

Supplementary Tables

Transcriptome analysis identifies differentially expressed genes involved in the metabolic regulatory network of progenies from the cross of low phytic acid *GmMIPS1* and *GmIPK1* soybean mutants

Hangxia Jin, Xiaomin Yu, Qinghua Yang, Xujun Fu, Fengjie Yuan *

Institute of Crop Science and Nuclear Technology Utilization, Zhejiang Academy of Agricultural Sciences, Hangzhou, Zhejiang, China

***Correspondence:**

Fengjie Yuan

fjyuanhz@126.com

Supplemental table legend

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Table S4: DEGs involved in PA metabolism

Table S5: DEGs involved in photosynthesis

Table S6: DEGs involved in starch and sucrose metabolism

Table S7: DEGs involved in defense mechanisms

Supplementary Table S1: Primers of qPCR

Gene	Size	Sequence(5'-3')
Glyma.11G238800	138 bp	F: GGTGGAAACAACGGCTCAAC
		R: GGACCCAACTCGGATAGCTG
Glyma.14G072200	100 bp	F: GACGCAGCTGACTGGGTTTA
		R: GTATGCGGACCACTTTCCCA
Glyma.16G065700	277 bp	F: AGCAAATGCTTTGTTGAAGTGGAA
		R: AGTGTTGAGATTGGATAAGGAACCA
Glyma.12G210600	159 bp	F: ACCTTCAAGAAGCTTGTGGCT
		R: TGTCAAACAATTCCTTATCCTTCCA
Glyma.08G109300	132 bp	F: AGCACATGACCGAGCTCAAA
		R: ACGAAGGTGCCATGTAAGCA
Glyma.12G232500	84 bp	F: GGAATCGTGTTAGGTTTAATTCCCA
		R: CAACTGATCACCTCGTCGGT
Glyma.16G214900	286 bp	F: TCATCGAAGGCAAGTTTAAAGAGT
		R: TAAGCTTCCTGCAACCAGCA
Glyma.09G073600	204 bp	F: TGGCCTCATCGAGACCTACA
		R: CCACCATTGCATGTGGCAAA
<i>ACT11</i>	213 bp	F: CAACCCAAAGGTCAACAG
		R: CAGCGAGATCCAAACGAA

Supplementary Table S2: Enriched GO terms associated with biological processes among DEGs between the *2mlpa* and 2MWT lines at five seed developmental stages

GO_ID	GOTerm	Gene Number In Term				
		Stage 1	Stage 2	Stage 3	Stage 4	Stage 5
GO:0001738	morphogenesis of a polarized epithelium	-	-	-	-	3
GO:0002009	morphogenesis of an epithelium	-	-	-	-	3
GO:0015691	cadmium ion transport	-	-	-	-	3
GO:0046108	uridine metabolic process	-	-	-	-	3
GO:0048729	tissue morphogenesis	-	-	-	-	3
GO:1901658	glycosyl compound catabolic process	-	-	-	-	3
GO:0002239	response to oomycetes	-	-	-	-	4
GO:0009403	toxin biosynthetic process	-	-	2	-	4
GO:0009700	indole phytoalexin biosynthetic process	-	-	2	-	4
GO:0015977	carbon fixation	-	-	-	-	4
GO:0035434	copper ion transmembrane transport	-	-	-	-	4
GO:0042435	indole-containing compound biosynthetic process	-	-	2	-	4
GO:0042548	regulation of photosynthesis, light reaction	-	-	-	-	4
GO:0043467	regulation of generation of precursor metabolites and energy	-	-	-	-	4
GO:0045682	regulation of epidermis development	-	-	2	-	4
GO:0046217	indole phytoalexin metabolic process	-	-	2	-	4
GO:0052314	phytoalexin metabolic process	-	-	2	-	4
GO:0052315	phytoalexin biosynthetic process	-	-	2	-	4
GO:0006658	phosphatidylserine metabolic process	2	-	-	-	4
GO:0015985	energy coupled proton transport, down electrochemical gradient	5	5	5	-	4
GO:0015986	ATP synthesis coupled proton transport	5	5	5	-	4
GO:0006536	glutamate metabolic process	-	-	-	-	5
GO:0006829	zinc II ion transport	-	-	-	-	5
GO:0010109	regulation of photosynthesis	-	-	-	-	5
GO:0032958	inositol phosphate biosynthetic process	-	-	-	-	5
GO:0046173	polyol biosynthetic process	-	-	-	-	5
GO:0072350	tricarboxylic acid metabolic process	-	-	-	-	5

GO:0009250	glucan biosynthetic process	-	-	-	-	7
GO:0009608	response to symbiont	-	-	-	-	7
GO:0009627	systemic acquired resistance	-	-	-	-	7
GO:0072506	trivalent inorganic anion homeostasis	-	-	2	-	7
GO:0006241	CTP biosynthetic process	-	-	-	-	8
GO:0009926	auxin polar transport	-	-	2	-	8
GO:0046036	CTP metabolic process	-	-	-	-	8
GO:1990066	energy quenching	-	-	-	-	8
GO:0015850	organic hydroxy compound transport	4	-	-	-	8
GO:0001934	positive regulation of protein phosphorylation	-	-	-	-	9
GO:0010562	positive regulation of phosphorus metabolic process	-	-	-	-	9
GO:0042327	positive regulation of phosphorylation	-	-	-	-	9
GO:0045937	positive regulation of phosphate metabolic process	-	-	-	-	9
GO:0055081	anion homeostasis	-	-	3	-	9
GO:0006220	pyrimidine nucleotide metabolic process	-	-	-	-	10
GO:0006221	pyrimidine nucleotide biosynthetic process	-	-	-	-	10
GO:0009218	pyrimidine ribonucleotide metabolic process	-	-	-	-	10
GO:0009220	pyrimidine ribonucleotide biosynthetic process	-	-	-	-	10
GO:0046132	pyrimidine ribonucleoside biosynthetic process	-	-	-	-	10
GO:0046134	pyrimidine nucleoside biosynthetic process	-	-	-	-	10
GO:0072528	pyrimidine-containing compound biosynthetic process	-	-	-	-	10
GO:0006825	copper ion transport	-	-	-	-	11
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	-	-	-	-	11
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	-	-	-	-	11
GO:0009208	pyrimidine ribonucleoside triphosphate metabolic process	-	-	-	-	11
GO:0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	-	-	-	-	11
GO:0009630	gravitropism	-	-	-	-	11
GO:0009814	defense response, incompatible interaction	-	-	-	-	11
GO:0031347	regulation of defense response	-	-	-	-	11
GO:0031401	positive regulation of protein modification process	-	-	-	-	11
GO:0032270	positive regulation of cellular protein metabolic process	-	-	-	-	11
GO:0051247	positive regulation of protein metabolic process	-	-	-	-	11

GO:0002252	immune effector process	-	-	-	-	12
GO:0006074	(1->3)-beta-D-glucan metabolic process	-	-	-	-	12
GO:0009629	response to gravity	-	-	-	-	12
GO:0015914	phospholipid transport	-	-	-	-	12
GO:0010466	negative regulation of peptidase activity	8	-	-	-	12
GO:0030162	regulation of proteolysis	8	-	-	-	12
GO:0045861	negative regulation of proteolysis	8	-	-	-	12
GO:0051346	negative regulation of hydrolase activity	8	-	-	-	12
GO:0052547	regulation of peptidase activity	8	-	-	-	12
GO:0006213	pyrimidine nucleoside metabolic process	-	-	-	-	13
GO:0009409	response to cold	-	-	-	-	13
GO:0010604	positive regulation of macromolecule metabolic process	-	-	-	-	13
GO:0031325	positive regulation of cellular metabolic process	-	-	-	-	13
GO:0046131	pyrimidine ribonucleoside metabolic process	-	-	-	-	13
GO:0048437	floral organ development	-	-	-	-	13
GO:0080134	regulation of response to stress	-	-	-	-	13
GO:0043086	negative regulation of catalytic activity	8	-	-	-	13
GO:0019220	regulation of phosphate metabolic process	-	-	-	-	14
GO:0043648	dicarboxylic acid metabolic process	-	-	-	-	14
GO:0051174	regulation of phosphorus metabolic process	-	-	-	-	14
GO:0051239	regulation of multicellular organismal process	-	-	4	-	14
GO:0031399	regulation of protein modification process	-	-	-	-	15
GO:0006869	lipid transport	-	-	-	-	16
GO:0009893	positive regulation of metabolic process	-	-	-	-	16
GO:0006972	hyperosmotic response	-	-	-	-	18
GO:0009167	purine ribonucleoside monophosphate metabolic process	9	10	10	-	18
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	9	10	10	-	18
GO:0009411	response to UV	-	-	-	-	19
GO:0098655	cation transmembrane transport	8	9	9	-	19
GO:0098660	inorganic ion transmembrane transport	8	9	9	-	19
GO:0098662	inorganic cation transmembrane transport	8	9	9	-	19
GO:1901698	response to nitrogen compound	-	-	5	-	20

GO:0009126	purine nucleoside monophosphate metabolic process	9	10	10	-	21
GO:0009127	purine nucleoside monophosphate biosynthetic process	9	10	10	-	21
GO:0009812	flavonoid metabolic process	12	4	-	-	21
GO:0009266	response to temperature stimulus	-	-	-	-	22
GO:0010876	lipid localization	-	-	-	-	22
GO:0098771	inorganic ion homeostasis	-	-	5	-	22
GO:0006633	fatty acid biosynthetic process	9	-	-	-	22
GO:0009156	ribonucleoside monophosphate biosynthetic process	9	10	11	-	22
GO:0009161	ribonucleoside monophosphate metabolic process	9	10	11	-	22
GO:0072330	monocarboxylic acid biosynthetic process	9	-	-	-	23
GO:0009914	hormone transport	-	-	-	-	25
GO:0050801	ion homeostasis	-	-	7	-	25
GO:0051273	beta-glucan metabolic process	12	-	-	-	25
GO:0009064	glutamine family amino acid metabolic process	10	-	-	-	25
GO:0009123	nucleoside monophosphate metabolic process	10	10	11	-	25
GO:0009124	nucleoside monophosphate biosynthetic process	10	10	11	-	25
GO:0060918	auxin transport	-	3	-	-	25
GO:0000302	response to reactive oxygen species	13	-	6	-	27
GO:0006955	immune response	-	-	-	-	28
GO:0045087	innate immune response	-	-	-	-	28
GO:0000041	transition metal ion transport	-	-	-	-	29
GO:0003002	regionalization	-	-	-	-	29
GO:0007389	pattern specification process	-	-	-	-	29
GO:0032268	regulation of cellular protein metabolic process	-	-	-	-	29
GO:0051246	regulation of protein metabolic process	-	-	-	-	29
GO:0009141	nucleoside triphosphate metabolic process	11	11	12	-	29
GO:0009639	response to red or far red light	-	-	-	-	30
GO:0048878	chemical homeostasis	-	-	8	-	30
GO:0034728	nucleosome organization	-	-	-	-	31
GO:0071824	protein-DNA complex subunit organization	-	-	-	-	31
GO:0015992	proton transport	12	13	13	-	31
GO:0010817	regulation of hormone levels	-	-	-	-	33

GO:0009908	flower development	-	-	-	-	34
GO:0006164	purine nucleotide biosynthetic process	13	12	13	-	36
GO:0009152	purine ribonucleotide biosynthetic process	13	12	13	-	36
GO:0002376	immune system process	-	-	-	-	38
GO:0009620	response to fungus	-	-	10	-	38
GO:0006818	hydrogen transport	16	15	16	-	38
GO:0072522	purine-containing compound biosynthetic process	14	13	14	-	38
GO:0015711	organic anion transport	19	-	-	-	39
GO:0015672	monovalent inorganic cation transport	15	13	14	-	39
GO:1901657	glycosyl compound metabolic process	13	13	15	-	41
GO:0006073	cellular glucan metabolic process	16	-	-	-	42
GO:0044264	cellular polysaccharide metabolic process	17	-	-	-	43
GO:0080090	regulation of primary metabolic process	-	-	-	-	46
GO:0009260	ribonucleotide biosynthetic process	15	13	15	-	46
GO:0046390	ribose phosphate biosynthetic process	15	13	15	-	46
GO:0032446	protein modification by small protein conjugation	-	-	-	-	48
GO:0090567	reproductive shoot system development	-	-	-	-	48
GO:0009165	nucleotide biosynthetic process	-	13	15	-	51
GO:1901293	nucleoside phosphate biosynthetic process	-	13	15	-	51
GO:0006325	chromatin organization	-	-	-	-	52
GO:0044042	glucan metabolic process	24	-	-	-	52
GO:0031323	regulation of cellular metabolic process	-	-	-	-	53
GO:0006952	defense response	-	-	11	-	54
GO:0009617	response to bacterium	-	-	-	-	55
GO:0071822	protein complex subunit organization	-	-	-	-	58
GO:0048608	reproductive structure development	-	-	-	-	59
GO:0061458	reproductive system development	-	-	-	-	59
GO:0090407	organophosphate biosynthetic process	19	14	16	-	60
GO:0048367	shoot system development	-	-	-	-	62
GO:1901137	carbohydrate derivative biosynthetic process	-	13	17	-	62
GO:0044262	cellular carbohydrate metabolic process	-	-	-	-	67
GO:0044702	single organism reproductive process	-	-	-	-	67

GO:0005976	polysaccharide metabolic process	34	-	-	-	75
GO:0009416	response to light stimulus	-	-	-	-	82
GO:0009314	response to radiation	-	-	-	-	94
GO:0009791	post-embryonic development	-	-	-	-	94
GO:0006970	response to osmotic stress	-	-	-	-	100
GO:0065008	regulation of biological quality	-	-	17	-	105
GO:0006812	cation transport	-	15	21	-	105
GO:0009725	response to hormone	-	-	-	-	111
GO:0001101	response to acid chemical	-	-	-	-	112
GO:0003006	developmental process involved in reproduction	-	-	-	-	124
GO:0048731	system development	-	-	-	-	125
GO:0009719	response to endogenous stimulus	-	-	22	-	126
GO:0043207	response to external biotic stimulus	-	-	24	-	134
GO:0051707	response to other organism	-	-	24	-	134
GO:0009607	response to biotic stimulus	-	-	24	-	138
GO:0005975	carbohydrate metabolic process	-	-	-	-	140
GO:0044711	single-organism biosynthetic process	55	19	24	-	147
GO:0010033	response to organic substance	-	-	30	-	149
GO:0051704	multi-organism process	-	-	28	-	161
GO:0006811	ion transport	71	20	31	-	172
GO:0009605	response to external stimulus	-	-	30	-	178
GO:0007275	multicellular organismal development	-	-	-	-	204
GO:0044707	single-multicellular organism process	-	-	-	-	225
GO:0032501	multicellular organismal process	-	-	-	-	231
GO:0009628	response to abiotic stimulus	-	-	-	-	251
GO:0044765	single-organism transport	111	33	46	-	269
GO:1902578	single-organism localization	112	33	47	-	272
GO:0042221	response to chemical	-	-	59	-	334
GO:0006950	response to stress	-	-	64	-	406
GO:0010467	gene expression	-	-	-	-	651
GO:0050896	response to stimulus	-	-	114	-	795
GO:0043170	macromolecule metabolic process	-	-	-	-	1199

GO:0071704	organic substance metabolic process	-	-	-	-	1635
GO:0009967	positive regulation of signal transduction	-	-	2	-	-
GO:0010039	response to iron ion	-	-	3	-	-
GO:0010647	positive regulation of cell communication	-	-	2	-	-
GO:0018130	heterocycle biosynthetic process	-	-	50	-	-
GO:0018871	1-aminocyclopropane-1-carboxylate metabolic process	-	-	2	-	-
GO:0019438	aromatic compound biosynthetic process	-	-	51	-	-
GO:0023056	positive regulation of signaling	-	-	2	-	-
GO:0034654	nucleobase-containing compound biosynthetic process	-	-	48	-	-
GO:0080135	regulation of cellular response to stress	-	-	2	-	-
GO:0098542	defense response to other organism	-	-	6	-	-
GO:1901362	organic cyclic compound biosynthetic process	-	-	51	-	-
GO:1901700	response to oxygen-containing compound	-	-	14	-	-
GO:1990267	response to transition metal nanoparticle	-	-	3	-	-
GO:2000026	regulation of multicellular organismal development	-	-	4	-	-
GO:0044699	single-organism process	517	-	-	-	-
GO:0006820	anion transport	32	-	-	-	-
GO:0065009	regulation of molecular function	29	-	-	-	-
GO:0044092	negative regulation of molecular function	27	-	-	-	-
GO:0033554	cellular response to stress	24	-	-	-	-
GO:0071554	cell wall organization or biogenesis	24	-	-	-	-
GO:0019748	secondary metabolic process	20	-	-	-	-
GO:0009698	phenylpropanoid metabolic process	19	-	-	-	-
GO:0044550	secondary metabolite biosynthetic process	17	-	-	-	-
GO:0009699	phenylpropanoid biosynthetic process	16	-	-	-	-
GO:0015849	organic acid transport	15	-	-	-	-
GO:0046942	carboxylic acid transport	15	-	-	-	-
GO:0006979	response to oxidative stress	13	-	-	-	-
GO:0015698	inorganic anion transport	13	-	-	-	-
GO:0048523	negative regulation of cellular process	10	-	-	-	-
GO:0030243	cellulose metabolic process	9	-	-	-	-
GO:0031324	negative regulation of cellular metabolic process	8	-	-	-	-

GO:0032269	negative regulation of cellular protein metabolic process	8	-	-	-	-
GO:0051248	negative regulation of protein metabolic process	8	-	-	-	-
GO:0009414	response to water deprivation	7	-	-	-	-
GO:0009415	response to water	7	-	-	-	-
GO:0055065	metal ion homeostasis	7	-	-	-	-
GO:0008272	sulfate transport	6	-	3	-	-
GO:0009808	lignin metabolic process	6	-	-	-	-
GO:0055076	transition metal ion homeostasis	6	-	3	-	-
GO:0072348	sulfur compound transport	6	-	3	-	-
GO:0006875	cellular metal ion homeostasis	5	-	-	-	-
GO:0009813	flavonoid biosynthetic process	5	-	-	-	-
GO:0030003	cellular cation homeostasis	5	-	3	-	-
GO:0034599	cellular response to oxidative stress	5	-	-	-	-
GO:0034614	cellular response to reactive oxygen species	5	-	-	-	-
GO:0046916	cellular transition metal ion homeostasis	5	-	-	-	-
GO:0006558	L-phenylalanine metabolic process	4	-	-	-	-
GO:0009685	gibberellin metabolic process	4	-	-	-	-
GO:0070542	response to fatty acid	4	-	2	-	-
GO:1902221	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process	4	-	-	-	-
GO:0000304	response to singlet oxygen	3	-	-	-	-
GO:0006476	protein deacetylation	3	-	-	-	-
GO:0016575	histone deacetylation	3	-	-	-	-
GO:0035601	protein deacylation	3	-	-	-	-
GO:0051552	flavone metabolic process	3	-	-	-	-
GO:0051553	flavone biosynthetic process	3	-	-	-	-
GO:0098732	macromolecule deacylation	3	-	-	-	-
GO:0006817	phosphate ion transport	2	-	-	-	-
GO:0007062	sister chromatid cohesion	2	-	-	-	-
GO:0010192	mucilage biosynthetic process	2	-	-	-	-
GO:0015750	pentose transport	2	-	-	-	-
GO:0071452	cellular response to singlet oxygen	2	-	-	-	-
GO:0044710	single-organism metabolic process	301	91	-	-	-

GO:0051179	localization	181	46	-	-	-
GO:0051234	establishment of localization	179	46	-	-	-
GO:0055086	nucleobase-containing small molecule metabolic process	-	20	-	-	-
GO:1901135	carbohydrate derivative metabolic process	-	20	-	-	-
GO:1901566	organonitrogen compound biosynthetic process	-	20	23	-	-
GO:0006753	nucleoside phosphate metabolic process	-	19	-	-	-
GO:0009117	nucleotide metabolic process	-	19	-	-	-
GO:0009259	ribonucleotide metabolic process	-	19	-	-	-
GO:0019693	ribose phosphate metabolic process	-	19	-	-	-
GO:0072521	purine-containing compound metabolic process	-	19	-	-	-
GO:0006163	purine nucleotide metabolic process	-	18	-	-	-
GO:0009150	purine ribonucleotide metabolic process	-	18	-	-	-
GO:0034220	ion transmembrane transport	-	10	10	-	-
GO:0055085	transmembrane transport	-	10	12	-	-
GO:1902600	hydrogen ion transmembrane transport	8	8	9	-	-
GO:0015980	energy derivation by oxidation of organic compounds	-	7	6	-	-
GO:0045333	cellular respiration	9	6	5	-	-
GO:0006461	protein complex assembly	-	5	-	-	-
GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient	-	5	6	-	-
GO:0022904	respiratory electron transport chain	-	5	3	-	-
GO:0070271	protein complex biogenesis	-	5	-	-	-
GO:0006835	dicarboxylic acid transport	-	3	-	-	-
GO:0015740	C4-dicarboxylate transport	-	3	-	-	-
GO:0006308	DNA catabolic process	-	2	-	-	-
GO:0009692	ethylene metabolic process	-	2	2	-	-
GO:0015936	coenzyme A metabolic process	-	2	2	-	-
GO:0015937	coenzyme A biosynthetic process	-	2	2	-	-
GO:0033865	nucleoside bisphosphate metabolic process	-	2	2	-	-
GO:0033866	nucleoside bisphosphate biosynthetic process	-	2	2	-	-
GO:0033875	ribonucleoside bisphosphate metabolic process	-	2	2	-	-
GO:0034030	ribonucleoside bisphosphate biosynthetic process	-	2	2	-	-
GO:0034032	purine nucleoside bisphosphate metabolic process	-	2	2	-	-

GO:0034033	purine nucleoside bisphosphate biosynthetic process	-	2	2	-	-
GO:0043449	cellular alkene metabolic process	-	2	2	-	-
GO:0051258	protein polymerization	-	2	2	-	-
GO:0051259	protein oligomerization	-	2	-	-	-
GO:1900673	olefin metabolic process	-	2	-	-	-
GO:0019752	carboxylic acid metabolic process	-	-	-	28	-
GO:0006508	proteolysis	68	-	-	27	-
GO:0006091	generation of precursor metabolites and energy	30	31	26	26	97
GO:0016485	protein processing	52	-	-	24	-
GO:0051604	protein maturation	52	-	-	24	-
GO:0010035	response to inorganic substance	40	-	18	19	123
GO:0010038	response to metal ion	-	-	-	17	108
GO:0055114	oxidation-reduction process	21	21	20	15	39
GO:0032787	monocarboxylic acid metabolic process	31	-	-	14	-
GO:0022900	electron transport chain	12	19	16	12	-
GO:0034660	ncRNA metabolic process	-	-	-	11	-
GO:0006631	fatty acid metabolic process	23	-	-	11	-
GO:0015979	photosynthesis	-	12	12	9	18
GO:0006399	tRNA metabolic process	-	-	-	9	-
GO:0019684	photosynthesis, light reaction	-	11	11	8	16
GO:0090305	nucleic acid phosphodiester bond hydrolysis	-	-	-	8	-
GO:0090501	RNA phosphodiester bond hydrolysis	8	-	-	8	-
GO:0031668	cellular response to extracellular stimulus	10	-	-	7	24
GO:0031669	cellular response to nutrient levels	10	-	-	7	24
GO:0071496	cellular response to external stimulus	10	-	-	7	24
GO:0009991	response to extracellular stimulus	-	-	-	7	25
GO:0031667	response to nutrient levels	-	-	-	7	25
GO:0034470	ncRNA processing	-	-	-	7	-
GO:0009267	cellular response to starvation	10	-	-	6	20
GO:0042594	response to starvation	10	-	-	6	20
GO:0008033	tRNA processing	-	-	-	6	-
GO:0048507	meristem development	-	-	-	6	-

GO:0009163	nucleoside biosynthetic process	12	13	14	5	28
GO:0042455	ribonucleoside biosynthetic process	12	13	14	5	28
GO:0009116	nucleoside metabolic process	12	13	14	5	32
GO:0009119	ribonucleoside metabolic process	12	13	14	5	32
GO:1901659	glycosyl compound biosynthetic process	13	13	15	5	34
GO:0015893	drug transport	10	-	-	5	-
GO:0042493	response to drug	10	-	-	5	-
GO:0009767	photosynthetic electron transport chain	-	7	6	5	-
GO:0019751	polyol metabolic process	-	3	-	4	14
GO:0010243	response to organonitrogen compound	-	-	5	4	15
GO:0042451	purine nucleoside biosynthetic process	10	12	12	4	18
GO:0046129	purine ribonucleoside biosynthetic process	10	12	12	4	18
GO:0046128	purine ribonucleoside metabolic process	10	12	12	4	19
GO:0042278	purine nucleoside metabolic process	10	12	12	4	20
GO:0009142	nucleoside triphosphate biosynthetic process	11	11	12	4	28
GO:0009199	ribonucleoside triphosphate metabolic process	11	11	12	4	28
GO:0009201	ribonucleoside triphosphate biosynthetic process	11	11	12	4	28
GO:0006457	protein folding	-	-	-	4	-
GO:0006754	ATP biosynthetic process	9	10	10	3	17
GO:0009144	purine nucleoside triphosphate metabolic process	9	10	10	3	17
GO:0009145	purine nucleoside triphosphate biosynthetic process	9	10	10	3	17
GO:0009205	purine ribonucleoside triphosphate metabolic process	9	10	10	3	17
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	9	10	10	3	17
GO:0046034	ATP metabolic process	9	10	10	3	17
GO:0010051	xylem and phloem pattern formation	-	-	-	3	-
GO:0043647	inositol phosphate metabolic process	5	-	-	3	-
GO:0009404	toxin metabolic process	-	-	2	2	5
GO:0006570	tyrosine metabolic process	-	-	-	2	-
GO:0009637	response to blue light	-	-	-	2	-
GO:0006020	inositol metabolic process	-	2	2	2	-

Supplementary Table S3: Enriched KEGG pathways between the *2mlpa* and 2MWT lines at five seed developmental stages

#Pathway	Gene Number In Pathway					
	Pathway ID	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5
Glycolysis / Gluconeogenesis	ko00010	18	3	3	9	39
Citrate cycle (TCA cycle)	ko00020	1			1	12
Pentose phosphate pathway	ko00030	6	2	3	2	19
Pentose and glucuronate interconversions	ko00040	15	3	2	6	31
Fructose and mannose metabolism	ko00051	4		1	2	17
Galactose metabolism	ko00052	15		1	3	26
Ascorbate and aldarate metabolism	ko00053	11	3	5	7	26
Fatty acid biosynthesis	ko00061	10	2	1		11
Fatty acid elongation	ko00062	4	1	3	3	6
Fatty acid metabolism	ko00071	9	3	3	5	19
Synthesis and degradation of ketone bodies	ko00072	1	1	1	1	2
Cutin, suberine and wax biosynthesis	ko00073	17	2	1	4	16
Steroid biosynthesis	ko00100	2			1	11
Ubiquinone and other terpenoid-quinone biosynthesis	ko00130	12		1		19
Oxidative phosphorylation	ko00190	25	30	29	7	67
Photosynthesis	ko00195	24	33	32	28	69
Photosynthesis - antenna proteins	ko00196	1			5	22
Purine metabolism	ko00230	37	11	19	12	104
Caffeine metabolism	ko00232					1
Pyrimidine metabolism	ko00240	39	9	19	12	100
Alanine, aspartate and glutamate metabolism	ko00250	6	2	3	6	31
Glycine, serine and threonine metabolism	ko00260	16	1	8	2	18
Cysteine and methionine metabolism	ko00270	11	3	9	7	24
Valine, leucine and isoleucine degradation	ko00280	4	2	2	2	15

Valine, leucine and isoleucine biosynthesis	ko00290	8		6		10
Lysine biosynthesis	ko00300					2
Lysine degradation	ko00310	6	3	2	3	21
Arginine and proline metabolism	ko00330	13	2	1	6	27
Histidine metabolism	ko00340	3	1		1	5
Tyrosine metabolism	ko00350	6	2	2	5	15
Phenylalanine metabolism	ko00360	22	2	4	5	39
Tryptophan metabolism	ko00380	10	2	3	5	12
Phenylalanine, tyrosine and tryptophan biosynthesis	ko00400	5	1		4	8
Benzoxazinoid biosynthesis	ko00402	6	2	3		5
beta-Alanine metabolism	ko00410	5	2		1	16
Taurine and hypotaurine metabolism	ko00430	7		1	2	7
Selenocompound metabolism	ko00450	2	3	2	3	7
Cyanoamino acid metabolism	ko00460	9	2	6	5	21
Glutathione metabolism	ko00480	11	4	5	1	25
Starch and sucrose metabolism	ko00500	30	5	14	14	75
N-Glycan biosynthesis	ko00510	3		2	1	9
Other glycan degradation	ko00511	21	1	2	3	21
Other types of O-glycan biosynthesis	ko00514				1	2
Amino sugar and nucleotide sugar metabolism	ko00520	9	1	6	3	38
Glycosaminoglycan degradation	ko00531	3				11
Glycerolipid metabolism	ko00561	10	1	2	1	16
Inositol phosphate metabolism	ko00562	8	4	5	5	31
Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	ko00563	12		5	3	29
Glycerophospholipid metabolism	ko00564	7		2		23
Ether lipid metabolism	ko00565	1				5
Arachidonic acid metabolism	ko00590	3		1		2
Linoleic acid metabolism	ko00591	9		2	2	16

alpha-Linolenic acid metabolism	ko00592	8		3	5	23
Sphingolipid metabolism	ko00600	6				15
Glycosphingolipid biosynthesis - globo series	ko00603	3				2
Glycosphingolipid biosynthesis - ganglio series	ko00604	3				7
Pyruvate metabolism	ko00620	17	5	4	6	36
Glyoxylate and dicarboxylate metabolism	ko00630	9	1	2	1	17
Propanoate metabolism	ko00640	14	4	2	3	23
Butanoate metabolism	ko00650	3	1	1	1	12
C5-Branched dibasic acid metabolism	ko00660					2
One carbon pool by folate	ko00670	2		1		5
Carbon fixation in photosynthetic organisms	ko00710	9	2	1	4	31
Thiamine metabolism	ko00730	1			1	2
Riboflavin metabolism	ko00740	2				8
Vitamin B6 metabolism	ko00750	3	2	1	2	9
Nicotinate and nicotinamide metabolism	ko00760					2
Pantothenate and CoA biosynthesis	ko00770	1		1	1	5
Biotin metabolism	ko00780					1
Lipoic acid metabolism	ko00785	1			1	2
Folate biosynthesis	ko00790	1				4
Porphyrin and chlorophyll metabolism	ko00860	7		3	1	19
Terpenoid backbone biosynthesis	ko00900	4	2	2	2	12
Indole alkaloid biosynthesis	ko00901	4		2		1
Monoterpenoid biosynthesis	ko00902					3
Limonene and pinene degradation	ko00903	19	3	4	8	29
Diterpenoid biosynthesis	ko00904	12	3	3	5	21
Brassinosteroid biosynthesis	ko00905	2		1		4
Carotenoid biosynthesis	ko00906	24		5	5	16
Zeatin biosynthesis	ko00908	6	3	5	4	13

Sesquiterpenoid and triterpenoid biosynthesis	ko00909	4	2	1		2
Nitrogen metabolism	ko00910	7	3	4	4	25
Sulfur metabolism	ko00920	2	2	2	1	9
Phenylpropanoid biosynthesis	ko00940	42	9	14	14	74
Flavonoid biosynthesis	ko00941	45	18	14	12	67
Anthocyanin biosynthesis	ko00942	2				1
Isoflavonoid biosynthesis	ko00943	9		3	2	8
Flavone and flavonol biosynthesis	ko00944	22	7	9	7	26
Stilbenoid, diarylheptanoid and gingerol biosynthesis	ko00945	28	6	10	9	43
Isoquinoline alkaloid biosynthesis	ko00950	3	1		2	9
Tropane, piperidine and pyridine alkaloid biosynthesis	ko00960	4	1		2	10
Betalain biosynthesis	ko00965					1
Glucosinolate biosynthesis	ko00966	5		2	1	4
Aminoacyl-tRNA biosynthesis	ko00970	3	1	1	2	10
Biosynthesis of unsaturated fatty acids	ko01040	6	1	1	2	12
Metabolic pathways	ko01100	361	108	153	138	794
Biosynthesis of secondary metabolites	ko01110	210	42	66	65	374
ABC transporters	ko02010	21	1	0	3	46
Ribosome biogenesis in eukaryotes	ko03008	14	2	3	15	45
Ribosome	ko03010	27	18	22	15	252
RNA transport	ko03013	26	2	9	16	61
mRNA surveillance pathway	ko03015	10	2	2	4	28
RNA degradation	ko03018	12	4	6	7	31
RNA polymerase	ko03020	28	6	15	6	58
Basal transcription factors	ko03022	2	2			4
DNA replication	ko03030	3	1	2	3	20
Spliceosome	ko03040	17	1	5	11	66
Proteasome	ko03050	1			1	6

Protein export	ko03060	6	1	3	3	30
Base excision repair	ko03410	7			2	16
Nucleotide excision repair	ko03420	3	1	1	2	20
Mismatch repair	ko03430	3	1	3	1	12
Homologous recombination	ko03440	9	3	6	1	22
Non-homologous end-joining	ko03450					2
Phosphatidylinositol signaling system	ko04070	7	2	5	3	37
Plant hormone signal transduction	ko04075	67	12	27	38	252
Ubiquitin mediated proteolysis	ko04120	13	1	8	9	64
Sulfur relay system	ko04122					1
SNARE interactions in vesicular transport	ko04130	2		1		22
Regulation of autophagy	ko04140	5		2		29
Protein processing in endoplasmic reticulum	ko04141	24	2	14	5	113
Endocytosis	ko04144	4	1	3	3	27
Phagosome	ko04145	12	2	3	1	47
Peroxisome	ko04146	12	1			33
Plant-pathogen interaction	ko04626	109	26	54	39	303
Natural killer cell mediated cytotoxicity	ko04650			2		7
Circadian rhythm - mammal	ko04710	2	1	1		9
Circadian rhythm - plant	ko04712	12	4	6	7	36

Supplementary Table S4: DEGs involved in PA metabolism

GeneID	log2Ratio(2mlp a-1/2M WT-1)	P-value	log2Ratio(2mlp a-2/2M WT-2)	P-value	log2Ratio(2mlp a-3/2 MWT-3)	P-value	log2Ratio(2mlp a-4/2M WT-4)	P-value	log2Ratio(2mlp a-5/2M WT-5)	P-value	Length	Pathway	GO Component	GO Function	GO Process	Blast nr
Glyma.04 G251700	-	-	-	-	1.4419	2.38 E-05	-	-	-	-	1819	ko00562//Inositol phosphate metabolism;ko03008//Ribosome biogenesis in eukaryotes;ko04070//Phosphatidyl inositol signaling system;ko01100//Metabolic pathways;ko04144//Endocytosis; ko04712//Circadian rhythm - plant	-	-	-	gi 356509438 ref XP_003523456.1 /0/PREDICTED: phosphatidylinositol 4-phosphate 5-kinase 4-like [Glycine max]
Glyma.05 G070400	1.1479	0.0074	-	-	-	-	-	-	-	-	4016	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidyl inositol signaling system;ko01100//Metabolic pathways	-	-	GO:0046488//phosphatidylinositol metabolic process;GO:0043647//inositol phosphate metabolic process;GO:0044707;GO:0044723; GO:0001101//response to acid chemical	gi 947109262 gb KRH57588.1 ;gi 947109263 gb KRH57589.1 ;gi 571454088 ref XP_006579677.1 ;gi 947109261 gb KRH57587.1 /0;0;0;0/hypothetical protein GLYMA_05G070400 [Glycine max];hypothetical protein GLYMA_05G070400 [Glycine max];PREDICTED: type I inositol polyphosphate 5-phosphatase 2-like [Glycine max];hypothetical protein GLYMA_05G070400 [Glycine max]
Glyma.07 G013900	-	-	-3.24	4.48 E-06	-3.276	5.75 E-06	-2.599	3.98 E-05	-	-	1625	ko00562//Inositol phosphate metabolism;ko00053//Ascorbate and aldarate metabolism	GO:0044424	GO:0046914//transition metal ion binding;GO:0016701//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	GO:0006020//inositol metabolic process	gi 947098691 gb KRH47183.1 ;gi 947098690 gb KRH47182.1 ;gi 947098692 gb KRH47184.1 /4.8486e-172;0;0/hypothetical protein GLYMA_07G013900 [Glycine max];hypothetical protein GLYMA_07G013900 [Glycine max];hypothetical protein GLYMA_07G013900 [Glycine max]
Glyma.17 G153000	-1.484	0.0028	-	-	-	-	-1.409	0.0012368	-	-	2721	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidyl inositol signaling system;ko01100//Metabolic pathways	-	-	GO:0046488//phosphatidylinositol metabolic process;GO:0043647//inositol phosphate metabolic process	gi 947054852 gb KRH04305.1 ;gi 356563443 ref XP_003549972.1 /0;0/hypothetical protein GLYMA_17G153000 [Glycine max];PREDICTED: type I inositol polyphosphate 5-phosphatase 2-like [Glycine max]
Glyma.18 G027200	-1.085	0.0021	-	-	-	-	-	-	-	-	2057	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidyl inositol signaling system;ko01100//Metabolic pathways	-	GO:0060089;GO:0046872//metal ion binding;GO:0004629//phospholipase C activity	GO:0007165//signal transduction;GO:0044238//primary metabolic process	gi 356568316 ref XP_003552358.1 ;gi 571542533 ref XP_006601952.1 /0;0/PREDICTED: phosphoinositide phospholipase C 6 isoform X2 [Glycine max];PREDICTED: phosphoinositide phospholipase C 6 isoform X1 [Glycine max]
Glyma.01 G016700	8.6673	1.87 E-42	11.304	2.50 E-38	9.9449	6.11 E-24	10.415	4.45 E-26	9.9027	1.85 E-15	1074	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidyl inositol signaling system;ko01100//Metabolic pathways	GO:0044464	GO:0046872//metal ion binding;GO:0051766//inositol trisphosphate kinase activity;GO:0051765//inositol tetrakisphosphate kinase activity;GO:0032550	GO:0043647//inositol phosphate metabolic process	gi 947126543 gb KRH74397.1 /0/hypothetical protein GLYMA_01G016700 [Glycine max]
Glyma.05 G224500	-	-	-	-	-	-	-	-	3.3182	0.002618	1497	ko00562//Inositol phosphate metabolism;ko00053//Ascorbate and aldarate metabolism	GO:0044424	GO:0046914//transition metal ion binding;GO:0016701//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	GO:0048646//anatomical structure formation involved in morphogenesis;GO:0006020//inositol metabolic process	gi 947111847 gb KRH60173.1 ;gi 947111848 gb KRH60174.1 ;gi 947111846 gb KRH60172.1 ;gi 734310448 gb KHM99828.1 /2.07501e-180;0;0/hypothetical protein GLYMA_05G224500 [Glycine max];hypothetical protein GLYMA_05G224500 [Glycine max];hypothetical protein GLYMA_05G224500 [Glycine max];Inositol oxygenase 4 [Glycine soja]

Glyma.03 G186300	-	-	-	-	-	-	-	-	2.9732	0.00 574 41	3274	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways;ko04144//Endocytosis	-	GO:0016307//phosp hatidylinositol phosphate kinase activity;GO:003255 0	GO:0046488//phosphatidylinositol metabolic process	gi 571446255 ref XP_006577040.1 /O/PREDICTED: phosphatidylinositol 4-phosphate 5-kinase 9-like [Glycine max]
Glyma.07 G266200	-	-	-	-	-	-	-	-	2.8717	0.00 144 03	1525	ko00562//Inositol phosphate metabolism;ko00053//Ascorbate and aldarate metabolism;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:00 44444; GO:00 16020// membr ane	GO:0070456	GO:0019852//L-ascorbic acid metabolic process;GO:0046488//phosphatidyl inositol metabolic process;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress	gi 734423661 gb KHN42287.1 ;gi 947102679 gb KRH5117 1.1 /O;0//Inositol monophosphatase 3 [Glycine soja] ;hypothetical protein GLYMA_07G266200 [Glycine max]
Glyma.05 G180600	-	-	-	-	-	-	-	-	2.6821	6.06 E-0 7	1864	ko00562//Inositol phosphate metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:00 44424	GO:0016872//intra molecular lyase activity	GO:0009642//response to light intensity;GO:0009620//response to fungus;GO:0000302//response to reactive oxygen species;GO:0006020//inositol metabolic process;GO:0009617//response to bacterium;GO:0006658//phosphatid ylserine metabolic process;GO:0002252;GO:0007275// multicellular organismal development;GO:0003006//develop mental process involved in reproduction;GO:0032958//inositol phosphate biosynthetic process;GO:0006644//phospholipid metabolic process	gi 947111062 gb KRH59388.1 ;gi 947111064 gb KRH5939 0.1 ;gi 947111063 gb KRH59389.1 ;gi 356512722 ref XP_0 03525065.1 /O;0;0;0//hypothetical protein GLYMA_05G180600 [Glycine max];hypothetical protein GLYMA_05G180600 [Glycine max];hypothetical protein GLYMA_05G180600 [Glycine max];PREDICTED: inositol-3-phosphate synthase [Glycine max]
Glyma.17 G259400	-	-	-	-	-	-	-	-	2.5304	0.00 140 5	984	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko04145//Phagosome	-	GO:0043169//cation binding	-	gi 734351221 gb KHN12631.1 /O/WD repeat and FYVE domain-containing protein 3 [Glycine soja]
Glyma.10 G218400	-	-	-	-	-	-	-	-	2.4082	5.02 E-0 6	5471	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko04145//Phagosome	-	GO:0016301//kinase activity;GO:003255 0	GO:0046488//phosphatidylinositol metabolic process;GO:0019538//protein metabolic process	gi 571484133 ref XP_006589464.1 /O/PREDICTED: putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1D isoform X1 [Glycine max]
Glyma.06 G096300	-	-	-	-	-	-	-	-	2.0648	7.46 E-0 5	3011	ko00562//Inositol phosphate metabolism;ko04140//Regulation of autophagy;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways;ko04145//Phagosome	-	GO:0032550;GO:00 52742	GO:0016192//vesicle-mediated transport;GO:0048017//inositol lipid-mediated signaling;GO:0006661//phosphatid ylinositol biosynthetic process;GO:0006970//response to osmotic stress;GO:0009555//pollen development	gi 734339581 gb KHN08996.1 /O/Phosphatidylinositol 3-kinase, nodule isoform [Glycine soja]
Glyma.19 G158700	-	-	-	-	-	-	-	-	2.0161	0.00 480 7	2946	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways	-	-	GO:0046488//phosphatidylinositol metabolic process	gi 734317079 gb KHN02561.1 ;gi 955389963 ref XP_01462 7585.1 ;gi 947045932 gb KRG95561.1 ;gi 947045936 gb K RG95565.1 ;gi 947045933 gb KRG95562.1 /O;0;0;0//Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 [Glycine soja] ;PREDICTED: type I inositol polyphosphate 5-phosphatase 4-like isoform X1 [Glycine max];hypothetical protein GLYMA_19G158700 [Glycine max];hypothetical protein GLYMA_19G158700 [Glycine max];hypothetical protein GLYMA_19G158700 [Glycine max]
Glyma.06 G013800	-	-	-	-	-	-	-	-	1.9627	2.11 E-0 7	6537	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways	GO:00 05911// cell-cel l unctio n;GO:0 016020 //memb	GO:0016772//transf erase activity, transferring phosphorus-containi ng groups;GO:1902936 ;GO:0003779//actin binding	GO:0046488//phosphatidylinositol metabolic process;GO:0048017//inositol lipid-mediated signaling;GO:0006464//cellular protein modification process	gi 947103164 gb KRH51547.1 ;gi 947103165 gb KRH5154 8.1 /O;0;0//hypothetical protein GLYMA_06G013800 [Glycine max];hypothetical protein GLYMA_06G013800 [Glycine max]

