1.35073E-07
Zinc finger (CCCH-type) family protein	-34.36363636	0.000762327	8.17325E-07
Protein of unknown function (DUF604)	-61.33587786	0.000212198	1.88788E-07
N/A	-84.65909091	0.000157021	1.29182E-07
glucose-6-phosphate/phosphate translocator	-34.26332288	0.000703795	7.34042E-07
glucose-6-phosphate/phosphate translocator	-29.71846847	3.68684E-11	2.92001E-15
glucose-6-phosphate/phosphate translocator	-33.24863884	0.000422084	4.52396E-07
STAS domain / Sulfate transporter family	-28.35820896	0.005104314	1.36236E-05
TBP-associated factor 15	-27.77777778	0.006638408	2.02113E-05
TBP-associated factor 15	-40	0.004244872	7.82592E-06
receptor like protein 6	-73.07692308	0.00012701	9.93217E-08

receptor like protein 6	-32.25806452	2.10036E-06	7.3091E-10
receptor like protein 6	-60.28514589	9.08552E-22	1.67033E-26
receptor like protein 6	-74.07407407	0.006111082	1.28843E-05
N/A	-53.75722543	2.43E-11	3.05611E-15
N/A	-81.25	3.22832E-07	7.1734E-11
Nucleotidyltransferase family protein	-31.66666667	0.000521764	1.70647E-06
N/A	-91.66666667	0.001242917	1.55316E-06
arginase	-70.1754386	0.000274874	2.21331E-07
N/A	-80	0.000425096	3.81258E-07
N/A	-25.33960293	0.004282959	1.05427E-05
N/A	-37.48902546	3.23074E-25	1.89539E-30
N/A	-52.17391304	3.61557E-13	1.64389E-17
RNA-binding (RRM/RBD/RNP motifs) family p	-52.17391304	3.61557E-13	1.64389E-17
RNA-binding (RRM/RBD/RNP motifs) family p	-27.53623188	0.000213257	1.9085E-07
RNA-binding (RRM/RBD/RNP motifs) family p	-37.48902546	3.23074E-25	1.89539E-30
protein binding	-27.53623188	0.000213257	1.9085E-07
protein binding	-52.17391304	3.61557E-13	1.64389E-17
protein binding	-37.48902546	3.23074E-25	1.89539E-30
xyloglucanase 113	-83.83380205	4.27E-48	2.17042E-54
xyloglucanase 113	-51.94424065	0.003368248	7.48107E-06
Histidine kinase-, DNA gyrase B-, and HSP90-l	-33.46613546	0.000651776	6.58117E-07
Histidine kinase-, DNA gyrase B-, and HSP90-l	-30.26819923	0.005036561	3.88024E-05
RNA polymerase II large subunit	-70.83333333	0.000213835	1.63087E-07
calcium-dependent protein kinase 16	-56.52173913	5.08029E-05	2.77928E-08
Phosphatidylinositol 3- and 4-kinase family pr	-25.69892473	0.007356445	6.72406E-05
Lactoylglutathione lyase / glyoxalase I family	-28.07129094	3.78E-12	3.33967E-16
Lactoylglutathione lyase / glyoxalase I family	-27.89048866	0.00183603	9.35492E-06
DNA binding;zinc ion binding;nucleic acid bin	-84.02985075	7.04898E-05	4.19747E-08
N/A	-75	0.004817982	9.29591E-06
Transducin/WD40 repeat-like superfamily pro	-25.52700415	5.31329E-05	8.81033E-08
cytochrome P450, family 81, subfamily D, pol	-32.12264151	6.59E-08	2.4484E-11
plastid ribosomal protein l11	-31.11367719	6.62E-12	6.51884E-16
N/A	-35.10278428	0.000804136	1.047E-06
SU(VAR)3-9 homolog 6	-39.47368421	0.004343744	8.06555E-06
RGPR-related	-47.05882353	0.002018826	2.99947E-06
alpha/beta-Hydrolases superfamily protein	-27.72277228	0.000310928	2.57869E-07
THUMP domain-containing protein	-30.97345133	6.66226E-06	2.36957E-09
RING/FYVE/PHD zinc finger superfamily prote	-90.90909091	0.001555015	2.07089E-06
CVP2 like 1	-63.63636364	0.000835286	9.35975E-07
Acyl-CoA N-acyltransferase with RING/FYVE/I	-56.03492553	0.000299513	2.45357E-07
somatic embryogenesis receptor-like kinase	-67.89772727	0.000395776	4.17858E-07
somatic embryogenesis receptor-like kinase	-92.45283019	1.47653E-11	1.02866E-15
somatic embryogenesis receptor-like kinase	-38.11398575	0.000376343	1.10204E-06
histone deacetylase 1	-71.21212121	0.006813334	2.09842E-05

Tetratricopeptide repeat (TPR)-like superfam	-91.66666667	0.004921546	9.61483E-06
RNA-binding (RRM/RBD/RNP motifs) family p	-25.24565382	6.0915E-05	1.04223E-07
ABC transporter 1	-32.11038961	0.004121823	7.53011E-06
Concanavalin A-like lectin protein kinase fam	-28.09237583	0.004623602	1.1785E-05
N/A	-83.33333333	0.003019842	5.0293E-06
zinc ion binding	-40	0.00494168	3.77477E-05
serine acetyltransferase 3;2	-37.39809783	9.00353E-05	5.59245E-08
TSL-kinase interacting protein 1	-96.96969697	1.40706E-05	5.73713E-09
FAD/NAD(P)-binding oxidoreductase family p	-72.58064516	0.000428819	3.85855E-07
Pyridoxal phosphate (PLP)-dependent transfe	-44.70066519	0.000293831	2.39396E-07
N/A	-75	0.002079785	3.11582E-06
Mitochondrial substrate carrier family protei	-59.41043084	1.94386E-05	8.48179E-09
microtubule-associated proteins 70-2	-28.71590153	0.000142361	9.86571E-08
HEAT repeat-containing protein	-74.72527473	0.001275399	1.60591E-06
DNA LIGASE 6	-67.35632184	0.002992509	1.86277E-05
phenylalanyl-tRNA synthetase class IIc family	-79.36507937	0.001417777	1.84133E-06
Ribosomal protein L12/ ATP-dependent Clp p	-100	0.00014754	1.03544E-07
Transmembrane amino acid transporter fami	-26.86567164	0.002172447	4.09378E-06
methionine aminopeptidase 1B	-43.86733417	0.004770682	9.17316E-06
NAC (No Apical Meristem) domain transcripti	-69.64285714	0.003941291	7.12658E-06
plant U-box 26	-25.5089717	0.008115221	7.76339E-05
N/A	-29.76190476	6.38129E-08	1.1044E-11
N/A	-41.37931034	1.20754E-05	4.7962E-09
peroxisomal adenine nucleotide carrier 1	-46.03174603	0.004452599	8.36236E-06
Transducin/WD40 repeat-like superfamily pr	-30.14090259	0.007160035	2.24435E-05
Pentatricopeptide repeat (PPR) superfamily p	-31.63265306	0.001500738	7.13074E-06
phosphoenolpyruvate carboxylase 4	-42.00971984	2.05118E-05	2.66259E-08
N/A	-37.66039029	8.71878E-13	5.95364E-17
N/A	-28.21081358	1.4755E-05	7.20785E-09
N/A	-37.33031674	9.291E-06	3.49424E-09
2-oxoglutarate (2OG) and Fe(II)-dependent o	-25.34246575	0.007649235	7.12959E-05
N/A	-25.89996814	6.28127E-07	1.83527E-10
N/A	-37.26133076	0.002967841	6.24153E-06
N/A	-39.52861953	1.6048E-16	3.88365E-21
N/A	-25.89996814	6.28127E-07	1.83527E-10
N/A	-37.26133076	0.002967841	6.24153E-06
N/A	-33.34991708	0.006922846	1.52166E-05
N/A	-92.30769231	0.004021801	9.61483E-06
galacturonosyltransferase 6	-60	0.000719383	7.61529E-07
alpha/beta-Hydrolases superfamily protein	-64.17910448	1.39619E-13	7.97546E-18
alpha/beta-Hydrolases superfamily protein	-77.6119403	2.00496E-14	6.46939E-19
methylcrotonyl-CoA carboxylase alpha chain,	-95.23809524	0.000301963	2.48015E-07
Zinc knuckle (CCHC-type) family protein	-30.89393939	0.003303984	2.14374E-05
Tetratricopeptide repeat (TPR)-like superfam	-36.53846154	0.000221818	1.70802E-07

basic region/leucine zipper motif 60	-32.78688525	0.000377032	3.29258E-07
N/A	-37.93103448	0.00496173	9.72244E-06
P-loop containing nucleoside triphosphate hy	-26.67390125	0.001742711	3.02304E-06
Protein of unknown function, DUF593	-100	0.000703795	7.39602E-07
N/A	-38.8712522	0.000134474	9.17121E-08
Thioesterase superfamily protein	-80.625	7.49481E-05	1.35694E-07
P-loop containing nucleoside triphosphate hy	-78.57142857	0.002670807	4.29893E-06
nudix hydrolase homolog 23	-57.5	0.001305715	1.65653E-06
NIMA-related kinase 2	-55.44715447	2.5401E-05	1.38594E-08
homeobox protein 22	-43.81377551	0.004526603	1.14635E-05
Protein of unknown function (DUF288)	-73.17073171	0.005653257	1.16786E-05
Cyclin-like family protein	-53.84615385	0.000848064	9.5216E-07
MAP kinase kinase 6	-38.63636364	0.00164928	2.23876E-06
S-adenosyl-L-methionine-dependent methylt	-73.91304348	0.007914422	1.81606E-05
Nucleic acid-binding, OB-fold-like protein	-90.69767442	7.37599E-05	5.13357E-08
RING-H2 group F2A	-38.23529412	5.94643E-06	2.47293E-09
N/A	-34.28571429	0.005815286	1.2085E-05
chaperone protein dnaJ-related	-35.13513514	0.004312652	7.98567E-06
Tetratricopeptide repeat (TPR)-like superfam	-70.34632035	5.94491E-10	5.79833E-14
Pseudouridine synthase family protein	-43.5483871	0.007691319	1.74682E-05
Golgi-body localisation protein domain ;RNA	-100	0.001933999	2.83514E-06
indole-3-acetic acid inducible 9	-52.38095238	0.009485397	2.32192E-05
N/A	-25.37252056	6.89461E-08	1.20841E-11
ribosomal protein S2	-83.09659091	9.4024E-06	3.54637E-09
Plant protein of unknown function (DUF828)	-39.03372646	8.26E-07	5.12771E-10
Pseudouridine synthase family protein	-30.95085568	0.00035838	1.03233E-06
nucleotide binding;protein binding	-73.91304348	2.79341E-06	8.46824E-10
Haloacid dehalogenase-like hydrolase (HAD)	-77.77777778	0.000930973	1.06641E-06
E3 ubiquitin ligase, putative	-85.65217391	0.001513714	2.49565E-06
Xanthine/uracil permease family protein	-100	0.000796198	8.74075E-07
serine/threonine protein phosphatase 2A 55	-27.11864407	0.007432213	1.67435E-05
Protein phosphatase 2A regulatory B subunit	-61.40350877	0.000156893	1.1241E-07
UDP-Glycosyltransferase superfamily protein	-50.15698587	1.83355E-05	2.30839E-08
Ethylene insensitive 3 family protein	-63.15789474	0.004931351	9.6376E-06
early nodulin-like protein 18	-46.26370625	4.06E-20	5.15698E-25
early nodulin-like protein 18	-76.92307692	1.5835E-06	5.33371E-10
auxin response factor 6	-100	0.000356554	3.05926E-07
protodermal factor 1	-33.63095238	0.009357303	3.33429E-05
hydroxyproline-rich glycoprotein family prote	-91.30434783	3.03144E-06	9.4007E-10
ENHANCED DOWNY MILDEW 2	-39.38215103	0.005552448	1.13808E-05
multidrug resistance-associated protein 3	-76.47058824	0.007749937	1.76354E-05
DNAJ heat shock N-terminal domain-containi	-67.14975845	0.001405002	1.8165E-06
N/A	-32.52608048	3.46E-09	8.2963E-13
Nucleotide-sugar transporter family protein	-25.92935479	0.002764235	4.49301E-06

SEC7-like guanine nucleotide exchange famil	-76.92307692	0.000765705	8.2338E-07
N/A	-38.7755102	0.003689797	8.49149E-06
RAS associated with diabetes protein 51C	-100	1.90164E-07	3.91869E-11
Protein of unknown function (DUF565)	-38.80034773	0.000411704	1.24385E-06
Protein of unknown function (DUF565)	-44.9376947	0.006687833	5.84878E-05
high mobility group	-58.72909699	0.000457565	4.18097E-07
Preprotein translocase Sec, Sec61-beta subur	-27.04100677	0.00032695	3.28019E-07
Protein phosphatase 2C family protein	-29.47368421	9.23401E-05	5.79656E-08
P-loop containing nucleoside triphosphate hy	-30.64516129	1.29933E-08	2.2949E-12
N/A	-45.11241447	0.00938922	3.34949E-05
Rhodanese/Cell cycle control phosphatase su	-72.72727273	0.008355196	2.8191E-05
regulatory particle AAA-ATPase 2A	-47.22222222	0.003908528	7.04246E-06
BCL-2-associated athanogene 6	-46.66666667	0.00495282	1.30847E-05
rubisco activase	-30.23255814	5.36E-12	5.1136E-16
mRNA capping enzyme family protein	-50.90909091	0.004776659	9.19516E-06
defective in exine formation protein (DEX1)	-69.04761905	0.000169544	1.23712E-07
RHOMBOID-like 1	-50	0.009259271	2.24824E-05
E3 Ubiquitin ligase family protein	-63.1372549	0.009984992	2.48229E-05
Protein kinase superfamily protein	-46.2962963	0.003213284	6.98768E-06
Cellulose-synthase-like C6	-100	4.05E-22	3.49343E-27
Chloroplast Ycf2;ATPase, AAA type, core	-34.97432606	1.00391E-07	1.86997E-11
Chloroplast Ycf2;ATPase, AAA type, coreMET	-38.07950192	1.23977E-10	1.34314E-14
N/A	-41.14583333	0.002814342	1.70141E-05
hAT dimerisation domain-containing protein	-94.28571429	2.12027E-06	6.07959E-10
DYNAMIN-like 1E	-34.95297806	0.000354245	1.01682E-06
basic helix-loop-helix (bHLH) DNA-binding su	-67.9791546	0.003976657	9.46497E-06
N/A	-27.47092057	0.003932664	9.30346E-06
Plant protein of unknown function (DUF247)	-36.90360273	0.000201432	4.8121E-07
alpha/beta-Hydrolases superfamily protein	-70.37037037	0.0048666	9.40399E-06
transcription regulators	-39.840842	1.93E-16	4.99224E-21
disproportionating enzyme 2	-83.72093023	0.00037888	3.3246E-07
lupeol synthase 2	-26.02678571	0.003070238	1.93314E-05
TGACG motif-binding factor 6	-72.81553398	0.000369017	3.20223E-07
P-loop containing nucleoside triphosphate hy	-63.88888889	0.001173157	1.42039E-06
N/A	-61.53846154	0.005825239	1.21236E-05
Transmembrane proteins 14C	-31.66410601	0.000111168	8.50027E-08
curculin-like (mannose-binding) lectin family	-90	0.008505711	2.01037E-05
N/A	-31.42857143	0.002345145	3.64596E-06
spindle pole body component 98	-75.30864198	0.002849701	4.67489E-06
Disease resistance-responsive (dirigent-like p	-26.01455698	0.000149301	3.26192E-07
alpha/beta-Hydrolases superfamily protein	-66.95116169	5.19212E-05	3.33749E-08
FUS3-complementing gene 1	-30.14705882	1.18264E-06	3.12219E-10
FASCICLIN-like arabinogalactan-protein 11	-44.93557087	4.94E-17	1.15309E-21
FASCICLIN-like arabinogalactan-protein 11	-50.67126966	0.000815725	9.05981E-07

Pyruvate kinase family protein	-90	0.008505711	2.01037E-05
RHOMBOID-like protein 15	-27.77991207	1.55638E-08	2.19141E-12
Chaperone DnaJ-domain superfamily protein	-76.92307692	0.000382766	3.37399E-07
N/A	-29.41176471	0.000672504	6.84616E-07
N/A	-27.11111111	4.62838E-12	2.81717E-16
N/A	-39.04761905	5.12743E-08	1.04702E-11
Protein phosphatase 2C family protein	-39.04761905	5.12743E-08	1.04702E-11
Protein phosphatase 2C family protein	-29.41176471	0.000672504	6.84616E-07
Protein phosphatase 2C family protein	-27.11111111	4.62838E-12	2.81717E-16
Protein of unknown function (DUF3511)	-27.62414511	0.000388687	1.15023E-06
regulatory particle triple-A ATPase 5A	-47.22772277	0.00047655	4.39476E-07
RNA polymerase II transcription mediators	-68	0.000331513	2.78606E-07
Li-tolerant lipase 1	-43.52501169	2.29482E-05	3.07559E-08
Glycosyl hydrolase superfamily protein	-70.83333333	0.001659154	2.25793E-06
Ankyrin repeat family protein	-36.36363636	0.000631379	6.29239E-07
FMN-linked oxidoreductases superfamily pro	-27.30141309	0.007329095	6.68789E-05
ATPase, F0/V0 complex, subunit C protein	-27.30141309	0.007329095	6.68789E-05
Sec14p-like phosphatidylinositol transfer fam	-73.91304348	0.007914422	1.81606E-05
Arabidopsis protein of unknown function (DU	-27.40925886	7.02E-12	6.98378E-16
Galactose oxidase/kelch repeat superfamily p	-66	0.000910494	1.03828E-06
Protein kinase superfamily protein	-69.13580247	0.005472757	1.11773E-05
N/A	-28.63636364	1.01E-07	4.08327E-11
glycosyl hydrolase 9B7	-66	0.001920592	2.72802E-06
Plant protein of unknown function (DUF869)	-48.8372093	0.006699323	1.4606E-05
xylem bark cysteine peptidase 3	-39.47368421	0.009184995	2.22279E-05
N/A	-64.28571429	0.004876312	9.44718E-06
RING/U-box superfamily protein	-55	0.000703795	7.37662E-07
RING/U-box superfamily protein	-81.81818182	5.77169E-05	3.27946E-08
homology to ABI1	-100	1.28339E-05	5.16698E-09
KNOTTED1-like homeobox gene 3	-37.82230806	1.00E-06	6.47962E-10
tyrosyl-DNA phosphodiesterase-related	-68.33333333	0.002539761	4.02655E-06
Phox (PX) domain-containing protein	-31.73935891	0.006206255	5.25008E-05
N/A	-100	0.001933999	2.83514E-06
Ribosomal protein S5 family protein	-28.40153195	3.81865E-05	2.27912E-08
Putative serine esterase family protein	-98	6.01066E-07	1.459E-10
CBL-interacting protein kinase 8	-55	0.002434174	3.82899E-06
Rho GTPase activation protein (RhoGAP) with	-60	0.001841775	2.57974E-06
binding	-29.67687075	2.53661E-09	3.73074E-13
binding	-39.00069396	0.001134112	1.69479E-06
binding	-72.22222222	0.000903423	1.02512E-06
ubiquitin-protein ligase 1	-33.9569161	3.89002E-07	1.05997E-10
ubiquitin-protein ligase 1	-31.55011655	0.000144838	1.16401E-07
APR-like 4	-31.41928494	0.001524982	2.51924E-06
alpha/beta-Hydrolases superfamily protein	-25.3968254	0.005467109	4.36687E-05

N/A	-91.66666667	0.004921546	9.61483E-06
chloride channel F	-25.90340208	0.009080022	3.19106E-05
N/A	-25.90340208	0.009080022	3.19106E-05
Ribosomal L32p protein family	-52.50982104	1.46832E-06	4.86861E-10
Ribosomal L32p protein family	-28.125	6.85703E-07	2.03501E-10
N/A	-38.26815642	3.14448E-08	6.15261E-12
peroxin 5	-37.35930736	0.004282959	1.05407E-05
Phosphoinositide phosphatase family protein	-47.64079148	1.69031E-05	8.47917E-09
N/A	-30.01808318	0.00065089	2.28647E-06
HAC13 protein (HAC13)	-80.13157895	4.46743E-05	7.05825E-08
zinc induced facilitator-like 1	-31.75501801	1.34583E-07	3.17232E-11
zinc induced facilitator-like 1	-27.21893491	0.000476624	4.40055E-07
alpha/beta-Hydrolases superfamily protein	-57.44047619	0.000510142	5.71431E-07
nuclear matrix protein-related	-56.71641791	0.000526401	4.97594E-07
ribosomal protein large subunit 27	-67.72727273	0.003020605	6.38621E-06
nucleoporin-related	-41.66666667	0.005157159	1.38256E-05
Family of unknown function (DUF566)	-48.40654608	0.009401203	3.35673E-05
Cytidine/deoxycytidylate deaminase family p	-100	0.001240448	1.54644E-06
cyclic nucleotide-gated channel 17	-71.16382506	3.04088E-12	1.8063E-16
transducin family protein / WD-40 repeat fan	-72.72727273	0.008355196	2.8191E-05
exocyst subunit exo70 family protein E2	-38.7477314	0.003825746	8.93749E-06
DDT domain superfamily	-74.64788732	0.000377032	3.29579E-07
Homeodomain-like superfamily protein	-90	0.005869408	1.22371E-05
ataxia-telangiectasia mutated	-64.61038961	0.002251172	4.3116E-06
ataxia-telangiectasia mutated	-39.3258427	6.2256E-05	4.16123E-08
Protein kinase superfamily protein	-37.5	9.8502E-05	6.29894E-08
alpha/beta-Hydrolases superfamily protein	-100	0.000440203	4.00618E-07
Pectin lyase-like superfamily protein	-28.87657058	0.002669057	1.58145E-05
glyceraldehyde-3-phosphate dehydrogenase	-44.3175853	0.009942255	0.000104024
nuclear protein X1	-43.33333333	0.000834933	9.34967E-07
RNA-metabolising metallo-beta-lactamase fa	-28.41234291	0.000269459	7.09819E-07
Protein kinase superfamily protein	-29.04233171	0.006237738	5.28551E-05
topoisomerase 3alpha	-51.72413793	0.009314196	2.27045E-05
Nucleotide-sugar transporter family protein	-71.53310105	0.000957331	3.86079E-06
plastid transcriptionally active7	-30.40229885	0.007264795	6.59934E-05
histone methyltransferases(H3-K4 specific);h	-53.74396135	0.002100986	3.15851E-06
putative protein kinase 1	-45.05882353	0.000476686	4.40462E-07
Transducin/WD40 repeat-like superfamily pro	-74.28571429	0.0059944	1.259E-05
sirohydrochlorin ferrochelatase B	-58	0.00471802	9.00616E-06
Tetratricopeptide repeat (TPR)-like superfam	-93.33333333	5.62741E-05	3.18177E-08
Transcription factor TFIIE, alpha subunit	-95.65217391	3.22857E-05	1.55791E-08
glycine-rich RNA-binding protein 3	-100	2.76356E-05	1.28935E-08
H(+)-ATPase 11	-68.18181818	2.69695E-08	4.11379E-12
DDT domain superfamily	-42.80661867	2.41711E-09	2.78293E-13

ARM repeat superfamily protein	-30.99415205	0.004700162	1.20881E-05
ARM repeat superfamily protein	-27.83018868	3.76748E-13	2.39947E-17
ARM repeat superfamily protein	-43.47826087	0.001784439	2.47774E-06
ARM repeat superfamily protein	-26.72998643	5.97584E-06	2.09037E-09
RNA-dependent RNA polymerase 2	-91.30434783	0.000695012	7.13043E-07
histone deacetylase 6	-100	3.22217E-05	1.55009E-08
ubiquitin-associated (UBA)/TS-N domain-con	-94.11764706	0.000303905	2.50501E-07
26S proteasome, regulatory subunit Rpn7;Pro	-36.86046512	0.003350142	7.42567E-06
26S proteasome, regulatory subunit Rpn7;Pro	-36.28909809	2.80E-06	2.30753E-09
AAA-type ATPase family protein	-73.91304348	0.006065956	1.27714E-05
MBOAT (membrane bound O-acyl transferase	-34	0.000697205	7.16826E-07
glycine-rich protein	-40.54580897	1.42E-07	6.16521E-11
O-fucosyltransferase family protein	-44.29123001	0.008480288	2.88426E-05
O-fucosyltransferase family protein	-36.97351828	0.00460798	8.72514E-06
plant glycogenin-like starch initiation protein	-33.19284802	0.004921377	1.29673E-05
hydroxyproline-rich glycoprotein family prote	-31.41025641	0.004395021	8.19299E-06
Histone H3 K4-specific methyltransferase SET	-39.09905426	0.008616815	2.94858E-05
Histone H3 K4-specific methyltransferase SET	-28.38333107	0.007936784	1.82194E-05
N/A	-91.42857143	0.000132304	8.96499E-08
Tetratricopeptide repeat (TPR)-like superfam	-59.09090909	0.008206862	1.91627E-05
AMP-dependent synthetase and ligase family	-93.33333333	9.09588E-05	5.65648E-08
AMP-dependent synthetase and ligase family	-93.33333333	9.09588E-05	5.65648E-08
Proteasome component (PCI) domain protein	-30.47504026	0.003248343	7.10017E-06
PIF1 helicase	-70.625	0.001759016	3.05715E-06
N/A	-70.625	0.001759016	3.05715E-06
histidine acid phosphatase family protein	-26.5625	0.001078932	1.28337E-06
histidine acid phosphatase family protein	-100	0.001933999	2.83514E-06
Transcription initiation factor IIF, beta subuni	-29.80769231	0.000466478	1.46927E-06
N/A	-27.65422859	1.19106E-05	4.71283E-09
WD-40 repeat family protein	-31.43079662	0.00015733	1.2954E-07
WD-40 repeat family protein	-27.53211629	0.000429667	4.64642E-07
WD-40 repeat family protein	-37.54813864	0.004517985	1.14357E-05
Tubulin/FtsZ family protein	-92.85714286	1.39579E-06	3.85892E-10
Pentatricopeptide repeat (PPR) superfamily p	-30.07493644	0.000112224	8.59907E-08
Ribosomal L32p protein family	-94.44444444	0.000775974	8.38216E-07
pumilio 7	-68.75	8.12321E-06	2.9845E-09
P-loop containing nucleoside triphosphate hy	-91.66666667	0.004921546	9.61483E-06
FAD-binding Berberine family protein	-36.08654076	1.04335E-05	1.15617E-08
N/A	-38.95877009	0.000971663	1.35124E-06
IAP-like protein 1	-47.91666667	0.008111141	1.88261E-05
Tic22-like family protein	-42.5	0.000137899	9.49584E-08
aspartate kinase-homoserine dehydrogenase	-71.64179104	0.000117533	7.85204E-08
Protein of unknown function, DUF538	-37.96440489	1.24E-10	1.93564E-14
NAD(P)-binding Rossmann-fold superfamily p	-28.87307458	0.006790648	5.98308E-05

5\'-3\' exonuclease family protein	-100	0.001933999	2.83514E-06
RNA-binding (RRM/RBD/RNP motifs) family p	-57.8125	0.000244683	1.93432E-07
N/A	-28.93081761	0.00245867	3.87474E-06
essential meiotic endonuclease 1B	-44.18604651	0.008099053	1.87862E-05
N/A	-42.9280397	0.007012912	1.55256E-05
signal recognition particle-related / SRP-relat	-46.08433735	0.000539075	5.1669E-07
P-loop nucleoside triphosphate hydrolases su	-100	3.88087E-07	9.04313E-11
RNA helicase, ATP-dependent, SK12/DOB1 pr	-78.125	0.006236312	1.3217E-05
N/A	-74.19354839	0.004402063	8.21257E-06
RNA-binding CRS1 / YhbY (CRM) domain prot	-29.36425339	2.45546E-15	9.83457E-20
RNA-binding CRS1 / YhbY (CRM) domain prot	-35.69601754	0.005428867	1.49176E-05
RNA-binding CRS1 / YhbY (CRM) domain prot	-42.23602484	6.51509E-18	1.8822E-22
RNA-binding CRS1 / YhbY (CRM) domain prot	-37.54696726	2.99552E-14	1.43578E-18
RNA-binding CRS1 / YhbY (CRM) domain prot	-38.21656051	9.62756E-14	5.1835E-18
annexin 5	-25.99302201	0.006942027	6.17816E-05
ARM repeat superfamily protein	-100	0.000115391	7.66995E-08
ARM repeat superfamily protein	-44	0.001134763	1.36392E-06
N/A	-75	0.002249117	3.46862E-06
Calcium-binding EF hand family protein	-75	0.002249117	3.46862E-06
N/A	-100	4.92908E-05	2.67079E-08
BED zinc finger ;hAT family dimerisation dom	-30.14853648	1.27E-08	3.72288E-12
Chaperone DnaJ-domain superfamily protein	-80	2.29E-07	1.09835E-10
RNA-binding protein 1	-51.16648993	0.001284776	1.62243E-06
P-type ATPase of Arabidopsis 2	-69.44136145	1.89E-16	4.79168E-21
WRKY DNA-binding protein 40	-26.76767677	0.006032049	5.04028E-05
Phox (PX) domain-containing protein	-79.6347032	8.97856E-06	3.99696E-09
RING/U-box superfamily protein	-37.58865248	0.000733326	2.67772E-06
RNA-binding KH domain-containing protein	-28.33333333	0.000548443	6.27749E-07
RNA-binding KH domain-containing protein	-25.19900498	0.009582246	3.47697E-05
RNA-binding KH domain-containing protein	-29.57746479	1.00554E-09	1.05419E-13
RNA-binding KH domain-containing protein	-36.95652174	0.000426023	3.82715E-07
Golgi-body localisation protein domain ;RNA	-100	0.000703795	7.39602E-07
Tetratricopeptide repeat (TPR)-like superfam	-66.07142857	0.004711596	8.9875E-06
Vacuolar sorting protein 9 (VPS9) domain	-25.83900227	8.24282E-07	2.48861E-10
MAPK/ERK kinase kinase 1	-36.36363636	0.007503301	1.69586E-05
YbaK/aminoacyl-tRNA synthetase-associated	-70.96774194	0.008206862	1.91627E-05
N/A	-26.20844564	7.18262E-05	1.28436E-07
IAA-leucine resistant (ILR)-like gene 6	-50.25031289	0.000491077	5.47173E-07
Chaperone DnaJ-domain superfamily protein	-40.625	0.004018222	7.31839E-06
global transcription factor group A2	-78.94736842	3.3141E-05	1.6089E-08
vacuolar protein sorting 45	-66.66666667	0.005925316	1.2389E-05
FTSH protease 11	-35.77694236	4.71E-08	1.66274E-11
plastid transcriptionally active7	-81.81818182	0.004303843	7.96305E-06
nascent polypeptide-associated complex sub	-29.54545455	0.003609909	6.36145E-06

disproportionating enzyme	-51.94805195	0.009736237	2.40475E-05
like COV 2	-39.28571429	0.00700902	1.55022E-05
Nucleotidyltransferase family protein	-25.15873016	0.000368267	3.19217E-07
ferrochelatase 2	-73.01587302	0.000175386	1.29518E-07
transducin family protein / WD-40 repeat fan	-100	0.000796198	8.74075E-07
glucan synthase-like 8	-100	0.000243473	1.92297E-07
glucan synthase-like 8	-54.08163265	6.45425E-05	4.38187E-08
glucan synthase-like 8	-31.66666667	0.00598506	1.2566E-05
N/A	-31.66666667	0.00598506	1.2566E-05
D111/G-patch domain-containing protein	-40.87504071	2.94E-06	2.44673E-09
GATA type zinc finger transcription factor fan	-58.90410959	0.000675074	8.28395E-07
Protein of unknown function (DUF962)	-43.24324324	0.000311801	3.0849E-07
Protein of unknown function (DUF962)	-40	3.94077E-06	1.29273E-09
Protein of unknown function (DUF962)	-34.87394958	1.81671E-22	1.86517E-27
Protein of unknown function (DUF962)	-27.84810127	5.06925E-19	1.36465E-23
Leucine-rich repeat protein kinase family pro	-25.44489093	0.000741281	9.36585E-07
SNF2 domain-containing protein / helicase do	-67.5	0.005918528	1.23612E-05
N/A	-100	7.87674E-06	2.87084E-09
U5 small nuclear ribonucleoprotein helicase	-33.76344086	0.004529719	1.14743E-05
P-loop containing nucleoside triphosphate hy	-44.68085106	0.000962609	1.33297E-06
ATPase E1-E2 type family protein / haloacid c	-25.58139535	0.001727111	2.37354E-06
homeodomain GLABROUS 2	-91.30434783	0.000695012	7.13043E-07
PIF1 helicase	-32.1291866	0.002717151	1.62016E-05
prenylated RAB acceptor 1.B4	-57.8125	1.24196E-07	2.42267E-11
Transducin/WD40 repeat-like superfamily pro	-57.8125	1.24196E-07	2.42267E-11
Stabilizer of iron transporter SufD / Polynucle	-74.11764706	0.002217143	3.40305E-06
Protein of unknown function (DUF803)	-28.29226848	0.002182126	4.12778E-06
Protein of unknown function (DUF803)	-31.12582781	4.65625E-06	1.84352E-09
Protein of unknown function (DUF803)	-48.10400867	2.05546E-07	4.34117E-11
Nucleotide/sugar transporter family protein	-52.94117647	0.001082744	1.59388E-06
Nucleotide/sugar transporter family protein	-47.31182796	3.20327E-06	1.19043E-09
Nucleotide/sugar transporter family protein	-45.45454545	0.003351354	5.77466E-06
signal recognition particle receptor alpha sub	-72.30769231	0.000926295	1.06037E-06
SET domain group 4	-38.38709677	0.000688034	2.45538E-06
cyclic nucleotide-gated channel 17	-100	0.001240448	1.54644E-06
DNAJ heat shock family protein	-36.80981595	2.99385E-06	1.09688E-09
DNAJ heat shock family protein	-26.41134557	4.65395E-05	2.89072E-08
DNAJ heat shock family protein	-39.13043478	0.000150272	1.06233E-07
N/A	-48.53603604	0.00482238	9.30793E-06
Ankyrin repeat family protein	-70.58823529	2.48778E-09	2.90078E-13
cytochrome P450, family 72, subfamily A, pol	-66.66666667	0.00022401	1.72805E-07
phytosylfokine-alpha receptor 2	-66.66666667	0.00022401	1.72805E-07
3-hydroxyacyl-CoA dehydrogenase family pro	-41.69398907	0.000591822	6.97507E-07
ribosomal protein L6 family protein	-45	0.007094679	1.57726E-05

cytochrome c oxidase 17	-100	5.09444E-06	1.74469E-09
pleiotropic drug resistance 12	-31.68119099	0.005614165	1.57091E-05
Galactose oxidase/kelch repeat superfamily	-31.1789905	0.002371301	4.6196E-06
Transducin/WD40 repeat-like superfamily pr	-43.56435644	0.004404594	3.20748E-05
Transducin/WD40 repeat-like superfamily pr	-96.15384615	1.20754E-05	4.80152E-09
ARF-GAP domain 5	-95.12195122	4.96095E-08	8.36756E-12
Disease resistance protein (TIR-NBS-LRR class	-38.31831832	0.005210367	1.04045E-05
Disease resistance protein (TIR-NBS-LRR class	-30.53626543	0.000623005	6.17971E-07
Disease resistance protein (TIR-NBS-LRR class	-50.94339623	0.000140179	9.70425E-08
Disease resistance protein (TIR-NBS-LRR class	-38.7804878	4.02392E-05	2.04203E-08
Disease resistance protein (TIR-NBS-LRR class	-34.32835821	3.18948E-06	1.01044E-09
disease resistance protein (TIR-NBS-LRR class	-51.26705653	0.000192914	1.67958E-07
BED zinc finger ;hAT family dimerisation dom	-64.46808511	4.18656E-05	2.15219E-08
disease resistance protein (TIR-NBS-LRR class	-41.66666667	0.000914884	1.04411E-06
Tetratricopeptide repeat (TPR)-like superfam	-74.41860465	0.000592594	5.79286E-07
ortholog of human splicing factor SC35	-74.41860465	0.000592594	5.79286E-07
Translation initiation factor SUI1 family prote	-33.79228954	0.000127505	8.6118E-08
N/A	-39.09294155	0.009285204	3.29824E-05
trehalose-phosphatase/synthase 7	-70.90909091	0.003036641	5.07286E-06
multiprotein bridging factor 1B	-29.72659486	0.004466416	3.27223E-05
protein kinase C substrate, heavy chain-relat	-25.64102564	0.000615827	2.12404E-06
O-methyltransferase family protein	-29.0805417	0.002067843	1.10711E-05
N/A	-44.44444444	0.004415854	1.10641E-05
Peptidase family M48 family protein	-90.90909091	0.004921546	9.61483E-06
Auxin-responsive GH3 family protein	-48.47094801	2.71881E-07	6.9442E-11
Core-2/I-branching beta-1,6-N-acetylglucosa	-33.02139037	0.00674261	1.47225E-05
N/A	-25.98357596	0.000576013	1.94708E-06
N/A	-100	6.22335E-07	1.52888E-10
TBP-associated factor 7	-73.51916376	0.000788288	1.02015E-06
nuclear factor Y, subunit C11	-54.05405405	8.74678E-05	5.4009E-08
N/A	-31.06796117	2.07E-30	3.15677E-36
NB-ARC domain-containing disease resistanc	-42.85714286	0.00731223	1.64102E-05
exocyst complex component 84B	-50	0.000987439	1.14557E-06
Phox-associated domain;Phox-like;Sorting ne	-56.21840243	0.000805269	8.87576E-07
translocon at the inner envelope membrane	-84.84848485	0.001249711	1.56624E-06
N/A	-57.47303544	9.89729E-06	3.76695E-09
Metallo-hydrolase/oxidoreductase superfam	-100	0.000796198	8.74075E-07
cation exchanger 5	-100	6.03462E-06	2.11536E-09
CemA-like proton extrusion protein-related	-28.38350377	0.002603975	5.21642E-06
CemA-like proton extrusion protein-related	-28.408713	0.00161963	2.19019E-06
Signal recognition particle, SRP54 subunit pr	-43.14345992	2.04894E-05	8.98538E-09
Ubiquitin system component Cue protein	-52.27272727	0.001906341	2.69927E-06
CASC3/Barentsz eIF4AIII binding	-43.75	0.002044314	3.04933E-06
aminopeptidase M1	-25.98484848	0.006262565	5.31393E-05

CCAAT-binding factor	-68	0.001192665	1.44926E-06
pectin methylesterase 3	-54.58669355	0.000115391	7.61307E-08
N/A	-64.17910448	4.30129E-05	2.22064E-08
CBL-interacting protein kinase 9	-38.42105263	0.007394621	6.77961E-05
cytochrome P450, family 86, subfamily A, pol	-62.5	8.96604E-08	1.99569E-11
cytochrome P450, family 86, subfamily A, pol	-67.5	6.4898E-07	1.60862E-10
Major facilitator superfamily protein	-55.51948052	0.000203014	1.53643E-07
RNAhelicase-like 8	-71.96969697	0.001680862	2.29642E-06
S-adenosyl-L-methionine-dependent methylt	-36.86868687	9.55052E-05	1.83175E-07
response regulator 2	-26.20155039	0.005708866	1.60698E-05
N/A	-26.20155039	0.005708866	1.60698E-05
N/A	-26.20155039	0.005708866	1.60698E-05
N/A	-26.20155039	0.005708866	1.60698E-05
Late embryogenesis abundant (LEA) hydroxyp	-27.47252747	3.26604E-05	4.78029E-08
MUTS homolog 7	-82.60869565	0.00161376	2.18107E-06
Plant protein of unknown function (DUF639)	-86.66666667	3.06456E-06	9.52884E-10
ATP-binding cassette A2	-38.89659958	8.95852E-12	5.84698E-16
BED zinc finger ;hAT family dimerisation dom	-38.56008055	3.75717E-09	5.89593E-13
Surfeit locus 1 cytochrome c oxidase biogene	-92.30769231	3.22857E-05	1.55791E-08
basic pentacysteine1	-92.30769231	1.89953E-08	2.73029E-12
Auxin efflux carrier family protein	-74.28571429	0.001547796	2.57826E-06
Fatty acid hydroxylase superfamily	-31.18762475	0.003062898	1.92727E-05
endoplasmic reticulum oxidoreductins 2	-30	0.007452525	6.85503E-05
Vacuolar sorting protein 39	-34.13105413	0.007936784	1.82336E-05
hexokinase 1	-28.7012987	0.009138996	3.22077E-05
hexokinase 1	-25.43847385	2.69E-12	2.25081E-16
nuclear RNA polymerase C2	-34.12277378	0.001057295	1.53075E-06
nuclear RNA polymerase C2	-27.14449601	1.17287E-08	2.06384E-12
N/A	-77.50206782	1.55393E-07	3.09961E-11
Alkaline-phosphatase-like family protein	-37.84652471	0.002136184	1.15577E-05
NAD(P)-binding Rossmann-fold superfamily p	-26.92307692	0.000639927	2.23658E-06
N/A	-95.45454545	1.90388E-10	1.63354E-14
LMBR1-like membrane protein	-28.92466935	0.001049893	1.51152E-06
N/A	-100	0.001240448	1.54644E-06
N/A	-67.64705882	6.46153E-07	1.59688E-10
Tautomerase/MIF superfamily protein	-55.85516179	2.36822E-05	1.06461E-08
SU(VAR)3-9 homolog 9	-33.66503368	0.000121424	2.49685E-07
N/A	-35.62172594	1.03E-08	2.91112E-12
ARM repeat superfamily protein	-67.34693878	0.000391002	3.46092E-07
RING-finger protein for embryogenesis	-29.58579882	0.002324156	3.6048E-06
DYNAMIN-like 1C	-67.21311475	6.07421E-06	2.13814E-09
Pentatricopeptide repeat (PPR-like) superfam	-65	3.05499E-07	6.74344E-11
Glutamyl-tRNA reductase family protein	-70.96774194	0.003804626	6.81339E-06
Transducin/WD40 repeat-like superfamily pro	-40	0.001455577	2.36062E-06

Protein of unknown function (DUF616)	-100	0.001240448	1.54644E-06
IQ-domain 9	-70.45454545	0.008742198	2.08614E-05
N/A	-39.34108527	0.005575491	1.14403E-05
Thioesterase/thiol ester dehydrase-isomeras	-97.2972973	1.8665E-06	5.31086E-10
2-oxoglutarate (2OG) and Fe(II)-dependent o	-47.72727273	4.57997E-05	7.27792E-08
cytochrome P450, family 707, subfamily A, p	-26.60347985	3.14E-09	7.42633E-13
Pentatricopeptide repeat (PPR) superfamily	-100	0.001240448	1.54644E-06
calmodulin-binding protein	-70	0.000151513	1.07333E-07
N/A	-60.17316017	0.00283208	4.63767E-06
RING/U-box superfamily protein	-50.67330211	6.59978E-07	1.65855E-10
N/A	-65.71428571	3.10585E-08	4.91972E-12
Glycosyl hydrolase superfamily protein	-41.66666667	0.00107249	1.27413E-06
N/A	-27.46443409	1.73E-07	7.86291E-11
tobamovirus multiplication 1	-100	0.001933999	2.83514E-06
ZCW7	-31.72774869	0.001509362	2.48748E-06
ZCW7	-38.88719357	1.41915E-08	1.96696E-12
Sec14p-like phosphatidylinositol transfer fam	-30.45751634	7.88398E-05	1.44188E-07
phosphate transporter 4;6	-44.93251243	2.16E-06	1.65923E-09
Smg-4/UPF3 family protein	-44.93251243	2.16E-06	1.65923E-09
DDT domain-containing protein	-30.83333333	0.007476304	1.68647E-05
Myosin heavy chain-related protein	-62.15447154	2.22958E-06	6.52382E-10
serine racemase	-100	0.001240448	1.54644E-06
RNA helicase, ATP-dependent, SK12/DOB1 pr	-46.53465347	0.005746026	1.1904E-05
phosphorylethanolamine cytidylyltransferase	-93.02325581	1.19359E-09	1.31296E-13
isoamylase 1	-72.22222222	0.004412727	8.23942E-06
BURP domain-containing protein	-27.13235294	1.61E-18	2.54054E-23
Fibronectin type III domain-containing protei	-27.45257453	4.93719E-05	8.04315E-08
CRS1 / YhbY (CRM) domain-containing protei	-83.33333333	3.10665E-12	1.86815E-16
CRS1 / YhbY (CRM) domain-containing protei	-36.99065792	0.000830814	9.28203E-07
associated molecule with the SH3 domain of	-100	3.22217E-05	1.55009E-08
Pyridoxal phosphate (PLP)-dependent transfe	-34.28571429	0.002980767	4.9511E-06
AGAMOUS-like 44	-100	9.291E-06	3.49531E-09
Protein phosphatase 2C family protein	-100	0.001933999	2.83514E-06
arginine/serine-rich zinc knuckle-containing	-55.453149	0.009092671	2.19311E-05
RNA-binding (RRM/RBD/RNP motifs) family p	-49.29577465	0.001190556	1.44408E-06
O-acetyltransferase family protein	-35.13513514	0.004312652	7.98567E-06
RECQ helicase l1	-47.54098361	0.000559946	5.41212E-07
ZIP metal ion transporter family	-100	0.000534009	5.09877E-07
ornithine-delta-aminotransferase	-96.96969697	2.02603E-10	1.76807E-14
Leucine-rich repeat protein kinase family pro	-80	0.000299187	2.44418E-07
G10 family protein	-85.71428571	0.003440723	5.98256E-06
protein binding	-40	0.001228867	1.50587E-06
general regulatory factor 9	-30.93407873	0.001406831	6.53368E-06
LETM1-like protein	-90	0.00295471	4.89482E-06