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Glyma.11 G041600	-	-	-	-	-	-	-	-	1.9501	0.00 176 78	3762	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways	-	-	GO:0046488//phosphatidylinositol metabolic process;GO:0043647//inositol phosphate metabolic process;GO:0044707;GO:0044723;GO:0001101//response to acid chemical	gi 571487238 ref XP_006590604.1 ;gi 734408756 gb KHN34863.1 ;gi 947079477 gb KRH28266.1 /0;0;0/PREDICTED: type I inositol polyphosphate 5-phosphatase 2-like [Glycine max];Type I inositol-1,4,5-trisphosphate 5-phosphatase 2 [Glycine soja];hypothetical protein GLYMA_11G041600 [Glycine max]
Glyma.01 G200500	-	-	-	-	-	-	-	-	1.8766	0.00 055 75	2276	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways	-	-	-	gi 947129377 gb KRH77231.1 /0/hypothetical protein GLYMA_01G200500 [Glycine max]
Glyma.20 G173200	-	-	-	-	-	-	-	-	1.8656	0.00 075 83	5623	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko04145//Phagosome	-	GO:0016301//kinase activity;GO:0032550	GO:0046488//phosphatidylinositol metabolic process;GO:0019538//protein metabolic process	gi 571568246 ref XP_006606196.1 /0/PREDICTED: putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1D isoform X1 [Glycine max]
Glyma.18 G018600	-1.302	2.09 E-1 0	-	-	-	-	-	-	1.7651	0.00 743 04	2095	ko00562//Inositol phosphate metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	-	GO:0016872//intra molecular lyase activity	GO:0009642//response to light intensity;GO:0009620//response to fungus;GO:0000302//response to reactive oxygen species;GO:0006020//inositol metabolic process;GO:0009617//response to bacterium;GO:0006658//phosphatid yserine metabolic process;GO:0002252;GO:0007275//multicellular organismal development;GO:0003006//developmental process involved in reproduction;GO:0032958//inositol phosphate biosynthetic process;GO:0006644//phospholipid metabolic process	gi 947048073 gb KRG97601.1 ;gi 947048074 gb KRG97602.1 ;gi 84311235 gb ABC55420.1 ;gi 947048072 gb KRG97600.1 /0;0;0;0/hypothetical protein GLYMA_18G018600 [Glycine max];hypothetical protein GLYMA_18G018600 [Glycine max];myo-inositol-1-phosphate synthase [Glycine max];hypothetical protein GLYMA_18G018600 [Glycine max]
Glyma.20 G013500	-	-	-	-	-	-	-	-	1.6738	5.93 E-0 6	6424	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko04145//Phagosome	-	GO:0043169//cation binding;GO:0016301//kinase activity;GO:0032550	GO:0046488//phosphatidylinositol metabolic process;GO:0019538//protein metabolic process	gi 955392583 ref XP_014628145.1 /0/PREDICTED: putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1C [Glycine max]
Glyma.17 G222600	-	-	-	-	-	-	-	-	1.591	0.00 251 68	4395	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system	-	-	-	gi 947055910 gb KRH05363.1 /0/hypothetical protein GLYMA_17G222600 [Glycine max]
Glyma.07 G273800	-	-	-	-	-	-	-	-	1.5463	0.00 852 08	3844	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways	-	GO:0046030//inositol triphosphate phosphatase activity	GO:0009888//tissue development;GO:0001101//response to acid chemical;GO:0046488//phosphatidylinositol metabolic process;GO:0009416//response to light stimulus;GO:0031667//response to nutrient levels;GO:0009756//carbohydrate mediated signaling;GO:0048878//chemical homeostasis;GO:0044723;GO:0022622//root system development;GO:0006950//response to stress	gi 571468135 ref XP_006584139.1 /0/PREDICTED: type I inositol polyphosphate 5-phosphatase 12-like isoform X2 [Glycine max]
Glyma.07 G216600	-	-	-	-	-	-	-	-	1.5295	7.62 E-0 5	6440	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling	-	GO:0043169//cation binding;GO:0016301//kinase	GO:0046488//phosphatidylinositol metabolic process;GO:0019538//protein	gi 955332007 ref XP_014633654.1 ;gi 947101860 gb KRH50352.1 /0;0/PREDICTED: putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1C

												system;ko04145//Phagosome		activity;GO:0032550	metabolic process	[Glycine max];hypothetical protein GLYMA_07G216600 [Glycine max]
Glyma.17 G102800	-1.159	7.45 E-07	-	-	-	-	-	-	1.5245	0.00 020 29	4611	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidylinositol signaling system	-	-	-	gi 955378570 ref XP_014625002.1 /0/PREDICTED: formin-like protein 20 [Glycine max]
Glyma.06 G089800	-	-	-	-	-	-	-	-	1.423	8.19 E-05	2250	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidylinositol signaling system;ko01100//Metabolic pathways	GO:0044464	GO:0046872//metal ion binding;GO:0051766//inositol trisphosphate kinase activity;GO:0051765//inositol tetrakisphosphate kinase activity;GO:0032550	GO:0043647//inositol phosphate metabolic process	gi 351721983 ref NP_001237484.1 /0/inositol phosphate kinase [Glycine max]
Glyma.08 G276400	-	-	-	-	-	-	-	-	1.3953	0.00 020 09	3700	ko00562//Inositol phosphate metabolism;ko00640//Propanoate metabolism;ko00410//beta-Alanine metabolism;ko01100//Metabolic pathways;ko00280//Valine, leucine and isoleucine degradation	-	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	GO:0008152//metabolic process	gi 955337351 ref XP_014634773.1 ;gi 955337353 ref XP_014634774.1 /0;0/PREDICTED: putative succinate-semialdehyde dehydrogenase C1002.12c [NADP(+)] isoform X1 [Glycine max];PREDICTED: putative succinate-semialdehyde dehydrogenase C1002.12c [NADP(+)] isoform X2 [Glycine max]
Glyma.04 G213400	-	-	-	-	-	-	-	-	1.3361	0.00 047 95	5026	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidylinositol signaling system;ko01100//Metabolic pathways	-	GO:0052742	GO:0046488//phosphatidylinositol metabolic process;GO:0048017//inositol lipid-mediated signaling;GO:0046474//glycerophospholipid biosynthetic process	gi 955317369 ref XP_014630360.1 ;gi 947115746 gb KRH64048.1 ;gi 947115749 gb KRH64051.1 ;gi 571451616 ref XP_006578790.1 /0;0;0/PREDICTED: phosphatidylinositol 4-kinase beta 1-like isoform X2 [Glycine max];hypothetical protein GLYMA_04G213400 [Glycine max];hypothetical protein GLYMA_04G213400 [Glycine max];PREDICTED: phosphatidylinositol 4-kinase beta 1-like isoform X1 [Glycine max]
Glyma.07 G045600	-	-	-	-	-	-	-	-	1.2135	0.00 185 72	7013	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidylinositol signaling system;ko04145//Phagosome	GO:0043231//intracellular membrane-bounded organelle	GO:0043169//cation binding;GO:0032550;GO:0016307//phosphatidylinositol phosphate kinase activity;GO:0016301//kinase activity	GO:0010118//stromal movement;GO:0006996//organelle organization;GO:0046488//phosphatidylinositol metabolic process;GO:0048229//gametophyte development;GO:0019538//protein metabolic process	gi 571464853 ref XP_006583187.1 ;gi 947099221 gb KRH47713.1 ;gi 947099222 gb KRH47714.1 /0;0;0/PREDICTED: 1-phosphatidylinositol-3-phosphate 5-kinase FAB1B-like [Glycine max];hypothetical protein GLYMA_07G045600 [Glycine max];hypothetical protein GLYMA_07G045600 [Glycine max]
Glyma.20 G218600	-	-	-	-	-	-	-	-	1.0042	0.00 435 65	3874	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidylinositol signaling system;ko01100//Metabolic pathways	-	-	GO:0046488//phosphatidylinositol metabolic process	gi 571569653 ref XP_006606425.1 ;gi 947042834 gb KRG92558.1 /0;0/PREDICTED: type II inositol polyphosphate 5-phosphatase 15-like [Glycine max];hypothetical protein GLYMA_20G218600 [Glycine max]
Glyma.08 G086800	-	-	-	-	-	-	-	-	-1.046	0.00 261 45	1665	ko00562//Inositol phosphate metabolism;ko00920//Sulfur metabolism;ko04070//Phosphatidylinositol signaling system;ko01100//Metabolic pathways	-	GO:0008252//nucleotidase activity	GO:0046488//phosphatidylinositol metabolic process	gi 356524978 ref XP_003531104.1 /0/PREDICTED: SAL1 phosphatase [Glycine max]
Glyma.02 G076500	-	-	-	-	-	-	-	-	-1.087	0.00 110 53	1436	ko00562//Inositol phosphate metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	-	GO:0003824//catalytic activity	GO:0044710	gi 356499161 ref XP_003518411.1 /0/PREDICTED: uncharacterized oxidoreductase At4g09670-like [Glycine max]
Glyma.08 G127700	-	-	-	-	-	-	-	-	-1.25	0.00 174 66	3280	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidylinositol signaling system;ko01100//Metabolic pathways;ko04144//Endocytosis	GO:0016020//membrane	GO:0016307//phosphatidylinositol phosphate kinase activity;GO:0032550	GO:0046488//phosphatidylinositol metabolic process	gi 356525381 ref XP_003531303.1 ;gi 571471155 ref XP_006585224.1 /0;0/PREDICTED: phosphatidylinositol 4-phosphate 5-kinase 7 isoform X1 [Glycine max];PREDICTED: phosphatidylinositol 4-phosphate 5-kinase 7 isoform X2 [Glycine max]

Glyma.14 G072200	-	-	-	-	-	-	-	-	-1.278	0.00 055 07	2575	ko00562//Inositol phosphate metabolism;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways	-	GO:0032550;GO:0051765//inositol tetrakisphosphate kinase activity	GO:0072502;GO:0009620//response to fungus;GO:0009617//response to bacterium;GO:0002252;GO:0032958//inositol phosphate biosynthetic process	gi 351727917 ref NP_001237433.1 /0/inositol pentakisphosphate 2-kinase [Glycine max]
Glyma.09 G011100	-	-	-	-	-	-	-	-	-1.507	0.00 123 27	1825	ko00562//Inositol phosphate metabolism;ko00053//Ascorbate and aldarate metabolism;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:0044444; GO:0016020//membrane	GO:0070456	GO:0019852//L-ascorbic acid metabolic process;GO:0046488//phosphatidylinositol metabolic process;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress	gi 734420434 gb KHN40821.1 ;gi 947087895 gb KRH36560.1 /0;4.89277e-157/Inositol monophosphatase 3 [Glycine soja] ;hypothetical protein GLYMA_09G011100 [Glycine max]
Glyma.11 G238800	-2.591	2.28 E-2 3	-3.016	4.24 E-1 3	-2.786	2.93 E-1 8	-2.887	2.17 E-1 4	-3.459	2.19 E-1 8	1945	ko00562//Inositol phosphate metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	-	GO:0016872//intramolecular lyase activity	GO:0009642//response to light intensity;GO:0009620//response to fungus;GO:0000302//response to reactive oxygen species;GO:0006020//inositol metabolic process;GO:0009617//response to bacterium;GO:0006658//phosphatidylserine metabolic process;GO:0002252;GO:0007275//multicellular organismal development;GO:0003006//developmental process involved in reproduction;GO:0032958//inositol phosphate biosynthetic process	gi 14764466 gb AAK72098.1 /0/myo-inositol-1-phosphate synthase [Glycine max]
Glyma.06 G213600	-5.258	### ### #	-5.849	1.29 E-4 3	-5.948	1.71 E-4 4	-4.886	1.05 E-1 4	-4.317	6.58 E-1 3	5148	ko00562//Inositol phosphate metabolism;ko03008//Ribosome biogenesis in eukaryotes;ko04070//Phosphatid ylinositol signaling system;ko01100//Metabolic pathways;ko04144//Endocytosis;ko04712//Circadian rhythm - plant	-	-	-	gi 947106465 gb KRH54848.1 /1.00594e-90/hypothetical protein GLYMA_06G213600 [Glycine max]

Supplementary Table S5: DEGs involved in photosynthesis

GeneID	log2Ratio (2mlpa-1/ 2MWT-1)	P-value	log2Ratio (2mlpa-2/ 2MWT-2)	P-value	log2Ratio (2mlpa-3/ 2MWT-3)	P-value	log2Ratio (2mlpa-4/ 2MWT-4)	P-value	log2Ratio (2mlpa-5/ 2MWT-5)	P-value	Length	Pathway	GO Component	GO Function	GO Process	Blast nr
Glyma.01 G050900	-2.3292	6.20E-06	-	-	-	-	-	-	-	-	936	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031976;GO:0009523//photosystem II	GO:0046872//metal ion binding;GO:0009055//electron carrier activity	GO:0022900//electron transport chain	gi 571434179 ref XP_003518016.2 /6.70419e-155/PR EDICTED: photosynthetic NDH subunit of luminal location 2, chloroplastic [Glycine max]
Glyma.01 G095900	-1.5306	4.04E-05	3.87635	1.67E-18	3.59217	1.29E-08	2.51069	1.12E-05	-	-	293	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009523//photosystem II;GO:0009507//chloroplast	-	GO:0015979//photosynthesis	gi 947127748 gb KRH75602.1 /3.04979e-23/hypothetical protein GLYMA_01G095900 [Glycine max]
Glyma.01 G153500	-1.5333	0.00125	3.85582	3.35E-13	4.15308	2.55E-09	2.95855	2.13E-05	-	-	750	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0009767//photosynthetic electron transport chain	gi 947128606 gb KRH76460.1 /0/hypothetical protein GLYMA_01G153500 [Glycine max]
Glyma.05 G073600	-	-	8.09189	2.08E-11	-	-	-	-	-	-	426	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0043231//intracellular membrane-bounded organelle	GO:0009055//electron carrier activity	GO:0009767//photosynthetic electron transport chain	gi 947109303 gb KRH57629.1 /2.58432e-118/hypothetical protein GLYMA_05G073600 [Glycine max]
Glyma.06 G217900	-2.0852	1.18E-07	3.69572	1.00E-14	4.21351	4.04E-15	3.21924	5.21E-08	-	-	507	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0009767//photosynthetic electron transport chain	gi 947106520 gb KRH54903.1 /3.69129e-118/hypothetical protein GLYMA_06G217900 [Glycine max]
Glyma.06 G224500	-	-	4.46157	1.14E-19	7.11534	1.38E-10	-	-	-	-	279	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0006464//cellular protein modification process;GO:0044710	gi 947106622 gb KRH55005.1 /1.83252e-63/hypothetical protein GLYMA_06G224500, partial [Glycine max]
Glyma.06 G229000	-2.3822	0.00074	2.7897	6.89E-09	4.99319	2.86E-10	-	-	-	-	417	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0033177//proton-transporting two-sector ATPase complex, proton-transporting domain;GO:0009534//chloroplast thylakoid	GO:0015077//monovalent inorganic cation transmembrane transporter activity;GO:0005488	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient;GO:0006754//ATP biosynthetic process	gi 947106696 gb KRH55079.1 /4.411e-37/hypothetical protein GLYMA_06G229000 [Glycine max]
Glyma.07 G143800	-	-	5.05164	5.42E-27	6.50017	9.31E-13	-	-	-	-	348	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0006464//cellular protein modification process;GO:0044710	gi 734395058 gb KHN28788.1 /1.56572e-70/Photosystem I P700 chlorophyll a apoprotein A1 [Glycine soja]

Glyma.08 G281300	-	-	3.99838	1.12E-19	5.44119	4.16E-20	2.99514	0.000186	-	-	324	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0034357;GO:0009536//plastid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process;GO:0022900//electron transport chain	gi 947096990 gb KRH4557.1 /1.40663e-74/hypothetical protein GLYMA_08G281300 [Glycine max]
Glyma.08 G363500	-1.3542	0.00236	4.01677	3.47E-16	3.98983	2.10E-09	2.57728	0.000109	-	-	621	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0034357	-	-	gi 947098318 gb KRH4690.3.1 /1.44663e-19/hypothetical protein GLYMA_08G363500 [Glycine max]
Glyma.11 G162200	-	-	3.7818	1.29E-19	3.51122	2.59E-09	1.71363	0.000303	-	-	699	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane	GO:0043169//cation binding;GO:0009055//electron carrier activity	GO:0009767//photosynthetic electron transport chain	gi 947081354 gb KRH3014.3.1 /9.45488e-155/hypothetical protein GLYMA_11G162200, partial [Glycine max]
Glyma.12 G169400	-1.3582	0.00317	-	-	-	-	-	-	-	-	1122	ko00195//Photosynthesis	GO:0009536//plastid	GO:0005488	-	gi 947077519 gb KRH2635.9.1 /3.82053e-90/hypothetical protein GLYMA_12G169400 [Glycine max]
Glyma.12 G202500	-	-	-	-	1.34376	0.0005	1.30934	4.46E-05	-	-	1010	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009534//chloroplast thylakoid	-	GO:0019684//photosynthesis, light reaction	gi 356543813 ref XP_003540354.1 /6.4337e-96/PREDICTED: photosystem II repair protein PSB27-H1, chloroplastic-like [Glycine max]
Glyma.12 G232700	-	-	5.52159	6.31E-28	5.20226	1.29E-10	3.29685	1.83E-06	-	-	429	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0009523//photosystem II;GO:0009534//chloroplast thylakoid	GO:0046914//transition metal ion binding;GO:0032550;GO:0016421//CoA carboxylase activity;GO:0046906//tetrapyrrole binding	GO:0015937//coenzyme A biosynthetic process;GO:0006351//transcription, DNA-templated;GO:0022900//electron transport chain;GO:0009765//photosynthesis, light harvesting;GO:0006631//fatty acid metabolic process	gi 947078548 gb KRH2738.8.1 /1.04111e-99/hypothetical protein GLYMA_12G232700 [Glycine max]
Glyma.13 G028200	-	-	3.83427	1.88E-21	2.99907	6.70E-06	1.79323	0.000164	-	-	816	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046914//transition metal ion binding;GO:0009055//electron carrier activity;GO:0003824//catalytic activity	GO:0006950//response to stress;GO:0009767//photosynthetic electron transport chain	gi 947069046 gb KRH1793.7.1 /0/hypothetical protein GLYMA_13G028200, partial [Glycine max]
Glyma.13 G088500	-	-	3.65135	7.24E-09	5.60027	5.33E-11	-	-	-	-	240	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0009534//chloroplast thylakoid	GO:0043169//cation binding;GO:0051536//iron-sulfur cluster binding;GO:0050136//NADH dehydrogenase (quinone) activity	GO:0009767//photosynthetic electron transport chain;GO:0022904//respiratory electron transport chain	gi 947070006 gb KRH1889.7.1 /6.89746e-54/hypothetical protein GLYMA_13G088500 [Glycine max]
Glyma.15 G114600	-1.4907	0.00038	3.91924	1.25E-19	5.49734	2.01E-20	3.02382	2.57E-05	-	-	1190	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0034357;GO:0009534//chloroplast thylakoid	GO:0009055//electron carrier activity;GO:0003824//catalytic activity	GO:0022900//electron transport chain	gi 947062266 gb KRH1152.7.1 /2.61757e-86/hypothetical protein GLYMA_15G114600 [Glycine max]
Glyma.15 G126100	-	-	4.07773	5.53E-20	4.93214	4.03E-10	3.73562	1.91E-07	-	-	363	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	-	GO:0044237//cellular metabolic process	gi 91214162 ref YP_53878.4.1 /4.7294e-24/photosystem I subunit IX [Glycine max]

Glyma.15 G208300	-	-	3.13165	5.67E-07	-	-	-	-	-	-	273	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	-	GO:0006091//generation of precursor metabolites and energy	gi 763745629 gb KJB1306.8.1 /1.93912e-15/hypothetical protein B456_002G055100 [Gossypium raimondii]
Glyma.15 G248600	-	-	3.14569	2.14E-09	2.81734	7.23E-05	-	-	-	-	342	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009536//plastid;GO:0009523//photosystem II	-	GO:0044237//cellular metabolic process	gi 947064317 gb KRH1357.8.1 /5.67331e-75/hypothetical protein GLYMA_15G248600 [Glycine max]
Glyma.17 G186400	-	-	3.90764	5.61E-08	5.2486	1.19E-08	-	-	-	-	207	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0043168//anion binding	GO:0044237//cellular metabolic process;GO:0031647//regulation of protein stability	gi 947055325 gb KRH0477.8.1 /3.72484e-44/hypothetical protein GLYMA_17G186400 [Glycine max]
Glyma.19 G054200	-2.0822	0.00014	2.22477	0.00014	4.32237	2.30E-06	-	-	-	-	318	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0033177//proton-transporting two-sector ATPase complex, proton-transporting domain;GO:0009534//chloroplast thylakoid	GO:0019829//cation-transporting ATPase activity;GO:0015077//monovalent inorganic cation transmembrane transporter activity	GO:0015986//ATP synthesis coupled proton transport	gi 947044351 gb KRG9398.0.1 /2.03094e-59/hypothetical protein GLYMA_19G054200 [Glycine max]
Glyma.20 G020600	1.57644	0.00398	-	-	-	-	-	-	-	-	925	ko00195//Photosynthesis	-	-	-	gi 571563659 ref XP_006605511.1 ;gi 955391318 ref XP_014627811.1 /1.21678e-120;1.45013e-102/PREDICTED: chloroplastic-like isoform X1 [Glycine max];PREDICTED: uncharacterized protein LOC100797820 isoform X2 [Glycine max]
Glyma.05 G099200	-2.654	3.46E-07	2.68556	1.85E-09	4.99906	1.21E-11	-	-	5.82843	3.79E-06	271	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0033177//proton-transporting two-sector ATPase complex, proton-transporting domain;GO:0009534//chloroplast thylakoid;GO:0009526//plastid envelope	GO:0015077//monovalent inorganic cation transmembrane transporter activity;GO:0005488	GO:0019684//photosynthesis, light reaction;GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient;GO:0006351//transcription, DNA-templated;GO:0006754//ATP biosynthetic process	gi 947109669 gb KRH5799.5.1 /7.86592e-52/hypothetical protein GLYMA_05G099200, partial [Glycine max]
Glyma.04 G095000	-2.2576	1.16E-07	3.87018	1.64E-15	4.11517	3.22E-14	3.56279	9.79E-11	4.10345	1.81E-06	711	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0043231//intracellular membrane-bounded organelle	GO:0043169//cation binding;GO:0009055//electron carrier activity	GO:0009767//photosynthetic electron transport chain	gi 947113933 gb KRH6223.5.1 /1.4233e-107/hypothetical protein GLYMA_04G095000 [Glycine max]
Glyma.12 G231900	-2.3851	8.45E-10	3.23154	1.60E-14	4.88738	3.62E-18	2.43866	0.000212	3.81275	1.12E-08	384	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0033177//proton-transporting two-sector ATPase complex, proton-transporting domain;GO:0009534//chloroplast thylakoid	GO:0032550;GO:0019829//cation-transporting ATPase activity;GO:0015077//monovalent inorganic cation transmembrane transporter activity	GO:0006818//hydrogen transport;GO:0006754//ATP biosynthetic process	gi 947078540 gb KRH2738.0.1 /1.10934e-66/hypothetical protein GLYMA_12G231900, partial [Glycine max]

Glyma.19 G109600	-2.573	1.09E-07	2.83652	3.41E-16	4.74518	2.94E-15	-	-	3.76104	1.27E-07	423	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0033177//proton-transporting two-sector ATPase complex, proton-transporting domain;GO:0009534//chloroplast thylakoid;GO:0009526//plastid envelope	GO:0019829//cation-transporting ATPase activity;GO:0015077//monovalent inorganic cation transmembrane transporter activity;GO:0005488	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient;GO:0015986//ATP synthesis coupled proton transport	gi 947045161 gb KRG94790.1 /9.26156e-42/hypothetical protein GLYMA_19G109600 [Glycine max]
Glyma.U0 16600	-	-	4.76174	6.26E-31	6.62145	1.61E-16	2.84707	0.000285	3.61362	0.00092	375	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding;GO:0046872//metal ion binding;GO:0051536//iron-sulfur cluster binding;GO:0003824//catalytic activity	GO:0006464//cellular protein modification process;GO:0044710	gi 947039131 gb KRG88966.1 /8.09939e-73/hypothetical protein GLYMA_U016600, partial [Glycine max]
Glyma.12 G232900	-2.3642	7.63E-21	3.57447	1.91E-19	5.67099	5.36E-20	2.3048	0.000369	3.57215	7.80E-09	1912	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0034357;GO:0009534//chloroplast thylakoid;GO:0016021//integral component of membrane	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding	GO:0044237//cellular metabolic process;GO:0044710	gi 91214155 ref YP_538777.1 /0/cytochrome f [Glycine max]
Glyma.12 G232500	-2.3405	3.08E-08	4.62078	2.89E-23	5.63807	2.47E-16	3.32027	1.64E-07	3.17592	0.00038	1023	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0034357;GO:0031224//intrinsic component of membrane;GO:0009532//plastid stroma;GO:0009534//chloroplast thylakoid	GO:0009055//electron carrier activity;GO:0043169//cation binding	GO:0019684//photosynthesis, light reaction;GO:0006351//transcription, DNA-templated;GO:0006412//translation;GO:0022900//electron transport chain;GO:0010038//response to metal ion;GO:0043623//cellular protein complex assembly;GO:0055076//transition metal ion homeostasis;GO:0009416//response to light stimulus	gi 11465978 ref NP_054520.1 /6.06418e-18/cytochrome b6/f complex subunit V [Nicotiana tabacum]
Glyma.01 G058600	-1.8677	1.42E-05	3.96422	1.97E-18	5.64774	4.80E-19	3.38744	2.16E-05	2.94009	0.00323	463	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0034357;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding;GO:0009055//electron carrier activity;GO:0003824//catalytic activity	GO:0022900//electron transport chain	gi 947127189 gb KRH75043.1 /2.29292e-78/hypothetical protein GLYMA_01G058600 [Glycine max]
Glyma.11 G114700	-1.6986	9.96E-06	3.78507	4.79E-17	4.29086	4.91E-13	2.74467	1.36E-07	2.5227	0.00244	408	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0034357;GO:0009536//plastid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process;GO:0022900//electron transport chain	gi 947080624 gb KRH29413.1 /2.22449e-94/hypothetical protein GLYMA_11G114700 [Glycine max]
Glyma.09 G090100	-1.3311	0.00415	4.85917	5.25E-26	6.41069	2.84E-13	4.45229	9.97E-08	2.52239	0.00569	558	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009536//plastid	-	GO:0044237//cellular metabolic process	gi 947089135 gb KRH37800.1 /7.49414e-119/hypothetical protein GLYMA_09G090100, partial [Glycine max]

Glyma.12 G096200	-2.6199	9.59E-15	2.01925	2.75E-08	4.32398	4.17E-12	-	-	2.46085	0.0001	318	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0033177//proton-transporting two-sector ATPase complex, proton-transporting domain;GO:0009534//chloroplast thylakoid	GO:0019829//cation-transporting ATPase activity;GO:0015077//monovalent inorganic cation transmembrane transporter activity	GO:0015986//ATP synthesis coupled proton transport	gi 947076502 gb KRH2534.2.1 /4.62789e-71/hypothetical protein GLYMA_12G096200, partial [Glycine max]
Glyma.12 G232000	-1.7611	9.52E-09	3.48479	3.66E-18	4.64109	5.21E-17	2.41548	3.46E-05	2.15131	2.10E-05	2784	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0033178//proton-transporting two-sector ATPase complex, catalytic domain;GO:0019866//organelle inner membrane;GO:0009534//chloroplast thylakoid	GO:0032550;GO:0019829//cation-transporting ATPase activity;GO:0015078//hydrogen ion transmembrane transporter activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient;GO:0015986//ATP synthesis coupled proton transport	gi 947078541 gb KRH2738.1.1 /0/hypothetical protein GLYMA_12G232000 [Glycine max]
Glyma.05 G074900	-1.8033	1.74E-06	3.92446	4.56E-17	4.21531	2.83E-13	3.45592	1.25E-09	2.06823	0.00579	439	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0016020//membrane;GO:0044424	-	GO:0044237//cellular metabolic process	gi 947109318 gb KRH5764.4.1 /8.28695e-19/hypothetical protein GLYMA_05G074900 [Glycine max]
Glyma.04 G066000	-	-	-	-	-	-	-	-	-1.0766	0.00597	1289	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0044434;GO:0044425;GO:0009579//thylakoid	-	GO:0044765	gi 351722297 ref NP_001237239.1 /7.45658e-115/unc characterized protein LOC100527009 [Glycine max]
Glyma.18 G241700	-	-	-	-	-	-	1.09562	0.00037	-1.1212	0.00138	1010	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009526//plastid envelope;GO:0031976;GO:0009570//chloroplast stroma;GO:0009522//photosystem I	-	GO:0044237//cellular metabolic process	gi 351724071 ref NP_001236277.1 /7.26819e-124/unc characterized protein LOC100500317 [Glycine max]
Glyma.11 G077600	-	-	-	-	-	-	-	-	-1.1864	0.00112	1442	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009526//plastid envelope;GO:0031976;GO:0044436;GO:0005576//extracellular region	GO:0009055//electron carrier activity;GO:0008187//poly-pyrimidine tract binding;GO:0003824//catalytic activity	GO:0009617//response to bacterium;GO:0022900//electron transport chain	gi 734422972 gb KHN4189.3.1 /0/Ferredoxin--NADP reductase, leaf isozyme, chloroplastic [Glycine soja]
Glyma.16 G127300	-	-	-	-	-	-	-	-	-1.1959	0.0074	1628	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009526//plastid envelope;GO:0031976;GO:0044436;GO:0005576//extracellular region	GO:0009055//electron carrier activity;GO:0008187//poly-pyrimidine tract binding;GO:0003824//catalytic activity;GO:0016731//oxidoreductase activity, acting on iron-sulfur proteins as donors, NAD or NADP as acceptor	GO:0009617//response to bacterium;GO:0022900//electron transport chain	gi 356559282 ref XP_003547929.1 ;gi 947058656 gb KRH08062.1 /0/PREDICTED: ferredoxin--NADP reductase, leaf isozyme, chloroplastic [Glycine max];hypothetical protein GLYMA_16G127300 [Glycine max]
Glyma.12 G089200	-	-	-	-	-	-	-	-	-1.2263	0.00141	784	ko00195//Photosynthesis	-	GO:0051536//iron-sulfur cluster binding;GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 351721230 ref NP_001238738.1 /2.55515e-92/unc characterized protein LOC100499711 [Glycine max]
Glyma.01 G238000	-	-	-	-	-	-	-	-	-1.2355	0.00761	818	ko00195//Photosynthesis	GO:0009536//plastid	GO:0051536//iron-sulfur cluster binding;GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 351725193 ref NP_001236060.1 /2.57228e-92/unc characterized protein LOC100500300 [Glycine

																	max]
Glyma.20 G110800	-	-	-	-	-	-	-	-	-	-1.3455	0.00089	988	ko00195//Photosynthesis	-	GO:0051536//iron-sulfur cluster binding;GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 351727909 ref NP_001236409.1 /2.3486e-111/uncharacterized protein LOC100500583 [Glycine max]
Glyma.13 G302900	-	-	-	-	-	-	-	-	-	-1.4536	0.00261	1060	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0009526//plastid envelope;GO:0031976;GO:0034357	GO:0043169//cation binding;GO:0015078//hydrogen ion transmembrane transporter activity;GO:0051536//iron-sulfur cluster binding;GO:0009055//electron carrier activity;GO:0052880	GO:1990066;GO:0044710;GO:0009617//response to bacterium;GO:0044237//cellular metabolic process;GO:0015992//proton transport	gi 947073587 gb KRH22478.1 ;gi 734413144 gb KHN36589.1 /1.21441e-85;1.16363e-156/hypothetical protein GLYMA_13G302900 [Glycine max];Cytochrome b6-f complex iron-sulfur subunit, chloroplastic [Glycine soja]
Glyma.20 G098500	-	-	-	-	-	-	-	-	-	-1.4605	0.00043	1412	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009523//photosystem II	GO:0046872//metal ion binding	GO:0044237//cellular metabolic process	gi 947040828 gb KRG90552.1 /0/hypothetical protein GLYMA_20G098500 [Glycine max]
Glyma.10 G042100	-	-	-	-	-	-	-	-	-	-1.4816	0.00025	1020	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0044434;GO:0009522//photosystem I	-	-	gi 351727413 ref NP_001236392.1 /1.41727e-61/uncharacterized protein LOC100499814 [Glycine max]
Glyma.08 G126800	-	-	-	-	-	-	-	-	-	-1.5198	2.97E-05	1086	ko00195//Photosynthesis	GO:0009536//plastid	GO:0043169//cation binding;GO:0051536//iron-sulfur cluster binding	GO:0022900//electron transport chain	gi 351720711 ref NP_001235138.1 /1.61599e-102/uncharacterized protein LOC100305932 [Glycine max]
Glyma.04 G215800	-	-	-	-	-	-	-	-	-	-1.5303	0.00103	1219	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009522//photosystem I;GO:0009534//chloroplast thylakoid;GO:0034357;GO:0009507//chloroplast;GO:0009579//thylakoid	GO:0005515//protein binding	GO:0006007//glucose catabolic process;GO:0006470//protein dephosphorylation;GO:0000097//sulfur amino acid biosynthetic process;GO:0009767//photosynthetic electron transport chain	gi 947115793 gb KRH64095.1 ;gi 947115794 gb KRH64096.1 ;gi 947115791 gb KRH64093.1 ;gi 351722715 ref NP_001235206.1 /1.61686e-78;4.64534e-50;3.80265e-116;6.1549e-101/hypothetical protein GLYMA_04G215800 [Glycine max];hypothetical protein GLYMA_04G215800 [Glycine max];hypothetical protein GLYMA_04G215800 [Glycine max];uncharacterized protein LOC100499729 [Glycine max]
Glyma.15 G016300	-	-	-	-	-	-	-	-	-	-1.5452	0.00413	1316	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031976;GO:0009570//chloroplast stroma;GO:0009522//photosystem I	-	GO:0044237//cellular metabolic process	gi 358248194 ref NP_001240092.1 /1.2461e-69/uncharacterized protein LOC100776789 [Glycine max]
Glyma.06 G150300	-	-	-	-	-	-	-	-	-	-1.5564	7.67E-05	1140	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0009534//chloroplast thylakoid;GO:0034357	GO:0005515//protein binding	GO:0044237//cellular metabolic process	gi 947105477 gb KRH53860.1 ;gi 351725111 ref NP_001236569.1 /2.80026e-87;1.3001e-109/hypothetical protein GLYMA_06G150300 [Glycine

																	max];uncharacterized protein LOC100306036 [Glycine max]
Glyma.08 G173700	-	-	-	-	-	-	-	-	-1.5775	2.26E-05	874	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009523//photosystem II;GO:0009534//chloroplast thylakoid	-	GO:0010207//photosystem II assembly	gi 351722140 ref NP_001235442.1 /2.65135e-85/uncharacterized protein LOC100499745 [Glycine max]	
Glyma.01 G180800	-	-	-	-	-	-	-	-	-1.5797	4.72E-06	1339	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0009523//photosystem II;GO:0019867//outer membrane	GO:0046872//metal ion binding	GO:0042548//regulation of photosynthesis, light reaction	gi 359806573 ref NP_001241522.1 /0/uncharacterized protein LOC100820458 [Glycine max]	
Glyma.05 G172300	-	-	-	-	-	-	-	-	-1.5846	7.39E-06	1447	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0044425	-	-	gi 359806150 ref NP_001240940.1 /3.50724e-96/uncharacterized protein LOC100779397 [Glycine max]	
Glyma.09 G250800	-	-	-	-	-	-	-	-	-1.6018	2.64E-05	1307	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009526//plastid envelope;GO:0031976;GO:0009570//chloroplast stroma;GO:0009522//photosystem I	-	GO:0044237//cellular metabolic process	gi 351726365 ref NP_001236868.1 /2.01874e-134/uncharacterized protein LOC100527240 [Glycine max]	
Glyma.10 G032200	-	-	-	-	-	-	1.55529	2.58E-06	-1.6047	9.86E-06	1332	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0016020//membrane;GO:0044424	-	-	gi 351721030 ref NP_001236684.1 /2.08586e-35/uncharacterized protein LOC100305788 [Glycine max]	
Glyma.15 G253700	-	-	-	-	-	-	-	-	-1.6737	7.91E-06	840	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009523//photosystem II;GO:0009534//chloroplast thylakoid	-	GO:0010207//photosystem II assembly	gi 351722402 ref NP_001236219.1 /1.48811e-84/uncharacterized protein LOC100305752 [Glycine max]	
Glyma.02 G047600	-	-	-	-	-	-	-	-	-1.6875	0.00759	1494	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009526//plastid envelope;GO:0031976;GO:0044436;GO:0005576//extracellular region	GO:0016731//oxidoreductase activity, acting on iron-sulfur proteins as donors, NAD or NADP as acceptor;GO:0009055//electron carrier activity;GO:0008187//polypyrimidine tract binding	GO:0009617//response to bacterium;GO:0022900//electron transport chain	gi 734312293 gb KHN00471.1 /0/Ferredoxin--NADP reductase, leaf isozyme, chloroplastic [Glycine soja]	
Glyma.04 G112800	-	-	-	-	-	-	-	-	-1.6901	3.70E-05	1366	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009522//photosystem I;GO:0009526//plastid envelope;GO:0031976	GO:0046906//tetrapyrrole binding	GO:0009767//photosynthetic electron transport chain;GO:0031647//regulation of protein stability;GO:0042548//regulation of photosynthesis, light reaction;GO:0006740//NADPH regeneration	gi 351722743 ref NP_001236650.1 /6.49139e-99/uncharacterized protein LOC100305786 [Glycine max]	
Glyma.11 G183300	-	-	-	-	-	-	-	-	-1.6983	0.0003	1620	ko00195//Photosynthesis	-	GO:0051536//iron-sulfur cluster binding;GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 359807123 ref NP_001241349.1 /2.88363e-100/uncharacterized protein LOC100785611 [Glycine max]	

Glyma.10 G249000	-	-	-	-	-	-	-	-	-1.7228	9.50E-06	1706	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009526//plastid envelope;GO:0031976;GO:0009570//chloroplast stroma;GO:0009522//photosystem I	-	GO:0044237//cellular metabolic process	gi 351727030 ref NP_001235355.1 /5.09919e-130 photosystem I subunit Psd [Glycine max]
Glyma.15 G194300	-	-	-	-	-	-	-	-	-1.7228	2.15E-06	1577	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521	GO:0046906//tetrapyrrole binding	GO:0044237//cellular metabolic process	gi 734325419 gb KHN05287.1 /2.64334e-76 Photosystem I reaction center subunit psak, chloroplastic [Glycine soja]
Glyma.20 G144700	-	-	-	-	-	-	1.38717	1.16E-05	-1.7241	9.00E-06	2825	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009526//plastid envelope;GO:0031976;GO:0009570//chloroplast stroma;GO:0009522//photosystem I	-	GO:0044237//cellular metabolic process	gi 734361807 gb KHN15781.1 ;gi 947041551 gb KRG91275.1 /4.18381e-149;2.80762e-107 Photosystem I reaction center subunit II, chloroplastic [Glycine soja] ;hypothetical protein GLYMA_20G144700 [Glycine max]
Glyma.13 G299200	-	-	-	-	-	-	-	-	-1.7771	4.73E-06	982	ko00195//Photosynthesis;ko01100//Metabolic pathways	-	-	GO:0019684//photosynthesis, light reaction	gi 356549934 ref XP_003543345.1 /3.90749e-87 PRE-DICTED: photosystem II repair protein PSB27-H1, chloroplastic-like [Glycine max]
Glyma.13 G127200	-	-	-	-	-	-	-	-	-1.81	0.00045	1027	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009523//photosystem II	-	GO:0044237//cellular metabolic process	gi 734438132 gb KHN48946.1 /1.42389e-120 Photosystem II reaction center PSB28 protein, chloroplastic [Glycine soja]
Glyma.18 G114900	-	-	-	-	-	-	-	-	-1.8659	0.00807	1323	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009523//photosystem II;GO:0009534//chloroplast thylakoid	GO:0046872//metal ion binding	GO:0044237//cellular metabolic process	gi 734394466 gb KHN28540.1 /0/Oxygen-evolving enhancer protein 2, chloroplastic [Glycine soja]
Glyma.05 G022900	-	-	-	-	-	-	-	-	-1.8739	1.98E-07	1212	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009522//photosystem I	-	-	gi 356511909 ref XP_003524664.1 /1.03197e-134 PRE-DICTED: photosystem I reaction center subunit III, chloroplastic [Glycine max]
Glyma.11 G181100	-	-	-	-	-	-	1.04059	0.001002	-1.8837	6.96E-06	826	ko00195//Photosynthesis	-	-	-	gi 351734544 ref NP_001236146.1 /7.06598e-79 uncharacterized protein LOC100305746 [Glycine max]
Glyma.09 G087700	-	-	-	-	-	-	-	-	-1.8851	0.00079	842	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521	GO:0046906//tetrapyrrole binding	GO:0044237//cellular metabolic process	gi 734421586 gb KHN41353.1 /8.16956e-79 Photosystem I reaction center subunit psak, chloroplastic [Glycine soja]
Glyma.17 G154900	-	-	-	-	-	-	-	-	-1.9216	0.00013	950	ko00195//Photosynthesis	GO:0009536//plastid	GO:0051536//iron-sulfur cluster binding;GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 356565441 ref XP_003550948.1 /9.65017e-122 PRE-DICTED: ferredoxin-2-like [Glycine max]
Glyma.06 G067400	-	-	-	-	-	-	-	-	-1.936	2.36E-06	1358	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0033177//proton-transporting two-sector ATPase complex, proton-transporting domain;GO:0009534//chloroplast thylakoid	GO:1901363;GO:0036094//small molecule binding;GO:0015077//monovalent inorganic cation transmembrane transporter	GO:0006818//hydrogen transport;GO:0006754//ATP biosynthetic process	gi 571459243 ref XP_006581353.1 /5.72054e-113 PRE-DICTED: ATP synthase subunit b', chloroplastic-like [Glycine max]

														activity:GO:0097159//organic cyclic compound binding		
Glyma.11 G061300	-	-	-	-	-	-	-	-	-1.9456	1.02E-08	1703	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0009523//photosystem II;GO:0019867//outer membrane	GO:0046872//metal ion binding	GO:0042548//regulation of photosynthesis, light reaction	gi 358249094 ref NP_001239736.1 /0/uncharacterized protein LOC100798485 [Glycine max]
Glyma.06 G020400	-	-	-	-	-	-	-	-	-1.9641	8.07E-07	1253	ko00195//Photosynthesis	GO:0031976;GO:0044436;GO:0044434	-	-	gi 351727401 ref NP_001238695.1 /2.34942e-87/uncharacterized protein LOC100499708 [Glycine max]
Glyma.05 G112100	-	-	-	-	-	-	-	-	-1.9851	8.75E-07	839	ko00195//Photosynthesis	GO:0009536//plastid	GO:0051536//iron-sulfur cluster binding;GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 955320478 ref XP_003524714.3;gi 947109880 gb KRH58206.1;gi 947109881 gb KRH58207.1 /3.96943e-122;3.11608e-115;4.2284e-105/PREDICTED:ferredoxin-2-like isoform X2 [Glycine max];hypothetical protein GLYMA_05G112100 [Glycine max];hypothetical protein GLYMA_05G112100 [Glycine max]
Glyma.11 G245400	-	-	-	-	-	-	1.7987	1.35E-07	-2.0021	0.00605	1001	ko00195//Photosynthesis;ko01100//Metabolic pathways	-	-	-	gi 356540203 ref XP_003538579.1 /3.7911e-68/PREDICTED: photosystem II core complex proteins psbY, chloroplastic-like [Glycine max]
Glyma.12 G092000	-	-	-	-	-	-	-	-	-2.0302	5.95E-06	831	ko00195//Photosynthesis	-	-	-	gi 571492781 ref XP_006592347.1 /8.1433e-90/PREDICTED: photosystem I subunit O [Glycine max]
Glyma.02 G141700	-	-	-	-	-	-	-	-	-2.0322	2.37E-06	771	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0044424	-	-	gi 947123122 gb KRH71328.1 /2.16326e-65/hypothetical protein GLYMA_02G141700 [Glycine max]
Glyma.13 G129400	-	-	-	-	-	-	-	-	-2.0393	9.93E-06	757	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0044434;GO:0009522//photosystem I	-	-	gi 351722581 ref NP_001236993.1 /5.52099e-62/uncharacterized protein LOC100526993 [Glycine max]
Glyma.14 G031800	-	-	-	-	-	-	-	-	-2.0778	1.32E-07	1121	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid;GO:0009523//photosystem II;GO:0005576//extracellular region	GO:0008187//polypyrimidine tract binding;GO:0046872//metal ion binding	GO:0009617//response to bacterium;GO:004237//cellular metabolic process	gi 214011454 gb ACJ61477.1 /0/oxygen-evolving enhancer protein 2 [Glycine max]
Glyma.03 G114600	-	-	-	-	-	-	-	-	-2.0798	5.46E-06	1073	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009523//photosystem II	GO:0046872//metal ion binding	GO:0044237//cellular metabolic process	gi 351727615 ref NP_001236143.1 /6.80492e-156/uncharacterized protein LOC100499794 [Glycine max]

Glyma.06 G321900	-1.0182	2.38E-07	-	-	-	-	-	-	-2.0799	1.53E-07	785	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009522//photosystem I;GO:0009526//plastid envelope;GO:0031976	GO:0046906//tetrapyrrole binding	GO:0009767//photosynthetic electron transport chain;GO:0031647//regulation of protein stability;GO:0042548//regulation of photosynthesis, light reaction;GO:0006740//NADPH regeneration	gi 351725243 ref NP_001235038.1 /2.09257e-113/unc characterized protein LOC100499718 [Glycine max]
Glyma.07 G112000	-	-	-	-	-	-	-	-	-2.1165	5.57E-08	1062	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031976;GO:0009523//photosystem II;GO:0009532//plastid stroma	GO:0046872//metal ion binding	GO:0044237//cellular metabolic process	gi 214011474 gb ACJ61487.1 ;gi 947100285 gb KRH48777.1 /3.30313e-153;7.43809e-146/oxygen-evolving enhancer protein 3 [Glycine max];hypothetical protein GLYMA_07G112000 [Glycine max]
Glyma.02 G282500	-	-	-	-	-	-	-	-	-2.1721	3.91E-08	1217	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid;GO:0009523//photosystem II;GO:0005576//extracellular region	GO:0008187//polypyrimidine tract binding;GO:0046872//metal ion binding	GO:0009617//response to bacterium;GO:0044237//cellular metabolic process	gi 734416475 gb KHN38354.1 /0/Oxygen-evolving enhancer protein 2, chloroplastic [Glycine soja]
Glyma.10 G042000	-	-	-	-	-	-	-	-	-2.2129	1.99E-05	820	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0044434;GO:0009522//photosystem I	-	-	gi 947083556 gb KRH32277.1 /3.15973e-97/hypothetical protein GLYMA_10G042000 [Glycine max]
Glyma.12 G199400	-	-	-	-	-	-	-	-	-2.239	1.58E-08	1088	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031224//intrinsic component of membrane;GO:0009526//plastid envelope;GO:0031976;GO:0034357	GO:0043169//cation binding;GO:0015078//hydrogen ion transmembrane transporter activity;GO:0051536//iron-sulfur cluster binding;GO:0009055//electron carrier activity;GO:0052880	GO:1990066;GO:0044710;GO:0009617//response to bacterium;GO:0044237//cellular metabolic process;GO:0015992//proton transport	gi 734321874 gb KHN04299.1 /1.5483e-156/Cytochrome b6-f complex iron-sulfur subunit, chloroplastic [Glycine soja]
Glyma.13 G357300	-	-	-	-	-	-	1.34091	5.40E-06	-2.3494	1.61E-07	1254	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031976;GO:0009570//chloroplast stroma;GO:0009522//photosystem I	-	GO:0044237//cellular metabolic process	gi 734403802 gb KHN32624.1 /2.63003e-70/Photosystem I reaction center subunit V1, chloroplastic [Glycine soja]
Glyma.07 G019700	-	-	-	-	-	-	-	-	-2.3656	0.00014	884	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0031976;GO:0009570//chloroplast stroma;GO:0009522//photosystem I	-	GO:0044237//cellular metabolic process	gi 351726538 ref NP_001236618.1 ;gi 571463893 ref XP_006582847.1 /1.42596e-73;1.51029e-78/uncharacterized protein LOC100499832 [Glycine max];PREDICTED: uncharacterized protein LOC100499832 isoform X1 [Glycine max]
Glyma.13 G204800	-	-	-	-	-	-	-	-	-2.4727	5.26E-05	1800	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;	GO:0033178//proton-transporting two-sector ATPase complex, catalytic domain	GO:0015078//hydrogen ion transmembrane transporter	GO:0006754//ATP biosynthetic process	gi 734415192 gb KHN37604.1 /0/ATP synthase gamma chain, chloroplastic [Glycine soja]

												ko01100//Metabolic pathways		activity:GO:0019829/cation-transporting ATPase activity		
Glyma.15 G107900	-	-	-	-	-	-	-	-	-2.4995	4.16E-10	1892	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0033178//proton-transporting two-sector ATPase complex, catalytic domain	GO:0015078//hydrogen ion transmembrane transporter activity;GO:0019829/cation-transporting ATPase activity	GO:0006754//ATP biosynthetic process	gi 734404516 gb KHN33027.1 /0/ATP synthase gamma chain, chloroplastic [Glycine soja]
Glyma.12 G169600	-	-	-	-	-	-	-	-	-2.5352	6.82E-07	889	ko00195//Photosynthesis	GO:0009536//plastid	GO:0051536//iron-sulfur cluster binding	GO:0022900//electron transport chain	gi 356543418 ref XP_003540157.1 /6.45877e-93/PREDICTED: ferredoxin-A-like [Glycine max]
Glyma.04 G020300	-	-	-	-	-	-	-	-	-2.5573	1.76E-09	1273	ko00195//Photosynthesis	GO:0031976;GO:004436;GO:0044434	GO:0046872//metal ion binding	-	gi 734406057 gb KHN33826.1 /1.33719e-85/Plastocyanin, chloroplastic [Glycine soja]
Glyma.12 G169500	-	-	-	-	-	-	1.17486	0.000723	-3.199	3.16E-08	881	ko00195//Photosynthesis	GO:0009536//plastid	GO:0051536//iron-sulfur cluster binding	GO:0044710	gi 351723843 ref NP_001237037.1 /2.17897e-93/unc characterized protein LOC100500372 [Glycine max]
Glyma.02 G184000	1.45087	0.00018	2.18905	2.86E-07	1.89131	0.00124	-	-	-4.1015	4.19E-07	461	ko00195//Photosynthesis;ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0033178//proton-transporting two-sector ATPase complex, catalytic domain;GO:0009534//chloroplast thylakoid	GO:0032550;GO:0019829//cation-transporting ATPase activity;GO:0015078//hydrogen ion transmembrane transporter activity	GO:0015986//ATP synthesis coupled proton transport	gi 947123790 gb KRH71996.1 /1.26336e-85/hypothetical protein GLYMA_02G184000, partial [Glycine max]
Glyma.08 G082900	-	-	-	-	-	-	2.15566	5.66E-07	-	-	1357	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding;GO:0043169//cation binding	GO:0006464//cellular protein modification process;GO:0006091//generation of precursor metabolites and energy	gi 359806638 ref NP_001241277.1 /0/chlorophyll a-b binding protein 3, chloroplastic-like [Glycine max]
Glyma.16 G162600	-	-	-	-	-	-	2.70875	6.86E-05	-	-	511	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding;GO:0043169//cation binding	GO:0006464//cellular protein modification process;GO:0006091//generation of precursor metabolites and energy	gi 947059228 gb KRH08634.1 /2.29509e-86/hypothetical protein GLYMA_16G162600, partial [Glycine max]
Glyma.16 G165800	-1.6062	7.18E-10	-	-	-	-	2.70675	4.48E-12	-	-	1884	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0031976	GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 358248490 ref NP_001240146.1 /0/chlorophyll a-b binding protein 21, chloroplastic-like [Glycine max]
Glyma.05 G128000	-	-	-	-	-	-	2.23169	2.28E-06	-1.0987	0.00637	1131	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding;GO:0043169//cation binding	GO:0006464//cellular protein modification process;GO:0006091//generation of precursor metabolites and energy	gi 255646685 gb ACU23816.1 /0/unknown [Glycine max]

Glyma.15 G052400	-	-	-	-	-	-	-	-	-1.1359	0.00041	1645	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009526//plastid envelope;GO:0009570//chloroplast stroma;GO:0009534//chloroplast thylakoid	-	GO:1990066;GO:0006091//generation of precursor metabolites and energy	gi 734405712 gb KHN3351.4.1 /1.20949e-173/Chlorophyll a-b binding protein CP24 10A, chloroplastic [Glycine soja]
Glyma.16 G205200	-	-	-	-	-	-	-	-	-1.3178	0.001	1338	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009503;GO:0009523//photosystem II;GO:0009570//chloroplast stroma	GO:0043169//cation binding	GO:1990066;GO:0009639//response to red or far red light;GO:0006091//generation of precursor metabolites and energy	gi 734384942 gb KHN24427.1 /8.97488e-165/Chlorophyll a-b binding protein CP26, chloroplastic [Glycine soja]
Glyma.12 G219300	-	-	-	-	-	-	-	-	-1.3908	0.00061	1237	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009536//plastid	GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 359807444 ref NP_001240880.1 /0/uncharacterized protein LOC100779387 [Glycine max]
Glyma.08 G180000	-	-	-	-	-	-	-	-	-1.4136	5.47E-05	1328	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009526//plastid envelope;GO:0009570//chloroplast stroma;GO:0009534//chloroplast thylakoid	-	GO:1990066;GO:0006091//generation of precursor metabolites and energy	gi 734390448 gb KHN26736.1 /4.09065e-174/Chlorophyll a-b binding protein CP24 10A, chloroplastic [Glycine soja]
Glyma.03 G262300	-	-	-	-	-	-	-	-	-1.4695	9.53E-05	1398	ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009534//chloroplast thylakoid	GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 947120744 gb KRH68993.1 ;gi 358249066 ref NP_001239987.1 /0;0/hypothetical protein GLYMA_03G262300 [Glycine max];uncharacterized protein LOC100794944 [Glycine max]
Glyma.05 G119000	-	-	-	-	-	-	-	-	-1.4759	0.00909	732	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy	gi 947109970 gb KRH58296.1 /2.40783e-163/hypothetical protein GLYMA_05G119000 [Glycine max]
Glyma.06 G194900	-	-	-	-	-	-	-	-	-1.4808	3.12E-05	1114	ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009526//plastid envelope;GO:0031976;GO:0009570//chloroplast stroma	GO:0043169//cation binding	GO:0009628//response to abiotic stimulus;GO:0006091//generation of precursor metabolites and energy	gi 734389434 gb KHN26254.1 /0/Chlorophyll a-b binding protein P4, chloroplastic [Glycine soja]
Glyma.14 G008000	-	-	-	-	-	-	-	-	-1.5094	4.07E-05	1200	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009526//plastid envelope;GO:0044437;GO:0009534//chloroplast thylakoid;GO:0009570//chloroplast stroma	GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0006091//generation of precursor metabolites and energy;GO:0006464//cellular protein modification process;GO:0009639//response to red or far red light	gi 359806053 ref NP_001241179.1 /0/uncharacterized protein LOC100815789 [Glycine max]
Glyma.14 G003400	-	-	-	-	-	-	-	-	-1.575	5.65E-06	1290	ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009507//chloroplast	GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 734433643 gb KHN46884.1 /3.8163e-165/Chlorophyll a-b binding protein 3, chloroplastic [Glycine soja]

Glyma.13 G282000	-	-	-	-	-	-	-	-	-1.8672	2.16E-06	1245	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009536//plastid	GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 359806176 ref NP_001241200.1 /0/uncategorized protein LOC100790960 [Glycine max]
Glyma.10 G177200	-	-	-	-	-	-	-	-	-1.8739	1.03E-06	1123	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009503;GO:0009523//photosystem II;GO:0009570//chloroplast stroma	GO:0043169//cation binding	GO:1990066;GO:0009639//response to red or far red light;GO:0006091//generation of precursor metabolites and energy	gi 356535308 ref XP_003536189.1 /6.78912e-163/PR EDICTED: chlorophyll a-b binding protein CP26, chloroplastic [Glycine max]
Glyma.07 G047600	-	-	-	-	-	-	-	-	-1.8987	1.98E-06	1400	ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009534//chloroplast thylakoid	GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 734313594 gb KHN01491.1;gi 947099250 gb KRH47742.1 /0;0/Chlorophyll a-b binding protein 7, chloroplastic [Glycine soja] ,hypothetical protein GLYMA_07G047600 [Glycine max]
Glyma.20 G212900	-	-	-	-	-	-	-	-	-2.0117	3.38E-05	1076	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009503;GO:0009523//photosystem II;GO:0009570//chloroplast stroma	GO:0043169//cation binding	GO:1990066;GO:0009639//response to red or far red light;GO:0006091//generation of precursor metabolites and energy	gi 734324257 gb KHN05032.1 /7.10859e-173/Chlorophyll a-b binding protein CP26, chloroplastic [Glycine soja]
Glyma.02 G309500	-	-	-	-	-	-	-	-	-2.0384	3.99E-08	1945	ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009507//chloroplast	GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 734396929 gb KHN29869.1 /5.17725e-165/Chlorophyll a-b binding protein 3, chloroplastic [Glycine soja]
Glyma.02 G064700	-	-	-	-	-	-	-	-	-2.0793	6.02E-07	2033	ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009536//plastid	GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 947121839 gb KRH70045.1;gi 947121840 gb KRH70046.1;gi 734312433 gb KHN00611.1 /3.16771e-162;3.01752e-138;7.33888e-176/hypothetical protein GLYMA_02G064700 [Glycine max];hypothetical protein GLYMA_02G064700 [Glycine max];Chlorophyll a-b binding protein 6A, chloroplastic [Glycine soja]
Glyma.16 G145800	-	-	-	-	-	-	-	-	-2.0802	2.09E-06	1161	ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009536//plastid	GO:0043169//cation binding	GO:0006091//generation of precursor metabolites and energy	gi 955376843 ref XP_006599410.2 /2.30353e-164/PR EDICTED: chlorophyll a-b binding protein 6A, chloroplastic [Glycine max]
Glyma.09 G154700	-	-	-	-	-	-	1.16335	0.000718	-2.0875	2.44E-06	1191	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009503;GO:0009523//photosystem II;GO:0009570//chloroplast stroma	GO:0043169//cation binding	GO:1990066;GO:0009639//response to red or far red light;GO:0006091//generation of precursor metabolites and energy	gi 734392935 gb KHN27863.1 /2.73903e-164/Chlorophyll a-b binding protein CP26, chloroplastic [Glycine soja]
Glyma.18 G028400	-	-	-	-	-	-	-	-	-2.1646	3.76E-07	1218	ko01100//Metabolic pathways;ko001	GO:0009536//plastid	-	GO:0009639//response to red or far red light;GO:0006091//	gi 356568441 ref XP_00352419.1 /2.48927e-167/PR EDICTED: chlorophyll a-b

												96//Photosynthesis - antenna proteins			generation of precursor metabolites and energy	binding protein CP29.3, chloroplastic-like [Glycine max]
Glyma.08 G074000	-	-	-	-	-	-	-	-	-2.3629	8.30E-10	1090	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy	gi 734417899 gb KHN3921.1.1 /0/Chlorophyll a-b binding protein CP24 10A, chloroplastic [Glycine soja]
Glyma.02 G305400	-	-	-	-	-	-	-	-	-2.7984	3.57E-12	1322	ko01100//Metabolic pathways;ko00196//Photosynthesis - antenna proteins	GO:0009521;GO:0009526//plastid envelope;GO:0009570//chloroplast stroma;GO:0009534//chloroplast thylakoid;GO:0044437;GO:0031224//intrinsic component of membrane	GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0009639//response to red or far red light;GO:0006091//generation of precursor metabolites and energy;GO:0006464//cellular protein modification process	gi 947125798 gb KRH74004.1.1 ;gi 358248712 ref NP_01240183.1 /1.06595e-163;0/hypothetical protein GLYMA_02G305400 [Glycine max];chlorophyll a-b binding protein 151, chloroplastic-like [Glycine max]

Supplementary Table S6: DEGs involved in starch and sucrose metabolism

GeneID	log2Ratio(2mlpa-1/2M WT-1)	P-value	log2Ratio(2mlpa-2/2M WT-2)	P-value	log2Ratio(2mlpa-3/2M WT-3)	P-value	log2Ratio(2mlpa-4/2M WT-4)	P-value	log2Ratio(2mlpa-5/2M WT-5)	P-value	Length	Pathway	GO Component	GO Function	GO Process	Blast nr
Glyma.01G007300	1.24442	0.00119	-	-	-	-	-	-	-	-	2189	ko00051//Fructose and mannose metabolism;ko00500//Starch and sucrose metabolism;ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism;ko00052//Galactose metabolism	GO:0044437;GO:0031306//intrinsic component of mitochondrial outer membrane	GO:0046914//transition metal ion binding;GO:0032550;GO:0004396//hexokinase activity	GO:0006833//water transport;GO:0010118//stomatal movement;GO:0016310//phosphorylation;GO:0006091//generation of precursor metabolites and energy;GO:0009757//hexose mediated signaling;GO:0019318//hexose metabolic process;GO:0008219//cell death	gi 356495847 ref XP_003516783.1 /0/PREDICTED: hexokinase-1-like [Glycine max]
Glyma.01G209500	1.13084	3.17E-05	-	-	-	-	-	-	-	-	1443	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//external encapsulating structure	GO:0052689//carboxylic ester hydrolase activity	GO:0071555//cell wall organization	gi 356497141 ref XP_003517421.1 /0/PREDICTED: probable pectinesterase 68 [Glycine max]
Glyma.02G186800	-1.4574	4.16E-07	-	-	-1.4823	0.00069	-	-	-	-	1926	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0005911//cell-cell junction;GO:0005618//cell wall	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 734320135 gb KHN03708.1 /0/Lysosomal beta glucosidase [Glycine soja]
Glyma.02G272100	-1.2165	3.18E-06	-	-	-	-	-	-	-	-	2421	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0005911//cell-cell junction;GO:0005618//cell wall	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 955308958 ref XP_014625681.1 ;gi 947125214 gb KRH73420.1 ;gi 955308961 ref XP_014625684.1 /0;0/PREDICTED: beta-glucosidase BoGH3B-like isoform X1 [Glycine max];hypothetical protein GLYMA_02G272100 [Glycine max];PREDICTED: beta-glucosidase BoGH3B-like isoform X3 [Glycine max]
Glyma.03G214600	-3.6427	2.08E-07	-	-	-	-	-	-	-	-	1194	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0004857//enzyme inhibitor activity;GO:0052689//carboxylic ester hydrolase activity	GO:0003006//developmental process involved in reproduction;GO:0044092//negative regulation of molecular function	gi 356505586 ref XP_003521571.1 /8.44156e-131/PREDICTED: 21 kDa protein-like [Glycine max]
Glyma.04G103600	-	-	-	-	-	-	-1.7978	6.89E-06	-	-	1864	ko00500//Starch and sucrose metabolism	-	GO:0019203//carbohydrate phosphatase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0005991//trehalose metabolic process	gi 571450061 ref XP_003523824.2 /0/PREDICTED: probable trehalose-phosphate phosphatase J [Glycine max]
Glyma.05G216400	-	-	-	-	-	-	1.09973	0.00042	-	-	2663	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0005488;GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0044238//primary metabolic process	gi 734310523 gb KHM99903.1 /0/Endoglucanase 6 [Glycine soja]
Glyma.05G236400	-	-	-	-	1.20227	0.00027	2.30482	2.33E-09	-	-	2164	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0009536//plastid	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0009825//multidimensional cell growth;GO:0044238//primary metabolic process	gi 356513078 ref XP_003525241.1 /0/PREDICTED: endoglucanase 8-like [Glycine max]

Glym a.06G 31850 0	-1.404 8	8.58E -06	-	-	-	-	-	-	-	-	18 91	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0016160//amylase activity	GO:0005976//polysaccharide metabolic process	gi 902938 dbj BAA09462.1 /0/bet a-amylase [Glycine max]
Glym a.06G 31850 0	-1.242 2	0.000 11	-	-	-	-	-	-	-	-	23 99	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00052//Galactose metabolism	-	GO:0004558//alpha-1,4 -glucosidase activity	GO:0044238//primary metabolic process	gi 356515372 ref XP_003526374. 1 /0/PREDICTED: beta-fructofuranosidase, soluble isoenzyme 1-like [Glycine max]
Glym a.07G 04600 0	-1.562 8	1.03E -09	-	-	-	-	-	-	-	-	35 58	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0005618//cell wall;GO:0043231//i ntracellular membrane-bounded organelle;GO:00444 44;GO:0005576//ext racellular region;GO:0016020// membrane	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0044092//negative regulation of molecular function;GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process	gi 947099228 gb KRH47720.1 /0/ hypothetical protein GLYMA_07G046000 [Glycine max]
Glym a.08G 07470 0	-	-	-	-	1.332 49	4.12E -06	-	-	-	-	30 60	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0031012//extrac ellular matrix	GO:0004553//hydrolas e activity, hydrolyzing O-glycosyl compounds	GO:0000272//polysaccharide catabolic process	gi 947093612 gb KRH42197.1 ;gi 356524862 ref XP_003531047.1 / 0/hypothetical protein GLYMA_08G074700 [Glycine max];PREDICTED: beta-xylosidase/alpha-L-arabinofu ranosidase 2 [Glycine max]
Glym a.08G 12080 0	-2.111 2	1.92E -05	-	-	-	-	-	-	-	-	30 54	ko00500//Starch and sucrose metabolism	-	GO:0019203//carbohyd rate phosphatase activity;GO:0035251// UDP-glucosyltransferas e activity	GO:0006796//phosphate-containing compound metabolic process;GO:0005991//trehalose metabolic process	gi 955335317 ref XP_014634392. 1 /0/PREDICTED: alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1-like [Glycine max]
Glym a.09G 12200 0	-	-	-	-	-	-	1.252 88	0.001 04	-	-	83 8	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	-	-	gi 356530768 ref XP_003533952. 1 /4.81613e-96/PREDICTED: 21 kDa protein-like [Glycine max]
Glym a.09G 20820 0	-1.949 8	0.000 26	-2.309 9	0.000 61	-	-	-	-	-	-	43 34	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0031224//intrinsic component of membrane	GO:0016759//cellulose synthase activity	GO:0030243//cellulose metabolic process;GO:0009856//pollination	gi 734417458 gb KHN38958.1 /0/ Cellulose synthase-like protein D3 [Glycine soja]
Glym a.10G 07480 0	2.305 22	0.000 16	-	-	-	-	-	-	-	-	19 59	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00052//Galactose metabolism	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0005985//sucrose metabolic process;GO:0046903//secretion;GO: 0006073//cellular glucan metabolic process	gi 356534392 ref XP_003535739. 1 /0/PREDICTED: beta-fructofuranosidase, insoluble isoenzyme 1-like isoform X1 [Glycine max]
Glym a.10G 23090 0	-	-	-	-	-	-	3.421 96	0.000 3	-	-	15 77	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0004553//hydrolas e activity, hydrolyzing O-glycosyl compounds	GO:0044238//primary metabolic process	gi 356534103 ref XP_003535597. 1 /0/PREDICTED: probable polygalacturonase [Glycine max]
Glym a.11G 03940 0	-	-	-	-	-2.843 4	2.02E -05	-	-	-	-	20 28	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0009532//plasti d stroma	GO:0016160//amylase activity	GO:0006950//response to stress;GO:0005976//polysaccharide metabolic process;GO:0000023//maltose metabolic process	gi 734408776 gb KHN34883.1 /0/ Beta-amylase 3, chloroplastic [Glycine soja]
Glym a.11G 10130 0	-1.256 1	0.003 48	-	-	-	-	-	-	-	-	23 21	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds;GO:0005488;GO :0004553//hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0044238//primary metabolic process	gi 571487997 ref XP_006590804. 1 ;gi 947080369 gb KRH29158.1 ; gi 947080368 gb KRH29157.1 /0: 0/PREDICTED: endoglucanase 5-like [Glycine max];hypothetical protein GLYMA_11G101300 [Glycine max];hypothetical protein GLYMA_11G101300 [Glycine max]
Glym a.12G 00470 0	-	-	-4.097 2	3.19E -07	-	-	-	-	-	-	12 95	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 947074959 gb KRH23799.1 /0/ hypothetical protein GLYMA_12G004700 [Glycine max]

Glym a.14G 00610 0	-1.024 9	0.004 79	-	-	-	-	-	-	-	20 78	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0044238//primary metabolic process	gi 955362405 ref XP_014622079.1 ;gi 947064948 gb KRH14091.1 ;gi 356551512 ref XP_003544118.1 ;gi 947064949 gb KRH14092.1 /0;0;0/PREDICTED: polygalacturonase-like isoform X2 [Glycine max];hypothetical protein GLYMA_14G006100 [Glycine max];PREDICTED: polygalacturonase-like isoform X1 [Glycine max];hypothetical protein GLYMA_14G006100 [Glycine max]
Glym a.14G 02740 0	-1.192	0.001 21	-	-	-	-	-	-	-	20 94	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transferase activity	-	gi 356553593 ref XP_003545139.1 /0/PREDICTED: probable galacturonosyltransferase 15 [Glycine max]
Glym a.14G 02910 0	-1.212 2	3.64E -07	-	-	-1.352 6	4.48E -05	-	-	-	37 43	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0035251//UDP-glucosyltransferase activity	GO:0005984//disaccharide metabolic process	gi 356553609 ref XP_003545147.1 /0/PREDICTED: probable sucrose-phosphate synthase 3 [Glycine max]
Glym a.15G 14680 0	1.080 02	3.06E -05	-	-	-	-	-	-	-	20 96	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0005618//cell wall;GO:0043231//intracellular membrane-bounded organelle	GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0044238//primary metabolic process	gi 571518634 ref XP_006597719.1 /0/PREDICTED: probable polygalacturonase isoform X1 [Glycine max]
Glym a.15G 18430 0	-1.564 5	4.02E -07	-	-	-	-	-	-	-	19 56	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0016788//hydrolase activity, acting on ester bonds	GO:0008152//metabolic process	gi 356558481 ref XP_003547535.1 /0/PREDICTED: pectinesterase/pectinesterase inhibitor PPE8B-like [Glycine max]
Glym a.15G 22350 0	-1.533 5	2.50E -05	-	-	-	-	-	-	-	24 32	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//external encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//carboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysaccharide catabolic process;GO:0044092//negative regulation of molecular function	gi 571520749 ref XP_006598050.1 /0/PREDICTED: probable pectinesterase/pectinesterase inhibitor 47 [Glycine max]
Glym a.16G 03930 0	-	-	-	-	-	-	1.585 76	0.001 07	-	18 45	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 947057276 gb KRH06682.1 /0/hypothetical protein GLYMA_16G039300 [Glycine max]
Glym a.16G 11800 0	-6.915 5	1.85E -28	-6.280 2	2.06E -18	-5.522 1	2.62E -12	-4.894	1.01E -08	-	41 2	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0044238//primary metabolic process	gi 947058503 gb KRH07909.1 /1.98927e-57/hypothetical protein GLYMA_16G118000 [Glycine max]
Glym a.17G 13850 0	-	-	-	-	-	-	2.641 56	0.000 24	-	25 05	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00052//Galactose metabolism	GO:0005618//cell wall;GO:0043231//intracellular membrane-bounded organelle	GO:0004558//alpha-1,4-glucosidase activity	GO:0005984//disaccharide metabolic process;GO:0051707//response to other organism;GO:0048364//root development;GO:0009739//response to gibberellin	gi 947054630 gb KRH04083.1 ;gi 356563300 ref XP_003549902.1 /0;0/hypothetical protein GLYMA_17G138500 [Glycine max];PREDICTED: acid beta-fructofuranosidase [Glycine max]
Glym a.17G 18820 0	-	-	-	-	-2.354 4	0.000 18	-	-	-	21 33	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 356565758 ref XP_003551104.1 /0/PREDICTED: beta-glucosidase BoGH3B-like [Glycine max]
Glym a.18G 06540	-	-	-	-	3.063 12	2.84E -08	3.021 59	1.77E -06	-	19 68	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of	GO:0044444	GO:0016787//hydrolase activity	-	gi 947048791 gb KRG98319.1 /0/hypothetical protein GLYMA_18G065400 [Glycine

0												secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis				max]
Glym a.19G 002500	-4.0922	2.07E-10	-	-	-	-	-	-	-	294	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	-	-	gi 947043560 gb KRG93189.1 /4.91238e-68/hypothetical protein GLYMA_19G002500 [Glycine max]	
Glym a.19G 016100	-	-	-	-	-3.9277	0.00026	-	-	-	1822	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transferase activity	GO:0006950//response to stress	gi 356572000 ref XP_003554158.1 /0/PREDICTED: probable galacturonosyltransferase-like 10 [Glycine max]	
Glym a.19G 078400	-	-	-	-	-	-	-5.1015	2.31E-07	-	1712	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//external encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//carboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysaccharide catabolic process;GO:0044092//negative regulation of molecular function	gi 955387229 ref XP_003553884.2 /0/PREDICTED: probable pectinesterase/pectinesterase inhibitor 36 isoform X1 [Glycine max]	
Glym a.19G 223100	1.54648	0.00117	-	-	-	-	-	-	-	2289	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0009536//plastid	GO:0070566//adenylyltransferase activity	GO:0005982//starch metabolic process;GO:0005977//glycogen metabolic process	gi 571559815 ref XP_003553688.2 /0/PREDICTED: glucose-1-phosphate adenylyltransferase large subunit 1-like [Glycine max]	
Glym a.19G 231300	-1.0956	0.00487	-	-	-	-	-	-	-	2028	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//external encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//carboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysaccharide catabolic process;GO:0044092//negative regulation of molecular function	gi 356572956 ref XP_003554631.1 /0/PREDICTED: putative pectinesterase/pectinesterase inhibitor 22 [Glycine max]	
Glym a.20G 029100	-1.7867	2.00E-05	-	-	-	-	-	-	-	2119	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00052//Galactose metabolism	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0005985//sucrose metabolic process;GO:0046903//secretion;GO:0006073//cellular glucan metabolic process	gi 571563934 ref XP_006605559.1 ;gi 356577241 ref XP_003556736.1 /0;0/PREDICTED: beta-fructofuranosidase, insoluble isoenzyme 1-like isoform X2 [Glycine max];PREDICTED: beta-fructofuranosidase, insoluble isoenzyme 1-like isoform X1 [Glycine max]	
Glym a.12G 130200	-	-	-	-	-	-	-	-	8.47386	2.32E-05	1900	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 955354334 ref XP_003540006.2 /0/PREDICTED: cyanogenic beta-glucosidase-like [Glycine max]
Glym a.12G 053800	-	-	-	-	-	-	-	-	8.43265	2.44E-05	2190	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0043231//intracellular membrane-bounded organelle	GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds;GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 947075816 gb KRH24656.1 ;gi 734387515 gb KHN25278.1 /0;0/hypothetical protein GLYMA_12G053800 [Glycine max];Non-cyanogenic beta-glucosidase [Glycine soja]
Glym a.11G 129500	-	-	-	-	-	-	-	-	8.2002	3.81E-05	1893	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 734406299 gb KHN33931.1 /0/Beta-glucosidase 24 [Glycine soja]
Glym a.12G 054000	-	-	-	-	-	-	-	-	7.98202	5.82E-05	2046	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 734387513 gb KHN25276.1 /0/Beta-glucosidase 24 [Glycine soja]

Glym a.11G 24030 0	-	-	-	-	-	-	-	-	7.958 68	6.55E -08	19 21	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//extern al encapsulating structure;GO:00444 37	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process;GO:0044092//negative regulation of molecular function	gi 571436840 ref XP_006573891. 1 /0/PREDICTED: pectinesterase-like [Glycine max]
Glym a.11G 12970 0	-	-	-	-	-	-	-	-	7.370 99	0.000 12	18 52	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 734406297 gb KHN33929.1 /0/ Beta-glucosidase 24 [Glycine soja]
Glym a.01G 13770 0	-	-	-	-	-	-	-	-	7.215 13	0.000 16	19 73	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//extern al encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process;GO:0044092//negative regulation of molecular function	gi 356496344 ref XP_003517028. 1 /0/PREDICTED: pectinesterase 2-like [Glycine max]
Glym a.12G 05410 0	-	-	-	-	-	-	-	-	7.171 14	0.000 17	19 43	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 356544535 ref XP_003540705. 1 /0/PREDICTED: cyanogenic beta-glucosidase-like [Glycine max]
Glym a.03G 02940 0	-	-	-	-	-	-	-	-	7.147 73	0.000 18	11 85	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//extern al encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process;GO:0044092//negative regulation of molecular function	gi 571444145 ref XP_006576427. 1 /0/PREDICTED: pectinesterase 2-like [Glycine max]
Glym a.19G 21260 0	-1.540 5	1.49E -08	-1.465 5	1.04E -06	-	-	-	-	5.658 83	0.000 38	20 56	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//extern al encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process;GO:0044092//negative regulation of molecular function	gi 571559513 ref XP_003553658. 2 /0/PREDICTED: pectinesterase-like [Glycine max]
Glym a.17G 22790 0	2.139 04	0.003 23	-	-	-	-	-	-	5.222 7	0.000 22	23 33	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00052//Galactose metabolism	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 947055989 gb KRH05442.1 ;gi 571538935 ref XP_003549347.2 / 0 /0/hypothetical protein GLYMA_17G227900 [Glycine max];PREDICTED: fructan 6-exohydrolase-like [Glycine max]
Glym a.20G 02670 0	-	-	-	-	-	-	-	-	5.108 43	9.60E -06	35 57	ko00500//Starch and sucrose metabolism	-	GO:0043168//anion binding;GO:0004645//p hosphorylase activity	GO:0044238//primary metabolic process;GO:0006950//response to stress;GO:0009628//response to abiotic stimulus	gi 571563869 ref XP_006605545. 1 ;gi 356577161 ref XP_00355669 6.1 /0 /0/PREDICTED: alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic-like isoform X2 [Glycine max];PREDICTED: alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic-like isoform X1 [Glycine max]
Glym a.17G 06780 0	-	-	-	-	-	-	-	-	4.337 57	5.92E -05	34 85	ko00500//Starch and sucrose metabolism	GO:0043231//intrac ellular membrane-bounded organelle;GO:00444 44	-	GO:0005991//trehalose metabolic process	gi 955380139 ref XP_014625413. 1 ;gi 947053485 gb KRH02938.1 / 0 /0/PREDICTED: probable alpha, alpha-trehalose-phosphate synthase [UDP-forming] 11 [Glycine max];hypothetical protein GLYMA_17G067800 [Glycine max]
Glym a.16G 01410	-1.859 4	4.37E -13	-	-	-	-	-	-	4.296 22	1.01E -06	18 90	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic	GO:0005618//cell wall;GO:0005576//e xtracellular	GO:0030234//enzyme regulator activity;GO:0052689//c	GO:0071555//cell wall organization;GO:0051707//response to other	gi 955374748 ref XP_006599763. 2 /0/PREDICTED: pectinesterase-like [Glycine max]

0												pathways	region;GO:0016020/ /membrane;GO:004 4424	arboxylic ester hydrolase activity	organism;GO:0000272//polysaccharide catabolic process;GO:0044092//negative regulation of molecular function	
Glym a.13G 08830 0	-	-	-	-	-3.266 1	0.000 3	-	-	3.849 87	0.000 13	17 63	ko00500//Starch and sucrose metabolism	-	GO:0019203//carbohydrate phosphatase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0005991//trehalose metabolic process	gi 734371039 gb KHN19585.1 /O/ Trehalose-phosphate phosphatase [Glycine soja]
Glym a.18G 00220 0	-	-	-	-	-	-	-	-	3.655 48	1.44E -05	13 20	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0043231//intracellular membrane-bounded organelle	GO:0016854//racemase and epimerase activity;GO:0048037//c ofactor binding	GO:0044238//primary metabolic process	gi 947047820 gb KRG97348.1 /O/ hypothetical protein GLYMA_18G002200 [Glycine max]
Glym a.01G 20340 0	-	-	-	-	-	-	-	-	3.472 36	0.000 56	20 41	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0009532//plastid stroma	GO:0016160//amylase activity	GO:0006950//response to stress;GO:0005976//polysaccharide metabolic process;GO:0000023//maltose metabolic process	gi 571436239 ref XP_006573703. 1 /O/PREDICTED: beta-amylase 3, chloroplastic [Glycine max]
Glym a.11G 11660 0	-	-	-	-	-	-	-	-	3.399 44	5.88E -05	24 07	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0009536//plastid	GO:0070566//adenylate transferase activity	GO:0005982//starch metabolic process;GO:0005977//glycogen metabolic process	gi 734418875 gb KHN39792.1 /O/ Glucose-1-phosphate adenylate transferase large subunit 1 [Glycine soja]
Glym a.08G 10910 0	-	-	-	-	-	-	2.087 16	6.96E -08	3.276 83	3.49E -09	23 43	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0043231//intracellular membrane-bounded organelle	GO:0016854//racemase and epimerase activity;GO:0048037//c ofactor binding	GO:0044238//primary metabolic process	gi 571462885 ref XP_003532740. 2 /O/PREDICTED: UDP-glucuronate 4-epimerase 6-like [Glycine max]
Glym a.06G 31840 0	-	-	-	-	-	-	-	-	3.210 01	4.15E -05	22 52	ko00500//Starch and sucrose metabolism	-	GO:0019203//carbohydrate phosphatase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0005991//trehalose metabolic process	gi 571462885 ref XP_006582414. 1 ;gi 947107964 gb KRH56347.1 /O/ PREDICTED: trehalose-phosphate phosphatase A-like [Glycine max];hypothetical protein GLYMA_06G318400 [Glycine max]
Glym a.13G 06790 0	-	-	-	-	-3.590 6	2.72E -05	-	-	3.056 66	0.000 28	16 51	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transferase activity	GO:0006950//response to stress	gi 356550372 ref XP_003543561. 1 /O/PREDICTED: probable galacturonosyltransferase-like 10 [Glycine max]
Glym a.08G 15040 0	-	-	-	-	-	-	-	-	3.026 77	0.000 62	13 32	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0005975//carbohydrate metabolic process	gi 955335734 ref XP_014634459. 1 /O/PREDICTED: vicianin hydrolase [Glycine max]
Glym a.06G 10480 0	-1.135 1	0.003 92	-	-	-	-	-	-	2.918 27	0.000 59	21 51	ko00500//Starch and sucrose metabolism	-	GO:0019203//carbohydrate phosphatase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0005991//trehalose metabolic process	gi 947104706 gb KRH53089.1 ;gi 947104707 gb KRH53090.1 ;gi 35 6518491 ref XP_003527912.1 ;gi 571459884 ref XP_006581545.1 / O;0;0;0/hypothetical protein GLYMA_06G104800 [Glycine max];hypothetical protein GLYMA_06G104800 [Glycine max];PREDICTED: probable trehalose-phosphate phosphatase J isoform X2 [Glycine max];PREDICTED: probable trehalose-phosphate phosphatase J isoform X1 [Glycine max]
Glym a.04G 01190 0	-	-	-	-	-	-	-	-	2.885 59	0.002 1	21 97	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0009536//plastid	GO:0070566//adenylate transferase activity	GO:0005982//starch metabolic process;GO:0005977//glycogen metabolic process	gi 947112523 gb KRH60825.1 ;gi 734405977 gb KHN33746.1 /O;0/ hypothetical protein GLYMA_04G011900 [Glycine max];Glucose-1-phosphate adenylate transferase large subunit

																	1 [Glycine soja]
Glym a.09G 07360 0	-	-	-	-	-	-	-	-	2.708 81	9.43E -06	36 72	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0035251//UDP- glu cosyltransferase activity	GO:0005984//disaccharide metabolic process;GO:0044403//symbiosis, encompassing mutualism through parasitism	gi 356530467 ref XP_003533802. 1 ;gi 947088892 gb KRH37557.1 ; gi 947088893 gb KRH37558.1 /0; 0//PREDICTED: sucrose synthase [Glycine max];hypothetical protein GLYMA_09G073600 [Glycine max];hypothetical protein GLYMA_09G073600 [Glycine max]	
Glym a.04G 20160 0	-	-	3.139 64	0.000 38	3.223 01	0.000 34	3.014 98	1.71E -06	2.611 23	0.001 21	11 84	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 947115574 gb KRH63876.1 /3. 01797e-58/hypothetical protein GLYMA_04G201600 [Glycine max]	
Glym a.01G 01400 0	-1.294 4	0.003 29	-	-	-2.291 6	0.001 02	-	-	2.597 94	0.000 11	39 67	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0031224//intrinsic component of membrane	GO:0016759//cellulose synthase activity	GO:0030243//cellulose metabolic process;GO:0009856//pollination	gi 571433624 ref XP_006572955. 1 /0//PREDICTED: cellulose synthase-like protein D2 [Glycine max]	
Glym a.09G 03860 0	-	-	-	-	-	-	-	-	2.416 06	0.008 02	32 03	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0005618//cell wall;GO:0005576//e xtracellular region	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0003006//developmental process involved in reproduction;GO:0044238//primary metabolic process	gi 955340041 ref XP_003533205. 3 ;gi 947088349 gb KRH37014.1 / 0//PREDICTED: beta-D-xylosidase 1-like [Glycine max];hypothetical protein GLYMA_09G038600 [Glycine max]	
Glym a.09G 16830 0	-	-	-	-	-	-	-	-	2.398 35	3.74E -05	22 21	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0016160//amylase activity	GO:0005976//polysaccharide metabolic process	gi 356531040 ref XP_003534086. 1 /0//PREDICTED: beta-amylase 1, chloroplastic [Glycine max]	
Glym a.14G 17090 0	-	-	-	-	-	-	1.461 13	5.28E -05	2.393 6	9.41E -09	27 39	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00520//Amino sugar and nucleotide sugar metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0005911//cell-c ell junction;GO:000557 6//extracellular region;GO:0005618/ /cell wall;GO:0009536//p lastid	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 356552866 ref XP_003544783. 1 ;gi 947067550 gb KRH16693.1 / 0//PREDICTED: probable beta-D-xylosidase 7 [Glycine max];hypothetical protein GLYMA_14G170900 [Glycine max]	
Glym a.17G 24790 0	-	-	-	-	-	-	-	-	2.367 96	0.000 4	22 61	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transfera se activity	-	gi 356562321 ref XP_003549420. 1 /0//PREDICTED: probable galacturonosyltransferase-like 1 [Glycine max]	
Glym a.15G 13370 0	-	-	-	-	-	-	-	-	2.338 48	0.000 27	33 65	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00052//Galactose metabolism	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds;GO:0005488	GO:0044238//primary metabolic process	gi 947062578 gb KRH11839.1 /0/ hypothetical protein GLYMA_15G133700 [Glycine max]	
Glym a.15G 10800 0	-	-	-	-	-	-	-	-	2.336 6	5.71E -07	40 85	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0030247//polysacc haride binding;GO:0046527//g lucosyltransferase activity	GO:0006073//cellular glucan metabolic process;GO:0008152//metabolic process	gi 356555668 ref XP_003546152. 1 /0//PREDICTED: starch synthase 3, chloroplastic/amyloplastic-like isoform X3 [Glycine max]	
Glym a.02G 28760 0	-	-	-	-	-	-	-	-	2.280 77	0.003 44	21 35	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transfera se activity	-	gi 356499376 ref XP_003518517. 1 ;gi 955309155 ref XP_01462601 1.1 /0//PREDICTED: probable galacturonosyltransferase 15 isoform X1 [Glycine max];PREDICTED: probable galacturonosyltransferase 15	

																		isoform X2 [Glycine max]
Glym a.05G 05630 0	-	-	-	-	-	-	-	-	2.245 95	5.03E -05	26 56	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00052//Galactose metabolism	GO:0005618//cell wall;GO:0043231//i ntracellular membrane-bounded organelle	GO:0004558//alpha-1,4 -glucosidase activity	GO:0005984//disaccharide metabolic process;GO:0051707//response to other organism;GO:0048364//root development;GO:0009739//response to gibberellin	gi 947109026 gb KRH57352.1 ;gi 947109027 gb KRH57353.1 ;gi 35 6514218 ref XP_003525803.1 /0; 0/0/hypothetical protein GLYMA_05G056300 [Glycine max];hypothetical protein GLYMA_05G056300 [Glycine max];PREDICTED: acid beta-fructofuranosidase [Glycine max]		
Glym a.09G 07710 0	-	-	-	-	-	-	-	-	2.244 18	0.000 39	17 90	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//extern al encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process;GO:0044092//negative regulation of molecular function	gi 734344035 gb KHN10379.1 /0/ Pectinesterase/pectinesterase inhibitor PPE8B [Glycine soja]		
Glym a.15G 18260 0	-	-	-	-	-	-	-	-	2.234 71	0.001 85	30 02	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0035251//UDP-glu cosyltransferase activity	GO:0005984//disaccharide metabolic process;GO:0044403//symbiosis, encompassing mutualism through parasitism	gi 947063355 gb KRH12616.1 ;gi 571519746 ref XP_006597891.1 / 0/0/hypothetical protein GLYMA_15G182600 [Glycine max];PREDICTED: sucrose synthase-like [Glycine max]		
Glym a.04G 11970 0	-	-	-	-	-	-	-	-	2.226 26	0.009 54	19 63	ko00500//Starch and sucrose metabolism	-	GO:0019203//carbohyd rate phosphatase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0005991//trehalose metabolic process	gi 571450244 ref XP_006578369. 1 /0/PREDICTED: trehalose-phosphate phosphatase A isoform X2 [Glycine max]		
Glym a.06G 31420 0	-1.208 4	6.28E -08	-	-	-	-	-	-	2.178 88	0.006 52	20 67	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//extern al encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process;GO:0044092//negative regulation of molecular function	gi 955326411 ref XP_003527536. 3 /0/PREDICTED: probable pectinesterase/pectinesterase inhibitor 47 [Glycine max]		
Glym a.12G 04240 0	-	-	-	-	-	-	-	-	2.159 5	0.002 19	25 21	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0009536//plasti d	GO:0070566//adenylt ransferase activity	GO:0005982//starch metabolic process;GO:0005977//glycogen metabolic process	gi 734387621 gb KHN25384.1 /0/ Glucose-1-phosphate adenyltransferase large subunit 1 [Glycine soja]		
Glym a.06G 12850 0	-	-	-	-	-	-	-	-	2.147 33	2.52E -05	23 78	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//extern al encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process;GO:0044092//negative regulation of molecular function	gi 356516053 ref XP_003526711. 1 /0/PREDICTED: probable pectinesterase/pectinesterase inhibitor 34 [Glycine max]		
Glym a.06G 03460 0	-	-	-	-	-	-	-	-	2.103 68	0.007 83	19 09	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transfera se activity	GO:0003002//regionalization;GO:00 42545//cell wall modification;GO:0006950//response to stress;GO:0048827//phyllome development;GO:0000003//reproduc tion;GO:0010413//glucuronoxylan metabolic process	gi 356519066 ref XP_003528195. 1 /0/PREDICTED: probable galacturonosyltransferase-like 1 [Glycine max]		
Glym a.01G 23250 0	-	-	-	-	-	-	-	-	2.095 02	0.003 81	39 49	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0031224//intrins ic component of membrane	GO:0016759//cellulose synthase activity	GO:0030243//cellulose metabolic process	gi 356497399 ref XP_003517548. 1 /0/PREDICTED: cellulose synthase-like protein D2 [Glycine max]		
Glym a.09G 07150 0	-	-	-	-	-	-	-	-	2.090 74	0.002 12	21 10	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0004553//hydrolas e activity, hydrolyzing O-glycosyl compounds	GO:0044238//primary metabolic process	gi 356530447 ref XP_003533792. 1 /0/PREDICTED: probable polygalacturonase [Glycine max]		
Glym a.08G 18090 0	-	-	-	-	-	-	-	-	2.081 41	0.001 09	28 07	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0031012//extrac ellular matrix	GO:0004553//hydrolas e activity, hydrolyzing O-glycosyl compounds	GO:0000272//polysaccharide catabolic process	gi 734390440 gb KHN26728.1 ;gi 356525896 ref XP_003531557.1 / 0/0/Beta-xylosidase/alpha-L-arabi nofuranosidase 1 [Glycine soja];PREDICTED: beta-xylosidase/alpha-L-arabinofu ranosidase 1 [Glycine max]		

Glym a.09G 02800 0	-	-	-	-	-	-	-	-	2.067 65	0.007 18	33 12	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00052//Galactose metabolism	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds;GO:0005488	GO:0044238//primary metabolic process	gi 734428229 gb KHN44656.1 /O/ Alpha-glucosidase [Glycine soja]
Glym a.19G 11360 0	-	-	-	-	-	-	-	-	2.051 27	0.000 29	24 81	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 947045227 gb KRG94856.1 ;gi 571556301 ref XP_006604248.1 / O/hypothetical protein GLYMA_19G113600 [Glycine max];PREDICTED: beta-glucosidase BoGH3B-like [Glycine max]
Glym a.15G 14370 0	-1.175 6	4.93E -06	-	-	-	-	-	-	2.038 65	0.001 15	26 44	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0005618//cell wall;GO:0005576//e xtracellular region	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0003006//developmental process involved in reproduction;GO:0044238//primary metabolic process	gi 947062724 gb KRH11985.1 ;gi 356556038 ref XP_003546334.1 / O/hypothetical protein GLYMA_15G143700 [Glycine max];PREDICTED: beta-D-xylosidase 1 [Glycine max]
Glym a.15G 09810 0	-	-	-	-	-	-	-	-	1.971 6	0.005 19	20 35	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0016160//amylase activity	GO:0005976//polysaccharide metabolic process	gi 351726594 ref NP_001236364. 1 /O/inactive beta-amylase-like [Glycine max]
Glym a.07G 06690 0	-	-	-	-	-	-	-	-	1.937 25	0.001 84	21 25	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0004553//hydrolas e activity, hydrolyzing O-glycosyl compounds	GO:0044238//primary metabolic process	gi 356520375 ref XP_003528838. 1 /O/PREDICTED: probable polygalacturonase [Glycine max]
Glym a.19G 11350 0	-	-	-	-	-	-	-	-	1.872 99	0.005 66	21 93	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanoamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0016798//hydrolas e activity, acting on glycosyl bonds	GO:0044238//primary metabolic process	gi 571556289 ref XP_006604246. 1 /O/PREDICTED: beta-glucosidase BoGH3B-like [Glycine max]
Glym a.05G 12780 0	-	-	-	-	-	-	-	-	1.833 83	0.006	36 36	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0046527//glucosylt ransferase activity	GO:0006073//cellular glucan metabolic process	gi 356512165 ref XP_003524791. 1 /O/PREDICTED: probable starch synthase 4, chloroplastic/amyloplastic [Glycine max]
Glym a.08G 29680 0	-	-	-	-	-	-	-	-	1.789 94	1.57E -06	33 46	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0046872//metal ion binding;GO:0016160//a mylase activity	GO:0044238//primary metabolic process	gi 356526892 ref XP_003532050. 1 /O/PREDICTED: alpha-amylase 3, chloroplastic isoform X1 [Glycine max]
Glym a.16G 01400 0	-	-	-	-	-	-	-	-	1.756 83	0.002 43	21 23	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0005911//cell-c ell junction;GO:001602 0//membrane;GO:00 30312//external encapsulating structure;GO:00444 37	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process;GO:0044092//negative regulation of molecular function	gi 356559248 ref XP_003547912. 1 /O/PREDICTED: pectinesterase 3 [Glycine max]
Glym a.11G 25490 0	-	-	-	-	-	-	-	-	1.751 78	0.000 3	24 70	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0043231//intrac ellular membrane-bounded organelle	GO:0016854//racemase and epimerase activity;GO:0048037//c ofactor binding	GO:0044238//primary metabolic process	gi 356540097 ref XP_003538527. 1 /O/PREDICTED: UDP-glucuronate 4-epimerase 6-like [Glycine max]
Glym a.13G 21500 0	-	-	-	-	-1.737 1	0.000 33	-	-	1.747 53	0.003 67	20 55	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0016160//amylase activity	GO:0005976//polysaccharide metabolic process	gi 356549058 ref XP_003542915. 1 /O/PREDICTED: inactive beta-amylase 9 [Glycine max]
Glym a.16G 03300 0	-	-	-	-	-	-	-	-	1.694 14	0.002 32	32 41	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0004553//hydrolas e activity, hydrolyzing O-glycosyl compounds	GO:0044238//primary metabolic process	gi 571525292 ref XP_003548644. 2 ;gi 571525296 ref XP_00659894 1.1 /O/PREDICTED: probable polygalacturonase isoform X1 [Glycine max];PREDICTED: probable polygalacturonase

																	isoform X2 [Glycine max]
Glym a.02G 20800 0	-	-	-	-	-	-	-	-	1.645 38	0.002 33	26 96	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0048037//cofactor binding;GO:0016857//r acemase and epimerase activity, acting on carbohydrates and derivatives	GO:0044238//primary metabolic process	gi 356500703 ref XP_003519171. 1/0/PREDICTED: UDP-glucuronate 4-epimerase 1-like [Glycine max]	
Glym a.05G 15230 0	-	-	-	-	-	-	-	-	1.572 44	0.007 24	18 79	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0043231//intrac ellular membrane-bounded organelle	GO:0016854//racemase and epimerase activity;GO:0048037//c ofactor binding	GO:0044238//primary metabolic process	gi 356512447 ref XP_003524930. 1 gi 947110527 gb KRH58853.1 / 0/0/PREDICTED: UDP-glucuronate 4-epimerase 6-like [Glycine max];hypothetical protein GLYMA_05G152300 [Glycine max]	
Glym a.04G 03030 0	-	-	-	-	-	-	-	-	1.476 44	0.000 46	29 55	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0009536//plasti d	GO:0070566//adenylt ransferase activity	GO:0005982//starch metabolic process;GO:0005977//glycogen metabolic process	gi 947112837 gb KRH61139.1 gi 734431667 gb KHN45868.1 gi 94 7112838 gb KRH61140.1 gi 5714 48915 ref XP_006577992.1 /0;0;0 ;0/hypothetical protein GLYMA_04G030300 [Glycine max];Glucose-1-phosphate adenylyltransferase large subunit, chloroplastic/amyloplastic [Glycine soja];hypothetical protein GLYMA_04G030300 [Glycine max];PREDICTED: glucose-1-phosphate adenylyltransferase large subunit, chloroplastic/amyloplastic-like isoform X2 [Glycine max]	
Glym a.18G 26510 0	-	-	-	-	-	-	-	-	1.462 92	0.009 46	18 46	ko00053//Ascorbate and aldarate metabolism;ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0043231//intrac ellular membrane-bounded organelle;GO:00444 44;GO:0005576//ext racellular region	GO:0016616//oxidore ductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166// nucleotide binding	GO:0009226//nucleotide-sugar biosynthetic process;GO:0009664//plant-type cell wall organization	gi 734354133 gb KHN13571.1/0/ UDP-glucose 6-dehydrogenase [Glycine soja]	
Glym a.17G 06960 0	-	-	-	-	-	-	-	-	1.375 86	0.001 37	26 21	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0048037//cofactor binding;GO:0016857//r acemase and epimerase activity, acting on carbohydrates and derivatives	GO:0044238//primary metabolic process	gi 356562525 ref XP_003549520. 1/0/PREDICTED: UDP-glucuronate 4-epimerase 1 [Glycine max]	
Glym a.01G 03790 0	-	-	-	-	-	-	-	-	1.312 05	0.003 17	22 01	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transfera se activity	-	gi 356498063 ref XP_003517873. 1/0/PREDICTED: probable galacturonosyltransferase-like 9 [Glycine max]	
Glym a.14G 15960 0	-	-	-	-	-	-	-	-	1.259 84	0.000 81	23 87	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//extern al encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//c arboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysacc haride catabolic process;GO:0044092//negative regulation of molecular function	gi 955364443 ref XP_014622596. 1/0/PREDICTED: probable pectinesterase/pectinesterase inhibitor 61 isoform X1 [Glycine max]	
Glym a.06G 12940 0	-	-	-	-	-	-	-	-	1.145 75	0.010 4	20 48	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0009532//plasti d stroma	GO:0046527//glucosylt ransferase activity	GO:0009059//macromolecule biosynthetic process;GO:0006073//cellular glucan metabolic process	gi 947105123 gb KRH53506.1/0/ hypothetical protein GLYMA_06G129400, partial [Glycine max]	
Glym a.13G 16160 0	-	-	-	-	-	-	-	-	1.095 13	0.001 25	41 00	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0005911//cell-c ell junction;GO:004444 4;GO:0016020//me mbrane	GO:0035251//UDP-glu cosyltransferase activity	GO:0005985//sucrose metabolic process	gi 947071288 gb KRH20179.1 gi 356548520 ref XP_003542649.1 / 0/0/hypothetical protein GLYMA_13G161600 [Glycine max];PREDICTED: probable	

																	sucrose-phosphate synthase [Glycine max]	
Glyma.11G010400	-	-	-	-	-	-	-	-	1.01237	0.01038	4001	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	GO:0031224//intrinsic component of membrane	GO:0016759//cellulose synthase activity	GO:0030243//cellulose metabolic process		gi 356538575 ref XP_003537778.1 /0/PREDICTED: cellulose synthase-like protein D2 [Glycine max]	
Glyma.18G262500	-	-	-	-	-	-	-	-	-1.0727	0.00386	1745	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//external encapsulating structure	GO:0052689//carboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0010393		gi 571549278 ref XP_006602929.1 /0/PREDICTED: pectinesterase 31-like [Glycine max]	
Glyma.02G226600	-	-	-	-	-	-	-	-	-1.0739	0.00302	1688	ko00051//Fructose and mannose metabolism;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0032958//inositol phosphate biosynthetic process		gi 571441318 ref XP_003518306.2 /0/PREDICTED: inositol 3-kinase-like [Glycine max]	
Glyma.12G240000	-	-	-	-	-	-	-	-	-1.075	0.00544	1941	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanosamino acid metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0005618//cell wall;GO:0043231//intracellular membrane-bounded organelle;GO:0005911//cell-cell junction	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0071704//organic substance metabolic process;GO:0044238//primary metabolic process;GO:0000904//cell morphogenesis involved in differentiation		gi 734370810 gb KHN19426.1 /0/Beta-glucosidase 13 [Glycine soja]	
Glyma.04G008400	-	-	-	-	-	-	-	-	-1.5185	0.00171	2008	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process		gi 356509549 ref XP_003523510.1 /0/PREDICTED: endoglucanase 24-like [Glycine max]	
Glyma.05G236600	-	-	-	-	-	-	-	-	-1.618	0.00341	1125	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0030234//enzyme regulator activity;GO:0052689//carboxylic ester hydrolase activity	GO:0044092//negative regulation of molecular function		gi 356513076 ref XP_003525240.1 /2.77858e-145/PREDICTED: 21 kDa protein-like [Glycine max]	
Glyma.17G044700	-	-	-	-	-	-	-	-1.7428	3.65E-06	-1.7283	8.46E-05	2227	ko00040//Pentose and glucuronate interconversions;ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0030312//external encapsulating structure	GO:0030234//enzyme regulator activity;GO:0052689//carboxylic ester hydrolase activity	GO:0071555//cell wall organization;GO:0000272//polysaccharide catabolic process;GO:0044092//negative regulation of molecular function		gi 356564706 ref XP_003550590.1 /0/PREDICTED: putative pectinesterase/pectinesterase inhibitor 45 [Glycine max]
Glyma.05G163600	-	-	-	-	-	-	-	-	-2.3975	0.00121	3005	ko00500//Starch and sucrose metabolism	-	GO:0019203//carbohydrate phosphatase activity;GO:0035251//UDP-glucosyltransferase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0005991//trehalose metabolic process		gi 356510997 ref XP_003524218.1 /0/PREDICTED: alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1-like [Glycine max]	
Glyma.06G008200	-	-	-	-	-	-	-	-	-2.5764	9.36E-06	1895	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238//primary metabolic process		gi 356517881 ref XP_003527614.1 /0/PREDICTED: endoglucanase 24-like [Glycine max]	