UDP-glucose:glycoprotein glucosyltransferase	-27.41779497	0.002902342	6.0514E-06
binding	-41.3372093	0.008379863	2.83084E-05
bZIP transcription factor family protein	-34.48275862	0.004920032	1.29573E-05
cytochrome P450, family 71, subfamily B, pol	-26.19937695	7.75246E-05	1.415E-07
N/A	-100	0.001933999	2.83514E-06
Rad21/Rec8-like family protein	-71.76470588	0.000308141	2.54457E-07
Ribosomal protein S5/Elongation factor G/III/	-100	0.001933999	2.83514E-06
Trypsin family protein	-65.67164179	4.4312E-06	1.47206E-09
N/A	-53.57142857	0.000150272	1.0607E-07
Metallo-hydrolase/oxidoreductase superfam	-100	0.001933999	2.83514E-06
multidrug resistance-associated protein 6	-76.81818182	0.007707273	2.50495E-05
Leucine-rich repeat transmembrane protein k	-39.86842105	0.0033077	2.14733E-05
LETM1-like protein	-100	0.000534009	5.09877E-07
mRNA capping enzyme family protein	-100	3.09357E-06	9.64173E-10
alpha/beta-Hydrolases superfamily protein	-59.83333333	9.62541E-05	7.14785E-08
Low PSII Accumulation 3	-25.73336826	0.000991912	4.04559E-06
cyclin-dependent kinase B1;2	-27.20238095	0.001156348	4.97278E-06
O-fucosyltransferase family protein	-28.57142857	0.000115304	7.59321E-08
EAP30/Vps36 family protein	-52.44122966	0.000165817	1.20749E-07
Pentatricopeptide repeat (PPR) superfamily p	-36.92307692	5.94833E-05	3.93294E-08
Pentatricopeptide repeat (PPR) superfamily p	-46.15384615	0.000652308	6.59186E-07
Pentatricopeptide repeat (PPR) superfamily p	-31.76470588	1.38669E-06	3.81343E-10
Pentatricopeptide repeat (PPR) superfamily p	-28.08988764	3.57038E-05	1.76474E-08
Pentatricopeptide repeat (PPR) superfamily p	-38.88888889	9.90426E-06	4.49561E-09
Pentatricopeptide repeat (PPR) superfamily p	-48.88888889	4.07776E-18	8.37309E-23
Pentatricopeptide repeat (PPR) superfamily p	-58.71559633	5.2241E-15	1.57073E-19
Pentatricopeptide repeat (PPR) superfamily p	-41.22807018	8.19788E-11	8.39691E-15
GTP-binding protein-related	-72.36842105	0.004811332	1.25257E-05
Topoisomerase II-associated protein PAT1	-41.94444444	0.000314104	3.11625E-07
Topoisomerase II-associated protein PAT1	-54.28571429	1.09852E-07	2.51726E-11
Topoisomerase II-associated protein PAT1	-44.0885265	2.39163E-10	2.79516E-14
Topoisomerase II-associated protein PAT1	-44.44444444	0.000396144	3.51516E-07
FTSH protease 12	-40.74074074	0.006687884	1.45664E-05
P-loop containing nucleoside triphosphate hy	-55.81395349	1.58957E-05	6.57453E-09
P-loop containing nucleoside triphosphate hy	-34.48275862	0.003058728	5.12097E-06
SPla/RYanodine receptor (SPRY) domain-cont	-38.13559322	0.002997114	6.31521E-06
Phosphoinositide phosphatase family protein	-100	1.92012E-05	8.35004E-09
N/A	-35.3125	0.003405725	2.24019E-05
SNF1 kinase homolog 10	-27.8592545	3.52E-11	4.80513E-15
Tetratricopeptide repeat (TPR)-like superfam	-30	0.004183431	7.69118E-06
PIF1 helicase	-30.14824798	0.008425597	8.1874E-05
calmodulin-binding protein-related	-27.53623188	6.41886E-05	3.77518E-08
Malectin/receptor-like protein kinase family p	-27.27272727	3.04347E-08	4.79859E-12
DNA/RNA polymerases superfamily protein	-26.84620344	0.002697389	5.46377E-06

Protein phosphatase 2C family protein	-63.88888889	0.008180794	1.90718E-05
NB-ARC domain-containing disease resistanc	-63.88888889	0.008180794	1.90718E-05
phototropin 2	-28.90271493	0.000711638	2.56817E-06
phototropin 2	-73.70689655	0.001134112	1.69533E-06
RNA recognition motif (RRM)-containing prot	-39.73888209	6.70594E-06	2.86198E-09
Nucleic acid-binding, OB-fold-like protein	-27.89983538	0.004059176	2.86338E-05
ARF-GAP domain 8	-37.81773782	3.50E-16	9.76647E-21
N/A	-49.82275218	2.87662E-08	5.55295E-12
N/A	-42.55319149	0.000916451	1.24378E-06
Concanavalin A-like lectin protein kinase fam	-44.44444444	0.000222668	2.01904E-07
Concanavalin A-like lectin protein kinase fam	-43.5483871	1.21274E-07	2.3301E-11
Concanavalin A-like lectin protein kinase fam	-43.75	9.71966E-12	6.5576E-16
Concanavalin A-like lectin protein kinase fam	-32.43243243	0.008862698	3.07483E-05
Concanavalin A-like lectin protein kinase fam	-43.90243902	0.000908461	1.03396E-06
N/A	-33.95061728	3.28415E-14	1.59569E-18
N/A	-28.07268008	0.000435184	3.9254E-07
N/A	-25.79206701	7.3107E-12	4.66427E-16
Xanthine/uracil permease family protein	-25.41193182	0.007072412	2.20853E-05
Kinase interacting (KIP1-like) family protein	-26.08695652	0.006485021	1.39533E-05
kinesin like protein for actin based chloroplas	-26.28332232	0.000917646	1.24965E-06
kinesin like protein for actin based chloroplas	-32.79722485	7.40E-06	7.67216E-09
cyclin-relatedMETHYLATED_REGION_CpG_H	-28.94736842	0.001319136	1.68033E-06
Protein of Unknown Function (DUF239)	-38.83495146	3.22969E-05	1.56082E-08
spermidine synthase 1	-47.53623188	0.000354228	3.63526E-07
pentatricopeptide (PPR) repeat-containing pr	-57.26273726	4.1663E-08	8.39813E-12
open reading frame 204	-31.59003831	4.10791E-05	2.0967E-08
beta-1,2-xylosyltransferase	-66.64098613	9.73237E-05	6.21645E-08
Haloacid dehalogenase-like hydrolase (HAD)	-28.49878935	0.003753498	2.56922E-05
N/A	-28.20048309	0.000167035	1.40492E-07
dolichol-phosphate mannosyltransferase-rela	-38.59649123	5.06E-13	3.64692E-17
RINT-1 / TIP-1 family	-35.11689417	2.87E-16	7.639E-21
RINT-1 / TIP-1 family	-64.23537703	5.03038E-08	1.02059E-11
ENTH/VHS family protein	-41.66666667	0.007936784	1.8241E-05
Signal transduction histidine kinase, hybrid-ty	-84.12698413	6.59978E-07	1.65394E-10
indigoidine synthase A family protein	-100	0.000796198	8.74075E-07
pentatricopeptide (PPR) repeat-containing pr	-100	0.000703795	7.39602E-07
Sec14p-like phosphatidylinositol transfer fam	-93.33333333	0.000709141	7.4782E-07
Transducin/WD40 repeat-like superfamily pro	-80	0.001217272	1.48709E-06
galacturonosyltransferase 4	-73.33333333	0.001564441	2.09491E-06
Homeobox-leucine zipper family protein / lip	-70.73170732	0.009227131	2.2384E-05
Calcium-dependent ARF-type GTPase activati	-47.72727273	0.000756041	8.08922E-07
KRR1 family protein	-41.93548387	0.005815286	1.20901E-05
dicer-like 2	-100	0.005353107	1.08251E-05
FAD-binding Berberine family protein	-30.27108434	0.000939266	1.07798E-06

NAD(P)-binding Rossmann-fold superfamily p	-41.26984127	0.005508077	1.12793E-05
NAD(P)-binding Rossmann-fold superfamily p	-96.66666667	2.7736E-05	1.29769E-08
LYR family of Fe/S cluster biogenesis protein	-35.44180885	6.62E-06	6.6555E-09
N/A	-29.54545455	0.000135885	1.07313E-07
N/A	-30.43478261	1.87179E-07	3.82972E-11
cytochrome P450, family 81, subfamily D, pol	-36.56923405	0.002004305	1.0595E-05
lectin protein kinase family protein	-28.65693584	2.18E-06	1.67517E-09
Galactose oxidase/kelch repeat superfamily p	-84.3373494	2.15153E-05	9.51416E-09
villin 4	-36.42512077	0.004992772	1.32308E-05
pumilio 5	-100	1.34565E-05	5.44723E-09
membrane bound O-acyl transferase (MBOA	-27.91871766	0.000160042	1.32193E-07
membrane bound O-acyl transferase (MBOA	-31.22129989	1.6685E-05	8.32594E-09
alfin-like 5	-59.15254237	0.000126172	2.6342E-07
DEAD/DEAH box RNA helicase family protein	-94.73684211	1.97241E-05	8.62084E-09
protein kinase family protein / C-type lectin c	-46.76958262	0.003167086	5.37397E-06
N/A	-33.28379224	1.59E-07	7.07609E-11
N/A	-60.48076923	0.003538729	6.19514E-06
VPS54	-31.74369542	0.001876515	3.34761E-06
Outer arm dynein light chain 1 protein	-45.35857299	0.003115914	6.70221E-06
rRNA processing protein-related	-32.2290032	2.47103E-05	1.12532E-08
Cyclophilin-like peptidyl-prolyl cis-trans isom	-26.93346842	0.000586742	6.88438E-07
Aha1 domain-containing protein	-25.95238095	1.88453E-05	2.38788E-08
PYRIMIDINE B	-46.04166667	0.003441086	7.73159E-06
P-loop containing nucleoside triphosphate hy	-46.04166667	0.003441086	7.73159E-06
fatty acid desaturase 2	-36.70833333	0.000156609	3.48281E-07
N/A	-70	6.98183E-05	1.23782E-07
Chaperone DnaJ-domain superfamily protein	-93.33333333	0.001063149	1.55316E-06
DNA GYRASE A	-78.94736842	0.003758864	6.69009E-06
Protein kinase superfamily protein	-36.15384615	0.00572838	1.61806E-05
Caleosin-related family protein	-43.47670251	0.003425268	7.66658E-06
N/A	-25.92342342	0.000679328	2.41983E-06
plastidic pyruvate kinase beta subunit 1	-25.36873156	0.001271237	5.64769E-06
DNA primases	-50.78039927	0.00034223	3.48291E-07
Heavy metal transport/detoxification superfa	-39.61916462	6.46745E-07	1.89817E-10
2-oxoglutarate (2OG) and Fe(II)-dependent o	-76.19047619	0.000297757	2.9091E-07
zinc finger WD40 repeat protein 1	-92.30769231	8.08049E-08	1.45773E-11
GroES-like zinc-binding alcohol dehydrogenas	-27.08616011	1.52214E-05	7.45699E-09
hydroxymethylglutaryl-CoA synthase / HMG-	-68.18181818	0.002502691	3.95513E-06
Microtubule associated protein (MAP65/ASE	-33.02459763	1.22E-07	5.12659E-11
Tetratricopeptide repeat (TPR)-like superfam	-46.8627451	8.92759E-05	1.68344E-07
Dihydroxyacetone kinase	-69.23076923	0.00803061	1.85391E-05
embryo sac development arrest 7	-36.66666667	0.00490816	9.53829E-06
photosystem II reaction center protein M	-29.22033898	0.00097996	1.13546E-06
Reticulon family protein	-41.03899573	8.76E-08	3.43843E-11

associated molecule with the SH3 domain of	-37.47987118	0.000775922	2.89513E-06
Fibronectin type III domain-containing protei	-85.71428571	0.008526819	2.01911E-05
N/A	-73.9088729	3.36592E-05	1.6464E-08
Tesmin/TSO1-like CXC domain-containing prc	-100	0.001933999	2.83514E-06
S-adenosyl-L-methionine-dependent methylt	-26.86433528	4.16E-07	2.22759E-10
sugar transporter 14	-37.35909823	0.000920785	1.25675E-06
MSCS-like 2	-40	0.006316256	1.34698E-05
Glycosyl hydrolase family protein	-31.47239086	2.69086E-06	9.64667E-10
Glycosyl hydrolase family protein	-38.83784606	1.00554E-09	1.05448E-13
SAUR-like auxin-responsive protein family	-76.47058824	0.000366033	3.16743E-07
SAUR-like auxin-responsive protein family	-76.47058824	0.000366033	3.16743E-07
Uncharacterized protein	-44.11206078	0.008460663	1.99228E-05
N/A	-43.40909091	0.001098386	1.31376E-06
DNA binding;ATP binding;nucleic acid binding	-55.55555556	0.006463162	1.38826E-05
Pentatricopeptide repeat (PPR-like) superfam	-76.69902913	3.01362E-08	4.66499E-12
DNA-directed RNA polymerases	-69.6969697	3.38468E-07	7.69459E-11
zinc finger protein 1	-60	0.005907747	1.2333E-05
SKP1-like 21	-70.90909091	0.001604185	2.16343E-06
Protein of unknown function (DUF3741)	-81.25	0.000115162	7.57544E-08
Protein of unknown function (DUF3245)	-25.5036208	0.000594029	2.02488E-06
RNA-binding KH domain-containing protein	-100	0.001933999	2.83514E-06
SCAR homolog 2	-52.27272727	0.001906341	2.69927E-06
N/A	-26.6226138	0.003821711	2.63512E-05
Target SNARE coiled-coil domain protein	-33.95566922	0.001277483	1.98623E-06
Polyketide cyclase/dehydrase and lipid transp	-37.83783784	0.002053449	3.06747E-06
Zinc finger C-x8-C-x5-C-x3-H type family prote	-90.90909091	0.004921546	9.61483E-06
transducin family protein / WD-40 repeat fan	-83.33333333	0.004158833	7.63375E-06
Protein kinase family protein	-34.84617728	0.002748854	5.6023E-06
N/A	-28.94557823	0.00731223	1.64078E-05
Galactose oxidase/kelch repeat superfamily p	-67.56756757	0.005375249	1.0919E-05
Beige/BEACH domain ;WD domain, G-beta re	-60.86956522	0.001736793	2.39194E-06
Outer membrane OMP85 family protein	-27.07143361	2.99E-20	3.38267E-25
N/A	-30.4964539	0.005851584	4.81558E-05
Mitochondrial transcription termination facto	-35.02739467	0.007294819	1.63376E-05
phosphatidyl inositol monophosphate 5 kinas	-26.4957265	0.006325378	5.39165E-05
Folylpolyglutamate synthetase family protein	-40.875	0.006649015	2.02567E-05
demeter-like 1	-26.81218851	0.005410003	1.48334E-05
LETM1-like protein	-28.125	0.005116276	1.36824E-05
N/A	-28.18766393	0.000406849	1.2234E-06
ribosomal protein L2	-29.20458787	2.64846E-13	1.63461E-17
N/A	-95	4.60684E-05	2.44257E-08
nuclear RNA polymerase A1	-39.69639932	4.62287E-14	2.30684E-18
nuclear RNA polymerase A1	-28.44001897	0.00016537	1.38113E-07
nuclear RNA polymerase A1	-35.78646934	7.35679E-14	3.816E-18

nuclear RNA polymerase A1	-34.44770563	4.07335E-12	3.23616E-16
nuclear RNA polymerase A1	-29.05525847	0.004191551	1.02131E-05
kinesin 1	-32.53333333	0.00047896	4.43266E-07
N/A	-36.32607705	4.36783E-19	1.14715E-23
N/A	-33.51032448	3.37981E-15	9.41851E-20
N/A	-34.53199365	0.002964542	4.91328E-06
Arginyl-tRNA synthetase, class Ic	-57.20238095	3.26251E-08	5.2875E-12
Arginyl-tRNA synthetase, class Ic	-92.72727273	3.89581E-06	1.27085E-09
SERINE CARBOXYPEPTIDASE-LIKE 49	-29.50208706	0.001832074	3.23705E-06
Ran BP2/NZF zinc finger-like superfamily prot	-58.33333333	7.37312E-34	1.93644E-39
Leucine-rich repeat protein kinase family pro	-78.4591195	0.000362188	3.75959E-07
Protein kinase family protein with ARM repea	-57.33333333	0.000297765	2.43038E-07
VEFS-Box of polycomb protein	-26.87598116	0.007958909	2.62384E-05
ubiquitin-specific protease 13	-100	0.000703795	7.39602E-07
P-loop containing nucleoside triphosphate hy	-28.59459459	0.002241335	4.2854E-06
P-loop containing nucleoside triphosphate hy	-53.31991952	0.008189209	2.73471E-05
Protein of unknown function (DUF3411)	-40.1744186	0.003482089	6.07236E-06
Polynucleotidyl transferase, ribonuclease H-li	-49.15254237	0.000881934	9.95361E-07
mitochondrially targeted single-stranded DN	-38.28551913	0.000157291	1.13041E-07
RING/U-box superfamily protein	-100	0.000703795	7.39602E-07
N/A	-100	0.000703795	7.39602E-07
Transducin/WD40 repeat-like superfamily pr	-26.77433694	4.36662E-05	6.8502E-08
Nucleolar histone methyltransferase-related	-28.77894737	7.38867E-05	1.33172E-07
ARM repeat superfamily protein	-44.12818471	0.001741729	3.01682E-06
N/A	-29.62992889	0.004337158	3.14229E-05
RNA-binding (RRM/RBD/RNP motifs) family p	-48.57142857	0.009877328	2.44901E-05
RNA binding (RRM/RBD/RNP motifs) family p	-95.23809524	1.5665E-05	6.46563E-09
N/A	-41.66666667	0.000639597	2.2338E-06
fatty alcohol oxidase 3	-28.86102403	0.00042248	1.28714E-06
Uncharacterised protein family (UPF0497)	-38.70967742	0.008276243	1.93793E-05
Protein of unknown function (DUF810)	-25.75138009	0.006094715	1.28409E-05
N/A	-100	0.00014754	1.03544E-07
nudix hydrolase homolog 26	-36.43697019	5.48454E-05	3.06882E-08
ribosomal protein L6 family protein	-32.6899456	1.58E-06	1.13244E-09
Transmembrane amino acid transporter fami	-100	0.000703795	7.39602E-07
N/A	-100	0.001061922	1.54644E-06
Sec1/munc18-like (SM) proteins superfamily	-76.47058824	2.83675E-07	6.15771E-11
Zim17-type zinc finger protein	-47.02380952	1.44069E-05	5.8848E-09
Zinc finger (C2H2 type) family protein / trans	-55	8.96769E-05	5.55738E-08
VIRB2-interacting protein 1	-50.71895425	0.004230545	1.03554E-05
N/A	-38.59649123	8.94899E-07	2.72637E-10
N/A	-37.5	0.006961761	1.5362E-05
tubulin beta 8	-43.98335583	3.09E-09	7.28271E-13
DEAD box RNA helicase (PRH75)	-39.02439024	0.004346889	8.07457E-06

Aluminium induced protein with YGL and LRD	-27.59076531	2.50E-06	1.99762E-09
CVP2 like 1	-45.8781362	0.003782564	8.79935E-06
Cupredoxin superfamily protein	-54.24528302	0.000376448	1.1029E-06
Protein of unknown function (DUF630 and DU	-26.2987013	0.0003002	2.46346E-07
HMG (high mobility group) box protein with /	-59.84848485	0.003294694	7.24691E-06
tonneau 1b (TON1b)	-98.61111111	3.20131E-08	5.14192E-12
hydroxyproline-rich glycoprotein family prote	-27.43589744	0.004578929	1.16318E-05
target of rapamycin	-37.04274162	0.002895672	4.78003E-06
N/A	-100	0.000703795	7.39602E-07
Ribosomal protein S5 family protein	-27.44488412	0.00957227	9.84952E-05
Ribosomal protein S5 family protein	-26.52412281	4.04E-08	1.38629E-11
N/A	-45	0.001968856	3.59766E-06
pleckstrin homology (PH) domain-containing	-81.81818182	0.001278077	1.6121E-06
N/A	-44.44444444	0.00078803	8.54717E-07
ralf-like 34	-35.76923077	0.007671471	7.16356E-05
P-loop containing nucleoside triphosphate hy	-81.31868132	5.91799E-05	3.39379E-08
Pentatricopeptide repeat (PPR) superfamily p	-100	7.69704E-05	4.65676E-08
ACT-like protein tyrosine kinase family protei	-34.64912281	0.001955079	2.87321E-06
Pyridoxal phosphate (PLP)-dependent transfe	-32.49249249	1.28E-07	5.45277E-11
Ubiquitin-like superfamily protein	-40	0.009723744	2.40095E-05
N/A	-40	0.009723744	2.40095E-05
Plant protein of unknown function (DUF827)	-47.27272727	0.002980767	4.94903E-06
RING/FYVE/PHD zinc finger superfamily prote	-100	0.001933999	2.83514E-06
ATPase, F0/V0 complex, subunit C protein	-100	5.19877E-12	3.2406E-16
beta glucosidase 13	-26.49859944	2.55799E-05	3.52831E-08
SEC14 cytosolic factor family protein / phospl	-28.45827961	3.26E-06	2.78041E-09
Ribosomal RNA processing Brix domain prote	-100	0.001933999	2.83514E-06
cleavage and polyadenylation specificity facto	-33.67521368	1.40098E-05	1.66631E-08
homolog of histone chaperone HIRA	-32.45415207	0.003601836	2.42498E-05
tRNAisopentenyltransferase 2	-72.5	0.000646723	6.49273E-07
Ribosomal protein L24e family protein	-41.77927928	0.000224392	1.73442E-07
vacuolar protein sorting 41	-31.48148148	0.002847219	4.66873E-06
ribosomal protein L9	-100	9.19326E-05	5.75246E-08
DNA ligase 1	-28.8814751	4.66678E-05	7.46565E-08
ABC transporter family protein	-90.90909091	0.00327541	5.60865E-06
Phototropic-responsive NPH3 family protein	-28.91772735	1.79E-11	2.10584E-15
receptor kinase 3	-28.71496563	0.003330041	2.1669E-05
BTB/POZ/MATH-domains containing protein	-100	0.001240448	1.54644E-06
Yippee family putative zinc-binding protein	-100	4.32189E-05	2.25468E-08
N/A	-100	4.32189E-05	2.25468E-08
Galactose oxidase/kelch repeat superfamily p	-100	0.001933999	2.83514E-06
K-box region and MADS-box transcription fac	-37.45045188	0.001386338	6.40178E-06
RNA polymerase II transcription mediators	-28.8003663	0.005714746	1.61046E-05
AGC (cAMP-dependent, cGMP-dependent an	-72.22222222	0.000169274	1.23391E-07

AGC (cAMP-dependent, cGMP-dependent an	-53.84615385	0.000543244	5.21085E-07
N/A	-28.10522811	0.000191201	4.50652E-07
mitogen-activated protein kinase kinase kina	-90.47619048	0.001217272	1.48809E-06
Basic-leucine zipper (bZIP) transcription facto	-100	0.005353107	1.08251E-05
cytochrome BC1 synthesis	-34.86756106	8.21332E-05	1.51914E-07
RNA binding	-33.88648389	4.42115E-06	1.72431E-09
RNA binding	-37.5	0.009161264	2.2157E-05
RNA binding	-42.3661509	7.06526E-13	3.57506E-17
pfkB-like carbohydrate kinase family protein	-50.58201058	0.002499077	1.44749E-05
RING/U-box superfamily protein	-40.8496732	2.05E-10	3.41132E-14
N/A	-90	0.002116499	3.20046E-06
N/A	-90	0.002116499	3.20046E-06
DHBP synthase RibB-like alpha/beta domain	-100	5.43973E-09	6.94116E-13
NOT2 / NOT3 / NOT5 family	-43.83561644	0.005317911	1.06642E-05
Pheophorbide a oxygenase family protein wit	-42.64705882	0.00048679	4.51227E-07
PHD finger family protein	-31.22015915	0.001407023	1.82014E-06
cellulose synthase-like B3	-76	0.004139529	1.00211E-05
N/A	-44.83333333	0.006177282	1.81625E-05
PIF1 helicase	-25.77186964	0.003791286	2.60551E-05
Protein kinase superfamily protein	-33.33333333	0.000800279	1.04092E-06
Protein kinase superfamily protein	-100	0.000277356	2.24346E-07
kinesin 3	-51.84275184	0.004548366	8.56891E-06
Protein kinase superfamily protein	-25.36509176	0.00075029	8.00567E-07
S-locus lectin protein kinase family protein	-83.33333333	0.004158833	7.63375E-06
S-locus lectin protein kinase family protein	-41.50943396	3.51349E-05	5.22633E-08
ARF-GAP domain 5	-29.09132007	0.000281564	7.51431E-07
cyclic nucleotide gated channel 5	-29.16121801	0.005269453	1.42408E-05
Domain of unknown function (DUF3598)	-34.46691176	0.008463618	2.87525E-05
Leucine-rich repeat transmembrane protein l	-61.9047619	0.002483692	3.91964E-06
Uncharacterised BCR, YbaB family COG0718	-32.99284985	0.000136801	1.08146E-07
N/A	-26.19047619	0.005289772	1.43439E-05
homogentisate 1,2-dioxygenase	-100	0.001240448	1.54644E-06
shaggy-like protein kinase 41	-91.66666667	0.004921546	9.61483E-06
ARM repeat superfamily protein	-100	0.000440203	4.00618E-07
DNA/RNA helicase protein	-100	0.000163436	1.18536E-07
Exostosin family protein	-40.1299505	2.72583E-05	3.84011E-08
S-locus lectin protein kinase family protein	-34.04862317	6.03E-07	3.47802E-10
S-locus lectin protein kinase family protein	-45	0.001116707	1.33731E-06
zinc ion binding	-36.73245614	0.002133853	3.23296E-06
N/A	-100	0.001933999	2.83514E-06
RING 1A	-27.56699755	3.10227E-05	1.75582E-08
RING 1A	-59.36853002	0.000594354	5.82281E-07
global transcription factor group E4	-90.90909091	0.000902374	1.02306E-06
Tetratricopeptide repeat (TPR)-like superfam	-60.86956522	0.003804626	6.81339E-06

terpene synthase 21	-33.75764994	0.000309625	8.48334E-07
myosin 2	-65.43209877	0.001845373	2.58613E-06
Seven transmembrane MLO family protein	-46.66666667	1.56E-07	6.85519E-11
Yippee family putative zinc-binding protein	-72.89719626	0.003941291	7.1275E-06
N/A	-74.50980392	4.92908E-05	2.6642E-08
RAB GTPase homolog A1B	-63.15789474	0.001933999	2.76347E-06
Leucine-rich repeat transmembrane protein	-30.77211394	0.001515491	7.22162E-06
senescence-related gene 1	-28.06172322	0.00049531	1.59304E-06
eukaryotic translation initiation factor SUI1 f	-59.64285714	4.56796E-06	1.52419E-09
disease resistance family protein / LRR family	-25.92592593	0.003959094	9.39458E-06
homolog of yeast ADA2 2A	-62.5	0.005607374	1.15345E-05
N/A	-25.27718802	0.003624911	2.44862E-05
N/A	-25.89222615	8.78E-07	5.54152E-10
Endomembrane protein 70 protein family	-54.05405405	0.000115391	7.67513E-08
N/A	-47.50957854	0.005208049	1.40133E-05
N/A	-28.19875776	2.20482E-06	6.40286E-10
N/A	-49.33333333	7.20898E-13	3.70064E-17
N/A	-55.93220339	1.16646E-06	3.6686E-10
N/A	-45.3125	1.15695E-08	2.02824E-12
high mobility group B2	-55.93220339	1.16646E-06	3.6686E-10
high mobility group B2	-45.3125	1.15695E-08	2.02824E-12
high mobility group B2	-28.19875776	2.20482E-06	6.40286E-10
high mobility group B2	-49.33333333	7.20898E-13	3.70064E-17
P-loop containing nucleoside triphosphate hy	-86.36363636	0.000920785	1.25558E-06
alcohol dehydrogenase 1	-27.64204545	9.8674E-06	4.47039E-09
Target of Myb protein 1	-96.15384615	7.23175E-05	4.32753E-08
DNAJ heat shock N-terminal domain-containi	-51.28205128	0.002256342	3.48142E-06
Auxin efflux carrier family protein	-38.46153846	0.005600242	1.15116E-05
N/A	-37.75946276	2.28006E-05	3.05002E-08
N/A	-29	1.63281E-08	2.93751E-12
N/A	-29.18192918	0.002752875	4.46961E-06
N/A	-27.817005	6.69421E-05	3.95676E-08
N/A	-42.62295082	9.45991E-07	2.435E-10
BTB/POZ domain-containing protein	-25.09070449	6.37E-09	1.65325E-12
Malectin/receptor-like protein kinase family	-27.00743049	3.37756E-08	5.57303E-12
casein lytic proteinase B3	-64.86486486	0.007775091	1.77072E-05
EID1-like 2	-67.85714286	0.001764726	2.43946E-06
N/A	-64.19753086	3.18591E-09	4.87397E-13
PIF1 helicase	-25.8382832	0.005197601	4.0674E-05
NAC domain containing protein 100	-33.26367119	0.001049893	1.51174E-06
NAC domain containing protein 100	-35.93073593	0.000651776	6.57229E-07
cullin 3	-100	0.001933999	2.83514E-06
hydroxyproline-rich glycoprotein family prote	-59.26370548	8.63944E-08	1.58391E-11
protein kinase 2A	-62.85714286	0.000555182	5.35793E-07

Disease resistance protein (TIR-NBS-LRR class	-36.28318584	2.24047E-09	3.23635E-13
Disease resistance protein (TIR-NBS-LRR class	-28.57142857	0.00179871	2.50359E-06
3\'-5\' exonuclease domain-containing protei	-75	0.000174085	1.27536E-07
MAPK/ERK kinase kinase 1	-76.78571429	0.000695076	7.14128E-07
NOD26-like intrinsic protein 1;2	-40.77109897	4.36857E-05	6.85769E-08
lysine-ketoglutarate reductase/saccharopine	-37.40653863	0.000946387	3.79934E-06
HAD-superfamily hydrolase, subfamily IG, 5\'	-100	0.000534009	5.09877E-07
multidrug resistance-associated protein 5	-100	3.22217E-05	1.55009E-08
myosin 2	-100	5.09444E-06	1.74469E-09
GDSL-like Lipase/Acylhydrolase superfamily p	-35.12817125	3.91E-09	9.54433E-13
CLIP-associated protein	-98.14814815	3.25745E-07	7.26201E-11
N/A	-37.78901855	2.78E-11	3.58589E-15
HSP20-like chaperones superfamily protein	-73.45238095	1.23273E-05	4.94495E-09
heat shock cognate protein 70-1	-29.2334248	1.79916E-05	7.57336E-09
PIF1 helicase	-29.2334248	1.79916E-05	7.57336E-09
N/A	-29.76506252	3.56359E-05	5.34068E-08
Protein kinase superfamily protein	-76.66666667	0.000286403	2.32504E-07
Protein of unknown function (DUF1336)	-40.39316975	0.00032109	3.20664E-07
D111/G-patch domain-containing protein	-27.91664294	1.11E-07	4.56176E-11
D111/G-patch domain-containing protein	-39.57875458	0.000160123	1.32575E-07
BED zinc finger ;hAT family dimerisation dom	-91.66666667	0.004921546	9.61483E-06
Tetratricopeptide repeat (TPR)-like superfam	-39.44444444	0.005983362	4.97599E-05
Protein kinase superfamily protein	-29.95126706	0.000577716	6.73296E-07
Protein of unknown function (DUF1162)	-76.15384615	0.000576571	5.59818E-07
HAESA-like 1	-30.15777309	0.000246278	2.30427E-07
N/A	-57.44444444	0.003594702	8.19239E-06
cysteine-rich RLK (RECEPTOR-like protein kina	-70	0.002384256	3.72392E-06
Peptidase S24/S26A/S26B/S26C family protei	-50.02462448	9.24063E-12	6.09888E-16
Disease resistance protein (TIR-NBS-LRR class	-68.08510638	0.000173994	1.27341E-07
Phosphatidylinositol-4-phosphate 5-kinase fa	-100	0.001933999	2.83514E-06
nuclear RNA polymerase D1B	-57.57575758	0.002729491	4.41964E-06
uridine 5\'-monophosphate synthase / UMP	-54.76190476	6.33109E-05	3.70035E-08
CBS domain-containing protein with a domai	-100	0.000703795	7.39602E-07
auxin response factor 8	-48.17391304	0.00283208	4.63665E-06
Integrin-linked protein kinase family	-32.64051522	8.46318E-06	3.12802E-09
N/A	-27.63918252	0.003546663	6.22648E-06
glutamate receptor 2.7	-34.50292398	0.004743378	1.22429E-05
glutamate receptor 2.7	-51.35746606	0.002239627	3.44413E-06
Homeodomain-like transcriptional regulator	-28.62318841	8.59852E-06	3.18435E-09
Homeodomain-like transcriptional regulator	-51.51515152	0.001166073	5.03242E-06
callose synthase 5	-74.46808511	0.003426762	5.93818E-06
STRUBBELIG-receptor family 3	-88.37209302	3.00516E-05	1.41044E-08
pyrophosphorylase 6	-100	0.001933999	2.83514E-06
RING/U-box superfamily protein	-89.76190476	7.70025E-06	2.77828E-09

interactor of constitutive active rops 1	-31.88932981	8.90E-14	4.83429E-18
MATE efflux family protein	-28.47144457	0.000220413	1.69235E-07
P-loop containing nucleoside triphosphate hy	-43.33333333	3.01E-07	1.51503E-10
Nucleotidyltransferase family protein	-65.85365854	0.00338527	5.84145E-06
Leucine-rich repeat (LRR) family protein	-63.07692308	0.004223776	7.77154E-06
myosin 2	-52.56099832	7.75942E-08	1.37136E-11
BURP domain-containing protein	-30.27912621	0.001234475	1.51365E-06
BURP domain-containing protein	-80.71428571	0.001273263	1.97633E-06
BURP domain-containing protein	-45.95393253	1.25E-17	2.48234E-22
WRKY DNA-binding protein 69	-90	0.000525153	4.9603E-07
Protein kinase superfamily protein	-100	1.80662E-05	7.75047E-09
photosynthetic electron transfer C	-76.05633803	0.001240448	1.53359E-06
Receptor-like protein kinase-related family pr	-44.68085106	3.66052E-05	2.15089E-08
Receptor-like protein kinase-related family pr	-49.93257417	1.90841E-09	2.16925E-13
N/A	-91.17647059	2.43309E-06	7.30736E-10
4-hydroxy-3-methylbut-2-enyl diphosphate s	-77.22222222	0.001213165	1.47951E-06
N/A	-47.87878788	6.31017E-05	1.09279E-07
ETHYLENE-INSENSITIVE3-like 3	-53.03571429	0.000431551	3.88947E-07
Tetratricopeptide repeat (TPR)-like superfam	-48.29956156	1.51E-08	4.52304E-12
Calcium-dependent phosphotriesterase supe	-48.29956156	1.51E-08	4.52304E-12
RNA methyltransferase family protein	-38.88888889	0.002379863	1.35136E-05
ENTH/VHS family protein	-68.125	0.001408473	1.82508E-06
Leucine-rich repeat family protein	-29.30094386	1.03E-18	1.56201E-23
GPI transamidase component Gpi16 subunit	-25.12768131	0.001982337	1.04439E-05
N/A	-100	6.72491E-06	2.39678E-09
autoinhibited Ca(2+)-ATPase 9	-75.75757576	3.78E-12	3.38919E-16
autoinhibited Ca(2+)-ATPase 9	-53.48837209	4.74737E-05	2.97057E-08
microtubule-associated proteins 65-1	-43.24561404	0.004676298	8.89566E-06
polymerase gamma 2	-34.61538462	0.001632497	2.21119E-06
NPR1-like protein 3	-32.05808081	0.003347015	7.40115E-06
F-box protein 2	-33.33333333	0.000692662	2.47858E-06
F-box protein 2	-80	0.007209879	1.6121E-05
Structural maintenance of chromosomes (SM	-95.45454545	0.000221651	1.7051E-07
RNA-binding KH domain-containing protein	-41.51747656	0.005278573	1.42828E-05
sorting nexin 2B	-26.84556696	0.00032339	8.99516E-07
Regulator of chromosome condensation (RCC	-72.5	0.001141307	1.37346E-06
Pentatricopeptide repeat (PPR-like) superfam	-87.5	0.00077132	8.32057E-07
sec7 domain-containing protein	-71.23287671	0.00022659	1.75472E-07
THO complex, subunit 5	-96	9.45691E-05	5.99196E-08
N/A	-46.529723	3.43446E-09	4.13056E-13
Pseudouridine synthase family protein	-36.88311688	0.009989518	3.70912E-05
Transketolase family protein	-75	0.003437998	5.97278E-06
nucleotide binding protein 35	-34.11764706	5.68216E-09	7.29218E-13
Small nuclear ribonucleoprotein family prote	-38.25161887	0.003002729	4.99582E-06

N/A	-35.71428571	0.000850746	3.28016E-06
G protein alpha subunit 1	-100	0.000440203	4.00618E-07
Chalcone-flavanone isomerase family protein	-37.14285714	6.05681E-05	3.5045E-08
ACT-like protein tyrosine kinase family protei	-55.78378378	4.06196E-05	2.06729E-08
Peroxidase superfamily protein	-28.23335021	3.627E-12	2.81011E-16
cullin 1	-30.84571852	1.47E-09	3.15044E-13
ARF-GAP domain 15	-41.81818182	6.42181E-10	8.05349E-14
ARF-GAP domain 15	-48.55072464	5.47955E-05	3.55824E-08
N/A	-31.12033195	2.59439E-15	1.06758E-19
N/A	-43.24324324	0.003302396	5.66212E-06
N/A	-47.5	0.000950387	1.31487E-06
N/A	-43.36170213	0.00282938	4.62703E-06
delta1-pyrroline-5-carboxylate synthase 1	-38.46153846	0.005037736	1.33897E-05
TRS120	-100	0.000796198	8.74075E-07
N/A	-63.89578164	1.22614E-06	3.26402E-10
SET domain group 29	-63.89578164	1.22614E-06	3.26402E-10
Polynucleotidyl transferase, ribonuclease H-li	-31.93582649	3.16895E-06	1.17143E-09
Polynucleotidyl transferase, ribonuclease H-li	-27.12943275	1.27598E-07	2.99093E-11
Protein of unknown function, DUF593	-25.33125	0.00559587	1.56153E-05
alcohol dehydrogenase 1	-62.73465957	3.90416E-09	4.75272E-13
LisH dimerisation motif;WD40/YVTN repeat-l	-66.66666667	0.000865438	1.14982E-06
RING/U-box superfamily protein	-52.08333333	0.006823164	1.49361E-05
Protein of unknown function (DUF1218)	-31.02275538	7.41E-06	7.68396E-09
ubiquitin-specific protease 26	-36.80555556	0.006028518	1.26793E-05
ubiquitin-specific protease 26	-100	0.001240448	1.54644E-06
DNA topoisomerase, type IA, core	-34.16208791	0.000897336	1.01603E-06
N/A	-28.28455458	0.003180295	2.03587E-05
Ribosomal protein L14	-40.93406593	0.001023852	1.46013E-06
bromo-adjacent homology (BAH) domain-cor	-33.67256637	0.004803448	1.24831E-05
Tetratricopeptide repeat (TPR)-like superfam	-100	0.001933999	2.83514E-06
signal peptide peptidase	-55.53359684	0.006171873	1.81257E-05
appr-1-p processing enzyme family protein	-72.70114943	0.001833685	3.24351E-06
N/A	-58.01838611	0.005049871	1.34295E-05
disease resistance protein (TIR-NBS-LRR class	-42.37762238	0.001610535	7.84546E-06
Tetratricopeptide repeat (TPR)-like superfam	-40.06159015	0.006437877	1.38047E-05
Tetratricopeptide repeat (TPR)-like superfam	-36.02150538	3.33794E-05	1.62782E-08
Tetratricopeptide repeat (TPR)-like superfam	-76.92307692	0.009041152	2.17936E-05
Tetratricopeptide repeat (TPR)-like superfam	-46.31578947	3.05399E-12	2.32605E-16
N/A	-53.84615385	0.000498983	5.56771E-07
N/A	-37.28813559	3.41544E-10	4.059E-14
N/A	-33.68159204	0.000178546	1.32245E-07
DNAJ heat shock N-terminal domain-containi	-77.71929825	0.000281029	2.71281E-07
NADH-dependent glutamate synthase 1	-34.48275862	0.009612209	3.495E-05
NADH-dependent glutamate synthase 1	-34.93150685	5.21247E-07	1.49219E-10

NADH-dependent glutamate synthase 1	-63.63636364	2.02431E-10	2.326E-14
NADH-dependent glutamate synthase 1	-35.18156121	0.000290218	2.35814E-07
Ribonuclease II/R family protein	-28.82675439	1.87289E-08	3.44097E-12
Ribonuclease II/R family protein	-31.01265823	9.38846E-13	6.53421E-17
N/A	-33.63248967	0.000114373	8.80129E-08
N/A	-33.36627141	3.55252E-11	3.33554E-15
N/A	-32.74336283	1.12545E-09	1.4853E-13
N/AMETHYLATED_REGION	-46.35897436	0.005869797	1.67882E-05
O-fucosyltransferase family protein	-29.13806255	0.006909491	1.51757E-05
O-fucosyltransferase family protein	-37.96061723	3.49894E-11	2.71987E-15
ER lumen protein retaining receptor family pı	-37.61276374	6.80E-06	6.88697E-09
phosphoenolpyruvate carboxylase-related kiı	-27.20848057	4.31E-09	1.06025E-12
Target SNARE coiled-coil domain protein	-100	1.13095E-05	4.42884E-09
N/A	-54.88721805	0.001165037	1.408E-06
TRAF-type zinc finger-related	-75	0.009307931	2.26619E-05
Transketolase family protein	-47.54221388	0.001146058	1.38086E-06
RNAse E/G-like	-83.63636364	0.000206026	1.56375E-07
B-box type zinc finger protein with CCT doma	-27.94117647	0.000803199	8.84706E-07
phosphate transporter 4;3	-50.79365079	0.000937613	1.07539E-06
RNA recognition motif (RRM)-containing prot	-28.70286576	0.005958211	1.71565E-05
WRKY DNA-binding protein 4	-38.10786914	1.86E-08	5.71297E-12
Protein of unknown function (DUF567)	-52.13600697	0.000739207	7.86573E-07
O-methyltransferase family protein	-29.6875	1.67536E-05	2.06414E-08
O-methyltransferase family protein	-47.22222222	0.003166326	6.8523E-06
Basic-leucine zipper (bZIP) transcription facto	-55.83982202	0.000400739	3.55887E-07
N/A	-49.74025974	0.000107393	8.15837E-08
LYR family of Fe/S cluster biogenesis protein	-44.8630137	0.005976975	1.25358E-05
P-loop containing nucleoside triphosphate hy	-31.71101017	0.000241156	6.10833E-07
Molecular chaperone Hsp40/DnaJ family prot	-29.75743936	0.000404024	4.2975E-07
chitinase A	-30.15151515	0.001574304	2.11389E-06
Poly (ADP-ribose) glycohydrolase (PARG)	-30.80882353	0.000740004	7.88125E-07
beta galactosidase 1	-100	0.000703795	7.39602E-07
casein kinase 1-like protein 2	-38.63636364	0.000440203	3.97918E-07
casein kinase 1-like protein 2	-32.07920792	2.23E-28	6.78936E-34
ARM repeat superfamily protein	-26.02739726	0.003444049	7.74229E-06
N/A	-25.60825377	3.5484E-05	5.30169E-08
N/A	-28.15934066	0.000509566	1.65416E-06
ACT domain-containing protein	-62.98003072	0.002363058	3.67554E-06
emp24/gp25L/p24 family/GOLD family prote	-27.69024817	0.008824935	8.76413E-05
emp24/gp25L/p24 family/GOLD family prote	-34.30499325	0.005547905	1.53977E-05
Tetratricopeptide repeat (TPR)-like superfam	-30.55555556	0.000403249	3.58411E-07
pyruvate decarboxylase-2	-30.55555556	0.000403249	3.58411E-07
K-box region and MADS-box transcription fac	-41.0130719	6.29E-06	6.23898E-09
dynamin-related protein 3A	-100	0.000277356	2.24346E-07

aldehyde dehydrogenase 6B2	-46.04519774	2.18E-06	1.67225E-09
Aluminium induced protein with YGL and LRD	-27.56201129	0.000295801	8.00393E-07
glucan synthase-like 1	-75.71428571	0.001378557	1.77119E-06
protease-related	-25.10712894	0.001119278	1.6653E-06
Ankyrin repeat family protein	-40.29888551	2.64031E-11	2.0137E-15
chromatin remodeling factor17	-35.06979063	0.000320942	2.67369E-07
beta-amylase 3	-74.19354839	0.005032822	9.90604E-06
N/A	-37.81609195	0.000124483	8.37112E-08
Thymidine kinase	-55.31400966	0.00294017	4.85564E-06
Galactose oxidase/kelch repeat superfamily p	-100	0.000796198	8.74075E-07
PSAJ	-81.77777778	2.8487E-23	2.61859E-28
PSAJ	-95.85492228	4.21979E-28	1.85673E-33
PSAJ	-37.86163522	2.68576E-11	2.46881E-15
PSAJ	-78.37465565	4.31419E-06	1.43003E-09
NPR1-like protein 3	-44.96551724	0.009341857	3.32511E-05
Ubiquitin carboxyl-terminal hydrolase family	-66.15384615	5.61302E-05	3.65965E-08
Plant invertase/pectin methylesterase inhibit	-38.4496124	2.38E-07	1.15327E-10
Drought-responsive family protein	-29.07779791	2.70551E-05	3.79912E-08
homolog of yeast sucrose nonfermenting 4	-100	3.11045E-05	1.47354E-08
Protein kinase superfamily protein	-35.87301587	0.003911856	9.23625E-06
N/A	-27.08333333	0.004710357	1.21236E-05
DNA binding;DNA-directed RNA polymerases	-26.12179487	9.94E-07	6.4095E-10
homolog of CFIM-25	-37.44377811	0.000569755	1.91985E-06
nuclear factor Y, subunit A5	-30.82251082	0.002105683	3.16712E-06
N/A	-35.67176871	0.003042672	6.47753E-06
XS domain-containing protein / XS zinc finger	-34.06593407	1.71117E-09	1.91995E-13
XS domain-containing protein / XS zinc finger	-34.06593407	1.71117E-09	1.91995E-13
P-loop containing nucleoside triphosphate hy	-27.53623188	0.007946427	1.82794E-05
Riboflavin synthase-like superfamily protein	-36.14457831	3.64193E-07	9.73053E-11
Riboflavin synthase-like superfamily protein	-28.49162011	1.01598E-09	1.32749E-13
Riboflavin synthase-like superfamily protein	-29.92989452	1.10901E-16	3.85928E-21
Riboflavin synthase-like superfamily protein	-42.52960443	2.2436E-13	1.35527E-17
Riboflavin synthase-like superfamily protein	-38.23529412	1.36355E-06	3.73979E-10
Riboflavin synthase-like superfamily protein	-31.81818182	0.001853486	2.60158E-06
Riboflavin synthase-like superfamily protein	-25.97402597	0.005066751	9.98397E-06
VPS54	-69.56521739	0.000453169	4.9452E-07
VPS54	-57.28669846	8.48188E-05	6.09817E-08
Outer arm dynein light chain 1 protein	-26.70977011	0.001104377	4.66705E-06
cation-chloride co-transporter 1	-27.63377926	6.47E-07	3.78981E-10
binding;RNA binding	-54.16666667	0.001687678	2.31192E-06
Pentatricopeptide repeat (PPR) superfamily p	-30.30165913	1.78499E-18	3.53433E-23
Pentatricopeptide repeat (PPR) superfamily p	-35.71428571	1.00554E-09	1.05053E-13
Pentatricopeptide repeat (PPR) superfamily p	-28.57142857	0.005615953	1.15686E-05
Pentatricopeptide repeat (PPR) superfamily p	-33.33333333	0.000329424	3.30933E-07