Supplementary Table S7: DEGs involved in defense mechanisms

GeneID	log2Ratio(2mlp a-1/2M WT-1)	P-value	log2Ratio(2mlp a-2/2M WT-2)	P-value	log2Ratio(2mlp a-3/2M WT-3)	P-value	log2Ratio(2mlp a-4/2M WT-4)	P-value	log2Ratio(2mlp a-5/2M WT-5)	P-value	Length	Pathway	GO Component	GO Function	GO Process	Blast nr
Glyma_U035700	2.43731	7.73E-15	1.31096	0.000149	1.15885	0.00026	-	-	2.00447	0.00032	3324	ko04626//Plant-pathogen interaction	-	GO:0016462//pyrophosphatase activity;GO:0032550;GO:0036094//small molecule binding;GO:1901363;GO:0097159//organic cyclic compound binding	GO:0006950//response to stress;GO:0007154//cell communication	gi 947038010 gb KRG88494.1 ;gi 947038009 gb KRG88493.1 ;gi 947038006 gb KRG88490.1 ;gi 955395634 ref XP_014628764.1 ;gi 947038007 gb KRG88491.1 ;gi 947038002 gb KRG88486.1 ;gi 947038005 gb KRG88489.1 ;gi 947038004 gb KRG88488.1 ;gi 947038003 gb KRG88487.1 /0;0;0;0;0;0;0/hypothetical protein GLYMA_U035700, partial [Glycine max];hypothetical protein GLYMA_U035700, partial [Glycine max];hypothetical protein GLYMA_U035700, partial [Glycine max];PREDICTED: TMV resistance protein N-like, partial [Glycine max];hypothetical protein GLYMA_U035700, partial [Glycine max];hypothetical protein GLYMA_U035700, partial [Glycine max];hypothetical protein GLYMA_U035700, partial [Glycine max];hypothetical protein GLYMA_U035700, partial [Glycine max];hypothetical protein GLYMA_U035700, partial [Glycine max]
Glyma_20G061300	-	-	-	-	-	-	-	-	2.77513	0.00674	3489	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 947040285 gb KRG90009.1 ;gi 947040287 gb KRG90011.1 ;gi 947040286 gb KRG90010.1 /0;0;0/hypothetical protein GLYMA_20G061300 [Glycine max];hypothetical protein GLYMA_20G061300 [Glycine max];hypothetical protein GLYMA_20G061300 [Glycine max]
Glyma_20G050700	-1.3244	6.58E-05	-	-	-	-	-	-	-	-	4266	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 947040118 gb KRG89842.1 ;gi 356577440 ref XP_003556833.1 /0;0/hypothetical protein GLYMA_20G050700 [Glycine max];PREDICTED: putative disease resistance RPP13-like protein 1 isoform X1 [Glycine max]
Glyma_18G086900	-2.307	0.000137	-	-	-3.6406	9.15E-07	-	-	-	-	3010	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 947049112 gb KRG98640.1 /0/hypothetical protein GLYMA_18G086900 [Glycine max]
Glyma_18G086600	-	-	-	-	-	-	-	-	3.16077	5.28E-05	3221	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 955384422 ref XP_014626398.1 /0/PREDICTED: disease resistance protein RPM1-like [Glycine max]
Glyma_17G245500	-	-	-	-	-	-	-	-	2.83107	0.00242	2929	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0009617//response to bacterium;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress	gi 356564213 ref XP_003550350.1 /0/PREDICTED: probable disease resistance protein At4g33300 [Glycine max]

Glyma. 17G180 100	-	-	-	-	-2.4985	0.00028	-	-	1.83128	0.00059	3836	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 571537529 ref XP_006601011.1 /0/PREDICTED: probable disease resistance protein At5g66900 [Glycine max]
Glyma. 16G214 900	4.65642	9.36E-30	3.54707	1.78E-10	3.92223	3.43E-16	3.89277	1.63E-15	3.15223	2.29E-05	2927	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0016462//pyrophosphatase activity	GO:0050896//response to stimulus;GO:0006950//response to stress;GO:0007154//cell communication	gi 947060016 gb KRH09422.1 ;gi 571530234 ref XP_006599700.1 ;gi 947060020 gb KRH09426.1 /0;0/hypothetical protein GLYMA_16G214900 [Glycine max];PREDICTED: TMV resistance protein N-like isoform X4 [Glycine max];hypothetical protein GLYMA_16G214900 [Glycine max]
Glyma. 16G214 800	-	-	-	-	-	-	-	-	2.03844	0.00432	1197	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 947060014 gb KRH09420.1 /0/hypothetical protein GLYMA_16G214800 [Glycine max]
Glyma. 16G213 700	-	-	-	-	-	-	-	-	4.79466	3.85E-08	3445	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication;GO:0050896//response to stimulus	gi 571530198 ref XP_006599690.1 ;gi 571530196 ref XP_006599689.1 ;gi 955374931 ref XP_014624138.1 /0;0/PREDICTED: TMV resistance protein N-like isoform X2 [Glycine max];PREDICTED: TMV resistance protein N-like isoform X1 [Glycine max];PREDICTED: TMV resistance protein N-like isoform X3 [Glycine max]
Glyma. 16G210 800	-	-	-	-	-	-	-	-	3.60977	0.00024	4638	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0036094//small molecule binding;GO:1901363;GO:0097159//organic cyclic compound binding;GO:0016462//pyrophosphatase activity	GO:0050896//response to stimulus;GO:0006950//response to stress;GO:0007154//cell communication	gi 947059932 gb KRH09338.1 ;gi 947059931 gb KRH09337.1 ;gi 35172431 ref NP_001237821.1 /0;0/hypothetical protein GLYMA_16G210800 [Glycine max];hypothetical protein GLYMA_16G210800 [Glycine max];candidate disease-resistance protein [Glycine max]
Glyma. 16G210 600	-	-	-	-	-	-	-	-	3.33939	0.00524	4549	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0016462//pyrophosphatase activity	GO:0050896//response to stimulus;GO:0006950//response to stress;GO:0007154//cell communication	gi 356559997 ref XP_003548282.1 ;gi 947059928 gb KRH09334.1 ;gi 947059927 gb KRH09333.1 /0;0/PREDICTED: TMV resistance protein N [Glycine max];hypothetical protein GLYMA_16G210600 [Glycine max];hypothetical protein GLYMA_16G210600 [Glycine max]
Glyma. 16G087 100	-	-	-	-	-	-	-	-	2.42611	0.00242	3617	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication;GO:0050896//response to stimulus	gi 571526878 ref XP_006599163.1 ;gi 947058007 gb KRH07413.1 /0;0/PREDICTED: TMV resistance protein N-like [Glycine max];hypothetical protein GLYMA_16G087100 [Glycine max]
Glyma. 16G086 700	-	-	-	-	-	-	-	-	3.72714	0.00035	3682	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 571526864 ref XP_006599159.1 /0/PREDICTED: TMV resistance protein N-like [Glycine max]

												pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction				
Glyma.16G033900	-	-	-	-	-	-	-	-	1.22042	0.00321	3868	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 571525333 ref XP_006598947.1 ;gi 947057200 gb KRRH06606.1 ;gi 571525345 ref XP_006598950.1 /0;0;0/PREDICTED: TMV resistance protein N-like isoform X1 [Glycine max];hypothetical protein GLYMA_16G033900 [Glycine max];PREDICTED: TMV resistance protein N-like isoform X2 [Glycine max]
Glyma.16G006400	-	-	-	-	-	-	-	-	4.05615	8.10E-05	3809	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 571524432 ref XP_006598818.1 ;gi 947056747 gb KRRH06153.1 /0;0;0/PREDICTED: putative disease resistance protein At4g11170 [Glycine max];hypothetical protein GLYMA_16G006400 [Glycine max]
Glyma.15G230700	-	-	-	-	-	-	-	-	2.59016	0.00068	4001	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 571520977 ref XP_006598091.1 ;gi 947064056 gb KRRH13317.1 /0;0;0/PREDICTED: putative disease resistance protein At3g14460 isoform X1 [Glycine max];hypothetical protein GLYMA_15G230700 [Glycine max]
Glyma.15G168500	-	-	-	-	-	-	-	-	3.41448	8.30E-05	3138	ko04626//Plant-pathogen interaction	-	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006950//response to stress;GO:0008152//metabolic process	gi 571513784 ref XP_006596935.1 ;gi 351727306 ref NP_001237924.1 /0;0;0/PREDICTED: CC-NBS-LRR class disease resistance protein isoform X1 [Glycine max];CC-NBS-LRR class disease resistance protein [Glycine max]
Glyma.15G127100	-1.8283	3.99E-05	-	-	-	-	-	-	-	-	3857	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 571522550 ref XP_006598349.1 /0;0/PREDICTED: putative disease resistance protein RGA3 [Glycine max]
Glyma.14G079600	-	-	-	-	-	-	-	-	1.61914	0.00122	2732	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0009617//response to bacterium;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress	gi 356552172 ref XP_003544443.1 /0/PREDICTED: probable disease resistance protein At4g33300 [Glycine max]
Glyma.14G079500	-	-	-	-	-	-	-	-	3.46527	0.00046	3226	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//	-	GO:0032550	GO:0009617//response to bacterium;GO:0009628//response to abiotic stimulus;GO:0006950//respon	gi 947066147 gb KRRH15290.1 ;gi 571508169 ref XP_003544442.2 /0;0;0/hypothetical protein GLYMA_14G079500 [Glycine max];PREDICTED: probable disease

												Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction			se to stress	resistance protein At4g33300 [Glycine max]
Glyma.13G285500	-	-	-	-	-	-	-	-	2.08844	0.00018	2506	ko04626//Plant-pathogen interaction	GO:0016020//membrane	GO:0032550;GO:0005515//protein binding;GO:0004702//receptor signaling protein serine/threonine kinase activity	GO:0035556//intracellular signal transduction;GO:0032147//activation of protein kinase activity;GO:0006950//response to stress	gi 356549811 ref XP_003543284.1 /0/PREDICTED: probable leucine-rich repeat receptor-like serine/threonine-protein kinase At5g15730 [Glycine max]
Glyma.13G193300	-	-	-	-	-	-	-	-	2.68408	0.00202	2962	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 947071784 gb KRH20675.1 /0/hypothetical protein GLYMA_13G193300 [Glycine max]
Glyma.13G190800	-2.642	0.000329	-	-	-	-	-	-	-	-	6542	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 351724721 ref NP_001237835.1 /0/disease resistance protein [Glycine max]
Glyma.13G071900	-1.7804	2.90E-06	-	-	-	-	-	-	-	-	4266	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 356550917 ref XP_003543829.1 /0/PREDICTED: putative disease resistance RPP13-like protein 1 [Glycine max]
Glyma.12G216000	-	-	-	-	-	-	-	-	2.00009	0.00115	1938	ko04626//Plant-pathogen interaction	GO:0016020//membrane	GO:0032550;GO:0005515//protein binding;GO:0004702//receptor signaling protein serine/threonine kinase activity	GO:0035556//intracellular signal transduction;GO:0032147//activation of protein kinase activity;GO:0006950//response to stress	gi 359806757 ref NP_001241300.1 /0/probable leucine-rich repeat receptor-like serine/threonine-protein kinase At5g15730-like [Glycine max]
Glyma.11G072100	-	-	-	-	-	-	-	-	1.64713	0.00409	4775	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 734423019 gb KHN41940.1 /0/Disease resistance RPP8-like protein 3 [Glycine soja]
Glyma.10G152200	-	-	-	-	-	-	-	-	3.00807	0.00746	3529	ko04626//Plant-pathogen interaction	GO:0031224//intrinsic component of membrane	GO:0046872//metal ion binding;GO:0016209//antioxidant activity;GO:0050664//oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	GO:0044707;GO:0006950//response to stress;GO:0044710	gi 947085173 gb KRH33894.1 /0/hypothetical protein GLYMA_10G152200 [Glycine max]
Glyma.09G258200	-	-	-2.3569	0.000468	-	-	-	-	-	-	2703	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 947091771 gb KRH40436.1 /0/hypothetical protein GLYMA_09G258200 [Glycine max]

Glyma. 09G210 600	-	-	-	-	-	-	-	-	2.82882	0.00115	3243	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 947090963 gb KRH39628.1 ;gi 356531473 ref XP_003534302.1 /0/0/hypothetical protein GLYMA_09G210600 [Glycine max];PREDICTED: disease resistance protein RPM1-like [Glycine max]
Glyma. 09G204 500	-	-	-	-	-	-	-	-	1.86353	0.00076	2748	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	GO:0080090//regulation of primary metabolic process;GO:1901576;GO:1901700;GO:0009889//regulation of biosynthetic process;GO:0006950//response to stress	gi 571478541 ref XP_003534274.2 /0/PREDICTED: transcription factor MYC2-like [Glycine max]
Glyma. 08G301 200	-	-	-	-	-	-	-	-	2.4358	0.00107	4462	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 571473774 ref XP_006586027.1 /0/PREDICTED: TMV resistance protein N-like isoform X1 [Glycine max]
Glyma. 07G077 700	-	-	-	-	-	-	-	-	4.26459	7.67E-05	8284	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0016462//pyrophosphatase activity	GO:0006950//response to stress	gi 571465371 ref XP_006583342.1 /0/PREDICTED: uncharacterized protein LOC100797322 [Glycine max]
Glyma. 07G065 000	-	-	-	-	-	-	-	-	-1.4807	0.00335	8012	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0016462//pyrophosphatase activity	GO:0006950//response to stress	gi 955330113 ref XP_006583276.2 /0/PREDICTED: uncharacterized protein LOC100810455 isoform X1 [Glycine max]
Glyma. 07G064 100	-1.5576	1.56E-12	-	-	-	-	-	-	1.29957	0.00024	9014	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0016462//pyrophosphatase activity	GO:0006950//response to stress	gi 955330053 ref XP_014633259.1 /0/PREDICTED: uncharacterized protein LOC100780862 isoform X5 [Glycine max]
Glyma. 07G063 600	-1.3486	2.93E-09	-	-	-	-	-	-	1.92709	2.67E-06	6075	ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding;GO:1901363;GO:0032550;GO:0016462//pyrophosphatase activity	GO:0006950//response to stress	gi 947099532 gb KRH48024.1 ;gi 947099531 gb KRH48023.1 /0/0/hypothetical protein GLYMA_07G063600 [Glycine max];hypothetical protein GLYMA_07G063600 [Glycine max]
Glyma. 07G062 900	-2.9084	2.66E-19	-	-	-	-	-	-	2.7345	0.00014	8215	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0016462//pyrophosphatase activity	GO:0006950//response to stress	gi 947099522 gb KRH48014.1 ;gi 571465132 ref XP_006583266.1 ;gi 955330079 ref XP_014633271.1 /0/0/0/hypothetical protein GLYMA_07G062900 [Glycine max];PREDICTED: uncharacterized protein LOC100808315 isoform X1 [Glycine max];PREDICTED: uncharacterized protein LOC100808315 isoform X2 [Glycine max]
Glyma. 07G037 000	-	-	-	-	-	-	-	-	3.45257	0.00152	3965	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 571464738 ref XP_006583154.1 ;gi 947099087 gb KRH47579.1 /0/0/PREDICTED: disease resistance protein RML1A-like [Glycine max];hypothetical protein GLYMA_07G037000 [Glycine max]
Glyma. 06G267 300	-	-	-	-	-	-	-	-	3.01267	0.0039	3171	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 351722777 ref NP_001235720.1 /0/resistance protein KR3 [Glycine max]
Glyma. 06G261 500	-	-	-	-	-	-	-	-	1.69889	0.00331	3650	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//P	-	GO:0032550	GO:0006950//response to stress;GO:0008037//cell recognition;GO:0007154//cell communication	gi 571462237 ref XP_003526160.2 /0/PREDICTED: TMV resistance protein N-like [Glycine max]

												lant-pathogen interaction				
Glyma.06G260100	-	-	-	-	-	-	-	-	2.04977	6.58E-05	3893	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0008037//cell recognition;GO:0007154//cell communication	gi 356517237 ref XP_003527295.1 /0/PREDICTED: TMV resistance protein N [Glycine max]
Glyma.06G259800	-	-	-	-	-2.2682	0.00131	-	-	3.24167	0.00055	4077	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0008037//cell recognition;GO:0007154//cell communication;GO:0050896//response to stimulus	gi 947107122 gb KRRH55505.1;gi 947107121 gb KRRH55504.1 /0;0/hypothetical protein GLYMA_06G259800 [Glycine max];hypothetical protein GLYMA_06G259800 [Glycine max]
Glyma.06G259400	-	-	-	-	-	-	-	-	3.81531	1.43E-06	3959	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0008037//cell recognition;GO:0007154//cell communication;GO:0050896//response to stimulus	gi 947107112 gb KRRH55495.1;gi 947107117 gb KRRH55500.1;gi 947107116 gb KRRH55499.1;gi 947107115 gb KRRH55498.1;gi 947107113 gb KRRH55496.1;gi 947107114 gb KRRH55497.1 /0;0;0;0;0/hypothetical protein GLYMA_06G259400 [Glycine max];hypothetical protein GLYMA_06G259400 [Glycine max];hypothetical protein GLYMA_06G259400 [Glycine max];hypothetical protein GLYMA_06G259400 [Glycine max];hypothetical protein GLYMA_06G259400 [Glycine max];hypothetical protein GLYMA_06G259400 [Glycine max]
Glyma.05G082000	-	-	-	-	-	-	-	-	3.37412	1.43E-05	4316	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress;GO:0008037//cell recognition;GO:0007154//cell communication;GO:0050896//response to stimulus	gi 947107062 gb KRRH55445.1;gi 947107064 gb KRRH55447.1;gi 955325788 ref XP_014632205.1;gi 947107067 gb KRRH55450.1;gi 947107063 gb KRRH55446.1;gi 955325790 ref XP_014632206.1 /0;0;0;0;0/hypothetical protein GLYMA_06G256000 [Glycine max];hypothetical protein GLYMA_06G256000 [Glycine max];PREDICTED: disease resistance-like protein CSA1 isoform X1 [Glycine max];hypothetical protein GLYMA_06G256000 [Glycine max];hypothetical protein GLYMA_06G256000 [Glycine max];PREDICTED: disease resistance-like protein CSA1 isoform X2 [Glycine max]
Glyma.05G082500	-	-	-	-	-2.2138	0.00091	-	-	2.48655	0.00114	3736	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 571454745 ref XP_006579882.1 /0/PREDICTED: probable disease resistance protein At5g66900 [Glycine max]

												interaction				
Glyma. 05G082 400	-	-	-	-	-1.2847	9.67E-0 5	-	-	-	-	2976	ko00230//Purine metabolism;ko00240//P yrimidine metabolism;ko01100// Metabolic pathways;ko03020//RN A polymerase;ko04626//P lant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 571454747 ref XP_006579883.1 /0/PREDIC TED: probable disease resistance protein At5g66900 [Glycine max]
Glyma. 05G082 200	-	-	-	-	-1.6823	0.00043	-	-	2.29377	0.00314	3498	ko04626//Plant-pathoge n interaction	-	GO:0032550	GO:0006950//response to stress	gi 356511730 ref XP_003524576.1 /0/PREDIC TED: probable disease resistance protein At5g66900 isoform X1 [Glycine max]
Glyma. 04G134 700	-1.6685	2.87E-1 1	-	-	-	-	-	-	2.32564	0.00019	2957	ko04626//Plant-pathoge n interaction	GO:00432 31//intrac ellular membrane -bounded organelle	GO:0046914//transition metal ion binding;GO:0016301//kina se activity;GO:0032550;GO: 0005515//protein binding;GO:0019787//ubiq uitin-like protein transferase activity;GO:0050136//NA DH dehydrogenase (quinone) activity	GO:0040007//growth;GO:190 2582;GO:0032446//protein modification by small protein conjugation;GO:0006950//res ponse to stress;GO:0009738//abscisic acid-activated signaling pathway;GO:0046903//secreti on;GO:0022904//respiratory electron transport chain	gi 947114519 gb KRH62821.1 /0/hypothetical protein GLYMA_04G134700 [Glycine max]
Glyma. 03G236 300	-	-	-	-	-	-	-	-	3.67642	0.00059	3154	ko04626//Plant-pathoge n interaction	GO:00312 24//intrinsic component of membrane	GO:0046872//metal ion binding;GO:0016209//anti oxidant activity;GO:0050664//oxid oreductase activity, acting on NAD(P)H, oxygen as acceptor	GO:0044707;GO:0006950//re sponse to stress;GO:0044710	gi 356505839 ref XP_003521697.1 ;gi 947120 277 gb KRH68526.1 /0;0/PREDICTED: respiratory burst oxidase homolog protein B-like [Glycine max];hypothetical protein GLYMA_03G236300 [Glycine max]
Glyma. 03G087 500	4.67502	2.13E-1 3	3.878	2.10E-0 8	1.88006	4.47E-0 5	-	-	2.60263	2.70E-0 6	3462	ko00230//Purine metabolism;ko00240//P yrimidine metabolism;ko01100// Metabolic pathways;ko03020//RN A polymerase;ko04626//P lant-pathogen interaction	-	GO:0032550	GO:0050896//response to stimulus;GO:0006950//respon se to stress;GO:0007154//cell communication	gi 947117919 gb KRH66168.1 ;gi 947117917 g b KRH66166.1 ;gi 947117918 gb KRH66167.1 /0;0;0/hypothetical protein GLYMA_03G087500 [Glycine max];hypothetical protein GLYMA_03G087500 [Glycine max];hypothetical protein GLYMA_03G087500 [Glycine max]
Glyma. 03G075 200	-	-	-	-	-	-	-	-	1.67137	0.00106	4750	ko00230//Purine metabolism;ko00240//P yrimidine metabolism;ko01100// Metabolic pathways;ko03020//RN A polymerase;ko04626//P lant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 351723333 ref NP_001237787.1 /0/NB-LRR type disease resistance protein [Glycine max]
Glyma. 02G041 800	-1.0331	0.00533 4	-	-	-	-	-	-	-	-	4056	ko04626//Plant-pathoge n interaction	-	GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 571438700 ref XP_006574650.1 ;gi 571438 704 ref XP_006574651.1 /0;0/PREDICTED: TMV resistance protein N-like isoform X1 [Glycine max];PREDICTED: TMV resistance protein N-like isoform X2 [Glycine max]
Glyma. 01G244 500	-	-	-	-	-	-	-	-	-1.6733	0.00048	1475	ko04626//Plant-pathoge n interaction	GO:00059 11//cell-ce ll	-	GO:0006950//response to stress	gi 356497514 ref XP_003517605.1 /7.23568e- 107/PREDICTED: protein SRC2 homolog [Glycine max]

														junction;GO:0044444			
Glyma.01G183400	-	-	-	-	-	-	-	1.21537	0.00257	3041	ko00230//Purine metabolism;ko00240//P yrimidine metabolism;ko01100// Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 356495456 ref XP_003516593.1 /0/PREDICTED: probable disease resistance protein At5g66900 [Glycine max]		
Glyma.01G039000	-1.5056	0.000133	-	-	-	-	-	-	-	4612	ko04626//Plant-pathogen interaction	-	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 571434029 ref XP_006573080.1 ;gi 947126871 gb KRH74725.1 /0;0/PREDICTED: TMV resistance protein N-like [Glycine max];hypothetical protein GLYMA_01G039000 [Glycine max]		
Glyma.01G010500	-	-	-	-	-3.5148	1.77E-05	-	-	-	3423	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0006950//response to stress	gi 351721361 ref NP_001235671.1 /0/NBS-LRR type disease resistance protein [Glycine max]		
Glyma.01G013500	-1.6818	0.000117	-	-	-	-	-	-	-	2710	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity	GO:0044237//cellular metabolic process	gi 356497629 ref XP_003517662.1 /0/PREDICTED: putative receptor-like protein kinase At4g00960 [Glycine max]		
Glyma.01G019700	-	-	-	-	-	-	-1.2556	0.00045	-	1586	ko04075//Plant hormone signal transduction;ko04626// Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 918463553 gb AL.A09121.1 ;gi 947126586 gb KRH74440.1 ;gi 571433718 ref XP_006572984.1 /0;0;0/bHLH transcription factor, partial [Glycine max];hypothetical protein GLYMA_01G019700 [Glycine max];PREDICTED: transcription factor bHLH93-like isoform X2 [Glycine max]		
Glyma.01G169500	-	-	-	-	-	-	1.34073	0.00063	-	1949	ko04626//Plant-pathogen interaction	-	-	-	gi 571435744 ref XP_003516553.2 /0/PREDICTED: leucine-rich repeat receptor-like protein kinase PXL2 [Glycine max]		
Glyma.02G030500	1.34889	0.004014	-	-	-	-	-	-	-	1808	ko00230//Purine metabolism;ko00240//P yrimidine metabolism;ko01100// Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 734394680 gb KHN28666.1 /0/Disease resistance RPP13-like protein 4 [Glycine soja]		
Glyma.02G060800	-	-	-	-	-	-	3.3442	2.71E-06	-	519	ko04075//Plant hormone signal transduction;ko04626// Plant-pathogen interaction	-	-	-	gi 571438947 ref XP_003519913.2 /1.87092e-112/PREDICTED: STS14 protein-like [Glycine max]		
Glyma.02G122000	-1.6118	0.001313	-	-	-	-	-	-	-	2634	ko04626//Plant-pathogen interaction	GO:0071944//cell periphery; GO:0044464	GO:0032550;GO:0004672//protein kinase activity	GO:0006464//cellular protein modification process;GO:0044767;GO:0006796//phosphate-containing compound metabolic process	gi 571439797 ref XP_003520131.2 ;gi 947122773 gb KRH70979.1 /0;0/PREDICTED: receptor-like protein kinase FERONIA [Glycine max];hypothetical protein GLYMA_02G122000 [Glycine max]		
Glyma.02G133000	-	-	-	-	-	-	-1.1072	0.00022	-	1274	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0016491//oxidoreductase activity	-	gi 351721626 ref NP_001235680.1 /2.1097e-124/uncharacterized protein LOC100499763 [Glycine max]		
Glyma.02G186900	-3.6771	5.81E-08	-	-	-3.7279	6.25E-06	-	-	-	780	ko04626//Plant-pathogen interaction	-	-	-	gi 947123831 gb KRH72037.1 /1.48469e-120/hypothetical protein GLYMA_02G186900 [Glycine max]		

Glyma. 02G189 800	-7.1847	7.47E-1 8	-	-	-8	1.60E-0 6	-	-	-	-	1077	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity	GO:0044237//cellular metabolic process	gi 947123865 gb KRRH72071.1 /0/hypothetical protein GLYMA_02G189800 [Glycine max]
Glyma. 02G228 300	-	-	-	-	-3.0422	0.0009	-	-	-	-	1506	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity	GO:0044238//primary metabolic process;GO:0044260;GO:0016310//phosphorylation	gi 734432078 gb KHN46141.1 /0/Mitogen-activated protein kinase kinase 2 [Glycine soja]
Glyma. 02G263 900	-1.0188	0.00297 7	-	-	-	-	-	-	-	-	2483	ko04626//Plant-pathogen interaction	GO:003124//intrinsic component of membrane	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356499209 ref XP_003518434.1 /0/PREDICTED: probable inactive receptor-like protein kinase At3g56050 [Glycine max]
Glyma. 03G037 300	-1.7241	8.08E-0 5	-	-	-	-	-	-	-	-	4743	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 571444245 ref XP_006576452.1 /0/PREDICTED: putative disease resistance protein At3g14460 isoform X1 [Glycine max]
Glyma. 03G087 600	-1.0887	0.00035	-	-	-	-	-	-	-	-	3387	ko04626//Plant-pathogen interaction	-	-	-	gi 947117921 gb KRRH66170.1;gi 947117920 gb KRRH66169.1 /0;0/hypothetical protein GLYMA_03G087600, partial [Glycine max];hypothetical protein GLYMA_03G087600, partial [Glycine max]
Glyma. 03G165 800	-3.1109	3.90E-0 6	-	-	-	-	-	-	-	-	4009	ko04626//Plant-pathogen interaction	GO:003124//intrinsic component of membrane	GO:0004672//protein kinase activity;GO:0032550	GO:0006468//protein phosphorylation	gi 571445952 ref XP_003520610.2 /0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At4g08850 [Glycine max]
Glyma. 03G225 000	-2.187	0.00087 6	-	-	-	-	-	-	-	-	2036	ko04075//Plant hormone signal transduction;ko04712//Circadian rhythm - plant;ko04626//Plant-pathogen interaction	-	-	-	gi 571446784 ref XP_003520776.2 /0/PREDICTED: transcription factor PIF3-like [Glycine max]
Glyma. 03G232 500	-	-	-	-	-2.101	0.00129	-	-	-	-	2258	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-pathogen interaction	-	-	-	gi 356505783 ref XP_003521669.1;gi 571446892 ref XP_006577216.1 /0;0/PREDICTED: calmodulin-binding protein 60 B isoform X1 [Glycine max];PREDICTED: calmodulin-binding protein 60 B isoform X2 [Glycine max]
Glyma. 04G054 200	4.36501	2.66E-1 3	-	-	-	-	-	-	-	-	987	ko04626//Plant-pathogen interaction	-	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0050896//response to stimulus;GO:0050794//regulation of cellular process;GO:0006351//transcription, DNA-templated	gi 356507032 ref XP_003522275.1 /5.63141e-118/PREDICTED: probable WRKY transcription factor 50 [Glycine max]
Glyma. 04G090 100	1.39161	0.00180 6	-	-	-	-	-	-	-	-	1549	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 947113857 gb KRRH62159.1 /0/hypothetical protein GLYMA_04G090100 [Glycine max]
Glyma. 04G136 200	-	-	-	-	-5.5982	2.78E-0 5	-	-	-	-	919	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	-	gi 947114537 gb KRRH62839.1 /1.15828e-96/hypothetical protein GLYMA_04G136200 [Glycine max]
Glyma. 04G188 700	-	-	-	-	-	-	1.43891	1.01E-0 6	-	-	1936	ko04626//Plant-pathogen interaction	GO:0031981//nuclear lumen;GO	GO:0032550;GO:0017111//nucleoside-triphosphatase activity;GO:0008135//tran	GO:0006412//translation;GO:0009154//purine ribonucleotide catabolic process	gi 356508726 ref XP_003523105.1 /0/PREDICTED: elongation factor Tu, chloroplastic-like [Glycine max]

														:0005576//extracellular region;GO:0009534//chloroplast thylakoid;GO:0009526//plastid envelope	slation factor activity, nucleic acid binding		
Glyma.05G021100	-1.1036	3.09E-05	-	-	-	-	-	-	-	-	3526	ko04626//Plant-pathogen interaction	GO:003124//intrinsinc component of membrane	GO:0046872//metal ion binding;GO:0016651//oxidoreductase activity, acting on NAD(P)H;GO:0016209//antioxidant activity	GO:0044710	gi 571453402 ref XP_006579505.1 /0/PREDICTED: respiratory burst oxidase homolog protein A-like isoform X1 [Glycine max]	
Glyma.05G085200	-	-	-	-	-2.5529	7.52E-06	-	-	-	-	3109	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	-	gi 734386654 gb KHN25017.1 /2.19482e-121/Calmodulin-like protein 1 [Glycine soja]	
Glyma.06G147100	8.34201	1.33E-15	-	-	-	-	-	-	-	-	1180	ko04626//Plant-pathogen interaction	-	-	GO:0009987//cellular process	gi 356516303 ref XP_003526835.1 /1.14509e-118/PREDICTED: probable WRKY transcription factor 51 [Glycine max]	
Glyma.06G147500	1.2473	6.42E-05	-	-	-	-	-	-	-	-	1417	ko04626//Plant-pathogen interaction	-	-	-	gi 571460585 ref XP_003526838.2 ;gi 955324384 ref XP_014631935.1 ;gi 571460587 ref XP_006581742.1 /2.30138e-139;1.08246e-113;8.10111e-123/PREDICTED: probable WRKY transcription factor 13 isoform X1 [Glycine max];PREDICTED: probable WRKY transcription factor 13 isoform X3 [Glycine max];PREDICTED: probable WRKY transcription factor 13 isoform X2 [Glycine max]	
Glyma.06G155500	-	-	-	-	-	-	1.24487	0.00087	-	-	2762	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0050896//response to stimulus;GO:0006464//cellular protein modification process	gi 356516377 ref XP_003526871.1 /0/PREDICTED: probable receptor-like serine/threonine-protein kinase At5g57670 [Glycine max]	
Glyma.06G176900	-	-	-	-	-	-	1.30953	1.99E-05	-	-	2054	ko04626//Plant-pathogen interaction	GO:0031981//nuclear lumen;GO:0005576//extracellular region;GO:0009534//chloroplast thylakoid;GO:0009526//plastid envelope	GO:0032550;GO:0017111//nucleoside-triphosphatase activity;GO:0008135//translation factor activity, nucleic acid binding	GO:0006412//translation;GO:0009154//purine ribonucleotide catabolic process	gi 356516623 ref XP_003526993.1 /0/PREDICTED: elongation factor Tu, chloroplastic [Glycine max]	
Glyma.06G256600	-2.2655	0.000243	-	-	-	-	-	-	-	-	2728	ko04626//Plant-pathogen interaction	-	-	-	gi 947107079 gb KRNH55462.1 ;gi 947107078 gb KRNH55461.1 /0;0/hypothetical protein GLYMA_06G256600 [Glycine max];hypothetical protein GLYMA_06G256600 [Glycine max]	
Glyma.07G003200	-	-	-	-	-	-	1.33451	0.00048	-	-	2281	ko04626//Plant-pathogen interaction	GO:0043231//intracellular membrane-bounded organelle	GO:0032550;GO:0004672//protein kinase activity	GO:0045682//regulation of epidermis development;GO:0045087//innate immune response;GO:0006464//cellular protein modification process;GO:0006796//phosphate-containing compound	gi 356521707 ref XP_003529493.1 /0/PREDICTED: mitogen-activated protein kinase kinase 4 [Glycine max]	

																metabolic process;GO:0090567	
Glyma.07G101100	-	-	-	-	-	-	1.64321	6.92E-05	-	-	911	ko04626//Plant-pathogen interaction	GO:0016020//membrane;GO:0043231//intracellular membrane-bounded organelle	GO:0046872//metal ion binding	-	gi 356520641 ref XP_003528969.1 /3.56334e-128/PREDICTED: probable calcium-binding protein CML18 [Glycine max]	
Glyma.07G143500	2.64784	0.000726	-	-	-	-	-	-	-	-	3222	ko04626//Plant-pathogen interaction	-	-	-	gi 947100766 gb KRH49258.1 /0/hypothetical protein GLYMA_07G143500 [Glycine max]	
Glyma.07G148500	-1.0211	0.00404	-	-	-	-	-	-	-	-	1859	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 571466375 ref XP_006583644.1 /0/PREDICTED: putative serine/threonine-protein kinase isoform X1 [Glycine max]	
Glyma.07G188800	-1.1234	0.004431	-	-	-	-	-	-	-	-	3106	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 356519528 ref XP_003528424.1 ;gi 947101435 gb KRH49927.1 /0;0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase B120 isoform X1 [Glycine max];hypothetical protein GLYMA_07G188800 [Glycine max]	
Glyma.07G229500	3.72869	2.51E-09	-	-	-	-	-	-	-	-	671	ko04626//Plant-pathogen interaction	-	-	-	gi 571467514 ref XP_006583962.1 /3.62461e-119/PREDICTED: probable calcium-binding protein CML45 [Glycine max]	
Glyma.08G089100	-1.1854	0.004227	-	-	-	-	-	-	-	-	2077	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 734395411 gb KHN28921.1 /0/Transcription factor bHLH91 [Glycine soja]	
Glyma.08G140900	-1.259	1.42E-06	-	-	-	-	-	-	-	-	2896	ko04626//Plant-pathogen interaction	GO:0009526//plastid envelope	GO:0016740//transferase activity	-	gi 356525527 ref XP_003531376.1 /0/PREDICTED: uncharacterized protein sl1770-like [Glycine max]	
Glyma.08G300900	-	-	4.05723	7.94E-12	-	-	-	-	-	-	804	ko04626//Plant-pathogen interaction	GO:0043231//intracellular membrane-bounded organelle	-	-	gi 947097334 gb KRH45919.1 /0/hypothetical protein GLYMA_08G300900 [Glycine max]	
Glyma.08G317400	-1.281	0.004056	-	-	-	-	-	-	-	-	4364	ko04626//Plant-pathogen interaction	-	-	-	gi 955337909 ref XP_014634887.1 /0/PREDICTED: disease resistance protein RPM1-like [Glycine max]	
Glyma.09G048300	-1.2898	9.83E-12	-	-	-	-	-	-	-	-	4435	ko04626//Plant-pathogen interaction	GO:0016020//membrane	GO:0036094//small molecule binding;GO:0004672//protein kinase activity;GO:1901363;GO:0097159//organic cyclic compound binding	GO:0006796//phosphate-containing compound metabolic process	gi 571476366 ref XP_003533521.2 /0/PREDICTED: LRR receptor-like serine/threonine-protein kinase GSO1 [Glycine max]	
Glyma.09G060200	-1.6886	0.000164	-	-	-2.2121	9.07E-06	-	-	-	-	1321	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 358248852 ref NP_001239951.1 /4.42554e-170/transcription factor bHLH35-like [Glycine max]	
Glyma.09G073200	-2.895	8.92E-08	-	-	-	-	-	-	-	-	3397	ko04626//Plant-pathogen interaction	GO:0031224//intracellular component of membrane	GO:0046872//metal ion binding;GO:0016651//oxidoreductase activity, acting on NAD(P)H;GO:0016209//antioxidant activity	GO:0044710	gi 947088885 gb KRH37550.1 ;gi 571476753 ref XP_006587062.1 /0;0/hypothetical protein GLYMA_09G073200 [Glycine max];PREDICTED: respiratory burst oxidase homolog protein E-like [Glycine max]	

Glyma. 09G131 500	-	-	-	-	-2.5086	6.29E-08	-	-	-	-	2458	ko04141//Protein processing in endoplasmic reticulum;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding;GO:0032550	GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process	gi 959092738 ref NP_001304616.1 /0/heat shock protein 83 [Glycine max]
Glyma. 09G173 800	-1.1171	0.000813	-	-	-	-	-	-	-	-	1965	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	GO:0005911//cell-cell junction;GO:0031224//intrinsic component of membrane;GO:004437	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947090375 gb KRH39040.1 /0/hypothetical protein GLYMA_09G173800 [Glycine max]
Glyma. 09G208 900	-1.4835	3.54E-05	-	-	-	-	-	-	-	-	2205	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 947090939 gb KRH39604.1 /0/hypothetical protein GLYMA_09G208900 [Glycine max]
Glyma. 09G216 400	-	-	8.34377	3.44E-12	-	-	-	-	-	-	4263	ko04626//Plant-pathogen interaction	GO:0031224//intrinsic component of membrane	GO:0004672//protein kinase activity;GO:0032550;GO:0016301//kinase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947091060 gb KRH39725.1 ;gi 571478728 ref XP_006587651.1 /0/0/hypothetical protein GLYMA_09G216400 [Glycine max];PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At3g47570 isoform X2 [Glycine max]
Glyma. 09G270 400	-1.2044	0.001246	-	-	-	-	-	-	-	-	1365	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	-	gi 955342880 ref XP_014617928.1 /7.75255e-114/PREDICTED: cysteine-rich receptor-like protein kinase 24 [Glycine max]
Glyma. 10G026 000	-1.035	2.29E-06	-	-	-	-	-	-	-	-	2818	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	GO:0044763;GO:0031326;GO:0006351//transcription, DNA-templated	gi 571481338 ref XP_006588626.1 /0/PREDICTED: basic helix-loop-helix protein A-like [Glycine max]
Glyma. 10G109 200	-1.9431	2.71E-07	-	-	-	-	-	-	-	-	2092	ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:0004672//protein kinase activity;GO:1901363;GO:0097159//organic cyclic compound binding;GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006464//cellular protein modification process	gi 571482431 ref XP_006588951.1 ;gi 947084513 gb KRH33234.1 ;gi 571482433 ref XP_006588952.1 ;gi 955345591 ref XP_014618594.1 ;gi 571482429 ref XP_006588950.1 /0/0/0/0/PREDICTED: cysteine-rich receptor-like protein kinase 19 isoform X2 [Glycine max];hypothetical protein GLYMA_10G109200 [Glycine max];PREDICTED: cysteine-rich receptor-like protein kinase 25 isoform X3 [Glycine max];PREDICTED: cysteine-rich receptor-like protein kinase 24 isoform X4 [Glycine max];PREDICTED: cysteine-rich receptor-like protein kinase 25 isoform X1 [Glycine max]
Glyma. 10G186 000	-1.1519	1.60E-06	-	-	-	-	-	-	-	-	1228	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 351723241 ref NP_001237016.1 /0/phosphoenolpyruvate-carboxylase [Glycine max]
Glyma. 10G195 700	1.37747	0.000323	2.14603	8.70E-05	-	-	-	-	-	-	3252	ko04626//Plant-pathogen interaction	GO:0031224//intrinsic component	GO:0004672//protein kinase activity;GO:0032550;GO:0016772//transferase	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356533862 ref XP_003535477.1 ;gi 734415812 gb KHN37899.1 /0/0/PREDICTED: receptor-like protein kinase [Glycine max];Receptor-like protein kinase [Glycine

														of membrane	activity, transferring phosphorus-containing groups		soja]
Glyma. 10G252 700	1.93406	0.00034 4	-	-	-	-	-	-	-	-	2254	ko04075//Plant hormone signal transduction;ko04626// Plant-pathogen interaction	-	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-cont aining compound metabolic process;GO:0006464//cellular protein modification process	gi 947086881 gb KRH35602.1 ;gi 571480841 r ef XP_006588454.1 ;gi 947086882 gb KRH35 603.1 /0;0;0/hypothetical protein GLYMA_10G252700 [Glycine max];PREDICTED: cysteine-rich receptor-like protein kinase 10-like isoform X1 [Glycine max];hypothetical protein GLYMA_10G252700 [Glycine max]
Glyma. 10G253 200	3.2775	5.20E-0 9	-	-	-	-	-	-	-	-	2615	ko04075//Plant hormone signal transduction;ko04626// Plant-pathogen interaction	-	-	-	-	gi 356534242 ref XP_003535666.1 /0/PREDIC TED: cysteine-rich receptor-like protein kinase 26 [Glycine max]
Glyma. 10G263 200	-	-	-	-	1.04849	0.00087	1.62627	2.85E-0 7	-	-	1670	ko04626//Plant-pathoge n interaction	-	-	-	-	gi 356536184 ref XP_003536619.1 /0/PREDIC TED: probable LRR receptor-like serine/threonine-protein kinase At4g20940 [Glycine max]
Glyma. 11G045 700	-	-	-	-	-	-	1.34784	3.23E-0 5	-	-	1666	ko04075//Plant hormone signal transduction;ko04626// Plant-pathogen interaction	-	-	-	-	gi 359806711 ref NP_001241548.1 /1.26439e- 162/LRR receptor-like serine/threonine-protein kinase GSO2-like precursor [Glycine max]
Glyma. 11G056 500	1.43199	0.00272 5	-	-	-	-	-	-	-	-	1480	ko04626//Plant-pathoge n interaction	-	-	GO:0046872//metal ion binding	-	gi 734423154 gb KHN42075.1 /2.89802e-135/ Calmodulin-like protein 1 [Glycine soja]
Glyma. 11G073 800	-	-	-	-	-	-	1.5327	1.36E-0 6	-	-	1986	ko04626//Plant-pathoge n interaction	-	-	-	-	gi 359807401 ref NP_001241130.1 /0/LRR receptor-like serine/threonine-protein kinase GSO1-like precursor [Glycine max]
Glyma. 12G143 000	-2.3424	0.00058 5	-	-	-	-	-	-	-	-	2742	ko04626//Plant-pathoge n interaction	-	-	GO:0016301//kinase activity;GO:0004672//prot ein kinase activity;GO:0032550	GO:0009987//cellular process;GO:0006464//cellular protein modification process	gi 734414229 gb KHN37217.1 ;gi 947077133 gb KRH25973.1 ;gi 571493480 ref XP_006592 565.1 ;gi 571493478 ref XP_006592564.1 /0;0; 0;0/G-type lectin S-receptor-like serine/threonine-protein kinase [Glycine soja];hypothetical protein GLYMA_12G143000 [Glycine max];PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase SD1-1 isoform X3 [Glycine max];PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X2 [Glycine max]
Glyma. 12G172 700	1.32281	0.00330 8	-	-	-	-	-	-	-	-	2039	ko04626//Plant-pathoge n interaction	-	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 571493920 ref XP_006592693.1 /0/PREDIC TED: serine/threonine-protein kinase CDL1-like [Glycine max]
Glyma. 12G175 300	-1.6315	1.28E-1 0	-	-	-	-	-	-	-	-	2971	ko04626//Plant-pathoge n interaction	GO:00444 40	GO:0032550;GO:0004672 //protein kinase activity;GO:0019899//enz yme binding	GO:0010087//phloem or xylem histogenesis;GO:0006464//cel lular protein modification process;GO:0006796//phosph ate-containing compound metabolic process	gi 955351956 ref XP_014619794.1 ;gi 947077 612 gb KRH26452.1 ;gi 351725463 ref NP_00 1237605.1 ;gi 955351954 ref XP_014619793.1 /0;0;0;0/PREDICTED: protein kinase family protein isoform X3 [Glycine max];hypothetical protein GLYMA_12G175300 [Glycine max];protein kinase family protein precursor [Glycine max];PREDICTED: protein kinase family protein isoform X2 [Glycine max]	
Glyma. 12G198 600	-1.2985	0.00195 3	-	-	-	-	-	-	-	-	2860	ko04075//Plant hormone signal transduction;ko04626// Plant-pathogen interaction	-	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-cont aining compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 955355212 ref XP_014620518.1 ;gi 571494 369 ref XP_006592830.1 /0;0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130 isoform X1 [Glycine max];PREDICTED: G-type lectin S-receptor-like

																serine/threonine-protein kinase At2g19130 isoform X2 [Glycine max]
Glyma.13G053700	4.07098	2.44E-16	2.81783	8.92E-06	-	-	-	-	-	-	3047	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947069467 gb KRRH18358.1 /0/hypothetical protein GLYMA_13G053700 [Glycine max]
Glyma.13G054300	-2.8374	1.24E-07	-2.5232	0.000178	-	-	-	-	-	-	2535	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 351727166 ref NP_001238431.1 /0/FERONIA receptor-like kinase precursor [Glycine max]
Glyma.13G080700	-1.5216	0.000874	-	-	-	-	-	-	-	-	1185	ko04626//Plant-pathogen interaction	GO:0031225//anchored component of membrane	GO:0005539//glycosaminoglycan binding	GO:0044036//cell wall macromolecule metabolic process;GO:0002376//immune system process	gi 947069872 gb KRRH18763.1 ;gi 947069871 gb KRRH18762.1 /0;0/hypothetical protein GLYMA_13G080700 [Glycine max];hypothetical protein GLYMA_13G080700 [Glycine max]
Glyma.13G184800	-1.6136	2.18E-06	-	-	-1.7479	0.00035	-1.9949	1.42E-05	-	-	4261	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 955358201 ref XP_014621131.1 /0/PREDICTED: putative disease resistance protein At3g14460 isoform X1 [Glycine max]
Glyma.13G190000	-2.2244	1.57E-07	-	-	-1.9935	0.00074	-2.0565	0.00053	-	-	3735	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 947071732 gb KRRH20623.1 /0/hypothetical protein GLYMA_13G190000 [Glycine max]
Glyma.13G195600	-1.4096	0.003179	-	-	-	-	-	-	-	-	3826	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 356546346 ref XP_003541587.1 /0/PREDICTED: putative disease resistance RPP13-like protein 1 isoform X1 [Glycine max]
Glyma.13G365900	-	-	-	-	1.39809	0.00012	1.54189	0.00031	-	-	1531	ko04626//Plant-pathogen interaction	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006796//phosphate-containing compound metabolic process;GO:0051301//cell division;GO:0001101//response to acid chemical	gi 947074694 gb KRRH23585.1 /0/hypothetical protein GLYMA_13G365900 [Glycine max]
Glyma.14G080100	-1.7885	2.52E-05	-	-	-	-	-	-	-	-	2915	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0032550;GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006464//cellular protein modification process	gi 947066158 gb KRRH15301.1 ;gi 571508197 ref XP_006595955.1 ;gi 356553923 ref XP_003545300.1 ;gi 571508200 ref XP_006595956.1 /0;0;0/hypothetical protein GLYMA_14G080100 [Glycine max];PREDICTED: mitogen-activated protein kinase kinase kinase 1-like isoform X2 [Glycine max];PREDICTED: MAP kinase kinase kinase mkh1-like isoform X1 [Glycine max];PREDICTED: mitogen-activated protein kinase kinase kinase YODA-like isoform X3 [Glycine max]