Major facilitator superfamily protein	-38.82896764	0.006502606	1.40293E-05
XH/XS domain-containing protein	-41.07142857	0.001781599	2.46801E-06
XH/XS domain-containing protein	-27.22359532	3.5589E-09	5.51469E-13
XH/XS domain-containing protein	-42.28221788	3.5242E-08	6.94185E-12
XH/XS domain-containing protein	-28.57603612	0.000566192	6.56148E-07
XH/XS domain-containing protein	-27.10341144	9.17156E-06	4.10697E-09
XH/XS domain-containing protein	-30.92497869	6.32629E-06	2.66257E-09
Ribosomal protein L13 family protein	-94.44444444	5.47806E-06	1.88812E-09
N/A	-48.33333333	6.53496E-05	4.45383E-08
guanyl-nucleotide exchange factors;GTPase b	-100	0.000440203	4.00618E-07
guanyl-nucleotide exchange factors;GTPase b	-54.13533835	0.002144564	3.25705E-06
myosin 2	-33.49078885	4.2188E-06	1.63154E-09
myosin 2	-35.48412144	2.53041E-06	8.97176E-10
cyclophilin 59	-27.96296296	0.007251536	2.28684E-05
S-locus lectin protein kinase family protein	-43.64295125	0.001448062	6.79174E-06
cycling DOF factor 1	-50	0.008532816	2.02116E-05
Ca(2)-dependent phospholipid-binding prote	-62.78801843	0.001061922	1.54889E-06
long-chain acyl-CoA synthetase 7	-31.89655172	0.004169739	1.01135E-05
beta galactosidase 9	-29.52586207	0.001981666	3.62628E-06
Disease resistance protein (TIR-NBS-LRR class	-32.84406141	0.008034062	1.85581E-05
N/A	-41.76319176	1.37E-07	5.91722E-11
nuclear RNA polymerase D1B	-96.77419355	7.75404E-06	2.80337E-09
N/A	-40	1.95441E-07	4.09612E-11
N/A	-48.53560931	1.80111E-23	1.58499E-28
N/A	-33.33333333	1.00118E-05	4.56866E-09
cytochrome P450, family 72, subfamily A, pol	-46.66877838	9.92563E-11	1.0537E-14
cytochrome P450, family 72, subfamily A, pol	-35.9375	0.006953375	2.1572E-05
cytochrome P450, family 72, subfamily A, pol	-28.16901408	0.006782381	2.08233E-05
cytochrome P450, family 72, subfamily A, pol	-52.11267606	1.24175E-07	2.41316E-11
cytochrome P450, family 72, subfamily A, pol	-48.24561404	4.63306E-12	2.85399E-16
cytochrome P450, family 72, subfamily A, pol	-34.42622951	0.000603677	5.95432E-07
Ribosomal protein L18ae family	-27.55102041	0.000917646	1.24812E-06
NB-ARC domain-containing disease resistanc	-25.96153846	0.008774511	8.68731E-05
photosystem II reaction center protein K prec	-29.04692082	0.004195621	1.02423E-05
photosystem II reaction center protein K prec	-46.38709981	7.9429E-17	1.8057E-21
Family of unknown function (DUF572)	-56.15079365	1.12E-06	7.35589E-10
glutathione S-transferase TAU 20	-41.74962293	0.000583123	6.81895E-07
Ribosomal protein L1p/L10e family	-31.62393162	2.66834E-08	4.03101E-12
N/A	-26.75	2.29779E-05	3.08073E-08
Lojap-related protein	-31.05921089	1.46572E-06	1.03319E-09
eukaryotic translation initiation factor 2 gam	-33.1443299	0.005499539	1.12481E-05
tetratricopeptide repeat (TPR)-containing pr	-58.33333333	0.004902405	9.50913E-06
N/A	-33.78378378	1.5665E-05	6.46763E-09
telomerase reverse transcriptase	-26.96629213	0.008716825	2.07434E-05

ATPases;nucleotide binding;ATP binding;nucl	-100	5.17853E-08	8.81988E-12
Transcription initiation factor TFIID subunit A	-100	0.001933999	2.83514E-06
Small nuclear ribonucleoprotein family prote	-71.83673469	0.004596086	8.6824E-06
exocyst complex component sec10	-52.5	1.32714E-06	3.60236E-10
pyruvate dehydrogenase E1 alpha	-84.72222222	2.59003E-05	1.1966E-08
Plant protein 1589 of unknown function	-40.12195122	0.003019842	5.02766E-06
ARM repeat superfamily protein	-85.48387097	1.03034E-05	3.92906E-09
ARM repeat superfamily protein	-49.73488865	0.002674408	4.30691E-06
adenosine-5\'-phosphosulfate (APS) kinase 3	-100	0.001933999	2.83514E-06
BED zinc finger ;hAT family dimerisation dom	-43.66197183	0.000209491	5.07566E-07
ARM repeat superfamily protein	-100	0.001933999	2.83514E-06
ENTH/VHS family protein	-63.26530612	5.57695E-05	3.1356E-08
N/A	-39.40985246	0.004639193	1.18491E-05
N/A	-41.74174174	3.0417E-05	1.71555E-08
regulatory particle triple-A 1A	-42.56542997	0.000258456	2.06595E-07
Alpha-L RNA-binding motif/Ribosomal protei	-88.46153846	0.00085171	1.12516E-06
GDSL-motif lipase 5	-50	0.009924873	3.67925E-05
GDSL-motif lipase 5	-92.85714286	1.45627E-05	5.95911E-09
alpha/beta-Hydrolases superfamily protein	-25.24938829	2.29E-07	1.10348E-10
NAC domain containing protein 85	-89.47368421	0.000353867	3.02268E-07
N/A	-81.48148148	0.002338159	3.62995E-06
Uncharacterised protein family (UPF0497)	-35.56231003	0.009235795	3.26674E-05
N/A	-44.52347084	0.003538729	6.19709E-06
translocase inner membrane subunit 17-2	-43.77300408	9.15E-08	3.64649E-11
Disease resistance protein (TIR-NBS-LRR class	-80.64516129	0.003948253	7.14299E-06
N/A	-30.6981982	0.000398413	4.21951E-07
N/A	-27.83411807	0.009386163	9.58036E-05
Protein of unknown function (DUF674)	-27.83411807	0.009386163	9.58036E-05
male gametophyte defective 3	-62.82051282	0.008480288	2.8838E-05
Ribosomal protein L13 family protein	-53.11594203	0.00839767	2.84237E-05
RNA recognition motif (RRM)-containing prot	-100	2.67194E-09	3.1547E-13
Leucine-rich repeat protein kinase family pro	-100	0.001240448	1.54644E-06
Endoribonuclease/protein kinase IRE1-like	-35.21380345	0.002058826	1.10079E-05
RNA polymerase I specific transcription initia	-28.0377735	5.82596E-09	9.45424E-13
RNA polymerase I specific transcription initia	-33.20261438	3.5453E-07	8.11174E-11
Glucose-6-phosphate/phosphate translocato	-40.95238095	0.001045479	1.50195E-06
Subtilase family protein	-48.71794872	0.009904325	3.66578E-05
ATPase, F0 complex, subunit B/B\', bacterial/	-49.24242424	0.009083579	3.19382E-05
ATP synthase subunit alpha	-49.24242424	0.009083579	3.19382E-05
diacylglycerol acyltransferase family	-26.4203985	0.003476223	7.8538E-06
diacylglycerol acyltransferase family	-28.4376672	0.00164362	2.78645E-06
Disease resistance protein (TIR-NBS-LRR class	-31.02380952	1.16155E-05	1.31833E-08
TSL-kinase interacting protein 1	-54.20899855	0.00272876	4.4147E-06
calcium-dependent protein kinase 28	-100	0.001240448	1.54644E-06

Protein of unknown function (DUF1640)	-52.59259259	0.008333981	2.80684E-05
S-adenosyl-L-methionine-dependent methylt	-37.14285714	0.005646928	1.16614E-05
N/A	-56.25	0.000137899	9.46457E-08
N/A	-50	0.009301166	3.30513E-05
ARM repeat superfamily protein	-43.47826087	0.004696663	8.95162E-06
ARM repeat superfamily protein	-95.23809524	6.30823E-05	3.66386E-08
Protein of unknown function (DUF677)	-55.73770492	0.005976975	1.25256E-05
Protein of unknown function (DUF1162)	-71.66666667	0.000594354	5.81537E-07
Disease resistance protein (TIR-NBS-LRR class	-38.46153846	0.005600242	1.15116E-05
nudix hydrolase homolog 12	-31.89908683	0.003007079	6.34577E-06
novel cap-binding protein	-100	0.005353107	1.08251E-05
glutathione-disulfide reductase	-61.29032258	0.004675962	8.88473E-06
disease resistance protein (TIR-NBS-LRR class	-33.33333333	7.82812E-05	4.7705E-08
HSP20-like chaperones superfamily protein	-42.15180545	0.000143484	1.149E-07
Protein Transporter, Pam16	-56.15989515	1.16384E-12	8.17656E-17
disease resistance family protein / LRR family	-36.87641723	0.000330287	3.32884E-07
multidrug resistance-associated protein 14	-52.50965251	0.004811332	1.25256E-05
disease resistance family protein / LRR family	-45.69892473	0.003522876	7.98475E-06
disease resistance family protein / LRR family	-28.73176207	0.008465582	2.87647E-05
Arabidopsis thaliana protein of unknown fun	-78.125	3.20131E-08	5.16483E-12
Myosin heavy chain-related protein	-57.67195767	0.002694784	4.35158E-06
CAP160 protein	-38.85714286	0.003460821	6.02766E-06
HXXXD-type acyl-transferase family protein	-25.62230335	0.000306799	8.36889E-07
RNA helicase family protein	-25.56536866	0.003871064	9.07894E-06
tRNA synthetase class I (I, L, M and V) family	-90.90909091	4.90256E-07	1.15767E-10
CBS domain-containing protein with a domai	-31.47514105	1.34359E-05	1.57827E-08
Galactose oxidase/kelch repeat superfamily	-98.46153846	1.4959E-08	2.09528E-12
CW-type Zinc Finger	-100	0.000440203	4.00618E-07
multifunctional protein 2	-27.40046838	2.26E-08	7.11949E-12
multifunctional protein 2	-100	1.79916E-05	7.62613E-09
ATP-citrate lyase B-1	-58.33333333	0.00391402	7.06096E-06
ubiquitin protein ligase 6	-52.38095238	0.005615459	1.15552E-05
pleiotropic drug resistance 9	-61.84210526	0.004592132	8.67156E-06
N/A	-75.65217391	0.008144325	2.70956E-05
Haloacid dehalogenase-like hydrolase (HAD)	-91.66666667	0.000188727	1.41723E-07
F-box family protein	-29.87109137	1.70661E-05	2.11217E-08
Auxin efflux carrier family protein	-26.63776114	6.56E-09	1.71198E-12
PA-domain containing subtilase family protei	-35.33204384	0.009569385	2.35301E-05
Core-2/I-branching beta-1,6-N-acetylglucosa	-28.18181818	0.003315973	2.15522E-05
Core-2/I-branching beta-1,6-N-acetylglucosa	-54.20168067	0.003901756	7.02676E-06
Transducin/WD40 repeat-like superfamily pr	-62.5	3.94347E-06	1.29846E-09
Phosphoribulokinase / Uridine kinase family	-78.125	0.000152866	1.09163E-07
tRNA synthetase beta subunit family protein	-93.75	0.000825161	9.20394E-07
Transducin family protein / WD-40 repeat fa	-100	0.001933999	2.83514E-06

N/A	-29.11681371	2.40E-10	4.08646E-14
N/A	-44.48346503	5.64E-06	5.44338E-09
plastid transcriptionally active 2	-29.71264368	0.000459098	5.03101E-07
plastid transcriptionally active 2	-58.82352941	0.001239085	1.52203E-06
malate dehydrogenase	-68.75	0.007623546	1.72863E-05
Ribosomal protein S5/Elongation factor G/III/	-59.72222222	0.000364128	3.14829E-07
Ypt/Rab-GAP domain of gyp1p superfamily pr	-30.34429099	0.000112111	2.24898E-07
RING/FYVE/PHD zinc finger superfamily prote	-42.57567105	0.003017536	1.888E-05
FUS3-complementing gene 2	-29.22374429	0.003167086	5.37439E-06
AAA-type ATPase family protein	-76.19047619	0.000115391	7.67359E-08
N/A	-33.51648352	2.63621E-10	3.09832E-14
N/A	-37.78284363	1.26164E-16	2.96068E-21
PPPDE putative thiol peptidase family protein	-80	0.001784439	2.47849E-06
ubiquitin C-terminal hydrolase 3	-100	0.000703795	7.39602E-07
N/A	-30.70265166	2.01837E-05	2.60873E-08
nicotinate/nicotinamide mononucleotide ade	-25.20325203	5.1489E-05	3.30295E-08
N/A	-80	0.005242606	1.04843E-05
Arabinanase/levansucrase/invertase	-50	0.007912596	1.8139E-05
Protein of unknown function (DUF579)	-50.5952381	0.009051124	3.17468E-05
kinase interacting (KIP1-like) family protein	-31.68316832	2.4918E-14	1.14526E-18
kinase interacting (KIP1-like) family protein	-27.43362832	3.66749E-07	9.84884E-11
kinase interacting (KIP1-like) family protein	-29.14107918	2.29193E-11	2.0767E-15
kinase interacting (KIP1-like) family protein	-48.60022396	8.54617E-09	1.45894E-12
kinase interacting (KIP1-like) family protein	-27.95698925	0.004582646	1.16469E-05
kinase interacting (KIP1-like) family protein	-45.04504505	0.005209895	1.40285E-05
phytochrome and flowering time regulatory	-28.53670886	0.000679526	6.95363E-07
dihydroflavonol 4-reductase	-25.46583851	1.48802E-06	4.95348E-10
N/A	-48.90510949	2.25816E-12	1.27512E-16
N/A	-27.05902638	5.5189E-08	9.47053E-12
Ribosomal protein S21 family protein	-83.60655738	0.000161894	1.16705E-07
nuclear RNA polymerase A2	-41.88311688	0.00866945	2.97575E-05
N/A	-50.64935065	1.11215E-24	8.15585E-30
N/A	-39.77272727	4.29438E-10	3.96804E-14
N/A	-43.47826087	2.04572E-08	2.98541E-12
N/A	-35.8974359	0.005825239	1.21236E-05
non-ATPase subunit 9	-88.23529412	0.002338548	3.63227E-06
Tetratricopeptide repeat (TPR)-like superfam	-40.54054054	0.001884159	2.6543E-06
Tetratricopeptide repeat (TPR)-like superfam	-31.05126269	3.89002E-07	1.0578E-10
ENTH/VHS/GAT family protein	-40.96385542	0.000204663	1.55191E-07
N/A	-39.57960644	0.005639884	1.16344E-05
N/A	-29.01234568	1.4686E-13	5.92341E-18
N/A	-27.63157895	7.61226E-05	5.34799E-08
RNA 2\'-phosphotransferase, Tpt1 / KptA fam	-36.11111111	0.001659154	2.25824E-06
Zinc finger protein 622	-61.66666667	0.005368098	1.08927E-05

ubiquitin-specific protease 26	-27.69230769	1.07017E-05	4.13588E-09
embryo defective 2410	-77.64705882	0.000691311	8.5743E-07
embryo defective 2410	-40.54054054	0.006637079	1.44167E-05
CBS domain-containing protein with a domai	-60.74766355	0.009828008	3.61495E-05
ankyrin repeat protein	-60.74766355	0.009828008	3.61495E-05
HXXXD-type acyl-transferase family protein	-37.93103448	0.002590829	5.17793E-06
N/A	-32.81509121	0.003397932	7.57662E-06
N/A	-28.26412138	2.96636E-07	6.4608E-11
N/A	-26.88172043	8.17472E-06	3.00942E-09
Exostosin family protein	-36.4673913	3.48577E-05	5.17095E-08
IQ-domain 19	-25.12820513	1.26675E-05	6.07164E-09
calcium-binding EF hand family protein	-39.43502825	3.04177E-08	4.7736E-12
aberrant lateral root formation 4	-100	2.98325E-07	6.51947E-11
CTC-interacting domain 7	-60	0.005553767	1.13916E-05
histidine kinase 5	-74.3902439	0.000319764	2.65918E-07
N/A	-52.60869565	0.006301595	1.87514E-05
TBP-associated factor 5	-33.67412828	0.000148109	1.20002E-07
Chalcone-flavanone isomerase family protein	-28.35820896	0.006488141	1.39743E-05
Protein of unknown function (DUF1218)	-54.65116279	3.93644E-10	4.78155E-14
Protein of unknown function (DUF1218)	-62	1.25154E-06	3.35917E-10
Protein of unknown function (DUF1218)	-26.78014865	0.006430787	1.93343E-05
RNA-binding protein 47C	-77.5	0.006603368	1.4286E-05
ADR1-like 1	-35.68438003	0.000448077	1.39175E-06
Protein phosphatase 2C family protein	-73.7704918	0.000646723	6.48445E-07
Erythronate-4-phosphate dehydrogenase fan	-100	0.001933999	2.83514E-06
UDP-Glycosyltransferase superfamily protein	-100	0.005353107	1.08251E-05
LSD1-like 3	-100	1.83775E-06	5.21557E-10
5\'-3\' exoribonuclease 3	-70.58823529	0.002394843	3.74781E-06
N/A	-51.09489051	1.13E-11	1.24256E-15
RNA polymerase II transcription mediators	-32.50547345	0.000538326	6.14665E-07
RNA polymerase II transcription mediators	-28.15100579	0.002276985	4.38346E-06
phragmoplast-associated kinesin-related prot	-27.83505155	0.000195624	1.47619E-07
ferritin 4	-37.33333333	4.57306E-06	1.79857E-09
ferritin 4	-31.81818182	2.15676E-08	3.16328E-12
ferritin 4	-30.8083177	0.000926295	1.06022E-06
Lojap-related protein	-31.5362841	6.51E-08	2.41075E-11
N/A	-73.61111111	0.004847211	9.36297E-06
N/A	-90.90909091	0.00327541	5.60865E-06
P-glycoprotein 18	-70.41420118	0.001984978	1.04649E-05
sphere organelles protein-related	-36.95652174	0.005426294	1.10705E-05
sphere organelles protein-related	-60	0.007151411	1.59483E-05
DNAJ heat shock family protein	-67.64705882	0.005381589	1.09359E-05
binding	-25.24312896	0.001956084	3.55891E-06
SGNH hydrolase-type esterase superfamily pı	-73.52941176	7.77224E-05	4.73075E-08

anthranilate synthase alpha subunit 1	-33.33333333	0.002800712	4.56988E-06
translocon at the inner envelope membrane	-100	2.76356E-05	1.28935E-08
potassium transporter 1	-37.8968254	0.000243157	1.9169E-07
peptide transporter 1	-100	0.001933999	2.83514E-06
Neutral/alkaline non-lysosomal ceramidase	-72.22222222	0.005009981	9.83638E-06
NB-ARC domain-containing disease resistanc	-25.35211268	0.004528533	3.33725E-05
NB-ARC domain-containing disease resistanc	-25.98690409	6.2445E-05	4.186E-08
NB-ARC domain-containing disease resistanc	-31.50684932	0.002942538	4.86309E-06
NB-ARC domain-containing disease resistanc	-47.82608696	0.000704473	7.41348E-07
NB-ARC domain-containing disease resistanc	-32.46753247	0.000811469	1.05921E-06
NB-ARC domain-containing disease resistanc	-45.26315789	1.04662E-06	2.73239E-10
EAP30/Vps36 family protein	-26.49350649	0.000414166	1.25234E-06
glucan synthase-like 7	-96.96969697	1.61356E-06	4.52016E-10
glucan synthase-like 7	-46.96969697	5.90648E-05	3.89364E-08
glucan synthase-like 7	-35.84507042	9.72511E-05	7.24742E-08
N/A	-42.72727273	1.70743E-05	7.11209E-09
N/A	-31.11111111	0.003980985	2.78746E-05
N/A	-61.29411765	0.00161732	2.7323E-06
Major facilitator superfamily protein	-25.75276445	0.00013003	2.73192E-07
alpha/beta-Hydrolases superfamily protein	-33.30827068	3.13055E-05	1.78005E-08
aminophospholipid ATPase 3	-29.48606272	0.000713932	8.94141E-07
N/A	-32.29376258	0.009976212	2.47938E-05
eukaryotic translation initiation factor 3G1	-42.54716981	0.003301486	2.14128E-05
UB-like protease 1D	-85.71428571	0.000743599	9.41324E-07
Plant protein of unknown function (DUF828)	-31.05128205	0.005967596	1.7199E-05
Plant protein of unknown function (DUF828)	-28.96212525	2.82727E-05	1.56862E-08
SOUL heme-binding family protein	-29.87711214	0.000553287	6.36309E-07
kinesin like protein for actin based chloroplas	-65.95744681	0.000910494	1.03814E-06
Xanthine/uracil permease family protein	-64.86318408	1.70E-06	1.23044E-09
UDP-Glycosyltransferase superfamily protein	-44.375	2.88148E-05	1.60059E-08
UDP-Glycosyltransferase superfamily protein	-45.19632414	0.001732018	2.99431E-06
Phototropic-responsive NPH3 family protein	-47.05882353	5.98645E-05	3.45062E-08
Signal recognition particle, SRP9/SRP14 subu	-26.95926872	0.000564005	6.52574E-07
Ribosomal protein S8e family protein	-30.30450908	2.5857E-06	9.23572E-10
Nuclear transport factor 2 (NTF2) family prot	-27.87787788	0.007337824	1.64985E-05
F-box family protein	-35.89256647	0.001854191	3.29462E-06
GPI transamidase component PIG-S-related	-33.00970874	9.77754E-06	4.42326E-09
GPI transamidase component PIG-S-related	-43.24324324	7.15679E-05	4.94342E-08
GPI transamidase component PIG-S-related	-33.05785124	6.33332E-07	1.56055E-10
dolichol-phosphate mannosyltransferase-rela	-32.00147984	0.007322684	1.6443E-05
N/A	-78.84615385	0.002157919	3.2805E-06
Protein kinase superfamily protein	-41.29554656	3.39505E-07	8.96119E-11
plant U-box 13	-30.6122449	0.003545459	6.21927E-06
N/A	-27.38828968	0.000107531	6.9867E-08

DIE2/ALG10 family	-31.99974395	3.03E-08	9.96807E-12
AAA-type ATPase family protein	-36.02614124	1.81671E-22	1.78575E-27
Protein of unknown function (DUF674)	-27.43902439	1.72039E-10	1.9316E-14
Protein of unknown function (DUF674)	-27.20462329	0.004434307	8.30525E-06
Yippee family putative zinc-binding protein	-26.32010354	1.46832E-06	4.85008E-10
Yippee family putative zinc-binding protein	-32.59504132	6.45494E-06	2.28163E-09
Protein of unknown function (DUF567)	-50.84745763	1.00554E-09	1.04438E-13
nuclear shuttle interacting	-32.73167358	0.000386208	1.14054E-06
Phosphoglycerate mutase, 2,3-bisphosphogly	-70.59961315	0.000703795	7.33411E-07
Serine/threonine-protein kinase Rio1	-56.25	0.001627191	2.20161E-06
Protein kinase superfamily protein	-72.22222222	0.008546843	2.02511E-05
binding	-100	0.0002397	1.88262E-07
Uncharacterized protein family (UPF0016)	-25.69007264	0.001114632	1.65253E-06
Uncharacterized protein family (UPF0016)	-40.87265231	4.77489E-07	1.34262E-10
ATPase, V1 complex, subunit B protein	-90	0.00295471	4.89482E-06
Protein kinase superfamily protein	-97.14285714	1.92469E-07	4.00852E-11
Pentatricopeptide repeat (PPR-like) superfam	-38.8185654	0.009486365	2.32324E-05
ARABIDILLO-1	-47.61904762	0.006746728	1.47391E-05
N/A	-29.56567242	0.008817792	3.04768E-05
little nuclei1	-32.72727273	0.009894751	2.45405E-05
mitogen-activated protein kinase phosphatas	-27.03801945	0.001768776	2.44766E-06
RNA-binding (RRM/RBD/RNP motifs) family p	-100	0.001933999	2.83514E-06
HEAT repeat-containing protein	-25.81578416	1.59077E-05	7.85449E-09
HEAT repeat-containing protein	-100	0.001933999	2.83514E-06
Major facilitator superfamily protein	-30.85585586	6.60E-07	3.8869E-10
REF4-related 1	-92.30769231	0.001904087	2.69215E-06
RNA-binding (RRM/RBD/RNP motifs) family p	-70	0.009734505	3.56521E-05
Pectin lyase-like superfamily protein	-26.5445801	4.25E-13	2.89179E-17
NHL domain-containing protein	-27.84008046	0.000534963	1.76322E-06
BAH domain ;TFIIS helical bundle-like domain	-75	0.004932456	9.64338E-06
Heavy metal transport/detoxification superfa	-53.94957983	0.000598497	5.87251E-07
SIN3-like 2	-80.55555556	0.000823006	9.16783E-07
Pentatricopeptide repeat (PPR) superfamily p	-41.57608696	2.43309E-06	7.31558E-10
HVA22-like protein K	-33.95983936	0.000330978	3.3445E-07
biotin carboxyl carrier protein 2	-96.66666667	1.38812E-06	3.82756E-10
PHD finger family protein	-47.10144928	0.001437431	1.87529E-06
N/A	-27.91255665	0.003708649	8.56653E-06
cell division protein ftsH, putative	-63.69047619	0.00010836	7.05647E-08
Proline-rich spliceosome-associated (PSP) fan	-77.35849057	1.78787E-08	2.54358E-12
RAB GTPase homolog A1D	-29.44175971	1.2481E-13	7.04763E-18
RAB GTPase homolog A1D	-50.79772995	7.78881E-31	3.06843E-36
RAB GTPase homolog A1D	-65.38835324	1.89176E-41	2.77461E-47
RAB GTPase homolog A1D	-47.23415682	6.7166E-12	5.46845E-16
golgin candidate 6	-34.92747253	0.000472038	5.2224E-07

auxin response factor 8	-60	0.005453457	1.50174E-05
CLIP-associated protein	-28.84615385	0.006424062	1.92998E-05
CLIP-associated protein	-28.35820896	2.47181E-05	1.34219E-08
peptide deformylase 1B	-25.47172588	0.000939253	1.29076E-06
SET domain group 29	-39.84848485	3.34188E-05	1.9237E-08
TLC ATP/ADP transporter	-34.98217469	0.006817451	2.10116E-05
Cytochrome C1 family	-79.41176471	0.000523011	4.93239E-07
Mitochondrial ribosomal protein L37	-47.36842105	0.001735936	2.38948E-06
Ribonuclease inhibitor	-100	0.000440203	4.00618E-07
DEAD-box protein abstrakt, putative	-90	0.005869408	1.22371E-05
ARM repeat superfamily protein	-83.33333333	0.000240795	1.89475E-07
N/A	-41.93548387	0.000308141	2.5444E-07
N/A	-80.95238095	7.73161E-05	4.70035E-08
MALE GAMETOPHYTE DEFECTIVE 2	-34.54829471	0.001051588	1.51487E-06
Protein of unknown function (DUF3754)	-53.04347826	0.004918235	1.29396E-05
Peptidase M50 family protein	-76.31578947	5.29223E-05	2.92629E-08
Core-2/I-branching beta-1,6-N-acetylglucosar	-29.57844251	2.22E-07	1.06075E-10
Cyclin/Brf1-like TBP-binding protein	-43.61702128	0.00284178	4.65641E-06
DHHC-type zinc finger family protein	-57.89473684	4.30994E-10	5.29183E-14
DHHC-type zinc finger family protein	-35.95505618	5.17298E-07	1.47749E-10
alpha-L-arabinofuranosidase 1	-54.54545455	0.004932584	3.76482E-05
mitochondrial RNAediting factor 1	-32.75862069	0.000649383	6.53373E-07
spindle pole body component 98	-70.14925373	0.005368098	1.08852E-05
receptor-like kinase in in flowers 3	-25.3968254	0.00909331	2.19393E-05
N/A	-70.83333333	3.35904E-08	5.51784E-12
N/A	-30.76443155	1.96E-08	6.07591E-12
myosin 2	-77.08333333	0.003785477	6.75967E-06
Lipin family protein	-100	3.68175E-05	1.83059E-08
endomembrane-type CA-ATPase 4	-60.86956522	0.006922846	1.52339E-05
N/A	-84.61538462	0.008526819	2.01911E-05
P-loop containing nucleoside triphosphate hy	-44	0.009296876	2.26282E-05
Ribosomal protein L13 family protein	-76.47058824	0.003960437	7.17084E-06
Nucleotide-diphospho-sugar transferases sup	-44.68085106	0.000833382	9.32619E-07
ACT-like superfamily protein	-59.3220339	5.08666E-05	2.7865E-08
alpha carbonic anhydrase 7	-31.89840723	2.26E-06	1.7561E-09
N/A	-26.54462243	0.001496817	1.97911E-06
UDP-glucosyl transferase 73C2	-26.54462243	0.001496817	1.97911E-06
Duplicated homeodomain-like superfamily pr	-35.32163743	0.001012789	4.14977E-06
peroxin 6	-86.36363636	2.43736E-05	1.1082E-08
NAD+ transporter 1	-100	0.000796198	8.74075E-07
WRKY DNA-binding protein 35	-100	2.29387E-06	6.79605E-10
N/A	-100	0.000703795	7.39602E-07
Translation initiation factor 2, small GTP-bind	-53.22580645	7.40109E-07	4.51417E-10
Protein kinase superfamily protein	-31.05413105	5.34E-06	5.07192E-09

Polynucleotidyl transferase, ribonuclease H-li	-30.06993007	1.67E-06	1.2086E-09
DHHC-type zinc finger family protein	-65.51724138	0.000944887	1.0865E-06
DNAJ heat shock N-terminal domain-containi	-55.31914894	0.000799921	8.79922E-07
plant glycogenin-like starch initiation protein	-78.26086957	0.003349409	7.41565E-06
transcription activators	-50	0.000554647	5.3487E-07
MuDR family transposase	-47.5	0.007842648	1.79097E-05
MuDR family transposase	-25.04862462	0.004100339	9.88589E-06
PIN domain-like family protein	-60	0.000877666	3.41605E-06
N/A	-60	0.000877666	3.41605E-06
N/A	-46.68067227	1.43E-14	6.62673E-19
zinc knuckle (CCHC-type) family protein	-51.73745174	0.008498885	2.00536E-05
RNA-binding (RRM/RBD/RNP motifs) family p	-76.38888889	9.28656E-05	5.84316E-08
P-loop containing nucleoside triphosphate hy	-53.64238411	4.0498E-10	4.94583E-14
N/AMETHYLATED_REGION	-36.36875123	4.02E-16	1.22356E-20
extra-large G-protein 1	-80.64516129	0.003261074	7.14299E-06
N/A	-45.92397275	2.58549E-05	3.57413E-08
FORMS APLOID AND BINUCLEATE CELLS 1C	-97.14285714	9.21935E-06	3.44807E-09
O-fucosyltransferase family protein	-49.50146628	0.000945072	1.08741E-06
DNAJ heat shock N-terminal domain-containi	-30.96660031	4.35097E-05	6.81901E-08
purin-rich alpha 1	-85.71428571	0.001933999	2.82117E-06
Plant protein of unknown function (DUF863)	-100	0.000796198	8.74075E-07
N/A	-37.23076923	0.000261045	6.79967E-07
N/A	-33.03240741	7.86E-09	2.12228E-12
EXS (ERD1/XPR1/SYG1) family protein	-36.84210526	5.11057E-05	3.26159E-08
Got1/Sft2-like vescicle transport protein fami	-96.2962963	5.60705E-05	3.15792E-08
zinc ion binding;nucleic acid binding	-75.71428571	0.002789447	5.73815E-06
RINT-1 / TIP-1 family	-66.9924812	0.000512793	4.81722E-07
hAT dimerisation domain-containing protein	-66.9924812	0.000512793	4.81722E-07
chitin elicitor receptor kinase 1	-100	0.000440203	4.00618E-07
N/A	-85.8974359	1.23273E-05	4.93644E-09
N/A	-50.79113924	0.004912718	1.29135E-05
ortholog of human splicing factor SC35	-50.79113924	0.004912718	1.29135E-05
N/A	-28.24899026	0.004622879	8.76014E-06
N/A	-27.74864025	0.001834553	3.24625E-06
GRAM domain family protein	-45.20833333	6.07347E-08	1.28406E-11
ubiquitin-specific protease 13	-25.31282051	4.60196E-14	2.2662E-18
BLISTER	-67.59259259	0.002982454	4.95609E-06
N/A	-67.59259259	0.002982454	4.95609E-06
TRAF-like superfamily protein	-48.88888889	0.003702328	6.57318E-06
pentatricopeptide (PPR) repeat-containing pr	-37.77777778	0.002427585	1.38818E-05
thioredoxin X	-42.29607251	2.26154E-05	3.01146E-08
N/A	-42.29607251	2.26154E-05	3.01146E-08
Arabidopsis phospholipase-like protein (PEAF	-90.90909091	0.004921546	9.61483E-06
ARM repeat superfamily protein	-36.36363636	0.00635582	1.35821E-05

N/A	-44.44444444	0.007447034	1.67823E-05
MBOAT (membrane bound O-acyl transferase	-65.54487179	0.005068597	9.99132E-06
Metallo-hydrolase/oxidoreductase superfam	-51.25	0.008757372	8.6617E-05
N/A	-25.24959368	0.007733475	1.75809E-05
Homeodomain-like protein with RING/FYVE/I	-40.8445577	0.001017712	1.19114E-06
transducin family protein / WD-40 repeat fan	-72.22222222	0.008968817	2.15798E-05
F-box family protein	-44.54545455	4.18748E-05	2.54599E-08
cysteine-rich RLK (RECEPTOR-like protein kina	-26.35332435	0.000255436	6.59259E-07
N/A	-80.90909091	0.000144904	1.01057E-07
Tesmin/TSO1-like CXC domain-containing pro	-55.88235294	4.67456E-06	1.56567E-09
Kinase interacting (KIP1-like) family protein	-31.05010661	0.002393079	3.74329E-06
phosphoglucomutase	-63.15789474	0.002793865	4.55665E-06
2-oxoglutarate (2OG) and Fe(II)-dependent o:	-25.32440019	0.000463193	4.24259E-07
N/A	-34.82772935	0.000979829	1.13459E-06
Regulator of chromosome condensation (RCC	-42.57164404	0.00047655	4.39637E-07
Pyridoxal phosphate (PLP)-dependent transfe	-36.42089094	2.75723E-08	4.22596E-12
FORMS APLOID AND BINUCLEATE CELLS 1A	-100	2.64011E-11	1.98005E-15
serine carboxypeptidase-like 27	-40.60606061	0.00046218	1.45194E-06
N/A	-33.15942029	0.000359561	1.03683E-06
Transmembrane Fragile-X-F-associated prote	-32.96296296	1.66982E-08	3.01506E-12
Transmembrane Fragile-X-F-associated prote	-54.05128205	1.72039E-10	1.92407E-14
Transmembrane Fragile-X-F-associated prote	-38.41269841	0.000454697	4.97332E-07
Transmembrane Fragile-X-F-associated prote	-72.16117216	5.42254E-09	6.87946E-13
Transmembrane Fragile-X-F-associated prote	-40.47619048	4.92908E-05	2.65406E-08
NAC (No Apical Meristem) domain transcripti	-59.28853755	0.009486365	2.32425E-05
N/A	-68.75	0.000620945	6.15197E-07
mRNA splicing factor, thioredoxin-like U5 snR	-96.15384615	1.03113E-09	1.08889E-13
phosphofructokinase 4	-60.81081081	3.20131E-08	5.14321E-12
N/A	-25.0113413	4.94954E-05	8.0688E-08
N/A	-62.16216216	0.004306119	1.06223E-05
N/A	-32.76315789	1.47339E-05	6.03996E-09
UBX domain-containing protein	-51.85185185	0.009192263	2.2259E-05
RING/FYVE/PHD zinc finger superfamily prote	-84.14634146	2.40672E-05	1.08897E-08
Eukaryotic aspartyl protease family protein	-100	0.000703795	7.39602E-07
MIRO-related GTP-ase 1	-93.33333333	0.002195562	3.36519E-06
P-loop containing nucleoside triphosphate hy	-33.60215892	2.33E-11	2.9228E-15
Chalcone-flavanone isomerase family protein	-66.00498487	1.13E-13	6.43181E-18
PRLI-interacting factor, putative	-62.05741627	2.55693E-17	5.4378E-22
lipase class 3 family protein	-30.12350265	0.004310897	1.06458E-05
BRI1 suppressor 1 (BSU1)-like 2	-82.8125	1.12951E-07	2.13706E-11
Protein of unknown function (DUF2296)	-28.30572508	0.002165398	4.07765E-06
N/A	-51.05359217	4.84E-44	3.54937E-50
Carbohydrate-binding-like fold	-36.07769424	1.79E-07	8.21974E-11
exocyst subunit exo70 family protein A1	-100	0.000440203	4.00618E-07

uricase / urate oxidase / nodulin 35, putative	-52.93040293	0.001240448	1.53019E-06
uricase / urate oxidase / nodulin 35, putative	-42.5990676	3.99E-07	2.1117E-10
nuclear RNA polymerase C1	-44.42724458	0.004503487	8.47115E-06
N/A	-72.91157441	7.19E-22	6.94041E-27
N/A	-83.33333333	2.14878E-12	1.1976E-16
GroES-like zinc-binding dehydrogenase famil	-80.95238095	0.003422193	2.25694E-05

Supplemental Table

GO term
GO:0005524
GO:0016772
GO:0001882
GO:0000166
GO:0016740
GO:0016773
GO:0004672
GO:0016790
GO:0004518
GO:0004221
GO:0003824
GO:0016462
GO:0004386
GO:0016817
GO:0005488
GO:0016887

10: Gene ontology enrichment analysis of the differentially hyper-methy

Description
ATP binding
transferase activity, transferring phosphorus-containing groups
nucleoside binding
nucleotide binding
transferase activity
phosphotransferase activity, alcohol group as acceptor
protein kinase activity
thiolester hydrolase activity
nuclease activity
ubiquitin thiolesterase activity
catalytic activity
pyrophosphatase activity
helicase activity
hydrolase activity, acting on acid anhydrides
binding
ATPase activity

lated genes.

Number in input list	Number in genome	%
85	3990	7.35
66	2985	5.71
94	4747	8.13
105	5459	9.08
96	4916	8.30
57	2624	4.93
52	2394	4.50
6	87	0.52
8	164	0.69
5	69	0.43
224	13905	19.38
30	1440	2.60
16	668	1.38
30	1480	2.60
268	17591	23.18
14	581	1.21

***P*-value**
9.50E-05
0.00025
0.00048
0.00058
0.00066
0.001
0.0017
0.002
0.003
0.0038
0.0058
0.026
0.033
0.035
0.04
0.042

Supplemental Table 11: Gene ontology enrichment analysis of the differer

GO term	Description
GO:0016817	hydrolase activity, acting on acid anhydrides
GO:0016462	pyrophosphatase activity
GO:0017111	nucleoside-triphosphatase activity
GO:0000166	nucleotide binding
GO:0003723	RNA binding
GO:0034062	RNA polymerase activity
GO:0005524	ATP binding
GO:0003899	DNA-directed RNA polymerase activity
GO:0005488	binding
GO:0035091	phosphoinositide binding
GO:0003843	1,3-beta-glucan synthase activity
GO:0016887	ATPase activity
GO:0016787	hydrolase activity
GO:0005515	protein binding
GO:0008017	microtubule binding
GO:0016779	nucleotidyltransferase activity
GO:0004386	helicase activity
GO:0008026	ATP-dependent helicase activity
GO:0008092	cytoskeletal protein binding
GO:0042623	ATPase activity, coupled
GO:0005543	phospholipid binding
GO:0060589	nucleoside-triphosphatase regulator activity
GO:0008047	enzyme activator activity
GO:0003777	microtubule motor activity
GO:0016853	isomerase activity
GO:0004518	nuclease activity
GO:0005083	small GTPase regulator activity
GO:0003676	nucleic acid binding
GO:0008289	lipid binding
GO:0016866	intramolecular transferase activity
GO:0005525	GTP binding
GO:0032561	guanyl ribonucleotide binding
GO:0008194	UDP-glycosyltransferase activity
GO:0043531	ADP binding
GO:0019001	guanyl nucleotide binding
GO:0009378	four-way junction helicase activity
GO:0004221	ubiquitin thiolesterase activity
GO:0003924	GTPase activity

ntially hypo-methylated genes.

Number in input list	Number in genome	*P* -value	%
72	1480	1.70E-06	3.71
70	1440	2.50E-06	3.61
69	1412	2.50E-06	3.55
198	5459	3.70E-06	10.20
30	486	4.30E-05	1.55
12	105	5.70E-05	0.62
145	3990	0.0001	7.47
11	98	0.00013	0.57
519	17591	0.00026	26.74
5	18	0.00027	0.26
5	23	0.00071	0.26
29	581	0.0015	1.49
153	4588	0.0025	7.88
201	6255	0.0026	10.36
13	189	0.0026	0.67
15	238	0.0028	0.77
31	668	0.0031	1.60
13	205	0.0049	0.67
14	238	0.0067	0.72
18	343	0.007	0.93
9	121	0.0071	0.46
10	154	0.011	0.52
7	87	0.011	0.36
10	155	0.012	0.52
13	238	0.015	0.67
10	164	0.016	0.52
9	142	0.018	0.46
127	3997	0.024	6.54
9	153	0.026	0.46
5	59	0.026	0.26
19	431	0.028	0.98
19	431	0.028	0.98
10	180	0.028	0.52
20	467	0.032	1.03
19	442	0.034	0.98
6	91	0.041	0.31
5	69	0.044	0.26
11	228	0.05	0.57

Supplemental Table 12: List of 93 syncytium-differentially hyper-methylated genes.