Glyma.14G173100	-1.7206	0.001058	-	-	-	-	-	-	-	-	909	ko04626//Plant-pathogen interaction	-	-	-	gi 947067578 gb KRRH16721.1 /0/hypothetical protein GLYMA_14G173100 [Glycine max]
Glyma.14G178000	-	-	-	-	-	-	-1.2401	0.0004	-	-	1985	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 356552929 ref XP_003544814.1 /0/PREDICTED: transcription factor bHLH96-like [Glycine max]
Glyma.14G186600	-1.5149	0.006118	-	-	-	-	-	-	-	-	4349	ko04626//Plant-pathogen interaction	-	-	-	gi 571511306 ref XP_006596398.1 /0/PREDICTED: probable disease resistance protein At4g27220 [Glycine max]
Glyma.14G199400	-2.7345	3.53E-10	-	-	-	-	-	-	-	-	2634	ko04626//Plant-pathogen interaction	-	-	-	gi 955362015 ref XP_014622020.1 /0/PREDICTED: disease resistance protein RPP13-like [Glycine max]
Glyma.14G215800	-1.686	2.05E-05	-	-	-	-	-	-	-	-	426	ko04626//Plant-pathogen interaction	GO:0016020//membrane	GO:0046872//metal ion binding	GO:0009642//response to light intensity;GO:0006952//defense response;GO:0010038//response to metal ion;GO:0001101//response to acid chemical;GO:0000302//response to reactive oxygen species;GO:0009908//flower development;GO:0009725//response to hormone;GO:0048571//long-day photoperiodism;GO:0051171//regulation of nitrogen compound metabolic process	gi 356553299 ref XP_003544994.1 /2.55184e-97/PREDICTED: probable calcium-binding protein CML18 [Glycine max]
Glyma.15G003300	-	-	-	-	-3.0234	6.87E-05	-	-	-	-	1619	ko04626//Plant-pathogen interaction	-	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0098542//defense response to other organism;GO:0006351//transcription, DNA-templated;GO:0010033//response to organic substance;GO:0050789//regulation of biological process	gi 947060391 gb KRRH09652.1 /0/hypothetical protein GLYMA_15G003300 [Glycine max]
Glyma.15G005100	-2.1938	1.92E-05	-	-	-	-	-	-	-	-	1293	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 947060425 gb KRRH09686.1;gi 356558556 ref XP_003547571.1 /0/hypothetical protein GLYMA_15G005100 [Glycine max];PREDICTED: transcription factor bHLH18-like [Glycine max]
Glyma.15G021300	-1.0055	0.000331	-	-	-	-	-	-	-	-	3188	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0016310//phosphorylation;GO:0006464//cellular protein modification process	gi 947060712 gb KRRH09973.1;gi 571514932 ref XP_006597179.1 /0/hypothetical protein GLYMA_15G021300 [Glycine max];PREDICTED: putative leucine-rich repeat receptor-like protein kinase At2g19210 [Glycine max]
Glyma.16G025400	1.45455	0.002021	-	-	-	-	-	-	-	-	2578	ko04626//Plant-pathogen interaction	GO:0031224//intrinsic component of membrane	GO:0005267//potassium channel activity	GO:0034220//ion transmembrane transport;GO:0051707//response to other organism;GO:0030001//metal ion transport	gi 571525040 ref XP_006598906.1 /0/PREDICTED: putative cyclic nucleotide-gated ion channel 13 [Glycine max]
Glyma.16G031700	-1.2156	7.50E-05	-	-	-	-	-	-	-	-	8487	ko04626//Plant-pathogen interaction	-	-	-	gi 947057171 gb KRRH06577.1 /0/hypothetical protein GLYMA_16G031700 [Glycine max]

Glyma. 16G137 300	-3.0028	2.00E-08	-	-	-	-	-	-	-	-	3711	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	GO:0050896//response to stimulus	gi 947058822 gb KRRH08228.1 /gi 947058821 gb KRRH08227.1 /0/hypothetical protein GLYMA_16G137300 [Glycine max];hypothetical protein GLYMA_16G137300 [Glycine max]
Glyma. 16G172 100	1.36638	0.005729	-	-	-	-	-	-	-	-	3246	ko04626//Plant-pathogen interaction	-	-	-	gi 947059346 gb KRRH08752.1 /0/hypothetical protein GLYMA_16G172100 [Glycine max]
Glyma. 16G174 400	-	-	2.82197	2.07E-09	3.5381	9.27E-06	2.91755	3.96E-06	-	-	1314	ko04626//Plant-pathogen interaction	-	-	-	gi 947059385 gb KRRH08791.1 /0/hypothetical protein GLYMA_16G174400 [Glycine max]
Glyma. 16G174 500	-	-	2.63316	2.74E-16	3.89368	2.36E-13	3.43608	1.18E-16	-	-	1698	ko04626//Plant-pathogen interaction	-	-	-	gi 947059386 gb KRRH08792.1 /0/hypothetical protein GLYMA_16G174500, partial [Glycine max]
Glyma. 16G178 800	-	-	-	-	-2.5748	3.91E-08	-	-	-	-	2787	ko04141//Protein processing in endoplasmic reticulum;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding;GO:0032550	GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process	gi 571529336 ref XP_006599549.1 /0/PREDICTED: heat shock protein 83-like [Glycine max]
Glyma. 16G202 400	4.13681	2.07E-09	-	-	-	-	-	-	-	-	2553	ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:0004672//protein kinase activity;GO:1901363;GO:0097159//organic cyclic compound binding;GO:0032550	GO:0006464//cellular protein modification process	gi 947059794 gb KRRH09200.1 /gi 947059792 gb KRRH09198.1 /gi 356561745 ref XP_003549139.1 /1.83213e-162;0/hypothetical protein GLYMA_16G202400 [Glycine max];hypothetical protein GLYMA_16G202400 [Glycine max];PREDICTED: cysteine-rich receptor-like protein kinase 10 [Glycine max]
Glyma. 16G214 600	-	-	3.12897	1.70E-06	-	-	-	-	-	-	3135	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0050896//response to stimulus	gi 947060012 gb KRRH09418.1 /0/hypothetical protein GLYMA_16G214600 [Glycine max]
Glyma. 17G085 000	-	-	-	-	-	-	1.37737	0.00018	-	-	2698	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356562682 ref XP_003549598.1 /0/PREDICTED: L-type lectin-domain containing receptor kinase S.1-like [Glycine max]
Glyma. 17G150 400	-1.8486	0.000146	-	-	-	-	-	-	-	-	882	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947054816 gb KRRH04269.1 /0/hypothetical protein GLYMA_17G150400 [Glycine max]
Glyma. 17G150 600	-1.4012	0.003606	-	-	-	-	-	-	-	-	2166	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 571536659 ref XP_003550928.2 /0/PREDICTED: probable L-type lectin-domain containing receptor kinase S.7 [Glycine max]
Glyma. 17G185 300	-1.8004	0.002111	-	-	6.25467	2.26E-09	-	-	-	-	516	ko04626//Plant-pathogen interaction	-	-	-	gi 947055314 gb KRRH04767.1 /1.54976e-111/hypothetical protein GLYMA_17G185300 [Glycine max]
Glyma. 17G187 200	-1.0292	4.88E-05	-	-	-	-	-	-	-	-	2779	ko04075//Plant hormone signal transduction;ko04626//	-	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular	gi 955377781 ref XP_014624839.1 /0/PREDICTED: probable inactive leucine-rich repeat receptor-like protein kinase At3g03770

												Plant-pathogen interaction			protein modification process	[Glycine max]
Glyma.18G026900	-12.34	2.08E-4 ₆	-9.977	4.88E-3 ₇	-10.577	9.89E-0 ₉	-3.3592	0.00107	-	-	1413	ko04626//Plant-pathogen interaction	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	-	gi 955382928 ref XP_003552842.3 /0/PREDICTED: putative serine/threonine-protein kinase-like protein CCR3 [Glycine max]
Glyma.18G076200	1.01857	0.00170 ₁	-	-	-	-	-	-	-	-	1764	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947048945 gb KRG98473.1 /0/hypothetical protein GLYMA_18G076200 [Glycine max]
Glyma.18G091800	-	-	-2.3481	0.00032 ₂	-	-	-2.8488	0.00028	-	-	2859	ko04626//Plant-pathogen interaction	-	-	-	gi 947049105 gb KRG98633.1 /5.16573e-129/hypothetical protein GLYMA_18G086300 [Glycine max]
Glyma.18G204500	-	-	-	-	5.03732	7.39E-2 ₇	6.40279	6.09E-2 ₈	-	-	3138	ko04626//Plant-pathogen interaction	-	-	-	gi 947050770 gb KRH00299.1 /0/hypothetical protein GLYMA_18G204500 [Glycine max]
Glyma.18G219800	-2.6256	6.49E-1 ₁	-	-	-	-	3.43879	9.85E-0 ₅	-	-	2944	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0036094//small molecule binding;GO:0004672//protein kinase activity;GO:1901363;GO:0097159//organic cyclic compound binding	GO:0044237//cellular metabolic process	gi 571548055 ref XP_006602745.1 ;gi 947051019 gb KRH00548.1 /0;0/PREDICTED: cysteine-rich receptor-like protein kinase 7 isoform X1 [Glycine max];hypothetical protein GLYMA_18G219800 [Glycine max]
Glyma.18G221400	-	-	-	-	2.33321	0.00077	-	-	-	-	2001	ko04626//Plant-pathogen interaction	GO:0043231//intracellular membrane-bounded organelle	GO:0005085//guanyl-nucleotide exchange factor activity	GO:0033124;GO:0009553//embryo sac development;GO:0032011//ARF protein signal transduction	gi 947051053 gb KRH00582.1 /1.48183e-178/hypothetical protein GLYMA_18G221400 [Glycine max]
Glyma.18G226300	-6.9116	4.87E-3 ₂	-	-	-	-	-6.3361	2.09E-1 ₃	-	-	9435	ko04626//Plant-pathogen interaction	-	-	-	gi 947051119 gb KRH00648.1 /0/hypothetical protein GLYMA_18G226300 [Glycine max]
Glyma.18G226500	-10.449	1.13E-2 ₅	-	-	-8.3636	1.56E-0 ₆	-7.747	3.75E-1 ₃	-	-	1058 ₃	ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding;GO:1901363	-	gi 947051121 gb KRH00650.1 /0/hypothetical protein GLYMA_18G226500 [Glycine max]
Glyma.18G226800	-6.9125	2.43E-4 ₅	-	-	-4.311	1.55E-0 ₇	-4.3603	2.88E-1 ₂	-	-	6246	ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding;GO:1901363	-	gi 947051124 gb KRH00653.1 /0/hypothetical protein GLYMA_18G226800 [Glycine max]
Glyma.18G226900	-9.0754	1.98E-1 ₆	-	-	-	-	-	-	-	-	4664	ko04626//Plant-pathogen interaction	-	-	-	gi 947051125 gb KRH00654.1 /0/hypothetical protein GLYMA_18G226900 [Glycine max]
Glyma.18G270800	-	-	-	-	3.77425	7.90E-0 ₈	-	-	-	-	2730	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity	GO:0006796//phosphate-containing compound metabolic process	gi 947051816 gb KRH01345.1 /0/hypothetical protein GLYMA_18G270800 [Glycine max]
Glyma.18G281700	1.61515	0.00244 ₁	-	-	-	-	-	-	-	-	4047	ko04626//Plant-pathogen interaction	-	-	-	gi 571549792 ref XP_003551801.2 /0/PREDICTED: probable disease resistance protein At4g27220 [Glycine max]
Glyma.18G287000	-	-	-2.3485	5.02E-0 ₅	-	-	-	-	-	-	3158	ko04626//Plant-pathogen interaction	-	-	-	gi 571549977 ref XP_006603027.1 /0/PREDICTED: disease resistance protein RPP13-like [Glycine max]

Glyma. 20G034 200	6.78477	1.36E-2 5	-	-	-	-	-	-	-	-	828	ko04626//Plant-pathogen interaction	-	-	-	gi 947039863 gb KRG89587.1 ;gi 734395097 gb KHN28802.1 /2.21565e-122;3.13952e-127/hypothetical protein GLYMA_20G034200 [Glycine max];Putative calcium-binding protein CML45 [Glycine soja]
Glyma. 20G132 400	-	-	-	-	-1.0367	0.00092	-	-	-	-	1141	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006796//phosphate-containing compound metabolic process	gi 955390929 ref XP_014627745.1 /1.80076e-124/PREDICTED: somatic embryogenesis receptor kinase 1-like isoform X1 [Glycine max]
Glyma. U00890 0	-1.4994	0.00050 7	-	-	-	-	-	-	-	-	2589	ko04626//Plant-pathogen interaction	-	-	-	gi 947038196 gb KRG88521.1 /0/hypothetical protein GLYMA_U008900 [Glycine max]
Glyma. U00880 0	5.37147	1.07E-2 2	5.18968	1.69E-2 4	-	-	-	-	10.5015	2.00E-1 0	1738	ko04626//Plant-pathogen interaction	-	-	-	gi 947038195 gb KRG88520.1 /0/hypothetical protein GLYMA_U008800 [Glycine max]
Glyma. 06G125 600	-	-	-	-	-	-	-	-	7.82888	9.42E-0 6	1743	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 959092742 ref NP_001304644.1 /0/probable WRKY transcription factor 53 [Glycine max]
Glyma. 10G002 200	-	-	-	-	-	-	-	-	7.59311	8.50E-0 5	1062	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	GO:0019932//second-messenger-mediated signaling	gi 351727589 ref NP_001236910.1 /1.00985e-102/uncharacterized protein LOC100526987 [Glycine max]
Glyma. 16G137 600	3.06089	4.26E-0 5	2.32125	3.36E-0 6	-	-	3.371	2.26E-0 6	6.77516	1.60E-1 6	3555	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	GO:0050896//response to stimulus	gi 955374830 ref XP_003548883.2 /0/PREDICTED: TMV resistance protein N-like [Glycine max]
Glyma. 16G026 400	-	-	-	-	-	-	-	-	5.61978	6.51E-1 1	1825	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 918463837 gb ALA09263.1 /0/WRKY transcription factor, partial [Glycine max]
Glyma. 09G005 700	-	-	-	-	-	-	-	-	5.51639	5.20E-0 8	1942	ko04626//Plant-pathogen interaction	-	-	-	gi 356532095 ref XP_003534609.1 /0/PREDICTED: probable WRKY transcription factor 31 [Glycine max]
Glyma. 20G137 900	-	-	-	-	-	-	-	-	5.32995	1.07E-0 5	2338	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0004672//protein kinase activity	-	gi 356575757 ref XP_003556003.1 ;gi 947041445 gb KRG91169.1 /0;0/PREDICTED: putative receptor-like protein kinase At4g00960 [Glycine max];hypothetical protein GLYMA_20G137900 [Glycine max]
Glyma. 09G099 900	-	-	-	-	-	-	-	-	4.98321	1.33E-1 1	3235	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 955340766 ref XP_006587157.2 ;gi 955340768 ref XP_014617538.1 /0;0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g56130 isoform X1 [Glycine max];PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g56130 isoform X2 [Glycine max]
Glyma. 12G011 700	-	-	-	-	-	-	-	-	4.85284	5.67E-1 2	3539	ko04626//Plant-pathogen interaction	-	-	-	gi 571491619 ref XP_006591996.1 /0/PREDICTED: disease resistance protein RPP13-like [Glycine max]
Glyma. 03G054 900	-	-	-	-	-	-	-	-	4.77784	1.80E-0 6	3248	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell	gi 571444460 ref XP_006576519.1 ;gi 571444463 ref XP_006576520.1 /0;0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X1 [Glycine max];PREDICTED:

																recognition	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X3 [Glycine max]
Glyma.16G137200	1.91235	0.000121	-	-	-	-	-	-	4.77561	7.66E-06	1648	ko04626//Plant-pathogen interaction	-	-	-	-	gi 955374835 ref XP_003547976.2 /0/PREDICTED: TMV resistance protein N [Glycine max]
Glyma.11G163300	-	-	-	-	-	-	-	-	4.73518	0.001	2355	ko04626//Plant-pathogen interaction	-	-	-	-	gi 356539680 ref XP_003538323.1 /0/PREDICTED: probable WRKY transcription factor 25 [Glycine max]
Glyma.07G078000	-	-	-	-	-	-	-	-	4.40047	0.00015	3561	ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding;GO:1901363	-	-	gi 955328410 ref XP_014632873.1 /0/PREDICTED: disease resistance protein RPS2-like [Glycine max]
Glyma.04G078400	-	-	-	-	-	-	-	-	4.29879	1.95E-05	955	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	-	-	gi 351721210 ref NP_001236178.1 /6.40392e-110/uncharacterized protein LOC100527700 [Glycine max]
Glyma.15G110300	-	-	-	-	-	-	-	-	4.29237	0.0001	2099	ko04626//Plant-pathogen interaction	-	-	-	-	gi 356555684 ref XP_003546160.1 /0/PREDICTED: probable WRKY transcription factor 31 [Glycine max]
Glyma.13G266100	-	-	-	-	-	-	-	-	4.22161	6.33E-05	3569	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	-	gi 734413477 gb KHN36922.1 /0/Putative leucine-rich repeat receptor-like serine/threonine-protein kinase [Glycine soja]
Glyma.13G303900	-	-	-	-	-	-	-	-	4.15709	3.46E-05	965	ko04626//Plant-pathogen interaction	-	-	-	-	gi 356547045 ref XP_003541928.1 /1.29939e-69/PREDICTED: calcium-binding protein PBP1-like [Glycine max]
Glyma.08G229100	-	-	1.83596	1.93E-10	2.12347	5.74E-11	-	-	4.08162	2.23E-14	3020	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process	-	gi 571472730 ref XP_006585700.1 /0/PREDICTED: probable inactive leucine-rich repeat receptor-like protein kinase At3g03770 [Glycine max]
Glyma.07G001400	2.29703	1.07E-05	3.38976	2.07E-11	3.1603	9.54E-10	3.1691	4.00E-05	4.06632	5.32E-06	2996	ko04626//Plant-pathogen interaction	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	-	-	gi 571464153 ref XP_006582973.1 /0/PREDICTED: U-box domain-containing protein 35-like isoform X1 [Glycine max]
Glyma.18G141500	-1.3615	0.000655	-	-	-	-	-	-	4.055	1.77E-06	2617	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	GO:0005911//cell-cell junction;GO:0016020//membrane	GO:0004672//protein kinase activity;GO:0032550	GO:0006468//protein phosphorylation;GO:0000302//response to reactive oxygen species	-	gi 571545655 ref XP_003551216.2 /0/PREDICTED: cysteine-rich receptor-like protein kinase 2 [Glycine max]
Glyma.01G204400	-	-	-	-	-	-	-	-	4.0261	3.69E-05	1572	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	-	gi 734424424 gb KHN42652.1 ;gi 947129438 gb KRH77292.1 /7.232e-138;1.9617e-107/Prot ein TIFY 10B [Glycine soja];hypothetical protein GLYMA_01G204400 [Glycine max]
Glyma.07G127100	-	-	-	-	-	-	-	-	4.01405	1.43E-05	3329	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	-	gi 571463975 ref XP_006582888.1 ;gi 955328256 ref XP_014632820.1 /0;0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At4g29180-like isoform X1 [Glycine max];PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At4g29180-like isoform X2 [Glycine max]
Glyma.09G182200	-	-	-	-	-	-	-	-	3.98403	6.48E-05	1785	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity	-	-	gi 947090495 gb KRH39160.1 /0/hypothetical protein GLYMA_09G182200 [Glycine max]

Glyma.08G142400	1.38593	0.004566	-	-	-	-	-	-	3.90859	1.61E-14	1059	ko04626//Plant-pathogen interaction	-	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0050896//response to stimulus;GO:0006351//transcription, DNA-templated	gi 255639287 gb ACU19941.1/1.44336e-110/unknown [Glycine max]
Glyma.05G215900	-	-	-	-	-	-	-	-	3.90576	0.00018	1807	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 356513295 ref XP_003525349.1 /0/PREDICTED: probable WRKY transcription factor 41 [Glycine max]
Glyma.08G235900	-	-	-	-	-	-	-	-	3.84501	0.00738	3545	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356526421 ref XP_003531816.1 /0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g56130 isoform X1 [Glycine max]
Glyma.03G047700	-	-	-	-	-	-	-	-	3.78387	8.11E-05	2490	ko04626//Plant-pathogen interaction	-	-	GO:0050896//response to stimulus	gi 947117339 gb KRH65588.1 /0/hypothetical protein GLYMA_03G047700, partial [Glycine max]
Glyma.11G075200	-	-	-	-	-	-	-	-	3.70245	2.53E-05	4641	ko04626//Plant-pathogen interaction	GO:0031224//intracellular component of membrane	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 955349679 ref XP_014619378.1 /0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At4g36180 [Glycine max]
Glyma.16G127900	-	-	-	-	-	-	-	-	3.69577	4.64E-08	7518	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0050896//response to stimulus	gi 947058663 gb KRH08069.1 ;gi 947058664 gb KRH08070.1 ;gi 947058662 gb KRH08068.1 /0;0;0/hypothetical protein GLYMA_16G127900 [Glycine max];hypothetical protein GLYMA_16G127900 [Glycine max];hypothetical protein GLYMA_16G127900 [Glycine max]
Glyma.01G117900	-	-	-	-	-	-	-	-	3.67399	0.00036	4216	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 571435020 ref XP_006573359.1 ;gi 947128048 gb KRH75902.1 ;gi 571435014 ref XP_006573356.1 ;gi 947128051 gb KRH75905.1 ;gi 947128060 gb KRH75914.1 /0;0;0;0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X2 [Glycine max];hypothetical protein GLYMA_01G117900 [Glycine max];PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X1 [Glycine max];hypothetical protein GLYMA_01G117900 [Glycine max];hypothetical protein GLYMA_01G117900 [Glycine max]
Glyma.07G023300	-	-	-	-	-4.0866	0.00042	-	-	3.67244	0.00039	1692	ko04626//Plant-pathogen interaction	-	-	GO:0098542//defense response to other organism;GO:0010033//response to organic substance;GO:0050789//regulation of biological process;GO:0009987//cellular process	gi 918463825 gb ALA09257.1/8.85387e-180/WRKY transcription factor, partial [Glycine max]
Glyma.18G281600	-	-	-	-	-	-	-	-	3.67154	0.00016	3793	ko04626//Plant-pathogen interaction	-	-	-	gi 947051977 gb KRH01506.1 /0/hypothetical protein GLYMA_18G2816002, partial [Glycine max]
Glyma.05G119500	-	-	-	-	-3.3414	0.00015	-	-	3.57315	0.0002	2761	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen	GO:0032991//macromolecular complex;G	GO:0005102//receptor binding;GO:0032550;GO:0004672//protein kinase activity;GO:0046983//prot	GO:0006984//ER-nucleus signaling pathway;GO:0009620//response to	gi 356510695 ref XP_003524071.1 /0/PREDICTED: BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like [Glycine max]

												interaction	O:0043231//intracellular membrane-bounded organelle; GO:0031224//intrinsic component of membrane	ein dimerization activity	fungus;GO:0040007//growth; GO:0010260//organ senescence;GO:0002239//response to oomycetes;GO:0009617//response to bacterium;GO:0006605//protein targeting;GO:0048580;GO:0006796//phosphate-containing compound metabolic process;GO:0010243//response to organonitrogen compound;GO:0002252;GO:0043401//steroid hormone mediated signaling pathway;GO:0006464//cellular protein modification process;GO:0009626//plant-type hypersensitive response	
Glyma.08G044400	-	-	-	-	-	-	-	-	3.54849	5.37E-05	2095	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-pathogen interaction	GO:0043231//intracellular membrane-bounded organelle	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0002831;GO:0010337//regulation of salicylic acid metabolic process;GO:0006351//transcription, DNA-templated	gi 947093104 gb KRH41689.1 ;gi 356524378 ref XP_003530806.1 /0//hypothetical protein GLYMA_08G044400 [Glycine max];PREDICTED: protein SAR DEFICIENT 1 [Glycine max]
Glyma.06G265000	-	-	-	-	-	-	-	-	3.47598	0.00051	3933	ko04626//Plant-pathogen interaction	-	-	-	gi 955326975 ref XP_014632562.1 /0//PREDICTED: disease resistance protein TAO1-like [Glycine max]
Glyma.13G181400	-	-	-	-	-	-	-	-	3.38634	5.12E-07	1719	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 571498823 ref XP_006594324.1 /0//PREDICTED: putative serine/threonine-protein kinase [Glycine max]
Glyma.09G274000	-	-	-	-	-	-	-	-	3.33606	0.00369	1194	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 937500778 ref NP_001302438.1 /0//probable WRKY transcription factor 70-like [Glycine max]
Glyma.10G178400	-	-	-	-	-	-	-	-	3.24413	0.00016	1548	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	GO:0019932//second-messenger-mediated signaling	gi 351726666 ref NP_001237902.1 /1.76727e-103/calmodulin [Glycine max]
Glyma.08G039400	-	-	-	-	-	-	-	-	3.21692	0.0003	2865	ko04626//Plant-pathogen interaction	-	-	-	gi 356527793 ref XP_003532491.1 /0//PREDICTED: leucine-rich repeat extensin-like protein 4 [Glycine max]
Glyma.06G255900	-	-	-	-	-	-	-	-	3.19763	0.00047	2845	ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:0004672//protein kinase activity;GO:1901363;GO:0097159//organic cyclic compound binding	GO:0006796//phosphate-containing compound metabolic process	gi 356514857 ref XP_003526119.1 /0//PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At1g11300 [Glycine max]
Glyma.03G046500	-1.4483	0.000234	-	-	1.29715	0.00065	-	-	3.19249	9.50E-05	3498	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 955310888 ref XP_006577442.2 /0//PREDICTED: putative disease resistance RPP13-like protein 1 [Glycine max]
Glyma.05G237200	2.50182	0.000159	-	-	-	-	-	-	3.17974	0.00137	2018	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-	GO:0043231//intracellular	GO:0001071//nucleic acid binding transcription factor	GO:0002831;GO:0010337//regulation of salicylic acid metabolic	gi 356513070 ref XP_003525237.1 /0//PREDICTED: protein SAR DEFICIENT 1-like [Glycine max]

												pathogen interaction	membrane-bound organelle	activity;GO:0003677//DNA binding	process;GO:0006351//transcription, DNA-templated	
Glyma.12G103600	-	-	-	-	-	-	-	-	3.16545	2.50E-05	1075	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	-	gi 734380494 gb KHN22869.1 /4.28219e-76/Calcium-binding protein PBP1 [Glycine soja]
Glyma.11G157200	-	-	-	-	-	-	-	-	3.15232	0.00203	816	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	-	gi 947081295 gb KRH30084.1 /4.03735e-97/hypothetical protein GLYMA_11G157200 [Glycine max]
Glyma.02G232600	-	-	-	-	-	-	-	-	3.13126	2.66E-06	2179	ko04626//Plant-pathogen interaction	-	-	-	gi 356500910 ref XP_003519273.1 /0/PREDICTED: probable WRKY transcription factor 25 [Glycine max]
Glyma.14G199800	-1.3358	0.001056	-	-	-	-	-	-	3.12085	0.00119	1328	ko04626//Plant-pathogen interaction	-	-	GO:0009987//cellular process	gi 571511635 ref XP_006596452.1 /0/PREDICTED: uncharacterized protein LOC102667674 [Glycine max]
Glyma.14G200200	-	-	-	-	-3.8331	0.00015	-	-	3.11345	0.00081	2778	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 356553124 ref XP_003544908.1 ;gi 947067983 gb KRH17126.1 /0;0/PREDICTED: probable WRKY transcription factor 25 [Glycine max];hypothetical protein GLYMA_14G200200 [Glycine max]
Glyma.19G229400	-	-	-	-	-	-	-	-	3.09356	0.00074	2279	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-pathogen interaction	-	-	-	gi 57155977 ref XP_006604792.1 /0/PREDICTED: calmodulin-binding protein 60 D isoform X1 [Glycine max]
Glyma.02G150600	-	-	-	-	-	-	-	-	3.0682	0.00046	2237	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356502836 ref XP_003520221.1 /0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase RKF3 [Glycine max]
Glyma.10G113300	-	-	-	-	-	-	-	-	3.06199	0.00077	708	ko04626//Plant-pathogen interaction	GO:0005622//intracellular	GO:0097159//organic cyclic compound binding;GO:1901363	GO:0071704//organic substance metabolic process;GO:0044238//primary metabolic process;GO:0044237//cellular metabolic process	gi 356537413 ref XP_003537222.1 /5.59253e-109/PREDICTED: elongation factor Tu, chloroplastic-like [Glycine max]
Glyma.08G021900	-	-	-	-	-	-	-	-	3.05728	0.0035	1990	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 918463829 gb ALAO9259.1 /0/WRKY transcription factor [Glycine max]
Glyma.06G142000	-	-	-	-	-	-	-	-	3.05627	0.00207	1605	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 356516231 ref XP_003526799.1 /0/PREDICTED: probable WRKY transcription factor 70 [Glycine max]
Glyma.11G043700	-	-	-	-	-	-	-	-	3.01001	0.00418	1758	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	gi 356540613 ref XP_003538782.1 /0/PREDICTED: transcription factor bHLH25-like [Glycine max]
Glyma.20G169000	-	-	-	-	-	-	-	-	2.9442	1.53E-07	2125	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0016310//phosphorylation;GO:0006464//cellular protein modification process	gi 351723997 ref NP_001238066.1 /0/serine/threonine protein kinase-like protein [Glycine max]
Glyma.18G281500	-	-	-	-	-	-	-	-	2.93243	0.00026	4414	ko04626//Plant-pathogen interaction	-	-	-	gi 955383602 ref XP_014626225.1 /0/PREDICTED: probable disease resistance protein At5g47250 isoform X1 [Glycine max]
Glyma.11G207500	-	-	-	-	-	-	-	-	2.90831	0.00068	2592	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356537805 ref XP_003537415.1 /0/PREDICTED: cysteine-rich receptor-like protein kinase 2 [Glycine max]

												interaction				
Glyma. 05G139 500	-	-	-	-	-	-	-	-	2.90743	0.00015	1643	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 955320825 ref XP_014631147.1 ;gi 734432012 gb KHN46091.1 /0;0/PREDICTED: cysteine-rich receptor-like protein kinase 10 isoform X2 [Glycine max];Cysteine-rich receptor-like protein kinase 10 [Glycine soja]
Glyma. 15G064 900	-	-	-	-	-	-	-	-	2.90364	0.00227	2760	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 955366151 ref XP_006597385.2 /0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X2 [Glycine max]
Glyma. 13G316 100	-	-	-	-	-	-	-	-	2.88609	0.0017	1153	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	-	gi 947073780 gb KRH22671.1 ;gi 947073781 gb KRH22672.1 /7.33047e-134;3.22811e-132/hypothetical protein GLYMA_13G316100 [Glycine max];hypothetical protein GLYMA_13G316100 [Glycine max]
Glyma. 02G100 300	-	-	-	-	-	-	-	-	2.85311	0.00188	2319	ko04626//Plant-pathogen interaction	-	GO:0001871;GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 351725961 ref NP_001238646.1 /0/stress-induced receptor-like kinase precursor [Glycine max]
Glyma. 17G062 300	-	-	-	-	-	-	-	-	2.82178	0.0016	1829	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947053400 gb KRH02853.1 ;gi 947053399 gb KRH02852.1 ;gi 351724607 ref NP_001238599.1 /0;0;0/hypothetical protein GLYMA_17G062300 [Glycine max];hypothetical protein GLYMA_17G062300 [Glycine max];protein kinase family protein [Glycine max]
Glyma. 01G118 300	-1.3246	0.000513	-	-	-	-	-	-	2.81805	0.0014	1776	ko04626//Plant-pathogen interaction	-	-	-	gi 947128075 gb KRH75929.1 ;gi 947128074 gb KRH75928.1 /0;0/hypothetical protein GLYMA_01G118300 [Glycine max];hypothetical protein GLYMA_01G118300 [Glycine max]
Glyma. 07G057 400	-	-	-	-	-	-	-	-	2.79984	0.00379	1907	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 918463827 gb ALAO9258.1 /0/WRKY transcription factor [Glycine max]
Glyma. 18G260 700	-	-	-	-	-	-	-	-	2.7992	0.00068	1307	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	-	gi 955382091 ref XP_014625776.1 ;gi 571549120 ref XP_006602906.1 /1.78052e-91;1.33475e-135/PREDICTED: probable calcium-binding protein CML45 isoform X2 [Glycine max];PREDICTED: probable calcium-binding protein CML45 isoform X1 [Glycine max]
Glyma. 11G157 100	-	-	-	-	-	-	-	-	2.79134	0.00455	806	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	-	gi 947081294 gb KRH30083.1 /6.00745e-97/hypothetical protein GLYMA_11G157100 [Glycine max]
Glyma. 09G236 800	-	-	-	-	-	-	-	-	2.78314	0.00455	1250	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	-	gi 356531760 ref XP_003534444.1 /7.58254e-149/PREDICTED: probable calcium-binding protein CML45 [Glycine max]
Glyma. 18G213 200	-	-	-	-	-	-	-	-	2.77615	0.00754	1171	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 351725863 ref NP_001237619.1 /0/transcription factor [Glycine max]
Glyma. 12G073 000	-	-	-	-	-4.3858	4.89E-05	-	-	2.75161	2.02E-06	2041	ko04650//Natural killer cell mediated cytotoxicity;ko04626//Plant-pathogen interaction	-	GO:0004702//receptor signaling protein serine/threonine kinase activity;GO:0032550	GO:0045682//regulation of epidermis development;GO:0051707//response to other organism;GO:0009411//response to	gi 356542571 ref XP_003539740.1 /0/PREDICTED: mitogen-activated protein kinase 3 [Glycine max]

																UV;GO:0009700//indole phytoalexin biosynthetic process;GO:0010243//response to organonitrogen compound;GO:0090567;GO:0080135//regulation of cellular response to stress;GO:0000187//activation of MAPK activity	
Glyma.17G096000	-	-	-	-	-	-	-	-	2.74555	0.0005	2393	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356565063 ref XP_003550764.1 /0/PREDICTED: calcium-dependent protein kinase 10-like [Glycine max]	
Glyma.15G043800	-	-	-	-	-	-	-	-	2.7409	0.00023	1878	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356557471 ref XP_003547039.1 /0/PREDICTED: probable serine/threonine-protein kinase RLCKVII [Glycine max]	
Glyma.16G172300	-	-	-	-	-	-	-	-	2.7281	0.00374	3398	ko04626//Plant-pathogen interaction	-	-	-	gi 571529127 ref XP_006599514.1 /0/PREDICTED: leucine-rich repeat receptor protein kinase MSL1-like [Glycine max]	
Glyma.09G061900	-	-	-	-	-	-	-	-	2.71067	3.81E-06	1572	ko04626//Plant-pathogen interaction	-	-	-	gi 947088702 gb KRH37367.1 /1.4299e-148/hypothetical protein GLYMA_09G061900 [Glycine max]	
Glyma.04G245000	-	-	-	-	-	-	-	-	2.69679	0.00116	955	ko04626//Plant-pathogen interaction	-	-	-	gi 947116302 gb KRH64604.1 /1.88213e-99/hypothetical protein GLYMA_04G245000 [Glycine max]	
Glyma.05G157000	-	-	-	-	-	-	-	-	2.69023	0.00092	1648	ko04650//Natural killer cell mediated cytotoxicity;ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity;GO:0046983//protein dimerization activity	GO:0006351//transcription, DNA-templated	gi 351727477 ref NP_001237162.1 /8.92484e-99/bZIP transcription factor bZIP111 [Glycine max]	
Glyma.17G018800	-	-	-	-	-	-	-	-	2.67929	3.42E-06	2593	ko04650//Natural killer cell mediated cytotoxicity;ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004702//receptor signaling protein serine/threonine kinase activity;GO:0032550	GO:0035556//intracellular signal transduction;GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947052688 gb KRH02141.1 ;gi 947052687 gb KRH02140.1 /0;0/hypothetical protein GLYMA_17G018800 [Glycine max];hypothetical protein GLYMA_17G018800 [Glycine max]	
Glyma.06G068100	-	-	-	-	-	-	-	-	2.6787	0.00064	3397	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356518250 ref XP_003527792.1 /0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5 [Glycine max]	
Glyma.12G133700	-	-	-	-	-	-	-	-	2.6664	1.69E-06	2444	ko04626//Plant-pathogen interaction	-	-	-	gi 356545139 ref XP_003541002.1 /0/PREDICTED: cyclic nucleotide-gated ion channel 4-like isoform X1 [Glycine max]	
Glyma.17G167600	-	-	-	-	-	-	1.08213	0.00056	2.65017	0.00021	2795	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	GO:0016020//membrane	GO:0016301//kinase activity	GO:0044237//cellular metabolic process	gi 356563574 ref XP_003550036.1 /0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At4g37250 [Glycine max]	
Glyma.13G033500	-	-	-	-	-	-	-	-	2.57301	0.00362	2293	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0001871;GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 955361655 ref XP_014621916.1 ;gi 571497140 ref XP_006593813.1 /0;0/PREDICTED: probable receptor-like protein kinase At1g67000 isoform X2 [Glycine max];PREDICTED: probable receptor-like protein kinase At1g67000 isoform X1 [Glycine max]	

Glyma. 07G080 700	-	-	-	-	-	-	-	-	2.5727	0.00436	2840	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 571465418 ref XP_003529974.2 /0/PREDICTED: putative receptor protein kinase ZmPK1 [Glycine max]
Glyma. 03G044 000	-	-	-	-	-	-	-	-	2.56707	0.0004	3606	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 947117295 gb KRH65544.1 /0/hypothetical protein GLYMA_03G044000 [Glycine max]
Glyma. 06G275 000	-	-	-	-	-	-	-	-	2.55626	0.00041	1599	ko04626//Plant-pathogen interaction	-	-	-	gi 947107330 gb KRH55713.1 /0/hypothetical protein GLYMA_06G275000 [Glycine max]
Glyma. 14G062 100	-	-	-	-	-	-	-	-	2.5506	0.00265	2448	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	GO:0031461//cullin-RING ubiquitin ligase complex	-	GO:0006952//defense response;GO:0001101//response to acid chemical;GO:0043161//proteasome-mediated ubiquitin-dependent protein catabolic process;GO:0009620//response to fungus;GO:0009908//flower development;GO:0009617//response to bacterium;GO:0009755//hormone-mediated signaling pathway;GO:0009639//response to red or far red light	gi 947065850 gb KRH14993.1 ;gi 947065849 gb KRH14992.1 /0;0/hypothetical protein GLYMA_14G062100 [Glycine max];hypothetical protein GLYMA_14G062100 [Glycine max]
Glyma. 07G095 000	-	-	-	-	-	-	-	-	2.53735	0.00062	2645	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	gi 571465619 ref XP_006583417.1 /0/PREDICTED: probable receptor-like protein kinase Atlg67000 isoform X2 [Glycine max]
Glyma. 13G128 200	-	-	-	-	-	-	-	-	2.53242	0.00081	3095	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 947070756 gb KRH19647.1 ;gi 947070757 gb KRH19648.1 ;gi 571497907 ref XP_003541379.2 /0;0;0/hypothetical protein GLYMA_13G128200 [Glycine max];hypothetical protein GLYMA_13G128200 [Glycine max];PREDICTED: receptor-like serine/threonine-protein kinase ALE2 isoform X2 [Glycine max]
Glyma. 02G129 300	-	-	-	-	-	-	-	-	2.52908	9.51E-07	3294	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 955307115 ref XP_014622348.1 /0/PREDICTED: proline-rich receptor-like protein kinase PERK9 [Glycine max]
Glyma. 10G142 600	-	-	-	-	-	-	-	-	2.52666	1.90E-06	3434	ko04075//Plant hormone signal transduction;ko04712//Circadian rhythm - plant;ko04626//Plant-pathogen interaction	-	-	-	gi 947085014 gb KRH33735.1 ;gi 918463621 gb ALA09155.1 /0;0/hypothetical protein GLYMA_10G142600 [Glycine max];bHLH transcription factor, partial [Glycine max]
Glyma. 03G043 000	-1.3551	0.000207	-	-	-	-	-	-	2.5216	0.0037	3748	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic	-	-	-	gi 955310860 ref XP_014628983.1 /0/PREDICTED: putative disease resistance protein At3g14460 [Glycine max]

												pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction				
Glyma.01G093100	-1.0863	0.005497	-	-	-	-	-	-	2.5204	3.80E-07	2915	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 955302504 ref XP_003516269.2 /0/PREDICTED: proline-rich receptor-like protein kinase PERK10, partial [Glycine max]
Glyma.11G020700	-	-	-	-	-	-	-	-	2.51182	0.00031	4134	ko04626//Plant-pathogen interaction	GO:003124//intrinsinc component of membrane	GO:0046872//metal ion binding;GO:0016651//oxidoreductase activity, acting on NAD(P)H;GO:0016209//antioxidant activity	GO:0044710	gi 947079092 gb KRLH27881.1 ;gi 356539557 ref XP_003538264.1 /0;0/hypothetical protein GLYMA_11G020700 [Glycine max];PREDICTED: respiratory burst oxidase homolog protein A [Glycine max]
Glyma.04G076200	-	-	-	-	-	-	-	-	2.50612	0.0009	1659	ko04626//Plant-pathogen interaction	-	GO:0005488	GO:0050896//response to stimulus	gi 151934217 gb ABS18446.1 /1.29563e-158/WRKY50 [Glycine max]
Glyma.08G284100	-	-	-	-	-	-	-	-	2.49575	0.00626	2697	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0016310//phosphorylation;GO:0006464//cellular protein modification process	gi 571468833 ref XP_006584462.1 /0/PREDICTED: protein kinase family protein isoform X1 [Glycine max]
Glyma.13G341500	-	-	-	-	-	-	-	-	2.49335	6.07E-06	2209	ko04626//Plant-pathogen interaction	-	-	-	gi 359806061 ref NP_001240925.1 /0/DNA-damage-repair/tolerance protein DRT100-like precursor [Glycine max]
Glyma.13G283600	-	-	-	-	-4.0713	3.79E-06	-	-	2.49105	0.0005	1652	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	GO:0009725//response to hormone;GO:0009628//response to abiotic stimulus	gi 351727745 ref NP_001238195.1 /1.28283e-78/uncharacterized protein LOC100306396 [Glycine max]
Glyma.03G054800	-	-	-	-	-	-	-	-	2.46534	0.00109	3125	ko04626//Plant-pathogen interaction	-	-	-	gi 947117434 gb KRLH65683.1 /0/hypothetical protein GLYMA_03G054800 [Glycine max]
Glyma.17G209000	-	-	-	-	-	-	-	-	2.45987	0.00299	1364	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0016491//oxidoreductase activity	-	gi 571538353 ref XP_006601141.1 /1.5634e-173/PREDICTED: transcription factor MYC2-like [Glycine max]
Glyma.17G118300	-	-	-	-	-	-	-	-	2.45514	1.78E-05	2965	ko04626//Plant-pathogen interaction	GO:003124//intrinsinc component of membrane	GO:0005249//voltage-gated potassium channel activity;GO:0005515//protein binding	GO:0010119//regulation of stomatal movement;GO:0048588//developmental cell growth;GO:0006970//response to osmotic stress;GO:0071805//potassium ion transmembrane transport	gi 947054292 gb KRLH03745.1 ;gi 947054293 gb KRLH03746.1 /0;0/hypothetical protein GLYMA_17G118300 [Glycine max];hypothetical protein GLYMA_17G118300 [Glycine max]
Glyma.13G032100	-	-	-	-	-	-	-	-	2.45312	0.00093	2332	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356547489 ref XP_003542144.1 /0/PREDICTED: probable receptor-like protein kinase Atlg11050 [Glycine max]
Glyma.03G043600	-	-	-	-	-	-	-	-	2.45282	0.00876	3606	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 947117290 gb KRLH65539.1 /0/hypothetical protein GLYMA_03G043600 [Glycine max]

Glyma.18G283200	-	-	-	-	-	-	-	-	2.45281	0.00037	2511	ko04626//Plant-pathogen interaction	-	-	-	gi 947052005 gb KRR01534.1 /0/hypothetical protein GLYMA_18G283200 [Glycine max]
Glyma.12G198800	-	-	-	-	-	-	-	-	2.43841	0.00664	2355	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 947078031 gb KRR26871.1 /0/hypothetical protein GLYMA_12G198800 [Glycine max]
Glyma.12G236500	-	-	-	-	-	-	-	-	2.42635	0.01014	3554	ko04626//Plant-pathogen interaction	-	-	-	gi 571494846 ref XP_006592960.1 ;gi 571494848 ref XP_006592961.1 /0;0/PREDICTED: probable disease resistance protein At1g61300 isoform X1 [Glycine max];PREDICTED: probable disease resistance protein At1g61300 isoform X2 [Glycine max]
Glyma.07G096300	-	-	-	-	-	-	-	-	2.42266	0.01016	2095	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 947100059 gb KRR48551.1 /0/hypothetical protein GLYMA_07G096300, partial [Glycine max]
Glyma.07G078100	-	-	-	-	-	-	-	-	2.40109	0.00924	4442	ko04626//Plant-pathogen interaction	-	-	-	gi 571465379 ref XP_006583346.1 /0/PREDICTED: uncharacterized protein LOC100797869 isoform X2 [Glycine max]
Glyma.02G115200	-	-	-	-	-	-	-	-	2.40077	0.00017	1754	ko04626//Plant-pathogen interaction	-	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0006970//response to osmotic stress;GO:0006351//transcription, DNA-templated	gi 571439709 ref XP_006574933.1 /0/PREDICTED: transcription factor [Glycine max]
Glyma.02G075600	-	-	-	-	-	-	-	-	2.39931	0.00061	2511	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 356502317 ref XP_003519966.1 /0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300 [Glycine max]
Glyma.09G071600	-	-	-	-	-	-	-	-	2.38848	9.38E-05	1296	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	gi 947088863 gb KRR37528.1 ;gi 734350125 gb KHN12298.1 ;gi 947088864 gb KRR37529.1 /5,27161e-146;1.94042e-171;2.31796e-142/hypothetical protein GLYMA_09G071600 [Glycine max];Protein TIFY 10A [Glycine soja] ;hypothetical protein GLYMA_09G071600 [Glycine max]
Glyma.02G245700	-	-	-	-	-	-	-	-	2.38419	0.00332	1530	ko04626//Plant-pathogen interaction	GO:0016020//membrane	GO:0046872//metal ion binding	GO:0009642//response to light intensity;GO:0006952//defense response;GO:0010038//response to metal ion;GO:0001101//response to acid chemical;GO:0000302//response to reactive oxygen species;GO:0009908//flower development;GO:0009725//response to hormone;GO:0048571//long-day photoperiodism;GO:0051171//regulation of nitrogen compound metabolic process	gi 356501039 ref XP_003519336.1 /3.57948e-97/PREDICTED: probable calcium-binding protein CML18 [Glycine max]
Glyma.10G253000	-	-	-	-	-	-	-	-	2.33106	2.41E-05	2565	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 955347300 ref XP_014618865.1 /0/PREDICTED: cysteine-rich receptor-like protein kinase 10 isoform X1 [Glycine max]