Gene ID	Annotation	
		P value
Glyma.01G157600	-	1.21106E-05
Glyma.02G014200	CTP synthase family protein	1.54644E-06
Glyma.02G078600	NAD(P)-binding Rossmann-fold superfamily protein	2.31518E-05
Glyma.02G095000	ribosomal protein L23AB	2.85434E-08
Glyma.02G141500	DREB2A-interacting protein 2	-
Glyma.02G165800	Protein kinase superfamily protein	-
Glyma.02G211800	auxin F-box protein 5	2.83514E-06
Glyma.02G259000	Aldolase-type TIM barrel family protein	-
Glyma.03G008100	cytochrome P450, family 86, subfamily A, polypeptide 8	-
Glyma.03G013000	RNAhelicase-like 8	2.80843E-11
Glyma.03G140100	NIMA-related kinase 5	2.00027E-08
Glyma.03G219500	Prolyl oligopeptidase family protein	2.83514E-06
Glyma.04G014400	switch subunit 3	3.45642E-06
Glyma.04G057200	CTC-interacting domain 7	8.99497E-10
Glyma.04G132900	Ribosomal protein S19e family protein	7.39602E-07
Glyma.04G221900	ribonuclease II family protein	2.01037E-05
Glyma.04G236900	NADH-dependent glutamate synthase 1	4.70062E-06
Glyma.05G044200	MA3 domain-containing protein	-
Glyma.05G046400	homolog of nucleolar protein NOP56	3.77185E-08
Glyma.05G105000	Phototropic-responsive NPH3 family protein	2.32405E-05
Glyma.05G117000	Calmodulin-binding transcription activator protein with	2.18258E-14
Glyma.05G223100	Mitochondrial ATP synthase subunit G protein	2.01911E-05
Glyma.06G046000	autoinhibited Ca2+-ATPase 1	8.98773E-06
Glyma.06G061600	nuclear RNA polymerase D2A	-
Glyma.06G140200	alpha/beta-Hydrolases superfamily protein	1.24253E-05
Glyma.06G141300	-	4.29594E-08
Glyma.06G214100	-	1.18536E-07
Glyma.06G216700	nudix hydrolase homolog 19	7.20284E-06
Glyma.06G322700	SNARE-like superfamily protein	5.88812E-06
Glyma.07G059900	ribosomal protein L5 B	2.83514E-06
Glyma.07G099000	-	-
Glyma.07G256500	CBS domain-containing protein with a domain of unkno	9.82772E-06
Glyma.08G096300	Transketolase family protein	4.94387E-06
Glyma.08G109400	Chalcone and stilbene synthase family protein	2.03258E-07
Glyma.08G138800	aspartate aminotransferase	2.15798E-05
Glyma.08G209300	-	-
Glyma.09G023300	Intron maturase, type II family protein	5.5233E-08
Glyma.09G155200	ATP-dependent Clp protease	3.84506E-07

Glyma.09G182600	zinc finger protein-related	8.68221E-08
Glyma.09G217700	-	1.94654E-09
Glyma.10G058500	chloroplast RNA-binding protein 29	4.67291E-07
Glyma.10G106500	INO80 ortholog	1.86949E-07
Glyma.10G104900	ARM repeat superfamily protein	-
Glyma.10G124700	peroxisomal 3-ketoacyl-CoA thiolase 3	-
Glyma.10G188600	TRAF-like superfamily protein	-
Glyma.10G205500	phosphoenolpyruvate carboxylase 4	1.84582E-05
Glyma.11G135300	Tetratricopeptide repeat (TPR)-like superfamily protein	9.51905E-06
Glyma.11G158400	AICARFT/IMPCHase bienzyme family protein	-
Glyma.11G218000	DegP protease 7	1.76856E-07
Glyma.11G234200	-	4.51724E-06
Glyma.12G052800	cell division cycle protein 48-related / CDC48-related	7.62613E-09
Glyma.12G107000	NAD(P)H dehydrogenase B1	1.28935E-08
Glyma.12G154900	-	-
Glyma.12G174700	Nucleotide/sugar transporter family protein	-
Glyma.13G139100	Transducin/WD40 repeat-like superfamily protein	6.75522E-10
Glyma.13G207200	NAD(P)-binding Rossmann-fold superfamily protein	2.31716E-05
Glyma.13G336200	triosephosphate isomerase	1.83649E-05
Glyma.14G097800	S-adenosyl-L-methionine-dependent methyltransferases	2.08206E-05
Glyma.15G009500	Lactoylglutathione lyase / glyoxalase I family protein	-
Glyma.15G046400	Phosphatidylinositol-4-phosphate 5-kinase family protei	-
Glyma.15G091000	auxin response factor 8	3.21845E-06
Glyma.15G115500	Inositol monophosphatase family protein	9.60573E-09
Glyma.15G134800	Ribosomal protein L12/ ATP-dependent Clp protease ad	7.66995E-08
Glyma.15G177000	Mob1/phocein family protein	2.06864E-05
Glyma.15G275000	Cellulose synthase family protein	3.34038E-06
Glyma.16G036900	Ribosomal protein L25/Gln-tRNA synthetase, anti-codon	-
Glyma.16G082400	Sec23/Sec24 protein transport family protein	2.83514E-06
Glyma.16G092500	-	2.83514E-06
Glyma.16G144000	Protein kinase superfamily protein	1.31234E-06
Glyma.16G195300	F-box/RNI-like superfamily protein	8.01981E-06
Glyma.17G011500	Saposin-like aspartyl protease family protein	7.66995E-08
Glyma.17G030800	-	-
Glyma.17G031900	calmodulin binding;transcription regulators	8.65029E-10
Glyma.17G104100	dicer-like 4	-
Glyma.17G146400	Plant VAMP (vesicle-associated membrane protein) fam	1.76844E-06
Glyma.17G157100	-	6.86935E-18
Glyma.18G044200	Homeodomain-like superfamily protein	9.47969E-08
Glyma.18G047900	nodulin MtN21 /EamA-like transporter family protein	3.97809E-06
Glyma.18G085200	beta-1,2-xylosyltransferase	6.86686E-08

Glyma.19G053500	NAD-dependent glycerol-3-phosphate dehydrogenase fa	1.0201E-05
Glyma.19G064200	-	-
Glyma.19G242300	O-acetylserine (thiol) lyase (OAS-TL) isoform A1	-
Glyma.20G126800	Cyclase family protein	3.26481E-09
Glyma.20G168100	ribosomal protein 1	-
Glyma.20G179900	phosphoglucosamine mutase family protein	-
Glyma.01G168900	DNA binding;zinc ion binding;nucleic acid binding;nuclei	1.12889E-08
Glyma.01G245100	histone deacetylase 1	4.42884E-09
Glyma.06G286700	O-methyltransferase family protein	1.05951E-10
Glyma.07G157400	SU(VAR)3-9 homolog 9	1.96873E-05
Glyma.10G104300	SERINE CARBOXYPEPTIDASE-LIKE 49	6.20201E-14
Glyma.13G073900	protein kinase 2A	1.01758E-05
Glyma.19G239700	DNAJ heat shock N-terminal domain-containing protein	7.4782E-07
Glyma.20G130800	Homeodomain-like protein with RING/FYVE/PHD-type z	1.43753E-05

CpG Context			CHG C	
q value	Methylation Difference	Region	P value	q value
0.005823103	46.2962963	GENE BODY	-	-
0.001240448	100	GENE BODY	-	-
0.009463526	50	GENE BODY	-	-
5.18275E-05	90	PROMOTER	-	-
-	-	-	-	-
-	-	-	3.6583E-07	0.00035602
0.001933999	100	GENE BODY	-	-
-	-	-	-	-
-	-	-	5.0732E-06	0.00255424
1.41839E-07	100	GENE BODY	-	-
3.94734E-05	55.3030303	GENE BODY	-	-
0.001933999	100	GENE BODY	-	-
0.002243341	41.61573213	GENE BODY	-	-
2.92739E-06	97.14285714	GENE BODY	-	-
0.000703795	100	PROMOTER (187bp); 5'UTR (1	-	-
0.008505711	90	GENE BODY	-	-
0.00286027	44.23076923	GENE BODY	-	-
-	-	-	-	-
6.41886E-05	28.191246	PROMOTER	-	-
0.009486365	42.64705882	GENE BODY	-	-
2.45968E-10	93.33333333	GENE BODY	-	-
0.008526819	86.66666667	GENE BODY	-	-
0.004711596	66.66666667	GENE BODY	-	-
-	-	-	-	-
0.005934657	87.5	GENE BODY	-	-
7.19661E-05	54.16666667	GENE BODY (147bp); 3'UTR (5	-	-
0.000163436	100	GENE BODY	-	-
0.00397489	64.28571429	GENE BODY	-	-
0.003404756	46.55172414	GENE BODY	-	-
0.001933999	100	GENE BODY	-	-
-	-	-	4.1379E-06	0.00218428
0.005008332	39.53488372	GENE BODY	-	-
0.002979043	76.66666667	GENE BODY	-	-
0.000254749	28.18035427	GENE BODY	-	-
0.008968817	72.22222222	GENE BODY	-	-
-	-	-	-	-
8.92381E-05	91.89189189	GENE BODY	-	-
0.000427669	84.59459459	GENE BODY	-	-

0.000128408	56.66666667	GENE BODY	-	-
5.63119E-06	65.46610169	PROMOTER	-	-
0.000499771	77.27272727	GENE BODY	-	-
0.00023892	84.61538462	GENE BODY	-	-
-	-	-	6.0542E-06	0.00290234
-	-	-	1.665E-07	0.00019181
-	-	-	1.5639E-05	0.00560042
0.008002959	68.11594203	GENE BODY	-	-
0.004905666	76.92307692	GENE BODY	-	-
-	-	-	4.0474E-15	4.2808E-11
0.000227945	47.43961353	GENE BODY	-	-
0.002774689	58.20895522	3'UTR	-	-
1.79916E-05	100	GENE BODY	-	-
2.76356E-05	100	GENE BODY	-	-
-	-	-	2.5418E-07	0.00026533
-	-	-	-	-
2.29387E-06	68.88888889	PROMOTER (145bp); 5'UTR (5	-	-
0.009468768	51.46871009	GENE BODY	-	-
0.007970342	56.41025641	GENE BODY	-	-
0.008730732	37.14285714	GENE BODY	-	-
-	-	-	-	-
-	-	-	-	-
0.002126331	76.19047619	GENE BODY	-	-
2.16506E-05	68.29268293	GENE BODY	-	-
0.000115391	100	GENE BODY	-	-
0.008698249	53.84615385	GENE BODY	4.4413E-08	6.5312E-05
0.00218781	80	GENE BODY	-	-
-	-	-	-	-
0.001933999	100	GENE BODY	-	-
0.001933999	100	GENE BODY	-	-
0.001098386	51.2195122	PROMOTER (7bp); 5'UTR (193	-	-
0.00432082	44.11764706	3'UTR	-	-
0.000115391	100	GENE BODY	-	-
-	-	-	-	-
2.84235E-06	64.28571429	GENE BODY	-	-
-	-	-	8.5873E-08	0.00011217
0.001377202	75	GENE BODY	-	-
1.67271E-13	37.67292127	GENE BODY	-	-
0.000137899	37.89431384	GENE BODY	-	-
0.002513721	29.69866418	PROMOTER	2.5793E-05	0.00787429
0.000105925	51.66666667	GENE BODY	-	-

0.005138627	54.16666667	GENE BODY	-	-
-	-	-	2.1726E-07	0.00023551
-	-	-	-	-
8.79837E-06	92	3'UTR (151bp); GENE BODY (4	1.0104E-18	2.2302E-14
-	-	-	7.0929E-06	0.00324597
-	-	-	1.0261E-05	0.00420225
2.4749E-05	75.91836735	GENE BODY	-	-
1.13095E-05	100	GENE BODY	-	-
4.50083E-07	28.7049732	GENE BODY	-	-
0.00837369	49.89316239	GENE BODY	9.2141E-06	0.00390898
6.21853E-10	100	GENE BODY	-	-
0.005131118	36.1025641	GENE BODY	-	-
0.000709141	92.85714286	GENE BODY	-	-
0.006629474	70	GENE BODY	-	-

ontext		CHH context			
hylation Diffe	Region	P value	q value	% Methylation Differences	Region
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	2.10E-08	1.6971E-05	39.90863787	PROMOTER
28.0346288	GENE BODY	-	-	-	-
-	-	-	-	-	-
-	-	1.4356E-05	0.0024849	38.65327381	PROMOTER
53.4659433	GENE BODY	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	7.60E-07	0.00028388	37.11340206	PROMOTER
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	5.18E-06	0.00119179	35.88383838	PROMOTER
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
65.5737705	PROMOTER	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	8.03E-08	4.9359E-05	29.06131938	PROMOTER
-	-	-	-	-	-
-	-	-	-	-	-

-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
34.8148148	GENE BODY	-	-	-	-
78.8157895	GENE BODY	-	-	-	-
42.039312	GENE BODY	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
60.6060606	GENE BODY	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
50	PROMOTER	-	-	-	-
-	-	5.51E-07	0.00022254	25.77436524	GENE BODY
-	-	8.18E-16	7.7844E-12	37.10462287	PROMOTER (
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	8.49E-10	1.2525E-06	42.42424242	3'UTR
-	-	5.901E-05	0.00672815	25.42982563	PROMOTER
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
31.4295502	GENE BODY	-	-	-	-
-	-	-	-	-	-
-	-	5.74E-06	0.00128561	29.32118165	PROMOTER
-	-	-	-	-	-
-	-	-	-	-	-
-	-	1.94E-07	9.9989E-05	33.0977918	PROMOTER (
-	-	-	-	-	-
-	-	-	-	-	-
-	-	5.83E-14	3.2916E-10	35.11047895	PROMOTER
-	-	-	-	-	-
29.5338442	GENE BODY	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
47.6027397	PROMOTER	-	-	-	-
-	-	-	-	-	-

-	-	-	-	-	-
29.7340248	GENE BODY	-	-	-	-
-	-	4.20E-17	5.6978E-13	32.98980877	PROMOTER
87.012987	3'UTR (151bp	-	-	-	-
65.3061224	GENE BODY	-	-	-	-
33.4507997	PROMOTER	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
29.3561368	GENE BODY	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-
-	-	-	-	-	-

145bp); 5'UTR (55bp)

7bp); 5'UTR (193 bp)

Supplemental Table 13: List of 193 syncytium-differentially hypo-methylated genes.

Gene ID	Annotation	
		P value
Glyma.01G038600	myb-like transcription factor family protein	-
Glyma.01G038700	-	1.0651E-05
Glyma.02G021900	-	5.0293E-06
Glyma.02G056800	FAD/NAD(P)-binding oxidoreductase family protein	3.8586E-07
Glyma.02G098100	Ribosomal protein L12/ ATP-dependent Clp protease a	1.0354E-07
Glyma.02G138900	-	3.8837E-21
Glyma.02G161100	basic region/leucine zipper motif 60	3.2926E-07
Glyma.02G218100	indole-3-acetic acid inducible 9	2.3219E-05
Glyma.02G273400	UDP-Glycosyltransferase superfamily protein	-
Glyma.02G274600	Ethylene insensitive 3 family protein	9.6376E-06
Glyma.03G027600	RAS associated with diabetes protein 51C	3.9187E-11
Glyma.03G079800	RHOMBOID-like 1	2.2482E-05
Glyma.03G114700	Plant protein of unknown function (DUF247)	-
Glyma.03G133200	Transmembrane proteins 14C	-
Glyma.03G147700	Disease resistance-responsive (dirigent-like protein) fa	-
Glyma.03G235200	regulatory particle triple-A ATPase 5A	4.3948E-07
Glyma.03G256800	Glycosyl hydrolase superfamily protein	2.2579E-06
Glyma.04G007400	FMN-linked oxidoreductases superfamily protein	-
Glyma.04G018200	-	-
Glyma.04G065700	Phox (PX) domain-containing protein	-
Glyma.04G079800	Ribosomal protein S5 family protein	-
Glyma.04G116700	peroxin 5	-
Glyma.04G190500	alpha/beta-Hydrolases superfamily protein	4.0062E-07
Glyma.04G191100	Pectin lyase-like superfamily protein	-
Glyma.05G020900	glycine-rich RNA-binding protein 3	1.2893E-08
Glyma.05G030700	H(+)-ATPase 11	4.1138E-12
Glyma.05G031900	ARM repeat superfamily protein	-
Glyma.05G041600	ubiquitin-associated (UBA)/TS-N domain-containing pr	2.505E-07
Glyma.05G049500	MBOAT (membrane bound O-acyl transferase) family	7.1683E-07
Glyma.05G053000	glycine-rich protein	-
Glyma.05G004900	sirohydrochlorin ferrochelatase B	9.0062E-06
Glyma.05G075400	Proteasome component (PCI) domain protein	-
Glyma.05G075100	AMP-dependent synthetase and ligase family protein	5.6565E-08
Glyma.05G143100	IAP-like protein 1	1.8826E-05
Glyma.05G150300	Tic22-like family protein	9.4958E-08
Glyma.05G161000	NAD(P)-binding Rossmann-fold superfamily protein	-
Glyma.06G016700	Calcium-binding EF hand family protein	3.4686E-06
Glyma.06G056300	P-type ATPase of Arabidopsis 2	-

Glyma.06G115100	IAA-leucine resistant (ILR)-like gene 6	-
Glyma.06G126000	FTSH protease 11	-
Glyma.06G130800	plastid transcriptionally active7	7.9631E-06
Glyma.06G148600	like COV 2	1.5502E-05
Glyma.06G202500	U5 small nuclear ribonucleoprotein helicase	-
Glyma.06G208900	ATPase E1-E2 type family protein / haloacid dehaloge	2.3735E-06
Glyma.06G238500	cytochrome P450, family 72, subfamily A, polypeptide	1.7281E-07
Glyma.06G238700	phytosylfokine-alpha receptor 2	1.7281E-07
Glyma.06G268700	disease resistance protein (TIR-NBS-LRR class), putativ	1.0441E-06
Glyma.06G271800	-	-
Glyma.06G311400	nuclear factor Y, subunit C11	5.4009E-08
Glyma.07G029200	Signal recognition particle, SRP54 subunit protein	8.9854E-09
Glyma.07G072900	RNAhelicase-like 8	2.2964E-06
Glyma.07G077400	S-adenosyl-L-methionine-dependent methyltransfera	-
Glyma.07G107300	basic pentacysteine1	2.7303E-12
Glyma.07G119900	Vacuolar sorting protein 39	1.8234E-05
Glyma.07G156500	Tautomerase/MIF superfamily protein	1.0646E-08
Glyma.07G165700	-	-
Glyma.07G177100	Pentatricopeptide repeat (PPR-like) superfamily prote	6.7434E-11
Glyma.07G190600	Transducin/WD40 repeat-like superfamily protein	-
Glyma.07G197000	Protein of unknown function (DUF616)	1.5464E-06
Glyma.07G205900	Thioesterase/thiol ester dehydrase-isomerase superfa	5.3109E-10
Glyma.07G268700	Sec14p-like phosphatidylinositol transfer family prote	-
Glyma.08G036600	BURP domain-containing protein	-
Glyma.08G044900	associated molecule with the SH3 domain of STAM 1	1.5501E-08
Glyma.08G082500	O-acetyltransferase family protein	7.9857E-06
Glyma.08G139300	binding	-
Glyma.08G140400	cytochrome P450, family 71, subfamily B, polypeptide	-
Glyma.08G191200	-	1.0607E-07
Glyma.08G194600	multidrug resistance-associated protein 6	-
Glyma.08G222300	O-fucosyltransferase family protein	7.5932E-08
Glyma.08G265300	RNA recognition motif (RRM)-containing protein	-
Glyma.08G271700	ARF-GAP domain 8	-
Glyma.08G344800	-	-
Glyma.08G362400	ENTH/VHS family protein	1.8241E-05
Glyma.09G017000	galacturonosyltransferase 4	2.0949E-06
Glyma.09G024400	Calcium-dependent ARF-type GTPase activating prote	8.0892E-07
Glyma.09G030300	NAD(P)-binding Rossmann-fold superfamily protein	1.2977E-08
Glyma.09G057800	pumilio 5	5.4472E-09
Glyma.09G202900	Glycosyl hydrolase family protein	1.0545E-13
Glyma.09G259200	Protein of unknown function (DUF3741)	7.5754E-08

Glyma.10G023300	Protein kinase family protein	-
Glyma.10G025000	-	1.6408E-05
Glyma.10G030000	Beige/BEACH domain ;WD domain, G-beta repeat pro	2.3919E-06
Glyma.10G102200	-	4.9133E-06
Glyma.U032500	uricase / urate oxidase / nodulin 35, putative	1.5302E-06
Glyma.U032300	exocyst subunit exo70 family protein A1	4.0062E-07
Glyma.10G195900	nudix hydrolase homolog 26	3.0688E-08
Glyma.10G209600	Zinc finger (C2H2 type) family protein / transcription f	5.5574E-08
Glyma.10G235100	tubulin beta 8	-
Glyma.10G241900	DEAD box RNA helicase (PRH75)	8.0746E-06
Glyma.10G243300	Aluminium induced protein with YGL and LRDR motifs	-
Glyma.11G039900	pleckstrin homology (PH) domain-containing protein	1.6121E-06
Glyma.11G040000	-	8.5472E-07
Glyma.11G055200	ralf-like 34	-
Glyma.11G096200	Pyridoxal phosphate (PLP)-dependent transferases su	-
Glyma.11G110100	ATPase, F0/V0 complex, subunit C protein	3.2406E-16
Glyma.11G141100	SEC14 cytosolic factor family protein / phosphoglyceri	-
Glyma.U034000	nuclear RNA polymerase C1	8.4711E-06
Glyma.11G188900	Ribosomal protein L24e family protein	1.7344E-07
Glyma.11G152600	Ribosomal RNA processing Brix domain protein	2.8351E-06
Glyma.11G222900	BTB/POZ/MATH-domains containing protein	1.5464E-06
Glyma.12G137100	Protein kinase superfamily protein	8.0057E-07
Glyma.12G230600	RAB GTPase homolog A1B	2.7635E-06
Glyma.13G084100	MAPK/ERK kinase kinase 1	7.1413E-07
Glyma.13G078800	3\'-5\' exonuclease domain-containing protein	1.2754E-07
Glyma.13G166100	Protein kinase superfamily protein	-
Glyma.13G174900	HAESA-like 1	-
Glyma.13G194900	Disease resistance protein (TIR-NBS-LRR class) family	1.2734E-07
Glyma.13G225300	-	6.2265E-06
Glyma.13G253600	pyrophosphorylase 6	2.8351E-06
Glyma.13G259200	interactor of constitutive active rops 1	-
Glyma.13G275400	MATE efflux family protein	1.6924E-07
Glyma.13G277200	P-loop containing nucleoside triphosphate hydrolases	-
Glyma.13G278800	Leucine-rich repeat (LRR) family protein	7.7715E-06
Glyma.13G289400	WRKY DNA-binding protein 69	4.9603E-07
Glyma.13G328200	-	-
Glyma.13G345000	Tetratricopeptide repeat (TPR)-like superfamily protei	-
Glyma.13G367200	Leucine-rich repeat family protein	-
Glyma.14G018300	microtubule-associated proteins 65-1	8.8957E-06
Glyma.14G084400	-	4.1306E-13
Glyma.14G131700	Protein of unknown function (DUF1218)	-

Glyma.14G137100	DNA topoisomerase, type IA, core	1.016E-06
Glyma.14G142100	signal peptide peptidase	-
Glyma.14G121200	alcohol dehydrogenase 1	4.7527E-13
Glyma.14G162300	NADH-dependent glutamate synthase 1	2.3581E-07
Glyma.14G190400	B-box type zinc finger protein with CCT domain	8.8471E-07
Glyma.14G200600	Protein of unknown function (DUF567)	7.8657E-07
Glyma.14G204100	Basic-leucine zipper (bZIP) transcription factor family	3.5589E-07
Glyma.15G023800	beta galactosidase 1	7.396E-07
Glyma.15G071300	Aluminium induced protein with YGL and LRDR motifs	-
Glyma.15G076300	protease-related	-
Glyma.15G097000	chromatin remodeling factor17	2.6737E-07
Glyma.15G098100	beta-amylase 3	9.906E-06
Glyma.15G125700	Galactose oxidase/kelch repeat superfamily protein	8.7408E-07
Glyma.15G163200	-	-
Glyma.15G193400	cation-chloride co-transporter 1	-
Glyma.15G212800	guanyl-nucleotide exchange factors;GTPase binding;G	4.0062E-07
Glyma.15G219300	Ca(2)-dependent phospholipid-binding protein (Copin	-
Glyma.15G209000	Ribosomal protein L13 family protein	1.8881E-09
Glyma.15G248800	Family of unknown function (DUF572)	-
Glyma.15G255100	-	-
Glyma.15G255900	eukaryotic translation initiation factor 2 gamma subu	1.1248E-05
Glyma.15G271800	tetratricopeptide repeat (TPR)-containing protein	9.5091E-06
Glyma.16G014200	exocyst complex component sec10	3.6024E-10
Glyma.16G039900	ARM repeat superfamily protein	3.9291E-09
Glyma.16G049600	ARM repeat superfamily protein	2.8351E-06
Glyma.16G071500	-	3.63E-06
Glyma.16G073700	Uncharacterised protein family (UPF0497)	-
Glyma.16G078500	translocase inner membrane subunit 17-2	-
Glyma.16G115700	diacylglycerol acyltransferase family	-
Glyma.16G128600	calcium-dependent protein kinase 28	1.5464E-06
Glyma.16G153800	novel cap-binding protein	1.0825E-05
Glyma.17G017700	CBS domain-containing protein with a domain of unkn	-
Glyma.17G037600	ubiquitin protein ligase 6	1.1555E-05
Glyma.17G039300	pleiotropic drug resistance 9	8.6716E-06
Glyma.17G044200	Haloacid dehalogenase-like hydrolase (HAD) superfam	1.4172E-07
Glyma.17G059800	PA-domain containing subtilase family protein	2.353E-05
Glyma.17G089100	Transducin family protein / WD-40 repeat family prot	2.8351E-06
Glyma.17G100600	malate dehydrogenase	1.7286E-05
Glyma.17G188600	non-ATPase subunit 9	3.6323E-06
Glyma.17G213600	calcium-binding EF hand family protein	4.7736E-12
Glyma.17G215800	aberrant lateral root formation 4	6.5195E-11

Glyma.17G226600	Chalcone-flavanone isomerase family protein	1.3974E-05
Glyma.17G253700	UDP-Glycosyltransferase superfamily protein	1.0825E-05
Glyma.18G013300	sphere organelles protein-related	1.107E-05
Glyma.18G082200	NB-ARC domain-containing disease resistance protein	-
Glyma.18G131200	-	2.4794E-05
Glyma.18G133400	eukaryotic translation initiation factor 3G1	-
Glyma.18G142600	SOUL heme-binding family protein	-
Glyma.18G157300	Ribosomal protein S8e family protein	-
Glyma.18G209800	Protein of unknown function (DUF567)	1.0444E-13
Glyma.18G237100	Protein kinase superfamily protein	2.0251E-05
Glyma.18G247300	ATPase, V1 complex, subunit B protein	4.8948E-06
Glyma.18G280500	little nuclei1	2.4541E-05
Glyma.19G006200	Pectin lyase-like superfamily protein	-
Glyma.19G003900	RNA-binding (RRM/RBD/RNP motifs) family protein	-
Glyma.19G016300	SIN3-like 2	9.1678E-07
Glyma.19G217000	WRKY DNA-binding protein 35	6.796E-10
Glyma.19G250600	transcription activators	5.3487E-07
Glyma.20G025100	purin-rich alpha 1	2.8212E-06
Glyma.20G104000	thioredoxin X	-
Glyma.20G140100	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	-
Glyma.20G149100	Tesmin/TSO1-like CXC domain-containing protein	1.5657E-09
Glyma.20G162200	-	1.1346E-06
Glyma.20G233700	MIRO-related GTP-ase 1	3.3652E-06
Glyma.20G241600	Chalcone-flavanone isomerase family protein	-
Glyma.01G168900	DNA binding;zinc ion binding;nucleic acid binding;nucl	4.1975E-08
Glyma.01G245100	histone deacetylase 1	-
Glyma.06G286700	O-methyltransferase family protein	-
Glyma.07G157400	SU(VAR)3-9 homolog 9	-
Glyma.10G104300	SERINE CARBOXYPEPTIDASE-LIKE 49	-
Glyma.13G073900	protein kinase 2A	5.3579E-07
Glyma.19G239700	DNAJ heat shock N-terminal domain-containing protei	8.7992E-07
Glyma.20G130800	Homeodomain-like protein with RING/FYVE/PHD-type	1.1911E-06

CpG Context				
q value	% Methylation Differences	Region	P value	q value
-	-	-	-	-
0.00531437	-60.625	GENE BODY	-	-
0.00301984	-83.33333333	GENE BODY	-	-
0.00042882	-72.58064516	GENE BODY	-	-
0.00014754	-100	3'UTR(3bp); GEN	-	-
1.6048E-16	-39.52861953	PROMOTER	6.2415E-06	0.00296784
0.00037703	-32.78688525	GENE BODY	-	-
0.0094854	-52.38095238	GENE BODY	-	-
-	-	-	-	-
0.00493135	-63.15789474	GENE BODY	-	-
1.9016E-07	-100	GENE BODY	-	-
0.00925927	-50	GENE BODY	-	-
-	-	-	-	-
-	-	-	8.5003E-08	0.00011117
-	-	-	-	-
0.00047655	-47.22772277	GENE BODY	-	-
0.00165915	-70.83333333	GENE BODY	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	2.2791E-08	3.8187E-05
-	-	-	1.0541E-05	0.00428296
0.0004402	-100	GENE BODY	-	-
-	-	-	-	-
2.7636E-05	-100	GENE BODY	-	-
2.697E-08	-68.18181818	GENE BODY	-	-
-	-	-	1.2088E-05	0.00470016
0.00030391	-94.11764706	GENE BODY	-	-
0.0006972	-34	3'UTR	-	-
-	-	-	-	-
0.00471802	-58	GENE BODY	-	-
-	-	-	7.1002E-06	0.00324834
9.0959E-05	-93.33333333	GENE BODY	-	-
0.00811114	-47.91666667	GENE BODY	-	-
0.0001379	-42.5	GENE BODY	-	-
-	-	-	-	-
0.00224912	-75	GENE BODY	-	-
-	-	-	-	-

-	-	-	5.4717E-07	0.00049108
-	-	-	-	-
0.00430384	-81.81818182	5'UTR(73bp); GE	-	-
0.00700902	-39.28571429	GENE BODY	-	-
-	-	-	1.1474E-05	0.00452972
0.00172711	-25.58139535	GENE BODY	-	-
0.00022401	-66.66666667	GENE BODY	-	-
0.00022401	-66.66666667	GENE BODY	-	-
0.00091488	-41.66666667	GENE BODY	-	-
-	-	-	3.2982E-05	0.0092852
8.7468E-05	-54.05405405	GENE BODY	-	-
2.0489E-05	-43.14345992	GENE BODY	-	-
0.00168086	-71.96969697	GENE BODY	-	-
-	-	-	-	-
1.8995E-08	-92.30769231	PROMOTER	-	-
0.00793678	-34.13105413	GENE BODY	-	-
2.3682E-05	-55.85516179	GENE BODY	-	-
-	-	-	-	-
3.055E-07	-65	GENE BODY	-	-
-	-	-	2.3606E-06	0.00145558
0.00124045	-100	GENE BODY	-	-
1.8665E-06	-97.2972973	GENE BODY	-	-
-	-	-	-	-
-	-	-	-	-
3.2222E-05	-100	GENE BODY	-	-
0.00431265	-35.13513514	GENE BODY	-	-
-	-	-	2.8308E-05	0.00837986
-	-	-	-	-
0.00015027	-53.57142857	PROMOTER	-	-
-	-	-	2.505E-05	0.00770727
0.0001153	-28.57142857	GENE BODY	-	-
-	-	-	2.862E-09	6.7059E-06
-	-	-	-	-
-	-	-	1.4049E-07	0.00016704
0.00793678	-41.66666667	3'UTR(20bp); GE	-	-
0.00156444	-73.33333333	GENE BODY	-	-
0.00075604	-47.72727273	GENE BODY	-	-
2.7736E-05	-96.66666667	GENE BODY	-	-
1.3456E-05	-100	5'UTR(62bp); GE	-	-
1.0055E-09	-38.83784606	PROMOTER	9.6467E-10	2.6909E-06
0.00011516	-81.25	3'UTR(11bp); GE	-	-

-	-	-	5.6023E-06	0.00274885
0.00731223	-28.94557823	GENE BODY	-	-
0.00173679	-60.86956522	GENE BODY	-	-
0.00296454	-34.53199365	GENE BODY	-	-
0.00124045	-52.93040293	GENE BODY	-	-
0.0004402	-100	GENE BODY	-	-
5.4845E-05	-36.43697019	PROMOTER	-	-
8.9677E-05	-55	GENE BODY	-	-
-	-	-	-	-
0.00434689	-39.02439024	GENE BODY	-	-
-	-	-	-	-
0.00127808	-81.81818182	GENE BODY	-	-
0.00078803	-44.44444444	3'UTR(125bp); G	-	-
-	-	-	-	-
-	-	-	-	-
5.1988E-12	-100	GENE BODY	-	-
-	-	-	-	-
0.00450349	-44.42724458	GENE BODY	-	-
0.00022439	-41.77927928	GENE BODY	-	-
0.001934	-100	GENE BODY	-	-
0.00124045	-100	GENE BODY	-	-
0.00075029	-25.36509176	PROMOTER	-	-
0.001934	-63.15789474	GENE BODY	-	-
0.00069508	-76.78571429	GENE BODY	-	-
0.00017408	-75	GENE BODY	-	-
-	-	-	6.733E-07	0.00057772
-	-	-	2.3043E-07	0.00024628
0.00017399	-68.08510638	GENE BODY	-	-
0.00354666	-27.63918252	PROMOTER	-	-
0.001934	-100	GENE BODY	-	-
-	-	-	-	-
0.00022041	-28.47144457	GENE BODY	-	-
-	-	-	-	-
0.00422378	-63.07692308	GENE BODY	-	-
0.00052515	-90	PROMOTER	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
0.0046763	-43.24561404	GENE BODY	-	-
3.4345E-09	-46.529723	GENE BODY	-	-
-	-	-	-	-

0.00089734	-34.16208791	PROMOTER	-	-
-	-	-	1.8126E-05	0.00617187
3.9042E-09	-62.73465957	PROMOTER (173	-	-
0.00029022	-35.18156121	GENE BODY	1.4922E-10	5.2125E-07
0.0008032	-27.94117647	3'UTR(72bp); GE	-	-
0.00073921	-52.13600697	GENE BODY	-	-
0.00040074	-55.83982202	GENE BODY	-	-
0.0007038	-100	GENE BODY	-	-
-	-	-	-	-
-	-	-	1.6653E-06	0.00111928
0.00032094	-35.06979063	GENE BODY	-	-
0.00503282	-74.19354839	GENE BODY	-	-
0.0007962	-100	GENE BODY	-	-
-	-	-	1.2124E-05	0.00471036
-	-	-	-	-
0.0004402	-100	GENE BODY	-	-
-	-	-	1.5489E-06	-
5.4781E-06	-94.44444444	3'UTR(105bp); G	-	-
-	-	-	-	-
-	-	-	-	-
0.00549954	-33.1443299	GENE BODY	-	-
0.0049024	-58.33333333	GENE BODY	-	-
1.3271E-06	-52.5	PROMOTER	-	-
1.0303E-05	-85.48387097	GENE BODY	-	-
0.001934	-100	GENE BODY	-	-
0.00233816	-81.48148148	GENE BODY	-	-
-	-	-	3.2667E-05	0.00923579
-	-	-	-	-
-	-	-	7.8538E-06	0.00347622
0.00124045	-100	GENE BODY	-	-
0.00535311	-100	GENE BODY	-	-
-	-	-	-	-
0.00561546	-52.38095238	GENE BODY	-	-
0.00459213	-61.84210526	GENE BODY	-	-
0.00018873	-91.66666667	GENE BODY	-	-
0.00956938	-35.33204384	GENE BODY	-	-
0.001934	-100	GENE BODY	-	-
0.00762355	-68.75	GENE BODY	-	-
0.00233855	-88.23529412	PROMOTER	-	-
3.0418E-08	-39.43502825	PROMOTER	-	-
2.9833E-07	-100	GENE BODY	-	-

0.00648814	-28.35820896	3'UTR	-	-
0.00535311	-100	GENE BODY	-	-
0.00542629	-36.95652174	PROMOTER	-	-
-	-	-	-	-
0.00997621	-32.29376258	GENE BODY	-	-
-	-	-	-	-
-	-	-	6.3631E-07	0.00055329
-	-	-	9.2357E-10	2.5857E-06
1.0055E-09	-50.84745763	GENE BODY	-	-
0.00854684	-72.22222222	GENE BODY	-	-
0.00295471	-90	GENE BODY	-	-
0.00989475	-32.72727273	GENE BODY	-	-
-	-	-	-	-
-	-	-	3.5652E-05	0.00973451
0.00082301	-80.55555556	GENE BODY	-	-
2.2939E-06	-100	5'UTR(43bp); PR	-	-
0.00055465	-50	GENE BODY	-	-
0.001934	-85.71428571	GENE BODY	-	-
-	-	-	-	-
-	-	-	-	-
4.6746E-06	-55.88235294	GENE BODY	-	-
0.00097983	-34.82772935	PROMOTER	-	-
0.00219556	-93.33333333	GENE BODY	-	-
-	-	-	-	-
7.049E-05	-84.02985075	GENE BODY	-	-
-	-	-	2.0984E-05	-
-	-	-	-	-
-	-	-	-	-
-	-	-	3.2371E-06	0.00183207
0.00055518	-62.85714286	GENE BODY	-	-
0.00079992	-55.31914894	GENE BODY	-	-
0.00101771	-40.8445577	GENE BODY	-	-

CHG Context		CHH context		
% Methylation Differences	Region	P value	q value	% Methylation Differences
-	-	8.55033E-05	0.00867934	-42.30769231
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-37.26133076	PROMOTER	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	2.30839E-08	1.8335E-05	-50.15698587
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	4.8121E-07	0.00020143	-36.90360273
-31.66410601	GENE BODY	-	-	-
-	-	3.26192E-07	0.0001493	-26.01455698
-	-	-	-	-
-	-	-	-	-
-	-	6.68789E-05	0.0073291	-27.30141309
-	-	4.08327E-11	1.01E-07	-28.63636364
-	-	5.25008E-05	0.00620626	-31.73935891
-28.40153195	GENE BODY	-	-	-
-37.35930736	GENE BODY	-	-	-
-	-	-	-	-
-	-	1.58145E-05	0.00266906	-28.87657058
-	-	-	-	-
-	-	-	-	-
-30.99415205	GENE BODY	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	6.16521E-11	1.42E-07	-40.54580897
-	-	-	-	-
-30.47504026	GENE BODY	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	5.98308E-05	0.00679065	-28.87307458
-	-	-	-	-
-	-	4.79168E-21	1.887E-16	-69.44136145

-50.25031289	GENE BODY	-	-	-
-	-	1.66274E-11	4.71E-08	-35.77694236
-	-	-	-	-
-	-	-	-	-
-33.76344086	GENE BODY	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-39.09294155	GENE BODY	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	1.83175E-07	9.5505E-05	-36.86868687
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	2.91112E-12	1.03E-08	-35.62172594
-	-	-	-	-
-40	PROMOTER	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	1.44188E-07	7.884E-05	-30.45751634
-	-	2.54054E-23	1.61E-18	-27.13235294
-	-	-	-	-
-	-	-	-	-
-41.3372093	GENE BODY	-	-	-
-	-	1.415E-07	7.7525E-05	-26.19937695
-	-	-	-	-
-76.81818182	GENE BODY	-	-	-
-	-	-	-	-
-39.73888209	GENE BODY	-	-	-
-	-	9.76647E-21	3.50E-16	-37.81773782
-28.20048309	GENE BODY	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-	-	-	-	-
-31.47239086	PROMOTER	-	-	-
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-34.84617728	GENE BODY	-	-	-
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-	-	7.28271E-13	3.09E-09	-43.98335583
-	-	-	-	-
-	-	1.99762E-09	2.4958E-06	-27.59076531
-	-	-	-	-
-	-	-	-	-
-	-	7.16356E-05	0.00767147	-35.76923077
-	-	5.45277E-11	1.2828E-07	-32.49249249
-	-	-	-	-
-	-	2.78041E-09	0.00000326	-28.45827961
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-29.95126706	GENE BODY	-	-	-
-30.15777309	GENE BODY	-	-	-
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-	-	4.83429E-18	8.9E-14	-31.88932981
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-	-	1.51503E-10	3.01E-07	-43.33333333
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-	-	1.09279E-07	6.3102E-05	-47.87878788
-	-	4.52304E-12	1.51E-08	-48.29956156
-	-	1.56201E-23	1.03E-18	-29.30094386
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-	-	7.68396E-09	7.41E-06	-31.02275538

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-55.53359684	GENE BODY	-	-	-
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-34.93150685	GENE BODY	-	-	-
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-	-	6.47E-07	3.7898E-10	-27.63377926
-	-	-	-	-
-	-	8.00393E-07	0.0002958	-27.56201129
-25.10712894	GENE BODY	-	-	-
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-	-	-	-	-
-27.08333333	GENE BODY	-	-	-
-	-	3.78981E-10	6.47E-07	-27.63377926
-	-	-	-	-
-62.78801843	3'UTR	-	-	-
-	-	-	-	-
-	-	7.35589E-10	1.1168E-06	-56.15079365
-	-	3.08073E-08	2.2978E-05	-26.75
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-35.56231003	GENE BODY	-	-	-
-	-	3.64649E-11	9.15E-08	-43.77300408
-26.4203985	GENE BODY	-	-	-
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-	-	1.57827E-08	1.3436E-05	-31.47514105
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-	-	3.33725E-05	0.00452853	-25.35211268
-	-	-	-	-
-	-	2.14128E-05	0.00330149	-42.54716981
-29.87711214	PROMOTER	-	-	-
-30.30450908	5'UTR(73bp);	-	-	-
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-	-	2.89179E-17	4.25E-13	-26.5445801
-70	PROMOTER	-	-	-
-	-	-	-	-
-	-	-	-	-
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-	-	-	-	-
-	-	3.01146E-08	2.2615E-05	-42.29607251
-	-	6.59259E-07	0.00025544	-26.35332435
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-	-	-	-	-
-	-	-	-	-
-	-	6.43181E-18	1.13E-13	-66.00498487
-	-	-	-	-
-71.21212121	3'UTR(65bp)	-	-	-
-	-	1.10711E-05	0.00206784	-29.0805417
-	-	2.49685E-07	0.00012142	-33.66503368
-29.50208706	GENE BODY	-	-	-
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5'UTR(40bp); PROMOTER(160bp)
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PROMOTER
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GENE BODY
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3'UTR(163bp); GENE BODY (37bp)
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PROMOTER
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GENE BODY
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Supplemental Table 14: Primer sequences used in qPCR assays.

Gene ID	Direction	Sequence 5'-3'
Glyma.02G211800	Forward	GGG CAG ATT ACC TTC CCG CG
	Reverse	CGAAGCTCGCGCAAGTCCTT
Glyma.17G141300	Forward	CTTCCATGGCAGAACCTGCG
	Reverse	CCACAGGCTCCCAATGTAGC
Glyma.17G204200	Forward	GACCATGCAATGCCAGCAGG
	Reverse	GCCACTGTCACCAAGAACTT
Glyma.03G054100	Forward	GAT ACA TCG CCT CGT GGA GG
	Reverse	GCGAGTGGCTACACAAAGTC
Glyma.01G027100	Forward	AGGCTTGTTGGAACACCAGGC
	Reverse	GCTGGCTTCTTGGTTGTCAC
Glyma.01G140300	Forward	CTCAGACGGTCTTGACTGGC
	Reverse	CCAAGTCCTCGCTTTCCACG
Glyma.08G277400	Forward	GGG AAC TCC ACA CTT CCT TCG
	Reverse	GGCAGCATAGCCTATTGGGT
Glyma.05G058200	Forward	CCTTCAAGAGAGTCCCTTCCG
	Reverse	CGCTGCAATCGACGACGTTG
Glyma.11G096600	Forward	AAGACACCAAAAGCACTTGTG
	Reverse	GGAGCCAAGGACTATTCAACT
Glyma.13G084100	Forward	GCAGAGGTTATGGGCTTCCA
	Reverse	GTGGCTCACCTCTTCCGATT
Glyma.19G016300	Forward	CGCTTTAATGAGCGGGGTTC
	Reverse	CAGGGCGTTCAGCACTCATA
Glyma.15G204600	Forward	CCAGACTCGTGCTGAAGTGT
	Reverse	GACACCAGCGATCGAGTTCA
Glyma.13G129900	Forward	TCCTTAACGACACTGGCATCC
	Reverse	ATTCACGATTCGCTGAGCCT

Glyma.20G104000	Forward	TACAGTGGTGACATGCGGTG
	Reverse	GAGATGAGACGGCAAGGACC
Glyma.09G219600	Forward	TAAAGCGGTTTGTGATCCCTGT
	Reverse	AAGAACACAGCTTCTCTGCAA
Glyma.18G142600	Forward	TGTTTTGGTGCTGTGCCAAC
	Reverse	GTTCCTGAAACTCGGGCTGA
Glyma.13G305700	Forward	CCCAAGTCCATTGTTCCAAGC
	Reverse	ACTGGTTGATGAAGCTGACAAGT
Glyma.10G235100	Forward	TGAGCCTTACAATGCAACCC
	Reverse	CCCAAAGCTTGGAGTGGTGA
Glyma.09G068500	Forward	ACAGAAAGCGCCTGTTCACT
	Reverse	CCTCGCCCTTTTGAACTGGA
Glyma.08G241900	Forward	ACTTGCACTCCATTGCTCCA
	Reverse	GGGTATGGCCTGTCCATGTG
Glyma.12G096900	Forward	CCGGATTAGCTGGACTGCAA
	Reverse	TTCCTCGTCTGATATGCCGC
Glyma.15G015100	Forward	ACATCGCGCTGGGTGATAAT
	Reverse	GCCTAGCATCAGGAAACGGA
Glyma.19G214900	Forward	GCAAACGTGGTAGAACCAGC
	Reverse	CGGTCTCAAGTGGGGGTTTT
Glyma.01G245100	Forward	GCCTTTCAAGGAGATTTCATGCT
	Reverse	CATCTTGGCCTGTGATCAGAAAG
Glyma.20G141600	Forward	GTGTAATGTTGGATGTGTTCCC
	Reverse	ACACAA TTGAGTTCAACACAAACCG