Glyma. 18G050 700	-	-	-	-	-	-	-	-	2.32729	0.00104	3603	ko04626//Plant-pathogen interaction	GO:0031224//intrinsic component of membrane	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356569432 ref XP_003552905.1 /0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g06840 [Glycine max]
Glyma. 11G077 300	-	-	-	-	-	-	-	-	2.31765	8.47E-05	2362	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947080010 gb KRH28799.1 ;gi 356540813 ref XP_003538879.1 /0;0/hypothetical protein GLYMA_11G077300 [Glycine max];PREDICTED: calcium-dependent protein kinase 28-like [Glycine max]
Glyma. 15G179 600	-	-	-	-	-1.9649	0.00127	-	-	2.30492	1.76E-05	1680	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	gi 947063310 gb KRH12571.1 ;gi 947063309 gb KRH12570.1 ;gi 734424752 gb KHN42787.1 /7.42797e-148;1.06902e-172;0/hypothetical protein GLYMA_15G179600 [Glycine max];hypothetical protein GLYMA_15G179600 [Glycine max];Protein TIFY 10A [Glycine soja]
Glyma. 07G063 300	-2.2096	8.89E-20	-	-	-	-	-	-	2.28114	7.66E-06	6579	ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding;GO:1901363	-	gi 947099527 gb KRH48019.1 /0/hypothetical protein GLYMA_07G0633001, partial [Glycine max]
Glyma. 13G244 200	-	-	-	-	-	-	-	-	2.27949	0.00369	3079	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0016301//kinase activity	GO:0048827//phyllome development;GO:0009913//epidermal cell differentiation;GO:0006464//cellular protein modification process;GO:0006796//phosphate-containing compound metabolic process;GO:0001708//cell fate specification;GO:0009653//anatomical structure morphogenesis;GO:0003006//developmental process involved in reproduction	gi 571500270 ref XP_006594611.1 /0/PREDICTED: protein STRUBBELIG-RECEPTOR FAMILY 3-like [Glycine max]
Glyma. 08G271 900	-	-	-	-	-	-	-	-	2.27188	2.14E-07	2704	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	gi 356526715 ref XP_003531962.1 /0/PREDICTED: transcription factor MYC2 [Glycine max]
Glyma. 08G303 700	-	-	-	-	-	-	-	-	2.27129	0.00448	4369	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 356524185 ref XP_003530712.1 /0/PREDICTED: TMV resistance protein N-like isoform X2 [Glycine max]
Glyma. 16G031 600	-	-	-	-	-	-	-	-	2.24955	7.05E-05	8938	ko04626//Plant-pathogen interaction	-	-	-	gi 947057170 gb KRH06576.1 ;gi 947057169 gb KRH06575.1 ;gi 571525240 ref XP_003548632.2 /0;0/hypothetical protein GLYMA_16G031600 [Glycine max];hypothetical protein GLYMA_16G031600 [Glycine max];PREDICTED: uncharacterized protein LOC100809946 isoform X2 [Glycine max]
Glyma. 06G263 900	-	-	-	-	-	-	-	-	2.24884	0.00448	4654	ko00230//Purine metabolism;ko00240//Pyrimidine	-	-	-	gi 955325893 ref XP_014632232.1 /0/PREDICTED: disease resistance protein TAO1-like isoform X1 [Glycine max]

												metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction				
Glyma.15G168200	-	-	-	-	-	-	-	-	2.24855	6.12E-07	1264	ko04626//Plant-pathogen interaction	-	-	-	gi 571519233 ref XP_006597810.1 /1.06697e-143/PREDICTED: probable WRKY transcription factor 11 [Glycine max]
Glyma.02G037200	-1.7656	8.60E-08	-	-	-	-	-	-	2.23956	0.00123	2518	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006468//protein phosphorylation	gi 734312199 gb KHN00377.1 /0/Cysteine-rich receptor-like protein kinase 3 [Glycine soja]
Glyma.06G262700	-	-	-	-	-	-	-	-	2.21301	0.00241	3570	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity	GO:0006796//phosphate-containing compound metabolic process	gi 955325868 ref XP_014632226.1 ;gi 955325866 ref XP_014632225.1 /0;0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X2 [Glycine max];PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 isoform X1 [Glycine max]
Glyma.15G030000	-	-	-	-	-	-	-	-	2.20226	0.00691	2706	ko04626//Plant-pathogen interaction	GO:0016023//cytoplasmic membrane-bounded vesicle	GO:0032550;GO:0004672//protein kinase activity;GO:0046983//protein dimerization activity	GO:0048364//root development;GO:0006464//cellular protein modification process;GO:0008356//asymmetric cell division;GO:0009791//post-embryonic development;GO:0006796//phosphate-containing compound metabolic process;GO:0003006//developmental process involved in reproduction	gi 947060869 gb KRG10130.1 /0/hypothetical protein GLYMA_15G030000 [Glycine max]
Glyma.U021800	-	-	-	-	-4.4647	4.84E-06	-	-	2.1905	9.34E-05	2236	ko04650//Natural killer cell mediated cytotoxicity;ko04626//Plant-pathogen interaction	-	GO:0004702//receptor signaling protein serine/threonine kinase activity;GO:0032550	GO:0045682//regulation of epidermis development;GO:0051707//response to other organism;GO:0009411//response to UV;GO:0009700//indole phytoalexin biosynthetic process;GO:0010243//response to organonitrogen compound;GO:0090567;GO:0080135//regulation of cellular response to stress;GO:0000187//activation of MAPK activity	gi 734378345 gb KHN22030.1 ;gi 947039232 gb KRG89067.1 ;gi 947039231 gb KRG89066.1 /0;0;1.25479e-175/Mitogen-activated protein kinase 3 [Glycine soja];hypothetical protein GLYMA_U021800 [Glycine max];hypothetical protein GLYMA_U021800 [Glycine max]
Glyma.06G171700	-	-	-	-	-	-	-	-	2.17475	0.00317	3031	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356518897 ref XP_003528113.1 ;gi 947105826 gb KRG54209.1 /0;0/PREDICTED: probable inactive leucine-rich repeat receptor-like protein kinase At3g03770 isoform X1 [Glycine max];hypothetical protein GLYMA_06G171700 [Glycine max]
Glyma.12G217500	-	-	-	-	-	-	-	-	2.14759	1.86E-05	744	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	GO:0009725//response to hormone;GO:0009628//response to abiotic stimulus	gi 351722363 ref NP_001238521.1 /5.24239e-78/uncharacterized protein LOC100500465 [Glycine max]

Glyma. 01G166 100	-	-	-	-	-2.1941	0.00121	-	-	2.1374	4.51E-05	2572	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947128803 gb KRF76657.1 ;gi 571435690 ref XP_006573556.1 /0;0/hypothetical protein GLYMA_01G166100 [Glycine max];PREDICTED: calcium-dependent protein kinase 28-like [Glycine max]
Glyma. 09G172 500	-	-	-1.5482	0.000245	-	-	-	-	2.12165	0.0002	1444	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0004672//protein kinase activity;GO:0019887//protein kinase regulator activity	GO:0001934//positive regulation of protein phosphorylation;GO:0006351//transcription, DNA-templated;GO:0002239//response to oomycetes;GO:0009617//response to bacterium;GO:0009692;GO:0009700//indole phytoalexin biosynthetic process;GO:0006970//response to osmotic stress;GO:0000160//phosphorelay signal transduction system;GO:0060918//auxin transport;GO:0009627//systemic acquired resistance	gi 356531126 ref XP_003534129.1 /0/PREDICTED: mitogen-activated protein kinase kinase 9 [Glycine max]
Glyma. 17G218 500	-	-	-	-	-	-	-	-	2.10669	9.07E-06	2394	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356563936 ref XP_003550213.1 /0/PREDICTED: L-type lectin-domain containing receptor kinase IX.1-like [Glycine max]
Glyma. 03G047 000	-	-	-	-	-	-	-	-	2.07611	0.00894	5472	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 955310901 ref XP_006576474.2 /0/PREDICTED: putative disease resistance RPP13-like protein 1 [Glycine max]
Glyma. 16G136 600	-2.1744	1.09E-08	-	-	-3.2628	4.42E-06	-	-	2.07556	0.00594	4635	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 571528161 ref XP_006599364.1 /0/PREDICTED: protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1 [Glycine max]
Glyma. 09G191 300	-	-	-	-	-	-	-	-	2.06922	8.50E-05	2501	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550;GO:0005198//structural molecule activity	GO:0006468//protein phosphorylation	gi 571475633 ref XP_006586722.1 /0/PREDICTED: putative receptor protein kinase PERK1 isoform X1 [Glycine max]
Glyma. 14G013 300	-	-	-	-	-	-	-	-	2.06612	0.00472	1947	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 571506326 ref XP_006595690.1 /0/PREDICTED: probable L-type lectin-domain containing receptor kinase S.7 [Glycine max]
Glyma. 03G220 800	-	-	-	-	-	-	-	-	2.04961	0.00933	1466	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 918463819 gb ALA09254.1 /0/WRKY transcription factor, partial [Glycine max]
Glyma. 06G077 400	-	-	-	-	-	-	-	-	2.04228	0.00024	1510	ko04626//Plant-pathogen interaction	-	GO:0001071//nucleic acid binding transcription factor	GO:0009617//response to bacterium;GO:0010243//response to organonitrogen	gi 351726405 ref NP_001238661.1 /2.62285e-180/transcription factor [Glycine max]

															activity;GO:0003677//DNA binding;GO:0005515//protein binding	compound;GO:0006351//transcription, DNA-templated	
Glyma.20G211700	-	-	-	-	-	-	-	-	2.03992	0.01021	1000	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding	GO:0019932//second-messenger-mediated signaling	gi 734324268 gb KHN05043.1 /2.79458e-103/Calmodulin-like protein 11 [Glycine soja]	
Glyma.15G209300	-	-	-	-	-	-	2.01415	8.15E-07	2.03631	0.00073	1603	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	gi 358248196 ref NP_001239837.1 /0/polygalacturonase inhibitor 1-like precursor [Glycine max]	
Glyma.09G188600	-	-	-	-	-	-	-	-	2.012	3.63E-08	1689	ko04626//Plant-pathogen interaction	-	-	-	gi 947090594 gb KRH39259.1 /0/hypothetical protein GLYMA_09G188600 [Glycine max]	
Glyma.15G166800	-	-	-	-	-	-	-	-	1.98857	0.00304	1468	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 734359974 gb KHN15341.1 ;gi 947063074 gb KRH12335.1 /4.00382e-169;8.36369e-155/Transcription factor bHLH35 [Glycine soja] ,hypothetical protein GLYMA_15G166800 [Glycine max]	
Glyma.13G351500	-	-	-	-	-	-	-	-	1.96196	0.0004	2061	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006468//protein phosphorylation	gi 947074444 gb KRH23335.1 /0/hypothetical protein GLYMA_13G351500 [Glycine max]	
Glyma.08G018900	-	-	-	-	-	-	-	-	1.94321	0.00026	4160	ko04626//Plant-pathogen interaction	GO:0031224//intrinsic component of membrane	GO:0046872//metal ion binding;GO:0016651//oxidoreductase activity, acting on NAD(P)H;GO:0016209//antioxidant activity	GO:0044710	gi 356528819 ref XP_003532995.1 /0/PREDICTED: respiratory burst oxidase homolog protein A-like [Glycine max]	
Glyma.06G077300	-	-	-	-	-	-	-	-	1.92549	0.00109	2515	ko04626//Plant-pathogen interaction	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0006811//ion transport;GO:0044763	gi 356518290 ref XP_003527812.1 /0/PREDICTED: putative cyclic nucleotide-gated ion channel 18 [Glycine max]	
Glyma.03G130800	-	-	-	-	-	-	-	-	1.9233	0.0013	1292	ko04626//Plant-pathogen interaction	GO:0016020//membrane	GO:0046872//metal ion binding	-	gi 356504734 ref XP_003521150.1 /1.60881e-141/PREDICTED: probable calcium-binding protein CML36 [Glycine max]	
Glyma.07G056400	-	-	-	-	-	-	-	-	1.9013	0.00691	2697	ko04626//Plant-pathogen interaction	GO:0031224//intrinsic component of membrane	GO:0005267//potassium channel activity	GO:0034220//ion transmembrane transport;GO:0030001//metal ion transport	gi 571465040 ref XP_006583243.1 /0/PREDICTED: cyclic nucleotide-gated ion channel 1-like [Glycine max]	
Glyma.05G232000	-	-	-	-	-	-	-	-	1.89839	2.35E-05	2142	ko04626//Plant-pathogen interaction	-	-	-	gi 734377070 gb KHN21547.1 /0/Leucine-rich repeat extensin-like protein 5 [Glycine soja]	
Glyma.09G199900	-	-	-	-	-	-	-	-	1.8369	0.00246	2123	ko04626//Plant-pathogen interaction	GO:0044444	GO:0032550;GO:0004672//protein kinase activity;GO:0019899//enzyme binding	GO:0006468//protein phosphorylation;GO:0009723//response to ethylene;GO:0009610//response to symbiotic fungus;GO:0045087//innate immune response	gi 356531361 ref XP_003534246.1 /0/PREDICTED: receptor-like cytosolic serine/threonine-protein kinase RBK1 [Glycine max]	
Glyma.07G088300	-1.037	2.95E-05	-	-	-	-	-	-	1.82871	2.70E-07	1467	ko04626//Plant-pathogen interaction	-	-	-	gi 947099935 gb KRH48427.1 /0/hypothetical protein GLYMA_07G088300 [Glycine max]	
Glyma.06G161200	-	-	-	-	-	-	-	-	1.82348	5.84E-07	1974	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0004672//protein kinase activity;GO:0046872//metal ion binding	GO:0006464//cellular protein modification process;GO:0009755//hormone-mediated signaling	gi 734341045 gb KHN09683.1 /0/Calcium-dependent protein kinase SK5 [Glycine soja]	

																pathway;GO:0006796//phosphate-containing compound metabolic process	
Glyma.08G290200	-	-	-	-	-	-	-	-	1.8229	0.00302	2192	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 734345203 gb KHN10619.1 /0/Serine/threonine-protein kinase PBS1 [Glycine soja]	
Glyma.15G065200	-	-	-	-	-	-	-	-	1.78024	1.08E-05	3227	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 955372320 ref XP_014623591.1 ;gi 947061453 gb KRH10714.1 /0;0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase B120 [Glycine max];hypothetical protein GLYMA_15G065200 [Glycine max]	
Glyma.01G196000	-	-	-	-	-	-	-	-	1.76396	0.00241	1433	ko04626//Plant-pathogen interaction	-	-	-	gi 947129312 gb KRH77166.1 /1.33443e-161/hypothetical protein GLYMA_01G196000 [Glycine max]	
Glyma.15G023200	-	-	-	-	-	-	-	-	1.74923	0.00147	3534	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006468//protein phosphorylation	gi 571514979 ref XP_003546664.2 /0/PREDICTED: inactive protein kinase SELMODRAFT_444075-like [Glycine max]	
Glyma.11G246200	-	-	-	-	-	-	-	-	1.71692	0.01048	3308	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 955351777 ref XP_014619757.1 ;gi 356538111 ref XP_003537548.1 ;gi 947082611 gb KRH31400.1 ;gi 947082608 gb KRH31397.1 ;gi 947082610 gb KRH31399.1 ;gi 947082607 gb KRH31396.1 /0;0;0;0;0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g67720 isoform X2 [Glycine max];PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g67720 isoform X1 [Glycine max];hypothetical protein GLYMA_11G246200 [Glycine max];hypothetical protein GLYMA_11G246200 [Glycine max];hypothetical protein GLYMA_11G246200 [Glycine max];hypothetical protein GLYMA_11G246200 [Glycine max]	
Glyma.07G015300	-	-	-	-	-	-	-	-	1.71489	0.00012	2873	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0044036//cell wall macromolecule metabolic process	gi 571464387 ref XP_006583047.1 /0/PREDICTED: lysM domain receptor-like kinase 3 isoform X2 [Glycine max]	
Glyma.16G157400	-	-	-	-	-	-	-	-	1.6993	0.00871	3424	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 947059159 gb KRH08565.1 /0/hypothetical protein GLYMA_16G157400 [Glycine max]	
Glyma.18G185400	-	-	-	-	-	-	-	-	1.69531	0.00323	2562	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006468//protein phosphorylation	gi 734323185 gb KHN04723.1 /0/L-type lectin-domain containing receptor kinase IV.1 [Glycine soja]	
Glyma.16G085900	-	-	-	-	-	-	-	-	1.68542	4.80E-05	5021	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//P	-	-	GO:0050896//response to stimulus	gi 571526823 ref XP_003548631.2 ;gi 947057991 gb KRH07397.1 ;gi 947057995 gb KRH07401.1 ;gi 734363398 gb KHN16501.1 /0;0;0;0/PREDICTED: TMV resistance protein N-like [Glycine max];hypothetical protein GLYMA_16G085900 [Glycine max];hypothetical protein GLYMA_16G085900 [Glycine max];TMV	

												lant-pathogen interaction				resistance protein N [Glycine soja]
Glyma.14G161600	-	-	-	-	-	-	-	-	1.67161	0.00057	2733	ko04626//Plant-pathogen interaction	GO:0031224//intrinsinc component of membrane	GO:0005217//intracellular ligand-gated ion channel activity	GO:0044763;GO:0070838//divalent metal ion transport	gi 356551532 ref XP_003544128.1 /0/PREDICTED: cyclic nucleotide-gated ion channel 1-like [Glycine max]
Glyma.08G060500	-	-	-	-	-	-	-	-	1.65122	0.00695	3278	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 947093372 gb KRH41957.1 ;gi 947093371 gb KRH41956.1 /0;0/hypothetical protein GLYMA_08G060500 [Glycine max];hypothetical protein GLYMA_08G060500 [Glycine max]
Glyma.19G132800	-	-	-	-	-	-	-	-	1.64426	0.00042	1542	ko04626//Plant-pathogen interaction	GO:0016020//membrane	GO:0046872//metal ion binding	-	gi 356571963 ref XP_003554140.1 /8.59197e-143/PREDICTED: probable calcium-binding protein CML36 [Glycine max]
Glyma.08G259000	-1.145	0.000992	-	-	-	-	-	-	1.62578	0.00246	2737	ko04626//Plant-pathogen interaction	-	-	-	gi 571473175 ref XP_006585845.1 /0/PREDICTED: putative disease resistance RPP13-like protein 3 [Glycine max]
Glyma.U008300	1.95409	3.68E-09	1.94453	2.21E-05	-	-	-	-	1.62528	0.00067	3851	ko04626//Plant-pathogen interaction	-	-	GO:0050896//response to stimulus	gi 947038217 gb KRG88524.1 ;gi 955395582 ref XP_014628748.1 /0;0/hypothetical protein GLYMA_U008300 [Glycine max];PREDICTED: protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1-like isoform X1 [Glycine max]
Glyma.01G183300	-	-	-	-	-1.9253	0.00106	-	-	1.61762	0.00318	2893	ko04626//Plant-pathogen interaction	-	-	-	gi 571435938 ref XP_006573620.1 /0/PREDICTED: probable disease resistance protein At5g66900 [Glycine max]
Glyma.17G250800	-	-	-	-	-	-	-	-	1.61735	0.00638	4171	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356562351 ref XP_003549435.1 /0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At2g16250 [Glycine max]
Glyma.01G032900	-	-	-	-	-	-	-	-	1.61077	0.00705	3261	ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:1901363;GO:0097159//organic cyclic compound binding	-	gi 947126778 gb KRH74632.1 /0/hypothetical protein GLYMA_01G032900 [Glycine max]
Glyma.03G138000	-	-	-	-	-	-	-	-	1.60409	8.51E-05	2274	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0004674//protein serine/threonine kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356504799 ref XP_003521182.1 ;gi 947118710 gb KRH66959.1 /0;0/PREDICTED: calcium-dependent protein kinase 32-like [Glycine max];hypothetical protein GLYMA_03G138000 [Glycine max]
Glyma.08G223400	-	-	-	-	-	-	-	-	1.58341	0.00227	1927	ko04626//Plant-pathogen interaction	GO:0044424	GO:0032550;GO:0004672//protein kinase activity	GO:2000026//regulation of multicellular organismal development;GO:0006464//cellular protein modification process;GO:0006796//phosphate-containing compound metabolic process;GO:0090567	gi 356526330 ref XP_003531771.1 /0/PREDICTED: mitogen-activated protein kinase kinase 5-like [Glycine max]
Glyma.17G166200	-	-	-	-	-	-	-	-	1.57639	0.00599	3103	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 734391140 gb KHN27061.1 /0/Putative receptor-like protein kinase [Glycine soja]
Glyma.01G189100	-	-	-	-	-	-	-	-	1.56901	0.00711	1870	ko04626//Plant-pathogen interaction	-	-	-	gi 571436024 ref XP_006573647.1 ;gi 356496927 ref XP_003517316.1 /1.38499e-170;5.94037e-177/PREDICTED: probable WRKY transcription factor 15 isoform X2 [Glycine max];PREDICTED: probable WRKY transcription factor 15 isoform X1 [Glycine

																	max]
Glyma. 03G043 200	-	-	-	-	-	-	-	-	1.5684	0.00751	3597	ko00230//Purine metabolism;ko00240//P yrimidine metabolism;ko01100// Metabolic pathways;ko03020//RN A polymerase;ko04626//P lant-pathogen interaction	-	-	-	gi 955310862 ref XP_006577438.2 /0/PREDIC TED: putative disease resistance protein At3g14460 [Glycine max]	
Glyma. 12G053 400	-	-	-	-	-	-	-	-	1.56451	0.0046	2238	ko04626//Plant-pathoge n interaction	-	GO:0046872//metal ion binding;GO:0004674//prot ein serine/threonine kinase activity;GO:0032550	GO:0006796//phosphate-cont aining compound metabolic process;GO:0006464//cellular protein modification process	gi 356544533 ref XP_003540704.1 /0/PREDIC TED: calcium-dependent protein kinase 24-like [Glycine max]	
Glyma. 10G023 100	-	-	-	-	-	-	-	-	1.5572	0.00031	1206	ko04626//Plant-pathoge n interaction	-	GO:0016628//oxidoreduct ase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;GO:0016772//tra nsferase activity, transferring phosphorus-containing groups	GO:0044710;GO:0006796//p hosphate-containing compound metabolic process	gi 356536745 ref XP_003536896.1 /0/PREDIC TED: probably inactive leucine-rich repeat receptor-like protein kinase IMK2 [Glycine max]	
Glyma. 08G297 400	-	-	-	-	-	-	-	-	1.52401	0.00032	3139	ko04626//Plant-pathoge n interaction	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 955337649 ref XP_014634833.1 /0/PREDIC TED: probable LRR receptor-like serine/threonine-protein kinase At1g14390 [Glycine max]	
Glyma. 12G135 600	-	-	-	-	-	-	-	-	1.52116	3.34E-0 5	4421	ko04626//Plant-pathoge n interaction	-	-	-	gi 734430980 gb KHN45708.1 /0/TMV resistance protein N [Glycine soja]	
Glyma. 14G071 400	-	-	-	-	-	-	-	-	1.48845	0.00331	1733	ko04650//Natural killer cell mediated cytotoxicity;ko04626// Plant-pathogen interaction	-	-	-	gi 356551950 ref XP_003544335.1 /3.19685e- 83/PREDICTED: ocs element-binding factor 1 [Glycine max]	
Glyma. 06G036 400	-	-	-	-	-	-	-	-	1.4688	0.00658	2659	ko04626//Plant-pathoge n interaction	-	GO:0016301//kinase activity;GO:0032550;GO: 0036094//small molecule binding;GO:1901363;GO: 0097159//organic cyclic compound binding	GO:0006464//cellular protein modification process;GO:0044237//cellular metabolic process	gi 947103557 gb KRH51940.1 ;gi 571458793 r ef XP_006581230.1 /0/0/hypothetical protein GLYMA_06G036400 [Glycine max];PREDICTED: mitogen-activated protein kinase kinase kinase YODA-like [Glycine max]	
Glyma. 07G105 700	-	-	-	-	-	-	1.54223	5.88E-0 5	1.44889	0.00611	1376	ko04626//Plant-pathoge n interaction	-	GO:0032550;GO:0004672 //protein kinase activity;GO:0019887//prot ein kinase regulator activity	GO:0001934//positive regulation of protein phosphorylation;GO:0006351 //transcription, DNA-templated;GO:0002239 //response to oomycetes;GO:0009617//resp onse to bacterium;GO:0009692;GO:0 009700//indole phytoalexin biosynthetic process;GO:0006970//respons e to osmotic stress;GO:0000160//phosphor elay signal transduction system;GO:0060918//auxin transport;GO:0009627//syste mic acquired resistance	gi 356520673 ref XP_003528985.1 /0/PREDIC TED: mitogen-activated protein kinase kinase 9 [Glycine max]	

Glyma. 03G054 100	-	-	-	-	-	-	-	-	1.44814	0.00481	3425	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	GO:0036094//small molecule binding;GO:1901363;GO:0097159//organic cyclic compound binding	-	gi 947117426 gb KRH65675.1 ;gi 947117424 gb KRH65673.1 ;gi 947117423 gb KRH65672.1 ;gi 947117427 gb KRH65676.1 ;gi 947117425 gb KRH65674.1 /4.13447e-155;0;0;0/hypothetical protein GLYMA_03G054100 [Glycine max];hypothetical protein GLYMA_03G054100 [Glycine max];hypothetical protein GLYMA_03G054100 [Glycine max];hypothetical protein GLYMA_03G054100 [Glycine max];hypothetical protein GLYMA_03G054100 [Glycine max]
Glyma. 10G009 100	-	-	-	-	-	-	-	-	1.44445	0.00037	1920	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0004702//receptor signaling protein serine/threonine kinase activity	GO:0035556//intracellular signal transduction;GO:0032147//activation of protein kinase activity	gi 359811321 ref NP_001241285.1 /0/pt-inter acting protein 1-like [Glycine max]
Glyma. 06G319 700	-	-	-	-	-	-	-	-	1.42848	0.00687	2068	ko04626//Plant-pathogen interaction	GO:0005618//cell wall;GO:0009536//plastid	GO:0016491//oxidoreductase activity	GO:0009628//response to abiotic stimulus;GO:0008152//metabolic process	gi 351724553 ref NP_001235526.1 /0/disease resistance protein/LRR protein-related protein precursor [Glycine max]
Glyma. 03G043 500	-	-	-	-	-	-	-	-	1.40762	0.00445	5300	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 955310855 ref XP_014628981.1 /0/PREDICTED: putative disease resistance protein At3g14460 [Glycine max]
Glyma. 06G153 200	-	-	-	-	-	-	-	-	1.40116	3.16E-05	2548	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356516360 ref XP_003526863.1 /0/PREDICTED: mitogen-activated protein kinase kinase YODA-like [Glycine max]
Glyma. 02G000 400	-	-	-	-	-	-	-	-	1.39581	0.00149	2481	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0016310//phosphorylation;GO:0006464//cellular protein modification process;GO:0044036//cell wall macromolecule metabolic process	gi 356499893 ref XP_003518770.1 /0/PREDICTED: lysM domain receptor-like kinase 4 [Glycine max]
Glyma. 09G259 100	-	-	-	-	-	-	-	-	1.37109	0.00132	4213	ko04626//Plant-pathogen interaction	GO:0044424	GO:0004672//protein kinase activity;GO:0019787//ubiquitin-like protein transferase activity;GO:0032550	GO:0032446//protein modification by small protein conjugation	gi 571479402 ref XP_006587850.1 ;gi 356531997 ref XP_003534561.1 /0;0/PREDICTED: U-box domain-containing protein 33-like isoform X2 [Glycine max];PREDICTED: U-box domain-containing protein 33-like isoform X1 [Glycine max]
Glyma. 04G220 400	-	-	-	-	-	-	-	-	1.36427	0.00919	3932	ko04626//Plant-pathogen interaction	GO:0031224//intrinsically component of membrane;GO:0044444	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356509054 ref XP_003523267.1 /0/PREDICTED: probable inactive receptor kinase At5g10020 [Glycine max]
Glyma. 01G218 800	-	-	-	-	-	-	-	-	1.36221	0.01007	3590	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	GO:0031224//intrinsically component of membrane	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 947129672 gb KRH77526.1 ;gi 571436477 ref XP_006573774.1 /0;0/hypothetical protein GLYMA_01G218800 [Glycine max];PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g63430 [Glycine max]

Glyma. 02G037 100	-	-	-	-	-1.1594	0.00107	-	-	1.35489	0.00125	3167	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	GO:0005911//cell-cell junction;GO:0016020//membrane	GO:0004672//protein kinase activity;GO:0032550	GO:0006468//protein phosphorylation;GO:0000302//response to reactive oxygen species	gi 571437782 ref XP_006574321.1 /0/PREDICTED: protein kinase family protein isoform X1 [Glycine max]
Glyma. 06G267 400	-	-	-	-	-	-	-	-	1.35229	0.00013	4506	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0050896//response to stimulus	gi 947107241 gb KRH55624.1 ;gi 571457908 ref XP_006580944.1 /0;0/hypothetical protein GLYMA_06G267400 [Glycine max];PREDICTED: uncharacterized protein LOC100500528 isoform X1 [Glycine max]
Glyma. 03G037 000	-	-	-	-	-	-	-	-	1.33316	0.00315	4395	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 356506465 ref XP_003522002.1 /0/PREDICTED: putative disease resistance RPP13-like protein 1 [Glycine max]
Glyma. 13G112 000	-	-	-	-	-	-	-	-	1.31771	0.00145	2360	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	gi 918463851 gb ALA09270.1 /0/ZIM transcription factor, partial [Glycine max]
Glyma. 01G118 800	-	-	-	-	-	-	-	-	1.31486	0.00236	2442	ko04626//Plant-pathogen interaction	-	-	-	gi 955302776 ref XP_014630170.1 /0/PREDICTED: probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840 isoform X1 [Glycine max]
Glyma. 14G074 700	-	-	-	-	-	-	-	-	1.31383	0.00712	4087	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356552103 ref XP_003544410.1 /0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At2g16250 [Glycine max]
Glyma. 08G218 600	-	-	-	-	-3.5617	4.69E-06	-	-	1.27268	0.00373	1828	ko04626//Plant-pathogen interaction	-	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0098542//defense response to other organism;GO:0006351//transcription, DNA-templated;GO:0010033//response to organic substance;GO:0050789//regulation of biological process;GO:0051707//response to other organism;GO:0009987//cellular process;GO:0065007//biological regulation;GO:0006952//defense response	gi 255637165 gb ACU18913.1 ;gi 947095978 gb KRH44563.1 ;gi 571468821 ref XP_006584456.1 ;gi 947095977 gb KRH44562.1 /0;6.61464e-70;0;1.08096e-125/unknown [Glycine max];hypothetical protein GLYMA_08G218600 [Glycine max];PREDICTED: transcription factor isoform X1 [Glycine max];hypothetical protein GLYMA_08G218600 [Glycine max]
Glyma. 06G145 700	-	-	-	-	-	-	-	-	1.27244	0.0079	2947	ko04626//Plant-pathogen interaction	GO:0009526//plastid envelope	GO:0016740//transferase activity	-	gi 947105396 gb KRH53779.1 /0/hypothetical protein GLYMA_06G145700 [Glycine max]
Glyma. 11G054 600	-	-	-	-	-	-	-	-	1.27213	0.00834	1836	ko04075//Plant hormone signal transduction;ko04712//Circadian rhythm - plant;ko04626//Plant-pathogen interaction	-	-	GO:0007275//multicellular organismal development;GO:0048608//reproductive structure development;GO:0009628//response to abiotic stimulus;GO:0009791//post-embryonic development	gi 734423171 gb KHN42092.1 ;gi 947079665 gb KRH28454.1 ;gi 947079664 gb KRH28453.1 /0;6.4743e-165;0/Transcription factor SPATULA [Glycine soja];hypothetical protein GLYMA_11G0546001, partial [Glycine max];hypothetical protein GLYMA_11G0546001 [Glycine max]

Glyma. 13G266 300	-	-	-	-	-	-	-	-	1.26018	0.00725	3585	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0046914//transition metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 947073017 gb KRH21908.1 /0/hypothetical protein GLYMA_13G266300 [Glycine max]
Glyma. 10G159 500	-	-	-	-	-	-	-	-	1.22398	0.00048	5775	ko04626//Plant-pathogen interaction	-	-	-	gi 571483241 ref XP_006589174.1 ;gi 947085312 gb KRH34033.1 ;gi 571483243 ref XP_006589175.1 /0;0;0/PREDICTED: protein MON2 homolog isoform X1 [Glycine max];hypothetical protein GLYMA_10G159500 [Glycine max];PREDICTED: protein MON2 homolog isoform X2 [Glycine max]
Glyma. 15G001 500	-	-	-	-	-	-	-	-	1.21865	0.00162	3906	ko04626//Plant-pathogen interaction	GO:0031224//intrinsinc component of membrane	GO:0032550;GO:0004672//protein kinase activity	GO:0050896//response to stimulus;GO:0006464//cellular protein modification process;GO:0006796//phosphate-containing compound metabolic process	gi 571514319 ref XP_003546285.2 /0/PREDICTED: receptor-like protein kinase [Glycine max]
Glyma. 13G248 800	-	-	-	-	-	-	-	-	1.1914	0.00564	3053	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0008037//cell recognition	gi 571500423 ref XP_006594639.1 /0/PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase B120 isoform X1 [Glycine max]
Glyma. 06G223 800	-	-	-	-	-	-	-	-	1.18334	0.00204	2664	ko04626//Plant-pathogen interaction	GO:0031224//intrinsinc component of membrane	GO:0005267//potassium channel activity	GO:0034220//ion transmembrane transport;GO:0030001//metal ion transport	gi 571461788 ref XP_006582102.1 ;gi 955325484 ref XP_014632152.1 /0;0/PREDICTED: probable cyclic nucleotide-gated ion channel 17 isoform X1 [Glycine max];PREDICTED: probable cyclic nucleotide-gated ion channel 17 isoform X2 [Glycine max]
Glyma. 05G034 600	-	-	-	-	-	-	-	-	1.1776	0.00402	2410	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-pathogen interaction	-	-	-	gi 571453593 ref XP_006579554.1 /0/PREDICTED: calmodulin-binding protein 60 A-like isoform X1 [Glycine max]
Glyma. 19G140 800	-	-	-	-	-	-	-	-	1.17675	0.00579	2209	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0004674//protein serine/threonine kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356572042 ref XP_003554179.1 /0/PREDICTED: calcium-dependent protein kinase 32 [Glycine max]
Glyma. 13G102 000	-	-	-	-	-	-	-	-	1.16015	0.00302	1764	ko04626//Plant-pathogen interaction	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated	gi 947070229 gb KRH19120.1 /7.85339e-164/hypothetical protein GLYMA_13G102000 [Glycine max]
Glyma. 05G010 600	-	-	-	-	-	-	-	-	1.12633	0.00748	2947	ko04626//Plant-pathogen interaction	GO:0031224//intrinsinc component of membrane	GO:0005249//voltage-gated potassium channel activity;GO:0005515//protein binding	GO:0010119//regulation of stomatal movement;GO:0048588//developmental cell growth;GO:0006970//response to osmotic stress;GO:0071805//potassium ion transmembrane transport	gi 571454296 ref XP_003524528.2 /0/PREDICTED: potassium channel AKT1-like [Glycine max]
Glyma. 11G232 200	-	-	-	-	-	-	-	-	1.12323	0.00569	2463	ko04626//Plant-pathogen interaction	GO:0031224//intrinsinc component of membrane	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356537999 ref XP_003537493.1 /0/PREDICTED: probable inactive receptor-like protein kinase At3g56050 [Glycine max]
Glyma. 02G008 500	-	-	-	-	-	-	-	-	1.09708	0.00085	1853	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0004702//receptor signaling protein serine/threonine kinase activity	GO:0035556//intracellular signal transduction;GO:0032147//activation of protein kinase activity	gi 571438081 ref XP_006574465.1 ;gi 358248598 ref NP_001239908.1 /0;0/PREDICTED: pto-interacting protein 1-like isoform X1 [Glycine max];pto-interacting protein 1-like [Glycine max]

Glyma.05G014600	-	-	-	-	-	-	-	-	1.0923	0.00905	1818	ko04626//Plant-pathogen interaction	-	-	-	gi 734359148 gb KHN15161.1 /0/Piriformospora indica-insensitive protein 2 [Glycine soja]
Glyma.08G316500	-	-	-	-	-	-	-	-	1.07526	0.00663	2702	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 214011508 gb ACJ61504.1 /0/calcium-dependent protein kinase [Glycine max]
Glyma.03G075300	-	-	-	-	-	-	-	-	1.07027	0.00772	5431	ko04626//Plant-pathogen interaction	-	GO:0032550	GO:0050896//response to stimulus	gi 571444675 ref XP_006576576.1 /0/PREDICTED: TMV resistance protein N-like isoform X1 [Glycine max]
Glyma.09G215700	-	-	-	-	-	-	-	-	1.06993	0.00209	2750	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	GO:0031224//intrinsic component of membrane	GO:0032550;GO:0004713//protein tyrosine kinase activity	GO:0006468//protein phosphorylation;GO:0071555//cell wall organization;GO:0000902//cell morphogenesis	gi 358248000 ref NP_001239788.1 ;gi 734348233 gb KHN11811.1 /0;0/LRR receptor-like serine/threonine-protein kinase FEI 1 precursor [Glycine max];LRR receptor-like serine/threonine-protein kinase FEI 1 [Glycine soja]
Glyma.07G151000	-	-	-	-	-	-	-	-	1.04984	0.00622	2685	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0004674//protein serine/threonine kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356521026 ref XP_003529159.1 /0/PREDICTED: calcium-dependent protein kinase 13 [Glycine max]
Glyma.08G265200	-	-	-	-	-	-	-	-	-1.0116	0.00326	1614	ko04626//Plant-pathogen interaction	GO:0044424	GO:0046872//metal ion binding	-	gi 571469172 ref XP_006584629.1 /1.81094e-167/PREDICTED: uncharacterized protein LOC100820628 isoform X1 [Glycine max]
Glyma.18G166800	-	-	-	-	-	-	-	-	-1.0201	0.00267	1362	ko04626//Plant-pathogen interaction	-	-	-	gi 351723541 ref NP_001235235.1 /0/RIN4c protein [Glycine max]
Glyma.17G154500	-	-	-	-	-	-	-	-	-1.0432	0.00577	1888	ko04626//Plant-pathogen interaction	-	-	-	gi 734314283 gb KHN01686.1 /0/Leucine-rich repeat-containing protein 40 [Glycine soja]
Glyma.16G049400	-	-	-	-	-	-	-	-	-1.0439	0.00284	1935	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	gi 359806583 ref NP_001241268.1 ;gi 947057436 gb KRH06842.1 /0;0/transcription factor ICE1-like [Glycine max];hypothetical protein GLYMA_16G049400 [Glycine max]
Glyma.20G222600	-	-	-	-	-	-	1.28669	0.00069	-1.0641	0.00474	1224	ko04626//Plant-pathogen interaction	-	GO:0032550;GO:0004672//protein kinase activity	GO:0009314//response to radiation;GO:0009267//cellular response to starvation;GO:0006464//cellular protein modification process;GO:0010243//response to organonitrogen compound;GO:0006796//phosphate-containing compound metabolic process	gi 351727763 ref NP_001236660.1 /0/phosphoenolpyruvate carboxylase kinase [Glycine max]
Glyma.19G005700	-	-	-	-	-	-	1.83488	0.00051	-1.086	0.00784	2512	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356573321 ref XP_003554810.1 /0/PREDICTED: cysteine-rich receptor-like protein kinase 42 [Glycine max]
Glyma.09G203000	-	-	-	-	-	-	-1.0423	0.00122	-1.2186	0.00052	1485	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 571475524 ref XP_006586670.1 ;gi 947090855 gb KRH39520.1 /0;0/PREDICTED: uncharacterized protein LOC100784145 isoform X1 [Glycine max];hypothetical protein GLYMA_09G203000 [Glycine max]
Glyma.02G100000	-	-	-	-	-	-	-	-	-1.2253	0.00325	2109	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process;GO:0010109//regulation of photosynthesis;GO:0048511//	gi 356502478 ref XP_003520046.1 /0/PREDICTED: serine/threonine-protein kinase STN7, chloroplastic-like [Glycine max]

																	rhythmic process	
Glyma.14G219700	-	-	-	-	-	-	-	-	-1.2448	0.00024	3030	ko04141//Protein processing in endoplasmic reticulum;ko04626//Plant-pathogen interaction	GO:0009536//plastid;GO:004437;GO:005911//cell junction;GO:0005576//extracellular region;GO:0016020//membrane	GO:0032550;GO:0005515//protein binding	GO:0010038//response to metal ion;GO:0044267//cellular protein metabolic process;GO:0009933//meristem structural organization;GO:0010073//meristem maintenance;GO:0006970//response to osmotic stress;GO:0015031//protein transport	gi 947068301 gb KRH17444.1 ;gi 571512225 ref XP_006596543.1 ;gi 734418176 gb KHN39421.1 /0;0/hypothetical protein GLYMA_14G219700 [Glycine max];PREDICTED: endoplasmic homolog isoform X2 [Glycine max];Endoplasmic like [Glycine soja]		
Glyma.12G219000	-	-	-	-	-	-	-	-	-1.2588	0.00143	2275	ko04626//Plant-pathogen interaction	-	-	-	gi 356542246 ref XP_003539580.1 /0/PREDICTED: cyclic nucleotide-gated ion channel 4-like [Glycine max]		
Glyma.14G040600	-	-	-	-	-	-	-	-	-1.2752	0.00043	995	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-pathogen interaction	GO:004437;GO:0016020//membrane	GO:0046872//metal ion binding	GO:0019932//second-messenger-mediated signaling;GO:0006637//acyl-CoA metabolic process;GO:0009640//photomorphogenesis;GO:0009593//detection of chemical stimulus;GO:0009605//response to external stimulus	gi 413945839 gb AFW78488.1 /1.43783e-104/calmodulin1 [Zea mays]		
Glyma.03G240000	-	-	-	-	-	-	-	-	-1.2762	0.00036	2166	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 947120341 gb KRH68590.1 ;gi 571447011 ref XP_006577251.1 /0;0/hypothetical protein GLYMA_03G240000 [Glycine max];PREDICTED: transcription factor bHLH94-like [Glycine max]		
Glyma.19G216200	-	-	-	-	-	-	-	-	-1.281	0.00029	1266	ko04650//Natural killer cell mediated cytotoxicity;ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding;GO:0046983//protein dimerization activity	GO:0033554//cellular response to stress;GO:0051240;GO:0006351//transcription, DNA-templated	gi 351721812 ref NP_001237222.1 /1.50678e-94/bZIP transcription factor bZIP41 [Glycine max]		
Glyma.03G170300	-	-	-	-	-	-	-	-	-1.2884	0.00842	3015	ko04075//Plant hormone signal transduction;ko04712//Circadian rhythm - plant;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 918463563 gb ALA09126.1 ;gi 947119269 gb KRH67518.1 /0;0/bHLH transcription factor, partial [Glycine max] ,hypothetical protein GLYMA_03G170300 [Glycine max]		
Glyma.17G258700	-	-	-	-	-	-	-	-	-1.3062	8.68E-05	2887	ko04141//Protein processing in endoplasmic reticulum;ko04626//Plant-pathogen interaction	GO:0009536//plastid;GO:004437;GO:005911//cell junction;GO:0005576//extracellular region;GO:0016020//membrane	GO:0032550;GO:0005515//protein binding	GO:0010038//response to metal ion;GO:0044267//cellular protein metabolic process;GO:0009933//meristem structural organization;GO:0010073//meristem maintenance;GO:0006970//response to osmotic stress;GO:0015031//protein transport	gi 571539837 ref XP_006601356.1 ;gi 734351227 gb KHN12637.1 /0;0/PREDICTED: endoplasmic homolog isoform X2 [Glycine max];Endoplasmic like [Glycine soja]		
Glyma.15G100100	-	-	-	-	-	-	-	-	-1.3487	0.00032	1828	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen	GO:0042579//microbody	GO:0004672//protein kinase activity;GO:0032550;GO:0036094//small molecule	GO:0006468//protein phosphorylation	gi 947062043 gb KRH11304.1 ;gi 955369108 ref XP_014623058.1 /4.33873e-143;0/hypothetical protein GLYMA_15G1001002 [Glycine max];PREDICTED: receptor-like cytosolic		

												interaction		binding:GO:1901363;GO:0097159//organic cyclic compound binding		serine/threonine-protein kinase RBK2 [Glycine max]
Glyma.02G275600	-	-	-	-	-	-	-	-	-1.3904	0.00011	945	ko04070//Phosphatidylinositol signaling system;ko04626//Plant-pathogen interaction	GO:0044437;GO:0016020//membrane	GO:0046872//metal ion binding	GO:0019932//second-messenger-mediated signaling;GO:0006637//acyl-CoA metabolic process;GO:0009640//photomorphogenesis;GO:0009593//detection of chemical stimulus;GO:0009605//response to external stimulus	gi 413945839 gb AFW78488.1 /1.43783e-104/calmodulin1 [Zea mays]
Glyma.07G212000	-	-	-	-	-	-	-	-	-1.4109	0.00985	2030	ko04626//Plant-pathogen interaction	GO:0043231//intracellular membrane-bounded organelle	GO:0046872//metal ion binding	-	gi 574584784 ref NP_001276189.1 /1.00228e-123/uncharacterized protein LOC100803158 [Glycine max]
Glyma.15G161200	-	-	-	-	-	-	-	-	-1.4248	5.78E-05	1658	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356556186 ref XP_003546407.1 /0/PREDICTED: probable receptor-like serine/threonine-protein kinase At5g57670 [Glycine max]
Glyma.02G247900	-	-	-	-	-	-	-	-	-1.4861	0.00028	1012	ko04626//Plant-pathogen interaction	-	-	-	gi 351721110 ref NP_001235151.1 ;gi 947124831 gb KRRH73037.1 /1.61515e-111;6.5414e-125/uncharacterized protein LOC100500493 [Glycine max];hypothetical protein GLYMA_02G247900 [Glycine max]
Glyma.11G217400	-	-	-	-	-	-	-	-	-1.4973	0.0019	2085	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 947082168 gb KRRH30957.1 /0/hypothetical protein GLYMA_11G217400 [Glycine max]
Glyma.16G059700	-	-	-	-	-	-	-	-	-1.5447	0.00118	3377	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 571526053 ref XP_006599042.1 ;gi 571526049 ref XP_006599041.1 /0;0/PREDICTED: probable inactive leucine-rich repeat receptor-like protein kinase At3g03770 isoform X2 [Glycine max];PREDICTED: probable inactive leucine-rich repeat receptor-like protein kinase At3g03770 isoform X1 [Glycine max]
Glyma.04G013800	-	-	-	-	-	-	-	-	-1.5499	0.00949	918	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	-	-	gi 734405996 gb KHN33765.1 /8.27238e-149/Protein TIFY 10B [Glycine soja]
Glyma.13G035100	-	-	-	-	-	-	-	-	-1.6389	0.00304	1130	ko04626//Plant-pathogen interaction	-	-	-	gi 356547218 ref XP_003542013.1 /4.33954e-91/PREDICTED: probable calcium-binding protein CML44 [Glycine max]
Glyma.16G099600	-	-	-	-	-	-	-	-	-1.6533	5.97E-05	969	ko04626//Plant-pathogen interaction	-	GO:0046872//metal ion binding;GO:0016628//oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	GO:0044710	gi 356559132 ref XP_003547855.1 /8.65453e-114/PREDICTED: probable calcium-binding protein CML16 [Glycine max]
Glyma.13G370100	-	-	-	-	-	-	-	-	-1.6542	0.00019	1579	ko04626//Plant-pathogen interaction	-	-	-	gi 356550659 ref XP_003543702.1 /0/PREDICTED: probable WRKY transcription factor 40 [Glycine max]
Glyma.14G185100	-	-	-	-	-	-	-	-	-1.7714	0.00542	1692	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 734419257 gb KHN39978.1 /0/Transcription factor bHLH93 [Glycine soja]

Glyma. 15G078 200	-	-	-	-	-	-	-	-	-1.7774	0.00012	1808	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 955373512 ref XP_014623829.1 /0/PREDICTED: serine/threonine-protein kinase-like protein ACR4 [Glycine max]
Glyma. 19G181 200	-	-	-	-	-	-	-	-	-1.8218	0.00077	1608	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 571558485 ref XP_006604574.1 ;gi 947046350 gb KRG95979.1 ;gi 356570752 ref XP_003553549.1 /0;0;0/PREDICTED: putative serine/threonine-protein kinase isoform X3 [Glycine max];hypothetical protein GLYMA_19G181200 [Glycine max];PREDICTED: putative serine/threonine-protein kinase isoform X1 [Glycine max]
Glyma. 13G234 800	-	-	-	-	-	-	-	-	-1.832	0.0026	1843	ko04626//Plant-pathogen interaction	-	GO:0016301//kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process	gi 356549280 ref XP_003543022.1 /0/PREDICTED: serine/threonine-protein kinase-like protein ACR4 [Glycine max]
Glyma. 06G092 000	-	-	-	-	-	-	-	-	-1.9707	0.00501	1587	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0005515//protein binding	-	gi 734339619 gb KHN09034.1 /0/Transcription factor bHLH93 [Glycine soja]
Glyma. 14G206 500	-	-	-	-	-	-	-	-	-2.0492	0.00723	4627	ko04626//Plant-pathogen interaction	-	-	-	gi 734398662 gb KHN30617.1 /0/Disease resistance protein [Glycine soja]
Glyma. 06G271 200	-	-	-	-	-	-	-	-	-2.0504	0.00562	2469	ko04626//Plant-pathogen interaction	-	-	-	gi 356515024 ref XP_003526201.1 /0/PREDICTED: cyclic nucleotide-gated ion channel 4-like [Glycine max]
Glyma. 20G185 100	-	-	-	-	-	-	-	-	-2.238	0.00042	2296	ko04626//Plant-pathogen interaction	-	-	GO:0009608//response to symbiont;GO:0044419//interspecies interaction between organisms	gi 571568702 ref XP_003556257.2 /0/PREDICTED: piriformospora indica-insensitive protein 2-like [Glycine max]
Glyma. 03G148 800	-	-	-	-	-	-	-	-	-2.3239	6.41E-06	2137	ko04075//Plant hormone signal transduction;ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356504892 ref XP_003521228.1 /0/PREDICTED: receptor-like cytosolic serine/threonine-protein kinase RBK2 [Glycine max]
Glyma. 19G152 100	-	-	-	-	-	-	-	-	-2.44	0.00019	2285	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 947045825 gb KRG95454.1 ;gi 356570544 ref XP_003553445.1 /0;0/hypothetical protein GLYMA_19G152100 [Glycine max];PREDICTED: receptor-like cytosolic serine/threonine-protein kinase RBK2 [Glycine max]
Glyma. 18G039 400	-	-	-	-	-	-	-	-	-2.4444	1.98E-05	2076	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process	gi 356569560 ref XP_003552967.1 /0/PREDICTED: serine/threonine-protein kinase CDL1-like [Glycine max]
Glyma. 09G265 700	-	-	-	-	-	-	-	-	-2.4727	0.00336	3737	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase;ko04626//Plant-pathogen interaction	-	-	-	gi 955342818 ref XP_014617918.1 /0/PREDICTED: putative disease resistance protein RGA4 [Glycine max]
Glyma. 13G187 600	-	-	-	-	-	-	-3.5659	3.23E-08	-2.5846	0.00174	2287	ko04626//Plant-pathogen interaction	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006468//protein phosphorylation	gi 947071700 gb KRG20591.1 /0/hypothetical protein GLYMA_13G187600 [Glycine max]

Glyma.13G083700	-	-	-	-	-	-	-	-	-2.7088	0.00153	833	ko04070/Phosphatidylinositol signaling system;ko04626/Plant-pathogen interaction	-	GO:0046872/metal ion binding	-	gi 356548725 ref XP_003542750.1 /7.13349e-108/PREDICTED: probable calcium-binding protein CML29 [Glycine max]
Glyma.08G271000	-	-	-	-	-	-	-	-	-3.2491	3.55E-11	1909	ko04075/Plant hormone signal transduction;ko04626/Plant-pathogen interaction	-	GO:0005515/protein binding	-	gi 955337298 ref XP_014634765.1 /0/PREDICTED: transcription factor bHLH71-like isoform X1 [Glycine max]
Glyma.18G271000	-1.6706	0.000559	-1.9606	1.60E-05	-2.0219	4.61E-06	-	-	-3.4182	5.75E-05	2592	ko04626/Plant-pathogen interaction	-	GO:0004672/protein kinase activity	GO:0006796/phosphate-containing compound metabolic process	gi 571549488 ref XP_006602953.1 /0/PREDICTED: receptor-like protein kinase FERONIA [Glycine max]
Glyma.17G261000	-	-	-	-	-	-	-	-	-4.0149	7.89E-08	1809	ko04626/Plant-pathogen interaction	GO:0043231/intracellular membrane-bounded organelle; GO:0016020/membrane	GO:0046872/metal ion binding;GO:0004674/protein serine/threonine kinase activity;GO:0032550	GO:0006796/phosphate-containing compound metabolic process;GO:0006464/cellular protein modification process	gi 571539899 ref XP_003549475.2 /0/PREDICTED: calcium-dependent protein kinase 2-like [Glycine max]
Glyma.03G088100	-11.6	1.16E-58	-11.133	1.42E-39	-10.886	7.06E-38	-5.5575	2.36E-18	-4.2575	5.55E-10	4005	ko00230/Purine metabolism;ko00240/Pyrimidine metabolism;ko01100/Metabolic pathways;ko03020/RNA polymerase;ko04626/Plant-pathogen interaction	-	-	GO:0050896/response to stimulus	gi 947117928 gb KRH66177.1 ;gi 571443502 ref XP_006576200.1 ;gi 571443498 ref XP_006576198.1 /0;0/hypothetical protein GLYMA_03G088100 [Glycine max];PREDICTED: uncharacterized LOC100527480 isoform X2 [Glycine max];PREDICTED: uncharacterized LOC100527480 isoform X1 [Glycine max]
Glyma.15G209200	-12.016	2.53E-13	-11.865	1.38E-11	-10.627	8.23E-11	-	-	-4.6062	0.00013	1119	ko04626/Plant-pathogen interaction	-	-	-	gi 947063715 gb KRH12976.1 /0/hypothetical protein GLYMA_15G209200 [Glycine max]
Glyma.03G088000	-10.378	3.06E-31	-9.5189	1.88E-20	-9.4617	1.56E-21	-5.2323	1.81E-11	-5.2689	7.23E-09	3143	ko04626/Plant-pathogen interaction	-	-	-	gi 571444898 ref XP_006576646.1 ;gi 947117926 gb KRH66175.1 /0;0/PREDICTED: TMV resistance protein N-like isoform X3 [Glycine max];hypothetical protein GLYMA_03G088000 [Glycine max]
Glyma.16G065700	-4.0878	2.47E-10	-5.3886	3.68E-12	-5.2294	2.02E-13	-3.0335	2.23E-06	-8.6387	2.44E-10	4096	ko04626/Plant-pathogen interaction	-	GO:0016301/kinase activity	GO:0016310/phosphorylation	gi 955377186 ref XP_014624710.1 /0/PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At4g08850 [Glycine max]
Glyma.01G010200	-	-	-	-	-	-	-	-	-1.5559	0.00272	1827	ko01100/Metabolic pathways;ko00710/Carbon fixation in photosynthetic organisms	GO:0009532/plastid stroma;GO:0009526/plastid envelope;GO:0009534/chloroplast thylakoid;GO:0005576/extracellular region	GO:0032550;GO:0016301/kinase activity	GO:0044238/primary metabolic process;GO:0009617/response to bacterium;GO:0006796/phosphate-containing compound metabolic process;GO:0006950/response to stress	gi 356495988 ref XP_003516852.1 /0/PREDICTED: phosphoribulokinase, chloroplastic [Glycine max]
Glyma.01G153300	-	-	-	-	-3.0901	0.00016	-	-	-	-	2099	ko00906/Carotenoid biosynthesis	-	GO:0046906/tetrapyrrole binding;GO:0046914/transition metal ion binding;GO:0016709/oxidoreductase activity, acting on paired donors, with	GO:0010162/seed dormancy process;GO:0009620/response to fungus;GO:0009416/response to light stimulus;GO:0006714/sequi	gi 947128604 gb KRH76458.1 ;gi 947128603 gb KRH76457.1 /0;0/hypothetical protein GLYMA_01G153300 [Glycine max];hypothetical protein GLYMA_01G153300 [Glycine max]

														incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	terpenoid metabolic process;GO:0006950//response to stress	
Glyma.01G163100	-	-	-	-	-	-	-	-	2.47807	0.00109	1698	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 734411617 gb KHN36003.1 ;gi 947128754 gb KRH76608.1 /0;0/Peroxidase 64 [Glycine soja];hypothetical protein GLYMA_01G163100 [Glycine max]
Glyma.01G171100	-	-	-	-	-	-	-	-	4.48764	0.00016	1661	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0005618//cell wall	GO:0043169//cation binding;GO:0046906//tetrapyrrole binding;GO:0016209//antioxidant activity;GO:0003824//catalytic activity	GO:0010383;GO:0009699//phenylpropanoid biosynthetic process;GO:0044702//single organism reproductive process;GO:0006950//response to stress	gi 356496705 ref XP_003517206.1 /0/PREDICTED: peroxidase 72-like [Glycine max]
Glyma.01G203400	-	-	-	-	-	-	-	-	3.47236	0.00056	2041	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0009532//plastid stroma	GO:0016160//amylase activity	GO:0006950//response to stress;GO:0005976//polysaccharide metabolic process;GO:0000023//maltose metabolic process	gi 571436239 ref XP_006573703.1 /0/PREDICTED: beta-amylase 3, chloroplastic [Glycine max]
Glyma.01G214200	-1.6511	6.82E-11	-	-	-	-	-	-	4.63818	4.28E-25	1320	ko00941//Flavonoid biosynthesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	-	GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0009699//phenylpropanoid biosynthetic process;GO:0006950//response to stress;GO:0001101//response to acid chemical;GO:0006996//organellar organization	gi 358248024 ref NP_001239794.1 /0/anthocyanidin synthase [Glycine max]
Glyma.01G219400	-1.1738	5.77E-07	-	-	-	-	-	-	-	-	820	ko00480//Glutathione metabolism;ko00590//Arachidonic acid metabolism	-	GO:0004601//peroxidase activity	GO:0006950//response to stress;GO:0044710	gi 351727154 ref NP_001236895.1 /8.45814e-121/uncharacterized protein LOC100306570 [Glycine max]
Glyma.02G032300	-1.7307	4.20E-07	-	-	-	-	-	-	-	-	866	ko04075//Plant hormone signal transduction	-	-	GO:0006950//response to stress	gi 359807353 ref NP_001241124.1 /1.75331e-109/uncharacterized protein LOC100783267 [Glycine max]
Glyma.02G093000	-	-	-	-	-	-	-	-	-1.499	0.00924	1491	-	-	GO:0046983//protein dimerization activity;GO:0004661//protein geranylgeranyltransferase activity	GO:0018342//protein prenylation;GO:0006950//response to stress;GO:0009725//response to hormone;GO:0001101//response to acid chemical	gi 734391396 gb KHN27225.1 /0/Geranylgeranyl transferase type-1 subunit beta [Glycine soja]
Glyma.02G157900	2.17653	4.63E-14	-	-	-	-	-	-	-	-	1215	-	GO:0043231//intracellular membrane-bounded organelle	-	GO:0006950//response to stress	gi 947123394 gb KRH71600.1 ;gi 356500303 ref XP_003518972.1 /1.23787e-86;1.80694e-58/hypothetical protein GLYMA_02G157900 [Glycine max];PREDICTED: uncharacterized protein LOC100527260 [Glycine max]
Glyma.02G224100	-	-	-	-	-	-	-	-	-1.7523	0.00032	826	-	GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0044437;GO:0000785//chromatin;GO:0	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization;GO:0006950//response to stress	gi 475622287 gb EMT31824.1 /1.35134e-52/Histone H4 [Aegilops tauschii]

													005911//cell junction;GO:0016020//membrane			
Glyma.02G228200	-	-	-	-	-	-	-	-	2.69927	0.00104	1955	ko04075//Plant hormone signal transduction	GO:0043231//intracellular membrane-bounded organelle	GO:0043169//cation binding;GO:0004721//phosphoprotein phosphatase activity	GO:0009620//response to fungus;GO:0006464//cellular protein modification process;GO:0009755//hormone-mediated signaling pathway;GO:0006950//response to stress	gi 356500878 ref XP_003519257.1 ;gi 947124500 gb KRH72706.1 /0;9.96677e-128/PREDICTED: probable protein phosphatase 2C 25 [Glycine max];hypothetical protein GLYMA_02G228200 [Glycine max]
Glyma.02G255400	-	-	-	-	-	-	-	-	2.45564	0.00324	2207	-	-	-	GO:0006950//response to stress	gi 947124958 gb KRH73164.1 /0/hypothetical protein GLYMA_02G255400 [Glycine max]
Glyma.03G056700	-	-	-	-	-	-	-	-	1.71214	0.00042	2411	ko01040//Biosynthesis of unsaturated fatty acids	GO:0009526//plastid envelope	GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0006950//response to stress;GO:0044710;GO:0044238//primary metabolic process	gi 358249324 ref NP_001239777.1 /0/omega-3 fatty acid desaturase, chloroplastic-like [Glycine max]
Glyma.03G116600	-	-	-	-	-	-	-	-	-1.2228	0.00022	1885	ko04141//Protein processing in endoplasmic reticulum	-	GO:0043169//cation binding;GO:0005515//protein binding;GO:0032550	GO:0006950//response to stress;GO:0044267//cellular protein metabolic process	gi 734426241 gb KHN43746.1 /0/Chaperone protein dnaJ 2 [Glycine soja]
Glyma.03G144400	-1.1908	0.000171	-	-	-	-	-	-	-	-	767	-	-	-	GO:0006950//response to stress;GO:0009791//post-embryonic development	gi 351727178 ref NP_001236128.1 /1.64464e-90/soybean seed maturation polypeptides [Glycine max]
Glyma.03G253500	-	-	-	-	-	-	-	-	-1.2355	0.00138	2562	ko00906//Carotenoid biosynthesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:0031976;GO:0044436	GO:0016491//oxidoreductase activity	GO:0032787//monocarboxylic acid metabolic process;GO:0006950//response to stress;GO:0006778//porphyrin-containing compound metabolic process;GO:0016122//xanthophyll metabolic process	gi 359807530 ref NP_001241404.1 ;gi 571443623 ref XP_006576259.1 /0;0/violaxanthin de-epoxidase, chloroplastic-like precursor [Glycine max];PREDICTED: violaxanthin de-epoxidase, chloroplastic-like isoform X5 [Glycine max]
Glyma.04G015900	-	-	-	-	-	-	-	-	-1.2822	0.00762	1767	ko01100//Metabolic pathways;ko00710//Carbon fixation in photosynthetic organisms	GO:0009521;GO:0031224//intrinsinc component of membrane;GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid;GO:0005576//extracellular region	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0009314//response to radiation;GO:0010038//response to metal ion;GO:0019318//hexose metabolic process;GO:0015977//carbon fixation;GO:0034285;GO:0044237//cellular metabolic process;GO:0006950//response to stress	gi 358248146 ref NP_001240080.1 ;gi 947112595 gb KRH60897.1 /0;0/uncharacterized protein LOC100806482 [Glycine max];hypothetical protein GLYMA_04G015900 [Glycine max]
Glyma.04G042300	-	-	-	-	-	-	-	-	-1.715	8.19E-06	1307	-	-	GO:0003676//nucleic acid binding	GO:0001101//response to acid chemical;GO:0009725//response to hormone;GO:0006950//response to stress	gi 918463735 gb AL09212.1 /4.09473e-165/MYB/HD-like transcription factor, partial [Glycine max]

Glyma. 04G095 500	-	-	-	-	-	-	-	-	1.02603	0.00198	2834	-	GO:0042175//nuclear outer membrane-endoplasmic reticulum membrane network;GO:0043231//intracellular membrane-bounded organelle;GO:0044444	GO:0046914//transition metal ion binding;GO:0032553//ribonucleotide binding;GO:0016653//oxidoreductase activity, acting on NAD(P)H, heme protein as acceptor	GO:0006950//response to stress;GO:0044710;GO:0001101//response to acid chemical	gi 734336550 gb KHN08276.1 /0/NADPH--cytochrome P450 reductase [Glycine soja]
Glyma. 04G103 900	-	-	-	-	-	-	-	-	1.35648	0.00552	1940	-	-	GO:0003676//nucleic acid binding	GO:0009628//response to abiotic stimulus;GO:0006950//response to stress;GO:0006351//transcription, DNA-templated	gi 918463511 gb ALA09100.1 /6.86589e-168/AP2-EREBP transcription factor, partial [Glycine max]
Glyma. 04G171 800	-	-	-	-	-	-	-	-	-2.1105	1.72E-07	1156	-	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0044765;GO:0044763;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress	gi 947115071 gb KRH63373.1 /0/hypothetical protein GLYMA_04G171800 [Glycine max]
Glyma. 04G198 200	-2.6678	5.29E-07	-3.3658	6.42E-11	-2.741	3.18E-05	-3.0729	1.59E-07	-4.8711	1.08E-13	1469	-	-	-	GO:0006950//response to stress	gi 955317145 ref XP_014630314.1 ;gi 571451376 ref XP_006578711.1 ;gi 947115507 gb KRH63809.1 ;gi 947115506 gb KRH63808.1 /8.85606e-114;9.6204e-126;2.55023e-92;4.98088e-104/PREDICTED: protein TAPETUM DETERMINANT 1-like isoform X2 [Glycine max];PREDICTED: protein TAPETUM DETERMINANT 1-like isoform X1 [Glycine max];hypothetical protein GLYMA_04G198200 [Glycine max];hypothetical protein GLYMA_04G198200 [Glycine max]
Glyma. 04G234 900	-	-	-	-	-	-	-	-	-1.1283	0.00084	1920	-	GO:0044444	-	GO:0006950//response to stress;GO:0007165//signal transduction	gi 734370890 gb KHN19500.1 /0/PP2A regulatory subunit TAP46 [Glycine soja]
Glyma. 05G055 600	2.14597	1.57E-22	1.87087	1.70E-07	1.72717	8.21E-09	1.51907	5.33E-05	1.89239	0.00019	2415	-	GO:0044424	-	GO:0010035//response to inorganic substance;GO:0006950//response to stress;GO:0009628//response to abiotic stimulus	gi 356514200 ref XP_003525794.1 /0/PREDICTED: hsp70-Hsp90 organizing protein 1-like [Glycine max]
Glyma. 05G103 600	1.14818	1.02E-06	-	-	-	-	-	-	3.03169	0.00478	1511	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 734328591 gb KHN06005.1 /0/Peroxidase 73 [Glycine soja]
Glyma. 05G150 100	-	-	-	-	-	-	-	-	3.25457	0.00072	533	-	-	-	GO:0051707//response to other organism;GO:0001101//response to acid chemical;GO:0009694//jasmonic acid metabolic	gi 947110493 gb KRH58819.1 /3.72565e-46/hypothetical protein GLYMA_05G150100 [Glycine max]

																process;GO:0010243//response to organonitrogen compound;GO:0009755//hormone-mediated signaling pathway;GO:0006950//response to stress;GO:0006984//ER-nucleus signaling pathway	
Glyma.05G192800	1.11757	1.37E-06	1.20541	0.000287	1.06995	0.00074	-	-	-	-	1167	-	-	-	-	GO:0006950//response to stress;GO:0010118//stomatal movement	gi 571453058 ref XP_006579344.1 /3.27039e-180/PREDICTED: uncharacterized protein LOC100305573 isoform X2 [Glycine max]
Glyma.05G193500	-1.0648	7.82E-06	-	-	-	-	-	-	-	-	1538	-	-	GO:0046914//transition metal ion binding;GO:0003824//catalytic activity	GO:0009617//response to bacterium;GO:0006950//response to stress;GO:0009755//hormone-mediated signaling pathway;GO:0032446//protein modification by small protein conjugation	gi 734406748 gb KHN34095.1 /0/E3 ubiquitin-protein ligase RGLG1 [Glycine soja]	
Glyma.05G195000	-	-	-	-	-2.6388	0.00091	-	-	3.46722	1.71E-05	1488	-	GO:0009536//plastid	GO:0003676//nucleic acid binding;GO:0019901//protein kinase binding	GO:0009314//response to radiation;GO:0051707//response to other organism;GO:0001101//response to acid chemical;GO:0032535//regulation of cellular component size;GO:0034285;GO:0006950//response to stress;GO:0006351//transcription, DNA-templated	gi 959092818 ref NP_001304649.1 /0/NAC domain-containing protein 2 [Glycine max]	
Glyma.05G211700	-	-	#####	2.36E-05	#####	1.97E-08	-	-	-	-	2131	ko00270//Cysteine and methionine metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	-	GO:0043168//anion binding;GO:0005515//protein binding;GO:0016846//carbon-sulfur lyase activity	GO:0001101//response to acid chemical;GO:0010039//response to iron ion;GO:0009692;GO:0009725//response to hormone;GO:0018871;GO:0003006//developmental process involved in reproduction;GO:0006950//response to stress;GO:0009605//response to external stimulus	gi 351726068 ref NP_001236858.1 /0/1-amino cyclopropane-1-carboxylate synthase [Glycine max]	
Glyma.06G002000	-	-	-	-	-	-	-	-	1.70251	2.14E-05	2049	-	GO:0031224//intracellular component of membrane	GO:0005515//protein binding	GO:0006950//response to stress	gi 356517840 ref XP_003527594.1 /0/PREDICTED: MLO-like protein 1 [Glycine max]	
Glyma.06G034600	-	-	-	-	-	-	-	-	2.10368	0.00783	1909	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transferase activity	GO:0003002//regionalization;GO:0042545//cell wall modification;GO:0006950//response to stress;GO:0048827//phyllome development;GO:0000003//reproduction;GO:0010413//glucuronoxylan metabolic process	gi 356519066 ref XP_003528195.1 /0/PREDICTED: probable galacturonosyltransferase-like 1 [Glycine max]	
Glyma.06G058500	-	-	-	-	-	-	1.45219	0.00012	-	-	1998	ko00062//Fatty acid elongation;ko01110//Biosynthesis of secondary metabolites	GO:0043231//intracellular membrane-bounded organelle	GO:0016746//transferase activity, transferring acyl groups	GO:0009314//response to radiation;GO:0006950//response to stress;GO:0006631//fatty acid metabolic process	gi 356514790 ref XP_003526086.1 /0/PREDICTED: 3-ketoacyl-CoA synthase 10-like [Glycine max]	

Glyma. 06G114 400	-	-	-	-	-	-	-	-	1.75694	0.00525	1499	ko0053//Ascorbate and aldarate metabolism;ko00480// Glutathione metabolism	GO:00319 76	GO:0046906//tetrapyrrole binding;GO:0016209//anti oxidant activity	GO:0009409//response to cold;GO:0007165//signal transduction;GO:0044710;GO :0006950//response to stress;GO:0044699;GO:0050 896//response to stimulus	gi 947104871 gb KRH53254.1 ;gi 356515910 ef XP_003526640.1 ;gi 947104870 gb KRH53 253.1 /9.09605e-131;0/0/hypothetical protein GLYMA_06G114400 [Glycine max];PREDICTED: probable L-ascorbate peroxidase 6, chloroplastic isoform X1 [Glycine max];hypothetical protein GLYMA_06G114400 [Glycine max]
Glyma. 06G146 200	-	-	-	-	-	-	-	-	2.64031	3.46E-0 3	669	-	-	GO:0016462//pyrophosph atase activity;GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 947105410 gb KRH53793.1 /2.22017e-164/ hypothetical protein GLYMA_06G146200 [Glycine max]
Glyma. 06G157 400	-	-	-	-	-3.1491	8.92E-0 5	-	-	-	-	1609	-	GO:00095 36//plastid	GO:0003676//nucleic acid binding;GO:0019901//prot ein kinase binding	GO:0009314//response to radiation;GO:0051707//respo nse to other organism;GO:0001101//respo nse to acid chemical;GO:0032535//regula tion of cellular component size;GO:0034285;GO:000695 0//response to stress;GO:0006351//transcript ion, DNA-templated	gi 513044651 gb AGO14648.1 ;gi 947105577 gb KRH53960.1 /0/0/NAC transcription factor [Glycine max];hypothetical protein GLYMA_06G157400 [Glycine max]
Glyma. 06G160 300	-	-	-	-	-	-	-	-	-1.8168	0.00013	584	-	-	-	GO:0001906//cell killing;GO:0006950//response to stress;GO:0009620//response to fungus	gi 947105631 gb KRH54014.1 /2.52264e-26/h ypothetical protein GLYMA_06G160300 [Glycine max]
Glyma. 06G160 400	-	-	-	-	-	-	-	-	4.86255	6.53E-0 5	642	-	-	-	GO:0006950//response to stress	gi 734341038 gb KHN09676.1 /1.27287e-30/D efensin-like protein 6 [Glycine soja]
Glyma. 06G167 300	1.65043	1.31E-0 5	-	-	-	-	-	-	-	-	1714	-	-	-	GO:0006950//response to stress	gi 571460950 ref XP_006581852.1 /1.48014e- 100/PREDICTED: protein TAPETUM DETERMINANT 1-like [Glycine max]
Glyma. 06G179 200	-1.3003	0.0001	-	-	-	-	-	-	-	-	2618	ko00052//Galactose metabolism	GO:00095 36//plastid	GO:0008378//galactosyltra nsferase activity	GO:0006950//response to stress;GO:0001101//response to acid chemical;GO:0044238//prima ry metabolic process	gi 571461147 ref XP_003527005.2 ;gi 571461 149 ref XP_006581911.1 /0/0/PREDICTED: galactinol--sucrose galactosyltransferase isoform X1 [Glycine max];PREDICTED: galactinol--sucrose galactosyltransferase isoform X2 [Glycine max]
Glyma. 06G192 100	-	-	-	-	-3.0559	3.37E-0 6	-4.4806	1.14E-1 6	-5.5694	3.88E-1 0	1957	-	GO:00312 24//intrinsic component of membrane	GO:0005215//transporter activity	GO:0044763;GO:0009628//re sponse to abiotic stimulus;GO:0006950//respon se to stress	gi 356519052 ref XP_003528188.1 /0/PREDIC TED: organic cation/carnitine transporter 3-like [Glycine max]
Glyma. 06G203 800	-	-	-	-	-	-	-	-	1.96284	0.0008	2929	ko03015//mRNA surveillance pathway;ko03040//Spli ceosome	GO:00329 91//macro molecular complex;GO: 0019028//viral capsid	GO:0036094//small molecule binding;GO:0097159//orga nic cyclic compound binding;GO:0046914//tran sition metal ion binding;GO:0032550	GO:0006950//response to stress	gi 571461496 ref XP_006582018.1 ;gi 955325 195 ref XP_014632096.1 ;gi 571461494 ref XP _003528224.2 /0/0/0/PREDICTED: glycine-rich cell wall structural protein 1.8-like isoform X2 [Glycine max];PREDICTED: glycine-rich cell wall structural protein 1.8-like isoform X3 [Glycine max];PREDICTED: glycine-rich cell wall structural protein 1.8-like isoform X1 [Glycine max]
Glyma. 06G248 900	-	-	-	-	-3.8586	2.79E-0 5	-	-	-	-	1786	-	GO:00432 31//intrace llular membrane -bounded organelle	GO:0003676//nucleic acid binding	GO:0001101//response to acid chemical;GO:0006950//respo nse to stress;GO:0006351//transcript ion, DNA-templated	gi 564010296 gb AHB63576.1 /0/NAC transcription factor [Glycine max]

Glyma. 06G309 100	-	-	-	-	-	-	-	-	-1.2445	0.00242	1565	-	GO:0043231//intracellular membrane-bounded organelle	-	GO:0006950//response to stress	gi 571457925 ref XP_006580951.1 ;gi 351727048 ref NP_001237915.1 /1.7048e-78;1.30928e-53/PREDICTED: uncharacterized protein LOC100527051 isoform X1 [Glycine max];uncharacterized protein LOC100527051 [Glycine max]
Glyma. 07G026 300	-	-	-	-	-	-	-	-	-1.0438	0.0035	1418	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00940//Phenylpropanoid biosynthesis	-	GO:0048037//cofactor binding	GO:0008152//metabolic process;GO:0006950//response to stress;GO:0010038//response to metal ion;GO:0001101//response to acid chemical	gi 734313393 gb KHN01290.1 /0/Dihydroflavonol-4-reductase [Glycine soja]
Glyma. 07G151 300	-	-	-	-	-	-	-	-	1.40593	0.00181	2130	ko01040//Biosynthesis of unsaturated fatty acids	GO:0009941//chloroplast envelope	GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0006633//fatty acid biosynthetic process;GO:0006950//response to stress	gi 734428355 gb KHN44706.1 /0/Omega-3 fatty acid desaturase, chloroplastic [Glycine soja]
Glyma. 07G152 900	-	-	-	-	-	-	-	-	-1.5243	5.53E-06	2549	ko04141//Protein processing in endoplasmic reticulum	GO:0005911//cell-cell junction;GO:0044432	GO:0003824//catalytic activity	GO:0006950//response to stress;GO:0000904//cell morphogenesis involved in differentiation;GO:0044710	gi 356523332 ref XP_003530294.1 ;gi 947100925 gb KRH49417.1 /0;0/PREDICTED: dnaJ protein ERD3A-like [Glycine max];hypothetical protein GLYMA_07G152900 [Glycine max]
Glyma. 07G153 100	-	-	-	-	-	-	-	-	1.84364	1.86E-07	2322	ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:0044444	GO:0046872//metal ion binding;GO:0019842//vitamin binding	GO:0006950//response to stress	gi 356521044 ref XP_003529168.1 /0/PREDICTED: pyruvate decarboxylase 2 [Glycine max]
Glyma. 07G252 100	-	-	-	-	-	-	-	-	1.43578	0.00029	12033	-	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0003676//nucleic acid binding	GO:0048731//system development;GO:0009755//hormone-mediated signaling pathway;GO:0009966//regulation of signal transduction;GO:0008152//metabolic process;GO:0006950//response to stress	gi 571467801 ref XP_006584045.1 /0/PREDICTED: chromatin structure-remodeling complex protein SYD-like isoform X1 [Glycine max]
Glyma. 07G266 200	-	-	-	-	-	-	-	-	2.87174	0.00144	1525	ko00562//Inositol phosphate metabolism;ko00053//Ascorbate and aldarate metabolism;ko04070//Phosphatidylinositol signaling system;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:0044444;GO:0016020//membrane	GO:0070456	GO:0019852//L-ascorbic acid metabolic process;GO:0046488//phosphatidylinositol metabolic process;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress	gi 734423661 gb KHN42287.1 ;gi 947102679 gb KRH51171.1 /0;0/Inositol monophosphatase 3 [Glycine soja];hypothetical protein GLYMA_07G266200 [Glycine max]
Glyma. 07G273 800	-	-	-	-	-	-	-	-	1.5463	0.00852	3844	ko00562//Inositol phosphate metabolism;ko04070//Phosphatidylinositol signaling system;ko01100//Metabolic pathways	-	GO:0046030//inositol triphosphate phosphatase activity	GO:0009888//tissue development;GO:0001101//response to acid chemical;GO:0046488//phosphatidylinositol metabolic process;GO:0009416//response to light stimulus;GO:0031667//response to nutrient levels;GO:0009756//carbohydrate mediated signaling;GO:0048878//chemical	gi 571468135 ref XP_006584139.1 /0/PREDICTED: type I inositol polyphosphate 5-phosphatase 12-like isoform X2 [Glycine max]

																homeostasis;GO:0044723;GO:0022622//root system development;GO:0006950//response to stress	
Glyma.08G003900	-	-	-	-	-	-	-	-	7.60589	7.09E-06	2090	ko00564//Glycerophospholipid metabolism;ko04070//Phosphatidylinositol signaling system;ko00561//Glycerolipid metabolism;ko01100//Metabolic pathways	-	GO:0016301//kinase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0006950//response to stress;GO:0048827//phyllome development;GO:0007186//G-protein coupled receptor signaling pathway;GO:0022622//root system development	gi 734363861 gb KHN16922.1 /5.93051e-137//Diacylglycerol kinase 1 [Glycine soja]	
Glyma.08G018000	-	-	-	-	-3.58	2.36E-05	-	-	2.58475	0.01002	2236	ko00270//Cysteine and methionine metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	-	GO:0043168//anion binding;GO:0005515//protein binding;GO:0016846//carbon-sulfur lyase activity	GO:0001101//response to acid chemical;GO:0010039//response to iron ion;GO:0009692;GO:0009725//response to hormone;GO:0018871;GO:003006//developmental process involved in reproduction;GO:0006950//response to stress;GO:0009605//response to external stimulus	gi 947092656 gb KRH41241.1 /0//hypothetical protein GLYMA_08G018000 [Glycine max]	
Glyma.08G165500	-	-	-	-	-	-	-	-	-1.1441	0.00085	1946	ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00710//Carbon fixation in photosynthetic organisms	GO:0030312//external encapsulating structure;GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0005576//extracellular region	GO:0032550;GO:0016301//kinase activity	GO:0010038//response to metal ion;GO:0006091//generation of precursor metabolites and energy;GO:0006796//phosphate-containing compound metabolic process;GO:0006950//response to stress	gi 356525742 ref XP_003531482.1 /0//PREDICTED: phosphoglycerate kinase, cytosolic [Glycine max]	
Glyma.08G181500	-	-	-	-	-	-	-	-	1.45236	0.00429	1365	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 571471963 ref NP_006585454.1 /0//PREDICTED: peroxidase 43-like [Glycine max]	
Glyma.08G196800	-	-	-	-	-	-	-	-	1.92843	2.28E-05	1631	-	GO:0016020//membrane	GO:0010178//IAA-amino acid conjugate hydrolase activity	GO:0002831;GO:0006950//response to stress	gi 734347256 gb KHN11319.1 ;gi 947095629 gb KRH44214.1 /0;0//IAA-amino acid hydrolase ILR1-like 4 [Glycine soja] ;hypothetical protein GLYMA_08G196800 [Glycine max]	
Glyma.08G230500	-	-	-	-	-	-	-	-	10.4957	1.50E-13	790	-	-	-	GO:0006950//response to stress	gi 351726098 ref NP_001236859.1 /1.45163e-110//uncharacterized protein LOC100499848 [Glycine max]	
Glyma.08G346700	3.14144	1.95E-49	2.80158	9.56E-17	2.41662	2.60E-14	1.91113	4.83E-08	2.85661	6.60E-10	2216	-	GO:0043231//intracellular membrane-bounded	GO:0016859//cis-trans isomerase activity;GO:1902936	GO:0044707;GO:0018208//peptidyl-proline modification;GO:0006950//response to stress;GO:0010038//response	gi 955338317 ref XP_014634970.1 /0//PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP62-like [Glycine max]	

													organelle; GO:004444		to metal ion	
Glyma. 09G011100	-	-	-	-	-	-	-	-	-1.5069	0.00123	1825	ko00562//Inositol phosphate metabolism;ko00053//Ascorbate and aldarate metabolism;ko04070//Phosphatidylinositol signaling system;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:004444;GO:0016020//membrane	GO:0070456	GO:0019852//L-ascorbic acid metabolic process;GO:0046488//phosphatidylinositol metabolic process;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress	gi 734420434 gb KHN40821.1 ;gi 947087895 gb KRH36560.1 /0;4.89277e-157//Inositol monophosphatase 3 [Glycine soja] ;hypothetical protein GLYMA_09G011100 [Glycine max]
Glyma. 09G022300	-2.8098	1.83E-20	-	-	-	-	-	-	-	-	1289	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 351723793 ref NP_001238315.1 /0/peroxidase precursor [Glycine max]
Glyma. 09G022400	-	-	-	-	-	-	-	-	2.90683	0.00075	1409	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 255637517 gb ACU19085.1 /0/unknown [Glycine max]
Glyma. 09G023000	-	-	-	-	-	-	-	-	8.80154	1.13E-05	1449	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 734380812 gb KHN22992.1 /0/Peroxidase C3 [Glycine soja]
Glyma. 09G040600	-	-	-	-	-	-	-	-	8.06853	4.50E-05	936	-	-	GO:0003824//catalytic activity	GO:0006950//response to stress	gi 351726932 ref NP_001237911.1 /1.98544e-110/uncharacterized protein LOC100305867 [Glycine max]
Glyma. 09G048400	-5.5581	2.27E-17	-	-	-	-	-	-	-	-	945	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 947088498 gb KRH37163.1 /0/hypothetical protein GLYMA_09G048400 [Glycine max]
Glyma. 09G056300	-	-	-	-	-	-	-	-	1.39593	0.00325	3594	ko00190//Oxidative phosphorylation	GO:0031224//intrinsinc component of membrane;GO:0005911//cell-cell junction;GO:0043231//intracellular	GO:0032550;GO:0017111//nucleoside-triphosphatase activity;GO:0043169//cation binding;GO:0008324//cation transmembrane transporter activity;GO:0046872//metal ion binding	GO:0009152//purine ribonucleotide biosynthetic process;GO:0006970//response to osmotic stress;GO:0009154//purine ribonucleotide catabolic process;GO:0006811//ion transport;GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient;GO:0010118//stomat	gi 571476496 ref XP_006586984.1 ;gi 947088618 gb KRH37283.1 /0;0//PREDICTED: plasma membrane ATPase 4-like [Glycine max];hypothetical protein GLYMA_09G056300 [Glycine max]

														membrane-bounded organelle		movement;GO:0001101//response to acid chemical;GO:0006950//response to stress	
Glyma.09G195800	-	-	-	-	-	-	-	-	1.1164	0.00922	1663	-		-	GO:0004721//phosphoprotein phosphatase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0006950//response to stress;GO:0030522//intracellular receptor signaling pathway	gi 947090724 gb KRG39389.1 ;gi 356531319 ref XP_003534225.1 /0;0/hypothetical protein GLYMA_09G195800 [Glycine max];PREDICTED: serine/threonine-protein phosphatase 7-like [Glycine max]
Glyma.09G197000	-	-	-	-	-	-	-	-	1.23284	0.00143	3119		ko04141//Protein processing in endoplasmic reticulum	-	GO:0032550;GO:0004672//protein kinase activity;GO:0004518//nucleic acid metabolism	GO:0090501//RNA phosphodiester bond hydrolysis;GO:0006396//RNA processing;GO:0006468//protein phosphorylation;GO:0030968//endoplasmic reticulum unfolded protein response;GO:0010033//response to organic substance;GO:0006950//response to stress	gi 571478408 ref XP_003533406.2 ;gi 947090746 gb KRG39411.1 /0;0/PREDICTED: serine/threonine-protein kinase/endoribonuclease IRE1a-like isoform X1 [Glycine max];hypothetical protein GLYMA_09G197000 [Glycine max]
Glyma.09G202000	1.15195	0.003352	-	-	-	-	-	-	-	-	1905		ko00630//Glyoxylate and dicarboxylate metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00460//Cyanosulfonamide metabolism;ko00670//One carbon pool by folic acid;ko00260//Glycine, serine and threonine metabolism	GO:0005840//ribosome;GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0031976;GO:0005576//extracellular region;GO:0016020//membrane	GO:0008187//poly-pyrimidine tract binding;GO:0043168//anion binding;GO:0016742//hydroxymethyl-, formyl- and related transferase activity	GO:0009314//response to radiation;GO:0010038//response to metal ion;GO:0009069//serine family amino acid metabolic process;GO:0006730//one-carbon metabolic process;GO:0048511//rhythmic process;GO:0043094//cellular metabolic compound salvage;GO:0006950//response to stress	gi 734417401 gb KHN38901.1 ;gi 947090836 gb KRG39501.1 ;gi 947090837 gb KRG39502.1 /0;0;0/Serine hydroxymethyltransferase, mitochondrial [Glycine soja];hypothetical protein GLYMA_09G202000 [Glycine max];hypothetical protein GLYMA_09G202000 [Glycine max]
Glyma.09G210900	-	-	-	-	-	-	-	-	-1.2504	0.00378	1894		ko01100//Metabolic pathways;ko00710//Carbon fixation in photosynthetic organisms	GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid;GO:0005576//extracellular region	GO:0032550;GO:0016301//kinase activity	GO:0044238//primary metabolic process;GO:0009617//response to bacterium;GO:0006796//phosphate-containing compound metabolic process;GO:0006950//response to stress	gi 356495988 ref XP_003516852.1 /0/PREDICTED: phosphoribulokinase, chloroplastic [Glycine max]
Glyma.09G218600	-	-	-	-	-	-	-	-	2.90812	0.00085	2072		ko00906//Carotenoid biosynthesis	-	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding;GO:0016709//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;GO:0016491//oxid	GO:0010162//seed dormancy process;GO:0009620//response to fungus;GO:0009416//response to light stimulus;GO:0006714//sesquiterpene metabolic process;GO:0006950//response to stress;GO:0044710	gi 734348207 gb KHN11785.1 ;gi 947091113 gb KRG39778.1 ;gi 947091114 gb KRG39779.1 ;gi 947091112 gb KRG39777.1 ;gi 947091110 gb KRG39775.1 /0;0;0;0/Abscicic acid 8'-hydroxylase 1 [Glycine soja];hypothetical protein GLYMA_09G218600 [Glycine max];hypothetical protein GLYMA_09G218600 [Glycine max];hypothetical protein GLYMA_09G218600 [Glycine max];hypothetical protein GLYMA_09G218600 [Glycine max]

															oreductase activity		
Glyma. 10G001700	-	-	-	-	-	-	-	-	1.83199	1.06E-03	1812	ko04140//Regulation of autophagy	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006950//response to stress;GO:0006464//cellular protein modification process;GO:0007154//cell communication	gi 947082911 gb KRG31632.1 /0/hypothetical protein GLYMA_10G001700 [Glycine max]	
Glyma. 10G019000	-	-	-	-	-	-	-	-	2.03198	2.80E-06	6495	ko02010//ABC transporters	GO:0005911//cell-cell junction;GO:0031224//intrinsic component of membrane;GO:0044437	GO:0032550;GO:0017111//nucleoside-triphosphatase activity;GO:0015405;GO:0051183//vitamin transporter activity;GO:0016628//oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	GO:0006835//dicarboxylic acid transport;GO:0051707//response to other organism;GO:0009154//purine ribonucleotide catabolic process;GO:0006950//response to stress	gi 356536723 ref XP_003536885.1 /0/PREDICTED: ABC transporter C family member 4-like [Glycine max]	
Glyma. 10G050800	-	-	-	-	-3.2757	0.00016	-	-	-	-	1493	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0044444	GO:0046906//tetrapyrrole binding;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0003824//catalytic activity	GO:0006950//response to stress;GO:0044710;GO:0009620//response to fungus	gi 356537521 ref XP_003537275.1 /0/PREDICTED: peroxidase 21 [Glycine max]	
Glyma. 10G058500	-	-	-	-	-	-	-	-	-1.1006	0.00133	1495	ko03015//mRNA surveillance pathway;ko03040//Spliceosome	GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid	GO:0003676//nucleic acid binding;GO:0036094//small molecule binding	GO:0006950//response to stress	gi 356533254 ref XP_003535181.1 /4.03851e-170/PREDICTED: 29 kDa ribonucleoprotein A, chloroplastic [Glycine max]	
Glyma. 10G127800	-	-	-	-	-	-	-1.132	0.00019	-	-	2177	ko03018//RNA degradation	GO:0005840//ribosome;GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0044437;GO:004429;GO:0016020//membrane	GO:0032550;GO:0046914//transition metal ion binding	GO:0010038//response to metal ion;GO:0006457//protein folding;GO:0006950//response to stress	gi 734343222 gb KHN10297.1 /0/Chaperonin CPN60-2, mitochondrial [Glycine soja]	
Glyma. 10G139500	-2.3686	8.16E-19	-2.5732	1.67E-12	-2.4054	3.41E-08	-1.8652	0.0001	-	-	1869	-	GO:0044436;GO:0044434;GO:0009579//thylakoid	GO:0016853//isomerase activity	GO:0044267//cellular protein metabolic process;GO:0009628//response to abiotic stimulus;GO:1901700;GO:0006950//response to stress;GO:0010033//response to organic substance	gi 947084964 gb KRG33685.1 ;gi 947084962 gb KRG33683.1 ;gi 356534945 ref XP_003536011.1 /1.08891e-130;0;0/hypothetical protein GLYMA_10G139500 [Glycine max];hypothetical protein GLYMA_10G139500 [Glycine max];PREDICTED: peptidyl-prolyl cis-trans isomerase, chloroplastic [Glycine max]	
Glyma. 10G172600	-	-	-	-	-	-	-	-	4.92439	2.02E-07	2373	ko00564//Glycerophospholipid metabolism	GO:0031012//extracellular matrix	GO:0003824//catalytic activity	GO:0009059//macromolecule biosynthetic process;GO:0009688//abscisic acid biosynthetic process;GO:0006950//response	gi 947085533 gb KRG34254.1 ;gi 571483425 ref XP_003535395.2 /0;0/hypothetical protein GLYMA_10G172600 [Glycine max];PREDICTED: uncharacterized protein LOC100811400 [Glycine max]	

Glyma. 11G035 200	-1.0134	5.17E-0 6	-	-	-	-	-	-	1.68646	0.00065	2408	ko00071//Fatty acid metabolism;ko01040//Biosynthesis of unsaturated fatty acids;ko01100//Metabolic pathways;ko04146//Peroxisome;ko00592//alpha-Linolenic acid metabolism	GO:0042579//microbody;GO:005911//cell-cell junction	GO:0016634//oxidoreductase activity, acting on the CH-CH group of donors, oxygen as acceptor;GO:0000166//nucleotide binding	GO:0009625//response to insect;GO:0010038//response to metal ion;GO:0009694//jasmonic acid metabolic process;GO:0048229//gametophyte development;GO:0009062//fatty acid catabolic process;GO:0006950//response to stress	gi 947079359 gb KRN28148.1 ;gi 734408808 gb KHN34915.1 /0;0/hypothetical protein GLYMA_11G035200 [Glycine max];Peroxisomal acyl-coenzyme A oxidase 1 [Glycine soja]
Glyma. 11G039 400	-	-	-	-	-2.8434	2.02E-0 5	-	-	-	-	2028	ko00500//Starch and sucrose metabolism;ko01100//Metabolic pathways	GO:0009532//plastid stroma	GO:0016160//amylase activity	GO:0006950//response to stress;GO:0005976//polysaccharide metabolic process;GO:0000023//maltose metabolic process	gi 734408776 gb KHN34883.1 /0/Beta-amylase 3, chloroplastic [Glycine soja]
Glyma. 11G078 300	-	-	-	-	-	-	-	-	3.1502	0.00035	4585	ko04075//Plant hormone signal transduction	-	GO:0004673//protein histidine kinase activity;GO:0032550;GO:0004888//transmembrane signaling receptor activity	GO:0003002//regionalization;GO:0006796//phosphate-containing compound metabolic process;GO:0007165//signal transduction;GO:0044702//single organism reproductive process;GO:0006950//response to stress	gi 571487712 ref XP_006590729.1 ;gi 947080024 gb KRN28813.1 /0;0/PREDICTED: histidine kinase 1-like isoform X2 [Glycine max];hypothetical protein GLYMA_11G078300 [Glycine max]
Glyma. 11G080 300	-	-	-	-	-	-	-	-	2.73761	0.00021	1522	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 947080055 gb KRN28844.1 /0/hypothetical protein GLYMA_11G080300 [Glycine max]
Glyma. 11G107 200	-	-	-	-	-	-	-	-	1.80125	3.89E-0 4	1304	ko00053//Ascorbate and aldarate metabolism;ko00480//Glutathione metabolism	GO:0005911//cell-cell junction;GO:0009526//plastid envelope;GO:0044437	GO:0046906//tetrapyrrole binding;GO:0016209//antioxidant activity	GO:0006950//response to stress;GO:0044710	gi 356538634 ref XP_003537806.1 /0/PREDICTED: L-ascorbate peroxidase 3, peroxisomal [Glycine max]
Glyma. 11G111 100	-	-	-	-	-	-	-	-	-1.1788	0.00358	1962	ko00051//Fructose and mannose metabolism;ko00030//Phosphate pathway;ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00710//Carbon fixation in photosynthetic organisms	GO:0005840//ribosome;GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0031976;GO:0005576//extracellular region;GO:0044436	GO:0016832//aldehyde lyase activity	GO:0010038//response to metal ion;GO:0001101//response to acid chemical;GO:0006091//generation of precursor metabolites and energy;GO:0006950//response to stress	gi 356538694 ref XP_003537836.1 /0/PREDICTED: fructose-bisphosphate aldolase 1, chloroplastic [Glycine max]
Glyma. 11G153 800	-	-	-	-	-	-	-	-	-1.2154	0.00099	1575	-	-	GO:0046872//metal ion binding;GO:0005543//phospholipid binding;GO:0043167//ion binding	GO:0006970//response to osmotic stress;GO:0006950//response to stress;GO:0009628//response to abiotic stimulus	gi 571486420 ref XP_006590331.1 ;gi 947081231 gb KRN30020.1 ;gi 947081232 gb KRN30021.1 /0;3.81041e-174;0/PREDICTED: uncharacterized protein LOC100806472 isoform X1 [Glycine max];hypothetical protein GLYMA_11G153800 [Glycine max];hypothetical protein GLYMA_11G153800 [Glycine max]

Glyma.11G178100	-	-	-	-	-	-	-1.3773	0.00135	-	-	868	-	GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0044437;GO:0000785//chromatin;GO:0005911//cell-cell junction;GO:0016020//membrane	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization;GO:0006950//response to stress	gi 475622287 gb EMT31824.1 /1.35134e-52/Histone H4 [Aegilops tauschii]
Glyma.11G212900	-	-	-	-	-	-	-	-	8.84592	1.57E-38	1005	ko00480//Glutathione metabolism	GO:0000325//plant-type vacuole	GO:0043167//ion binding;GO:0016765//transferase activity, transferring alkyl or aryl (other than methyl) groups	GO:0006950//response to stress;GO:0009962//regulation of flavonoid biosynthetic process	gi 959092507 ref NP_001304475.1 /1.32038e-156/glutathione S-transferase F11-like [Glycine max]
Glyma.11G247600	1.56653	1.40E-10	-	-	-	-	-	-	1.77344	1.23E-05	1578	ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:0030312//external encapsulating structure;GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0005911//cell-cell junction;GO:0016020//membrane	GO:0046914//transition metal ion binding;GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors;GO:0000166//nucleotide binding	GO:0010038//response to metal ion;GO:0019318//hexose metabolic process;GO:0009617//response to bacterium;GO:0006950//response to stress	gi 359806082 ref NP_001241184.1 /0/uncharacterized protein LOC100807342 [Glycine max]
Glyma.11G252900	-	-	-	-	-	-	-	-	-2.371	0.00025	1685	ko03010//Ribosome	GO:0009532//plastid stroma	GO:0003676//nucleic acid binding;GO:0003824//catalytic activity	GO:0006950//response to stress	gi 947082755 gb KRN31544.1 ;gi 356538073 ref XP_003537529.1 /0;0/hypothetical protein GLYMA_11G252900 [Glycine max];PREDICTED: 30S ribosomal protein S1 homolog isoform X1 [Glycine max]
Glyma.12G037400	-	-	-	-	-	-	-	-	-1.0625	0.00433	1707	ko00051//Fructose and mannose metabolism;ko00030//Pentose phosphate pathway;ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00710//Carbon fixation in photosynthetic organisms	GO:0005840//ribosome;GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0031976;GO:0005576//extracellular region;GO:0044436	GO:0016832//aldehyde-lyase activity	GO:0010038//response to metal ion;GO:0001101//response to acid chemical;GO:0006091//generation of precursor metabolites and energy;GO:0006950//response to stress	gi 734387664 gb KHN25427.1 /0/Fructose-bisphosphate aldolase 1, chloroplastic [Glycine soja]
Glyma.12G064000	-	-	-	-	-	-	-	-	1.3953	0.00866	2285	ko04144//Endocytosis;ko04141//Protein processing in endoplasmic reticulum;ko03040//Spliceosome	GO:0005840//ribosome;GO:0030312//external encapsulating structure	GO:0032550;GO:0019899//enzyme binding	GO:0051707//response to other organism;GO:0010038//response to metal ion;GO:0009628//response to abiotic	gi 734402634 gb KHN32117.1 /0/Heat shock cognate 70 kDa protein [Glycine soja]

													ing structure; GO:0009526/plastid envelope; GO:004437;GO:0005911//cell-cell junction;GO:0005576/extracellular region;GO:0016020//membrane		stimulus;GO:0006950//response to stress	
Glyma.13G028200	-	-	3.83427	1.88E-21	2.99907	6.70E-06	1.79323	0.00016	-	-	816	ko00195//Photosynthesis;ko01100//Metabolic pathways	GO:0009521;GO:0031224//intrinsically component of membrane;GO:0009534//chloroplast thylakoid	GO:0046914//transition metal ion binding;GO:0009055//electron carrier activity;GO:0003824//catalytic activity	GO:0006950//response to stress;GO:0009767//photosynthetic electron transport chain	gi 947069046 gb KRH17937.1 /0/hypothetical protein GLYMA_13G028200, partial [Glycine max]
Glyma.13G058600	-	-	-	-	-	-	-	-	1.47973	4.86E-05	3288	-	GO:0009532//plastid stroma	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006950//response to stress;GO:0009657//plastid organization;GO:0051604//protein maturation	gi 734331638 gb KHN07152.1 /0/Chaperone protein ClpB3, chloroplastic [Glycine soja]
Glyma.13G067900	-	-	-	-	-3.5906	2.72E-05	-	-	3.05666	0.00028	1651	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transferase activity	GO:0006950//response to stress	gi 356550372 ref XP_003543561.1 /0/PREDICTED: probable galacturonosyltransferase-like 10 [Glycine max]
Glyma.13G088100	-	-	-	-	-	-	-	-	2.25151	0.0007	1919	-	-	-	GO:0009987//cellular process;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress	gi 356548125 ref XP_003542454.1 /2.69255e-175/PREDICTED: ethylene-responsive transcription factor RAP2-4 [Glycine max]
Glyma.13G112500	-	-	-	-	-	-	-	-	-1.5724	0.0004	1219	-	GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid;GO:0005576//extracellular region	GO:0032550;GO:0046914//transition metal ion binding	GO:0010038//response to metal ion;GO:0044267//cellular protein metabolic process;GO:0051353//positive regulation of oxidoreductase activity;GO:0006950//response to stress	gi 571497607 ref XP_006593958.1 /1.45306e-162/PREDICTED: 20 kDa chaperonin, chloroplastic [Glycine max]
Glyma.13G147000	-	-	-	-	-	-	-	-	-1.7739	8.30E-06	687	-	GO:0031981//nuclear lumen;GO:0009536//plastid;GO	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization;GO:0006950//response to stress	gi 475622287 gb EMT31824.1 /1.35134e-52/Histone H4 [Aegilops tauschii]

													:0044437; GO:00007 85//chrom atin;GO:0 005911//ce ll-cell junction;G O:001602 0//membra ne			
Glyma. 13G195 200	-	-	-	-	-	-	-	-	1.70917	5.94E-0 5	5403	-	GO:00432 31//intrac ellular membrane -bounded organelle	GO:0046914//transition metal ion binding;GO:0016301//kina se activity;GO:0032550;GO: 0005515//protein binding;GO:0019787//ubiq uitin-like protein transferase activity;GO:0050136//NA DH dehydrogenase (quinone) activity	GO:0040007//growth;GO:190 2582;GO:0032446//protein modification by small protein conjugation;GO:0006950//res ponse to stress;GO:0009738//abscisic acid-activated signaling pathway;GO:0046903//secreti on;GO:0022904//respiratory electron transport chain	gi 947071810 gb KRH20701.1 /0/hypothetical protein GLYMA_13G195200 [Glycine max]
Glyma. 13G196 600	-	-	-	-	-	-	-2.2378	8.30E-0 6	-2.2229	0.0008	1567	-	GO:00095 32//plastid stroma;GO :0016020// membrane ;GO:0009 536//plasti d	GO:0003824//catalytic activity	GO:0009617//response to bacterium;GO:0006970//resp onse to osmotic stress;GO:0044710;GO:0006 950//response to stress	gi 571495833 ref XP_006593398.1 ;gi 351722 504 ref NP_001237502.1 /4.24891e-129;1.451 89e-127/PREDICTED: uncharacterized protein LOC100527538 isoform X1 [Glycine max];uncharacterized protein LOC100527538 [Glycine max]
Glyma. 13G243 100	-	-	-	-	-	-	-	-	-1.3442	0.00026	1716	ko03010//Ribosome	GO:00159 34//large ribosomal subunit;G O:001602 0//membra ne;GO:004 4437;GO: 0009536// plastid;GO :0031981// nuclear lumen	GO:0005198//structural molecule activity	GO:0006950//response to stress;GO:0010467//gene expression	gi 734337622 gb KHN08559.1 /1.12516e-80/6 0S ribosomal protein L26-1 [Glycine soja]
Glyma. 13G301 600	2.80312	2.63E-1 0	-	-	-	-	-	-	-	-	720	-	GO:00432 31//intrac ellular membrane -bounded organelle	-	GO:0006950//response to stress	gi 351727659 ref NP_001238192.1 /1.19665e- 49/uncharacterized protein LOC100305628 [Glycine max]
Glyma. 13G325 900	-	-	-	-	-	-	-	-	-1.1247	0.00165	1652	-	GO:00312 24//intrinsi c component of membrane ;GO:0005 911//cell-c ell junction	GO:0005372//water transmembrane transporter activity	GO:0055085//transmembrane transport;GO:0001101//respo nse to acid chemical;GO:0048588//devel opmental cell growth;GO:0042044//fluid transport;GO:0006950//respo nse to stress;GO:0051234//establis hment of localization	gi 162457846 ref NP_001105639.1 ;gi 947073 999 gb KRH22890.1 /0;3.82382e-137/aquaporin PIP2-7 [Zea mays];hypothetical protein GLYMA_13G325900 [Glycine max]
Glyma. 13G367 000	-	-	-	-	-	-	-	-	-1.1564	0.00288	1219	ko00190//Oxidative phosphorylation;ko011 00//Metabolic pathways	GO:00057 46//mitoch ondrial respiratory chain	GO:0046914//transition metal ion binding;GO:0051536//iron -sulfur cluster binding;GO:0003824//cata lytic activity	GO:0006950//response to stress;GO:0044710	gi 947074709 gb KRH23600.1 ;gi 947074707 g b KRH23598.1 ;gi 947074708 gb KRH23599.1 /1.886e-169;0;0/hypothetical protein GLYMA_13G367000 [Glycine max];hypothetical protein GLYMA_13G367000 [Glycine

																	max];hypothetical protein GLYMA_13G367000 [Glycine max]
Glyma. 14G061 200	-	-	-	-	-3.4096	0.00087	-	-	3.54047	1.14E-0 5	1734	-	-	-	GO:0006950//response to stress	gi 571507539 ref XP_003545237.2 /0/PREDIC TED: nematode resistance protein-like HSPRO2 [Glycine max]	
Glyma. 14G078 600	-	-	-	-	-	-	1.27601	5.93E-0 4	2.69163	2.01E-0 7	1720	ko01100//Metabolic pathways;ko00592//alp ha-Linolenic acid metabolism	GO:00095 26//plastid envelope; GO:00095 34//chloro plast thylakoid	GO:0046906//tetrapyrrole binding;GO:0046914//tran sition metal ion binding;GO:0016491//oxid oreductase activity;GO:0016836//hydr o-lyase activity	GO:0051707//response to other organism;GO:0006631//fatty acid metabolic process;GO:0001101//respon se to acid chemical;GO:0006950//respo nse to stress	gi 947066131 gb KRH15274.1 /0/hypothetical protein GLYMA_14G078600 [Glycine max]	
Glyma. 14G084 700	-1.636	8.73E-1 0	-	-	-	-	-	-	-	-	1592	-	GO:00432 31//intrace llular membrane -bounded organelle	GO:0003676//nucleic acid binding;GO:0001071//nucl eic acid binding transcription factor activity	GO:0006950//response to stress;GO:0006351//transcri ption, DNA-templated	gi 351724471 ref NP_001235779.1 /2.00806e- 130/dehydration responsive element binding protein [Glycine max]	
Glyma. 14G088 300	-	-	-1.6406	0.00031 1	-3.5117	1.76E-0 5	-	-	2.38448	4.30E-0 5	1097	-	-	GO:0043169//cation binding	GO:0050789//regulation of biological process;GO:0001101//respon se to acid chemical;GO:0009719;GO:00 09628//response to abiotic stimulus;GO:0007275//multic ellular organismal development;GO:0006950//re sponse to stress;GO:0010033//response to organic substance	gi 390517035 ref NP_001254622.1 /2.3512e-1 31/zinc finger protein ZAT10-like [Glycine max]	
Glyma. 14G111 800	-	-	-	-	-	-	-1.4101	9.21E-0 5	-	-	2504	ko00270//Cysteine and methionine metabolism;ko00330// Arginine and proline metabolism;ko00960//T ropane, piperidine and pyridine alkaloid biosynthesis;ko01100// Metabolic pathways;ko01110//Bio synthesis of secondary metabolites;ko00360//P henylalanine metabolism;ko00250// Alanine, aspartate and glutamate metabolism;ko00400//P henylalanine, tyrosine and tryptophan biosynthesis;ko00950//I soquinoline alkaloid biosynthesis;ko00350// Tyrosine metabolism	GO:00095 32//plastid stroma;GO :0009526// plastid envelope; GO:00444 29;GO:00 05576//ext racellular region	GO:0043168//anion binding;GO:0070546	GO:0010038//response to metal ion;GO:0043648//dicarboxyli c acid metabolic process;GO:0009064//glutami ne family amino acid metabolic process;GO:0009066;GO:000 6950//response to stress	gi 734321388 gb KHN04158.1 ;gi 947066652 gb KRH15795.1 /0/0/Aspartate aminotransferase P2, mitochondrial [Glycine soja] ;hypothetical protein GLYMA_14G111800 [Glycine max]	
Glyma. 14G171 500	-	-	-	-	-1.8387	5.17E-0 5	-	-	-	-	1795	-	-	-	GO:0009987//cellular process;GO:0009628//respon se to abiotic stimulus;GO:0006950//respon se to stress	gi 571510835 ref XP_006596336.1 /6.02977e- 159/PREDICTED: ethylene-responsive transcription factor RAP2-4-like [Glycine max]	
Glyma. 14G176 700	-	-	-	-	-	-	-	-	2.10905	4.99E-0 3	1728	ko04075//Plant hormone signal transduction	GO:00432 31//intrace llular	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-cont aining compound metabolic process;GO:0009628//respon se to stress	gi 734344379 gb KHN10464.1 /0/Serine/threon ine-protein kinase SAPK2 [Glycine soja]	

													membrane-bounded organelle		e to abiotic stimulus;GO:0006950//response to stress;GO:0006464//cellular protein modification process	
Glyma.14G190800	-	-	-	-	-	-	-	-	-1.2147	0.00602	1491	-	GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0044437;GO:0000785//chromatin;GO:005911//cell-cell junction;GO:0016020//membrane	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization;GO:0006950//response to stress	gi 475622287 gb EMT31824.1 /1.35134e-52/Histone H4 [Aegilops tauschii]
Glyma.14G195200	-	-	-	-	-3.7808	3.31E-05	-	-	3.02087	0.00017	1825	ko04075//Plant hormone signal transduction	GO:0043231//intracellular membrane-bounded organelle	GO:0043169//cation binding;GO:0004721//phosphoprotein phosphatase activity	GO:0009620//response to fungus;GO:0006464//cellular protein modification process;GO:0009755//hormone-mediated signaling pathway;GO:0006950//response to stress	gi 356553088 ref XP_003544890.1 ;gi 947067914 gb KRH17057.1 /0;5.22623e-137/PREDICTED: probable protein phosphatase 2C 25 [Glycine max];hypothetical protein GLYMA_14G195200 [Glycine max]
Glyma.14G201700	1.10966	0.004665	-	-	-	-	-	-	-	-	1549	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 947068000 gb KRH17143.1 /0/hypothetical protein GLYMA_14G201700 [Glycine max]
Glyma.15G006400	-	-	-	-	-	-	-	-	-1.1887	0.00164	1964	ko00190//Oxidative phosphorylation;ko01100//Metabolic pathways	GO:0005746//mitochondrial respiratory chain	GO:0046914//transition metal ion binding;GO:0051536//iron-sulfur cluster binding;GO:0003824//catalytic activity	GO:0006950//response to stress;GO:0044710	gi 947074707 gb KRH23598.1 /0/hypothetical protein GLYMA_13G367000 [Glycine max]
Glyma.15G034000	-	-	-	-	-	-	-	-	1.3977	0.00982	3882	ko00230//Purine metabolism;ko00232//Caffeine metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko04146//Peroxisome	GO:0044444	GO:0046914//transition metal ion binding;GO:0051536//iron-sulfur cluster binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0006144//purine nucleobase metabolic process;GO:0006950//response to stress;GO:0006801//superoxide metabolic process	gi 947060936 gb KRH10197.1 /0/hypothetical protein GLYMA_15G034000 [Glycine max]
Glyma.15G052700	-	-	-	-	-	-	-	-	4.56792	0.00383	1267	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	GO:0043231//intracellular membrane-bounded organelle;GO:0030312//external encapsulating structure;GO:00059	GO:0043169//cation binding;GO:0046906//tetrapyrrole binding;GO:0016209//antioxidant activity;GO:0003824//catalytic activity	GO:0009620//response to fungus;GO:0009698//phenylpropanoid metabolic process;GO:0042743//hydrogen peroxide metabolic process;GO:0006950//response to stress	gi 955366031 ref XP_014622898.1 /0/PREDICTED: cationic peroxidase 2 [Glycine max]

													11//cell-cell junction;GO:0005576/extracellular region;GO:0016020//membrane			
Glyma.15G088000	-	-	-	-	-	-	1.6912	0.00012	2.7109	1.87E-06	2418	ko04144//Endocytosis; ko04141//Protein processing in endoplasmic reticulum; ko03040//Spliceosome	GO:0030312//external encapsulating structure; GO:0009536//plastid; GO:0016020//membrane	GO:0032550;GO:0016891//endoribonuclease activity, producing 5'-phosphomonoesters	GO:0051707//response to other organism;GO:0090501//RNA phosphodiester bond hydrolysis;GO:0006950//response to stress	gi 947061823 gb KRH11084.1 /0/hypothetical protein GLYMA_15G088000 [Glycine max]
Glyma.15G100700	-	-	-	-	-	-	-	-	-1.516	8.64E-05	833	-	-	GO:0016671//oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	GO:0044710;GO:0044267//cellular protein metabolic process;GO:0006950//response to stress	gi 351724743 ref NP_001237068.1 /4.00215e-99/uncharacterized protein LOC100305558 [Glycine max]
Glyma.15G124500	-	-	-	-	-	-	-	-	-2.3622	0.0076	1927	-	GO:0016020//membrane;GO:0031224//intrinsinc component of membrane	GO:0005515//protein binding	GO:0050896//response to stimulus;GO:0006950//response to stress	gi 947062437 gb KRH11698.1 ;gi 571518103 ref XP_006597646.1 /0;0/hypothetical protein GLYMA_15G124500 [Glycine max];PREDICTED: MLO-like protein 13 [Glycine max]
Glyma.15G128700	-	-	-	-	-	-	-	-	2.99002	0.00284	1464	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 734356908 gb KHN14345.1 /0/Peroxidase 22 [Glycine soja]
Glyma.15G132600	-	-	-	-	-	-	-	-	1.5412	0.01003	2044	ko00908//Zeatin biosynthesis	GO:0030312//external encapsulating structure; GO:0005911//cell-cell junction	GO:0046993;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0044710;GO:0000741//karyogamy;GO:0003006//developmental process involved in reproduction;GO:0006950//response to stress	gi 356555926 ref XP_003546280.1 /0/PREDICTED: inactive tetrahydrocannabinolic acid synthase-like [Glycine max]
Glyma.15G132800	-	-	-	-	-	-	-	-	3.43451	8.07E-05	2173	-	GO:0005911//cell-cell junction;GO:0005618//cell wall;GO:0043231//intracellular membrane-bounded organelle; GO:0044444;GO:0005576//extracellular	GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0006950//response to stress;GO:0044710	gi 734356870 gb KHN14307.1 /0/Reticuline oxidase-like protein [Glycine soja]

													region;GO:0016020//membrane			
Glyma.15G162600	-	-	-	-	-	-	-	-	1.31971	0.00704	3504	ko00190//Oxidative phosphorylation	GO:0005911//cell-cell junction;GO:0043231//intracellular membrane-bounded organelle;GO:003124//intrinsic component of membrane	GO:0032550;GO:0017111//nucleoside-triphosphatase activity;GO:0046872//metal ion binding;GO:0008324//cation transmembrane transporter activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient;GO:0009152//purine ribonucleotide biosynthetic process;GO:0010118//stomatal movement;GO:0001101//response to acid chemical;GO:0009154//purine ribonucleotide catabolic process;GO:0006950//response to stress	gi 356556196 ref XP_003546412.1 /0/PREDICTED: plasma membrane ATPase 4-like [Glycine max]
Glyma.15G217100	2.88696	3.31E-08	-	-	-	-	-	-	-	-	823	-	-	-	GO:0006950//response to stress	gi 351726383 ref NP_001235333.1 /4.13848e-109/uncharacterized protein LOC100306201 [Glycine max]
Glyma.15G218900	-	-	-	-	-	-	-	-	5.54997	0.00036	848	-	-	-	GO:0006950//response to stress	gi 734420599 gb KHN40931.1 /6.60831e-110/MLP-like protein 43 [Glycine soja]
Glyma.15G261900	-	-	-	-	-	-	-	-	-1.0382	0.00211	2027	ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00710//Carbon fixation in photosynthetic organisms	GO:0030312//external encapsulating structure;GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0005576//extracellular region	GO:0032550;GO:0016301//kinase activity	GO:0010038//response to metal ion;GO:0006091//generation of precursor metabolites and energy;GO:0006796//phosphate-containing compound metabolic process;GO:0006950//response to stress	gi 947064495 gb KRN13756.1 ;gi 356557028 ref XP_003546820.1 /0;0/hypothetical protein GLYMA_15G261900 [Glycine max];PREDICTED: phosphoglycerate kinase, cytosolic [Glycine max]
Glyma.15G274300	-	-	-	-	-	-	-	-	-2.6561	0.00072	720	-	GO:0009536//plastid	-	GO:0006950//response to stress	gi 734419109 gb KHN39933.1 /1.97483e-113/MLP-like protein 28 [Glycine soja]
Glyma.16G044900	-	-	-	-	-	-	-	-	-1.2431	0.00194	1619	ko01100//Metabolic pathways;ko00710//Carbon fixation in photosynthetic organisms	GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid;GO:0005576//extracellular region	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0009314//response to radiation;GO:0019318//hexose metabolic process;GO:0034285;GO:0006950//response to stress	gi 356561064 ref XP_003548805.1 /0/PREDICTED: glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic [Glycine max]
Glyma.16G055900	-	-	-	-	-	-	2.35556	0.00016	-	-	1382	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 571525981 ref XP_003548517.2 /0/PREDICTED: peroxidase 55-like [Glycine max]

												biosynthesis				
Glyma.16G080100	-	-	-	-	-	-	-	-	2.30011	0.00039	2340	-	GO:003124//intrinsic component of membrane	GO:0005515//protein binding	GO:0006950//response to stress	gi 947057895 gb KRN07301.1 ;gi 734311089 gb KHM99994.1 /0;0/hypothetical protein GLYMA_16G080100 [Glycine max];MLO-like protein 1 [Glycine soja]
Glyma.16G098700	-3.903	1.84E-10	-	-	-	-	-	-	-	-	1682	ko04141//Protein processing in endoplasmic reticulum	GO:0005911//cell-cell junction;GO:0044432	GO:0003824//catalytic activity	GO:0006950//response to stress;GO:0000904//cell morphogenesis involved in differentiation;GO:0044710	gi 955373994 ref XP_014623933.1 /0/PREDICTED: dnaJ protein ERD3A-like [Glycine max]
Glyma.16G100400	-	-	-	-	-	-	-	1.29943	0.00097	-	537	-	GO:0005911//cell-cell junction;GO:0016020//membrane;GO:0005618//cell wall	GO:0016787//hydrolase activity	GO:0016485//protein processing;GO:0006950//response to stress	gi 734383103 gb KHN23780.1 /2.1965e-29/Defensin SD2 [Glycine soja]
Glyma.16G129800	-	-	-	-	-	-	-	-	-1.1645	0.00248	1290	-	-	GO:0016671//oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	GO:0044710;GO:0044267//cellular protein metabolic process;GO:0006950//response to stress	gi 356559314 ref XP_003547945.1 /8.30954e-177/PREDICTED: peptide methionine sulfoxide reductase A5-like [Glycine max]
Glyma.16G159700	2.02261	8.96E-05	-	-	-	-	-	-	4.85712	3.48E-05	3395	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase	-	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 571528807 ref XP_006599456.1 /0/PREDICTED: TMV resistance protein N-like [Glycine max]
Glyma.16G164400	-	-	-	-	-	-	-	-	10.1391	2.44E-08	1424	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 947059246 gb KRN08652.1 ;gi 358249064 ref NP_001239731.1 /0;0/hypothetical protein GLYMA_16G164400 [Glycine max];uncharacterized protein LOC100795412 precursor [Glycine max]
Glyma.16G211400	-	-	-	-	-	-	-	-	3.37201	0.00075	5242	-	-	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 947059957 gb KRN09363.1 ;gi 947059961 gb KRN09367.1 ;gi 947059960 gb KRN09366.1 /0;0;0/hypothetical protein GLYMA_16G211400 [Glycine max];hypothetical protein GLYMA_16G211400 [Glycine max];hypothetical protein GLYMA_16G211400 [Glycine max]
Glyma.16G212300	-1.8558	0.000242	-	-	-	-	-	-	-	-	3786	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko01100//Metabolic pathways;ko03020//RNA polymerase	-	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006950//response to stress;GO:0007154//cell communication	gi 358248732 ref NP_001239675.1 /0/TMV resistance protein N-like [Glycine max]
Glyma.17G030000	-	-	-	-	-	-2.7144	0.00105	-	-	2.67176	0.00631	1005	-	-	GO:0006950//response to stress	gi 734319289 gb KHN03329.1 /1.47272e-115/Pathogenesis-related protein STH-2 [Glycine soja]

Glyma.17G030100	-	-	-	-	-	-	-	-	8.97181	8.60E-06	867	-	-	-	GO:0006950//response to stress	gi 734319288 gb KHN03328.1 /4.37402e-111/Major allergen Pru av 1 [Glycine soja]
Glyma.17G030200	-3.5199	3.28E-08	-	-	-	-	1.77618	0.00059	5.06797	8.56E-10	947	-	-	-	GO:0006950//response to stress	gi 351725047 ref NP_001236055.1 /4.96124e-92/uncharacterized protein LOC547916 [Glycine max]
Glyma.17G030300	-	-	-	-	-	-	-	-	9.30716	5.30E-06	896	-	-	-	GO:0006950//response to stress	gi 359807211 ref NP_001241617.1 /4.85297e-92/uncharacterized protein LOC100791036 [Glycine max]
Glyma.17G047200	-	-	-	-	-	-	-	-	-1.3922	0.00167	908	-	GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid;GO:0005576//extracellular region	GO:0032550;GO:0046914//transition metal ion binding	GO:0010038//response to metal ion;GO:0044267//cellular protein metabolic process;GO:0051353//positive regulation of oxidoreductase activity;GO:0006950//response to stress	gi 947053124 gb KRH02577.1 ;gi 947053123 gb KRH02576.1 /2.70356e-142;7.30452e-139/hypothetical protein GLYMA_17G047200 [Glycine max];hypothetical protein GLYMA_17G047200 [Glycine max]
Glyma.17G063200	-	-	-	-	-	-	-	-	-1.4648	0.00012	815	-	GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0044437;GO:0000785//chromatin;GO:0005911//cell-cell junction;GO:0016020//membrane	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization;GO:0006950//response to stress	gi 475622287 gb EMT31824.1 /1.35134e-52/Histone H4 [Aegilops tauschii]
Glyma.17G072400	-1.0878	2.04E-05	-	-	-	-	-	-	-	-	2310	ko04144//Endocytosis; ko04141//Protein processing in endoplasmic reticulum;ko03040//Spliceosome	GO:0016020//membrane;GO:0030312//external encapsulating structure;GO:0009536//plastid	GO:0032550	GO:0006950//response to stress;GO:0051707//response to other organism	gi 356562559 ref XP_003549537.1 /0/PREDICTED: heat shock 70 kDa protein [Glycine max]
Glyma.17G145100	-	-	-	-	-	-	-	-	3.21091	0.00114	2868	-	-	GO:0004551//nucleotide diphosphatase activity;GO:0016787//hydrolase activity;GO:0003824//catalytic activity	GO:0006950//response to stress	gi 571532280 ref XP_006600227.1 ;gi 947054735 gb KRH04188.1 ;gi 947054734 gb KRH04187.1 ;gi 359806679 ref NP_001241031.1 /0;0/PREDICTED: uncharacterized protein LOC100815507 isoform X1 [Glycine max];hypothetical protein GLYMA_17G145100 [Glycine max];hypothetical protein GLYMA_17G145100 [Glycine max];uncharacterized protein LOC100815507 [Glycine max]

Glyma. 17G218 700	-	-	-	-	-	-	-	-	1.35911	0.00956	3043	ko04075//Plant hormone signal transduction	-	GO:0043169//cation binding;GO:0004721//phosphoprotein phosphatase activity	GO:0009767//photosynthetic electron transport chain;GO:0001933//negative regulation of protein phosphorylation;GO:0009738//abscisic acid-activated signaling pathway;GO:0006950//response to stress;GO:0044763;GO:0006464//cellular protein modification process;GO:0031324//negative regulation of cellular metabolic process;GO:0006796//phosphate-containing compound metabolic process;GO:0009737//response to abscisic acid	gi 356563938 ref XP_003550214.1 ;gi 734373231 gb KHN20160.1 ;gi 947055849 gb KRN05302.1 ;gi 571538689 ref XP_006601194.1 /0;0;0/PREDICTED: protein phosphatase 2C 77-like isoform X3 [Glycine max];Protein phosphatase 2C 16 [Glycine soja];hypothetical protein GLYMA_17G218700 [Glycine max];PREDICTED: protein phosphatase 2C 77-like isoform X4 [Glycine max]
Glyma. 17G237 900	-	-	-	-	-	-	-	-	-1.2807	6.55E-04	2177	-	-	GO:0005488	GO:0010035//response to inorganic substance;GO:0051707//response to other organism;GO:0001101//response to acid chemical;GO:0009628//response to abiotic stimulus;GO:0009725//response to hormone;GO:0009966//regulation of signal transduction;GO:0006950//response to stress	gi 947056168 gb KRN05621.1 /3.38894e-144/hypothetical protein GLYMA_17G237900 [Glycine max]
Glyma. 17G246 500	-	-	-	-	-	-	1.31886	0.00049	2.51887	2.71E-09	2795	ko01100//Metabolic pathways;ko00592//alpha-Linolenic acid metabolism	GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding;GO:0016491//oxidoreductase activity;GO:0016836//hydrolyase activity	GO:0051707//response to other organism;GO:0006631//fatty acid metabolic process;GO:0001101//response to acid chemical;GO:0006950//response to stress	gi 351721547 ref NP_001236445.1 /0/allene oxide synthase [Glycine max]
Glyma. 18G009 700	1.38422	6.90E-11	-	-	-	-	-	-	-	-	3145	ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:0030312//external encapsulating structure;GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0005911//cell-cell junction;GO:0016020//membrane;GO:0043231//intracellular membrane-bounded organelle	GO:0046914//transition metal ion binding;GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors;GO:0000166//nucleotide binding;GO:0005488	GO:0010038//response to metal ion;GO:0019318//hexose metabolic process;GO:0009617//response to bacterium;GO:0006950//response to stress;GO:0050896//response to stimulus	gi 947047940 gb KRG97468.1 ;gi 358248010 ref NP_001240046.1 ;gi 947047937 gb KRG97465.1 ;gi 947047939 gb KRG97467.1 /2.43442e-146;0;0;0/hypothetical protein GLYMA_18G009700 [Glycine max];uncharacterized protein LOC100782924 [Glycine max];hypothetical protein GLYMA_18G009700 [Glycine max]

Glyma.18G043700	1.0456	0.005885	-	-	-	-	-	-	3.30405	7.82E-07	3445	ko00480//Glutathione metabolism	GO:0000325//plant-type vacuole	GO:0043167//ion binding;GO:0016765//transferase activity, transferring alkyl or aryl (other than methyl) groups	GO:0006950//response to stress;GO:0009962//regulation of flavonoid biosynthetic process	gi 359807572 ref NP_001241411.1 /1.0728e-157 glutathione S-transferase F11-like [Glycine max]
Glyma.18G055300	-1.8657	6.03E-09	-	-	-	-	-	-	-	-	1252	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 356565900 ref XP_003551174.1 /0/PREDICTED: peroxidase 4-like [Glycine max]
Glyma.18G118100	-	-	-	-	-	-	-	-	1.32268	0.00626	2113	ko00909//Sesquiterpenoid and triterpenoid biosynthesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:0031224//intrinsic component of membrane	GO:0016709//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;GO:0000166//nucleotide binding	GO:0006694//steroid biosynthetic process;GO:0006950//response to stress;GO:0001101//response to acid chemical;GO:0044710	gi 947049536 gb KRG99064.1 ;gi 356569981 ref XP_003553171.1 ;gi 947049537 gb KRG99065.1 /0;0/hypothetical protein GLYMA_18G118100 [Glycine max];PREDICTED: squalene epoxidase 3-like [Glycine max];hypothetical protein GLYMA_18G118100 [Glycine max]
Glyma.18G204000	-	-	-	-	-	-	-	-	-1.8469	6.16E-07	2159	-	GO:0005911//cell-cell junction;GO:0044432	GO:0003824//catalytic activity	GO:0006950//response to stress;GO:0000904//cell morphogenesis involved in differentiation;GO:0044710	gi 356566692 ref XP_003551564.1 /0/PREDICTED: dnaJ protein ERD13A [Glycine max]
Glyma.18G204200	-	-	-	-	-	-	-	-	1.55495	1.39E-05	2393	ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	GO:0044444	GO:0046872//metal ion binding;GO:0019842//vitamin binding	GO:0006950//response to stress	gi 356568132 ref XP_003552267.1 /0/PREDICTED: pyruvate decarboxylase 2 [Glycine max]
Glyma.18G215000	-	-	-	-	-	-	-	-	-1.2931	0.00044	1168	-	GO:0016020//membrane	-	GO:0006950//response to stress;GO:0048229//gametophyte development	gi 359806290 ref NP_001241475.1 ;gi 947050936 gb KRH00465.1 /2.96668e-150;6.13158e-117/uncharacterized protein LOC100810722 precursor [Glycine max];hypothetical protein GLYMA_18G215000 [Glycine max]
Glyma.18G219100	-	-	-	-	-	-	-	-	1.04107	0.00572	2336	ko00010//Glycolysis / Gluconeogenesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00260//Glycine, serine and threonine metabolism	GO:0031967;GO:0009536//plastid;GO:0005911//cell-cell junction;GO:0005576//extracellular region;GO:0016020//membrane	GO:0046914//transition metal ion binding;GO:0004619//phosphoglycerate mutase activity	GO:0010038//response to metal ion;GO:0044763;GO:0048229//gametophyte development;GO:0006091//generation of precursor metabolites and energy;GO:0006006//glucose metabolic process;GO:0006950//response to stress	gi 734420079 gb KHN40585.1 /0;2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Glycine soja]
Glyma.18G238500	-	-	-	-	-	-	-	-	-1.36	0.00195	1650	-	-	GO:0016301//kinase activity	GO:0019751//polyol metabolic process;GO:0006796//phosphate-containing compound metabolic process;GO:0006950//response to stress;GO:0007186//G-protein coupled receptor signaling pathway	gi 947051332 gb KRH00861.1 ;gi 356566923 ref XP_003551674.1 /0;0/hypothetical protein GLYMA_18G238500 [Glycine max];PREDICTED: sphingoid long-chain bases kinase 2, mitochondrial-like [Glycine max]

Glyma. 18G278 900	-	-	-	-	-	-	-	-	2.57163	0.00135	2019	ko00330//Arginine and proline metabolism;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites	-	GO:0016645//oxidoreductase activity, acting on the CH-NH group of donors	GO:0009617//response to bacterium;GO:0006560//proline metabolic process;GO:0006536//glutamate metabolic process;GO:0006950//response to stress	gi 356568869 ref XP_003552630.1 /0/PREDICTED: proline dehydrogenase 2, mitochondrial [Glycine max]
Glyma. 19G011 700	-	-	-	-	-	-	-	-	8.60825	1.84E-05	2324	ko00592//alpha-Linolenic acid metabolism	-	GO:0016209//antioxidant activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 734382169 gb KHN23570.1 /0/Prostaglandin G/H synthase 2 [Glycine soja]
Glyma. 19G016 100	-	-	-	-	-3.9277	0.00026	-	-	-	-	1822	ko00500//Starch and sucrose metabolism;ko01110//Biosynthesis of secondary metabolites;ko00520//Amino sugar and nucleotide sugar metabolism	-	GO:0016740//transferase activity	GO:0006950//response to stress	gi 356572000 ref XP_003554158.1 /0/PREDICTED: probable galacturonosyltransferase-like 10 [Glycine max]
Glyma. 19G066 200	-	-	-	-	-	-	-	-	2.37898	6.23E-05	1166	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 734305902 gb KHM98789.1 /0/Peroxidase 44 [Glycine soja]
Glyma. 19G091 800	-2.9749	1.32E-05	-	-	-	-	-	-	-	-	1509	ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko00360//Phenylalanine metabolism;ko00940//Phenylpropanoid biosynthesis	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress	gi 356571531 ref XP_003553930.1 /0/PREDICTED: peroxidase 55 [Glycine max]
Glyma. 19G105 100	-	-	-1.25	0.000682	-	-	2.71529	3.54E-11	-	-	1531	ko00941//Flavonoid biosynthesis;ko01100//Metabolic pathways;ko01110//Biosynthesis of secondary metabolites;ko04712//Circadian rhythm - plant	GO:0000325//plant-type vacuole	GO:0016746//transferase activity, transferring acyl groups	GO:0009411//response to UV;GO:0060918//auxin transport;GO:0001101//response to acid chemical;GO:0009718//anthocyanin-containing compound biosynthetic process;GO:0009725//response to hormone;GO:0006950//response to stress	gi 356571645 ref XP_003553986.1 /0/PREDICTED: chalcone synthase J-like [Glycine max]
Glyma. 19G172 500	-	-	-	-	-	-	-	-	-1.1328	0.00146	1082	-	GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0044437;GO:0000785//chromatin;GO:005911//cell-cell junction;GO:0016020//membrane	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization;GO:0006950//response to stress	gi 571558188 ref XP_006604532.1 /6.08435e-89/PREDICTED: histone H4-like [Glycine max]

Glyma. 19G181 300	-	-	-	-	-	-	-	-	-2.2821	5.65E-07	1588	-	GO:003124//intrinsic component of membrane;GO:0005911//cell-cell junction;GO:0009536//plastid	GO:0044389//ubiquitin-like protein ligase binding;GO:0005372//water transmembrane transporter activity	GO:0051707//response to other organism;GO:0042044//fluid transport;GO:0006950//response to stress;GO:0055085//transmembrane transport;GO:0001101//response to acid chemical	gi 947046352 gb KRG95981.1 ;gi 356572440 ref XP_003554376.1 /3.54333e-159;0/hypothetical protein GLYMA_19G181300 [Glycine max];PREDICTED: aquaporin PIP2-1 [Glycine max]
Glyma. 19G240 400	-	-	-	-	-	-	-	-	-1.0373	0.00366	1574	ko04146//Peroxisome	GO:0044424	GO:0043169//cation binding;GO:0016209//anti oxidant activity;GO:0003824//catalytic activity	GO:0009642//response to light intensity;GO:0010193//response to ozone;GO:0010224//response to UV-B;GO:0044710;GO:0009651//response to salt stress;GO:0072593//reactive oxygen species metabolic process;GO:0009617//response to bacterium;GO:0009744//response to sucrose;GO:0035194//posttranscriptional gene silencing by RNA;GO:0046688//response to copper ion;GO:0009987//cellular process;GO:0010035//response to inorganic substance;GO:0009628//response to abiotic stimulus;GO:0008152//metabolic process;GO:0006950//response to stress	gi 351725359 ref NP_001235298.1 ;gi 947047281 gb KRG96910.1 ;gi 947047280 gb KRG96909.1 /1.08219e-93;1.44827e-53;8.32826e-66/superoxide dismutase [Cu-Zn] [Glycine max];hypothetical protein GLYMA_19G240400 [Glycine max];hypothetical protein GLYMA_19G240400 [Glycine max]
Glyma. 20G017 900	5.90078	5.72E-14	-	-	-	-	-	-	-	-	1145	-	-	-	GO:0006950//response to stress	gi 359807343 ref NP_001240867.1 /1.92537e-1077/MLP-like protein 28-like [Glycine max]
Glyma. 20G026 700	-	-	-	-	-	-	-	-	5.10843	9.60E-06	3557	ko00500//Starch and sucrose metabolism	-	GO:0043168//anion binding;GO:0004645//phosphorylase activity	GO:0044238//primary metabolic process;GO:0006950//response to stress;GO:0009628//response to abiotic stimulus	gi 571563869 ref XP_006605545.1 ;gi 356577161 ref XP_003556696.1 /0;0/PREDICTED: alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic-like isoform X2 [Glycine max];PREDICTED: alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic-like isoform X1 [Glycine max]
Glyma. 20G053 700	-	-	-	-	-1.5643	0.00027	-	-	2.23282	0.00967	3225	ko00591//Linoleic acid metabolism;ko01100//Metabolic pathways;ko00592//alpha-Linolenic acid metabolism	GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid	GO:0046914//transition metal ion binding;GO:0016702//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;GO:0032550	GO:0051707//response to other organism;GO:0006633//fatty acid biosynthetic process;GO:0055114//oxidation-reduction process;GO:0001101//response to acid chemical;GO:0006950//response to stress	gi 947040160 gb KRG89884.1 ;gi 356575019 ref XP_003555640.1 /0;0/hypothetical protein GLYMA_20G053700 [Glycine max];PREDICTED: linoleate 13S-lipoxygenase 2-1, chloroplastic-like [Glycine max]
Glyma. 20G079 300	-	-	-	-	-	-	-1.0971	0.0003	-	-	2229	ko03018//RNA degradation	GO:0005840//ribosome;GO:0009532//pl	GO:0032550;GO:0046914//transition metal ion binding	GO:0010038//response to metal ion;GO:0006457//protein folding;GO:0006950//response	gi 734401136 gb KHN31621.1 /0/Chaperonin CPN60-2, mitochondrial [Glycine soja]

													stid stroma;GO :0009526// plastid envelope; GO:00444 37;GO:00 44429;GO :0016020// membrane		e to stress	
Glyma. 20G080 000	-1.6661	0.00097 2	-	-	-	-	-	-	-3.5159	4.17E-0 5	1899	ko00380//Tryptophan metabolism	-	GO:0000166//nucleotide binding;GO:0016709//oxid oreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	GO:0009683//indoleacetic acid metabolic process;GO:0006950//respon se to stress	gi 571565271 ref XP_003555725.2 /0/PREDIC TED: probable indole-3-pyruvate monooxygenase YUCCA7 [Glycine max]
Glyma. 20G083 800	-	-	-	-	-	-	-	-	-1.2725	0.00064	1088	-	GO:00319 81//nuclea r lumen;GO :0009536// plastid;GO :0044437; GO:00007 85//chrom atin;GO:0 005911//ce ll-cell junction;G O:001602 0//membra ne	GO:0003676//nucleic acid binding;GO:0046983//prot ein dimerization activity	GO:0034728//nucleosome organization;GO:0006950//re sponse to stress	gi 475622287 gb EMT31824.1 /1.35134e-52/H istone H4 [Aegilops tauschii]
Glyma. 20G122 500	-	-	-	-	-	-	-	-	1.76847	1.93E-0 6	1694	ko00051//Fructose and mannose metabolism;ko00030//P entose phosphate pathway;ko00010//Gly colysis / Gluconeogenesis;ko011 00//Metabolic pathways;ko01110//Bio synthesis of secondary metabolites;ko00710//C arbon fixation in photosynthetic organisms	GO:00319 76;GO:00 09532//pla stid stroma	GO:0016832//aldehyde-ly ase activity	GO:0006950//response to stress;GO:0010038//response to metal ion;GO:0006091//generation of precursor metabolites and energy	gi 947041204 gb KRG90928.1 /0/hypothetical protein GLYMA_20G122500 [Glycine max]
Glyma. 20G133 200	-	-	-1.4898	0.00079 8	-3.1996	0.00043	-	-	1.3797	0.00326	1580	-	-	-	GO:0009628//response to abiotic stimulus;GO:0006950//respon se to stress	gi 918463665 gb AL.A09177.1 /2.67846e-160/ C2H2-Zn transcription factor, partial [Glycine max]
Glyma. 20G169 200	-	-	-	-	-	-	1.27701	0.00011	-	-	1364	ko01100//Metabolic pathways;ko01110//Bio synthesis of secondary metabolites;ko00360//P henylalanine metabolism;ko00940//P henylpropanoid biosynthesis	GO:00059 11//cell-ce ll junction;G O:000561 8//cell wall	GO:0003824//catalytic activity;GO:0016209//anti oxidant activity;GO:0043169//cati on binding;GO:0046906//tetra pyrrole binding	GO:0044710;GO:0006950//re sponse to stress	gi 356576075 ref XP_003556160.1 /0/PREDIC TED: peroxidase 12-like [Glycine max]
Glyma. 20G197 100	-	-	-	-	-	-	-1.0367	0.00127	-	-	2151	ko03018//RNA degradation	GO:00058 40//riboso me;GO:00 09532//pla	GO:0032550;GO:0046914 //transition metal ion binding	GO:0010038//response to metal ion;GO:0006457//protein folding;GO:0006950//respon se to stress	gi 356576411 ref XP_003556325.1 /0/PREDIC TED: chaperonin CPN60-2, mitochondrial [Glycine max]

													stid stroma;GO :0009526// plastid envelope; GO:00444 37;GO:00 44429;GO :0016020// membrane		e to stress	
Glyma. 20G210 800	-	-	-	-	-	-	-	-	2.68797	0.00053	1691	ko04140//Regulation of autophagy	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-cont aining compound metabolic process;GO:0006950//respon se to stress;GO:0006464//cellular protein modification process;GO:0007154//cell communication	gi 356576545 ref XP_003556391.1 /0/PREDIC TED: CBL-interacting serine/threonine-protein kinase 4-like [Glycine max]
Glyma. 20G230 900	-	-	-	-	-	-	-	-	1.73223	0.00694	2490	-	-	-	GO:0006950//response to stress	gi 947043086 gb KRG92810.1 ;gi 947043085 g b KRG92809.1 /0/0/hypothetical protein GLYMA_20G230900 [Glycine max];hypothetical protein GLYMA_20G230900 [Glycine max]
Glyma. U03300 0	-2.5662	9.41E-0 8	-	-	-	-	-	-	-	-	2316	ko00062//Fatty acid elongation;ko01110//Bi osynthesis of secondary metabolites	GO:00432 31//intrac ellular membrane -bounded organelle	GO:0016746//transferase activity, transferring acyl groups	GO:0009314//response to radiation;GO:0006950//respo nse to stress;GO:0006631//fatty acid metabolic process	gi 947038781 gb KRG88669.1 /0/hypothetical protein GLYMA_U033000 [Glycine max]