**SUPPORTING INFORMATION**

# Transcriptomic and proteomic research to explore bruchid-resistant genes in mungbean isogenic lines

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**Supplementary Table S1. The seed nutrients of VC1973A and VC6089A**

| | VC1973A | VC6089A |
|---|---|---|
| 100 seeds weight (g) | 5.89±0.24 | 5.79±0.09 |
| Soluble sugar content (mg/gDW) | 51.58±1.58 | 44.63±1.50 |
| Soluble protein content (mg/gFW) | 97.68±9.31 | 80.89±2.64 |

**Supplementary Table S2. All defferintial expression genes between seeds of mungbean isogenic lines VC6089A and VC1973A**

| ID[a] | Description | Accession | Query cover | E value | Ident | Fold change | Avg TPM of VC6089A | Location | Functional category |
|---|---|---|---|---|---|---|---|---|---|
| g27780.t1 | Callose synthase-like protein [Medicagotruncatula] | KEH38459.1 | 99% | 0 | 84% | Inf[b] | 0.23 | Vr05 | Defense-related protein |
| g21777.t1 | Flavonol synthase [Glycine max] | NP_001237419.1 | 99% | 0 | 90% | Inf[b] | 0.89 | Vr06 | Defense-related protein |
| g4739.t1 | Polyprotein, putative [Solanum demissum] | AAT38747.2 | 72% | 3.00E-49 | 66% | Inf[b] | 1.54 | scaffold_160 | Other |
| g34480.t1 | Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Glycine soja] | KHN06274.1 | 45% | 4.00E-42 | 49% | Inf[b] | 1.36 | Vr05 | Other |
| g39181.t1 | Resistant specific protein-1(4) [Vignaradiata] | BAC22498.1 | 99% | 7.00E-117 | 47% | Inf[b] | 0.89 | Vr05 | Other |
| g11456.t1 | Unknow | | | | | Inf[b] | 10.09 | Vr06 | Unknow |
| g34458.t1 | Gag/pol polyprotein [Pisumsativum] | AAQ82037.1 | 76% | 0 | 59% | 2165.06 | 75.91 | Vr01 | Other |
| g39185.t1 | Resistant specific protein-1(4) [Vignaradiata] | BAC22498.1 | 99% | 0 | 83% | 1304.69 | 1748.70 | Vr05 | Other |
| g28439.t1 | Wound-responsive family protein [Medicagotruncatula] | KEH29602.1 | 98% | 2.00E-36 | 75% | 29.30 | 59.37 | Vr02 | Stress-related |
| g39310.t1 | Putative callose synthase 8 [Glycine soja] | KHN15554.1 | 97% | 0 | 90% | 26.54 | 2.40 | Vr05 | Defense-related protein |
| g8360.t1 | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, putative [Theobroma cacao] | XP_007036095.1 | 88% | 2.00E-11 | 52% | 25.29 | 117.17 | Vr04 | Enzyme |
| g1755.t1 | Cyclic nucleotide gated channel [Medicagotruncatula] | XP_003610842.1 | 92% | 4.00E-21 | 45% | 22.12 | 4.85 | Vr01 | Transporter |
| g12224.t1 | Early nodulin-93 [Glycine soja] | KHN27413.1 | 98% | 1.00E-45 | 92% | 16.40 | 21.04 | Vr07 | Other |
| g1131.t1 | Receptor-like kinase [Medicagotruncatula] | AES92207.2 | 76% | 0 | 86% | 14.47 | 4.27 | Vr07 | Signal transduction |
| g8726.t1 | Heat stress transcription factor A-6b [Glycine soja] | KHN03824.1 | 90% | 4.00E-151 | 78% | 12.86 | 2.43 | Vr08 | Chaperone |
| g10506.t2 | Extra-large G-like protein [Medicagotruncatula] | KEH17297.1 | 98% | 0 | 59% | 10.53 | 0.47 | scaffold_83 | Defense-related protein |
| g11735.t1 | RNA-directed DNA polymerase (Reverse transcriptase); Chromo; Zinc finger, CCHC-type; Peptidase aspartic, active site; Polynucleotidyl transferase, Ribonuclease H fold | ABN06064.1 | 81% | 0 | 55% | 10.06 | 2.97 | Vr11 | Enzyme |

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|---|---|---|---|---|---|---|---|---|---|
| | [Medicagotruncatula] | | | | | | | | |
| g14236.t1 | Heat shock factor protein HSF30-like [Glycine max] | NP_001274388.1 | 99% | 0 | 83% | 9.78 | 38.24 | Vr05 | Chaperone |
| g17827.t1 | LOB domain-containing protein 41 [Theobroma cacao] | XP_007033275.1 | 87% | 7.00E-111 | 66% | 9.73 | 59.47 | Vr04 | Gene expression and regulation |
| g15438.t1 | Indole-3-acetic acid-amidosynthetase GH3.3 [Medicagotruncatula] | XP_003611653.1 | 99% | 0 | 85% | 8.61 | 9.79 | Vr11 | Hormone response |
| g5213.t1 | Selection and upkeep of intraepithelial T-cells protein 6, putative [Theobroma cacao] | XP_007046553.1 | 99% | 3.00E-96 | 58% | 8.19 | 3.18 | Vr07 | Other |
| g35151.t1 | Stearoyl-ACP desaturase [Glycine max] | NP_001236391.1 | 99% | 0 | 85% | 8.10 | 2.46 | Vr06 | Enzyme |
| g24175.t1 | Sucrose synthase 2 [Glycine soja] | KHN41027.1 | 99% | 0 | 94% | 8.09 | 0.69 | Vr06 | Enzyme |
| g1413.t2 | Pyruvate decarboxylase [Medicagotruncatula] | XP_003593734.1 | 98% | 0 | 84% | 7.63 | 8.45 | Vr10 | Enzyme |
| g21928.t1 | Heat stress transcription factor A-2 [Glycine soja] | KHN37042.1 | 99% | 5.00E-156 | 69% | 7.55 | 4.48 | Vr06 | Chaperone |
| g32890.t1 | Wound-responsive family protein [Medicagotruncatula] | KEH38819.1 | 98% | 6.00E-36 | 76% | 7.28 | 118.61 | scaffold_170 | Stress-related |
| g11137.t1 | RNA-directed RNA polymerase [Medicagotruncatula] | KEH40642.1 | 99% | 0 | 67% | 7.28 | 3.87 | Vr11 | Enzyme |
| g5437.t1 | Longifolia protein [Medicagotruncatula] | KEH25068.1 | 98% | 0 | 48% | 7.25 | 0.59 | Vr04 | Cell skeleton |
| g29069.t1 | F-box protein PP2-B10 [Glycine soja] | KHN20969.1 | 99% | 5.00E-119 | 71% | 7.16 | 34.95 | Vr06 | Signal transduction |
| g11137.t2 | RNA-directed RNA polymerase [Medicagotruncatula] | KEH40645.1 | 99% | 0 | 67% | 6.91 | 3.40 | Vr11 | Enzyme |
| g13845.t1 | ATP-dependent zinc metalloprotease FTSH 6 [Arabidopsis thaliana] | NP_568311.2 | 96% | 0 | 77% | 6.89 | 5.96 | Vr04 | Enzyme |
| g779.t1 | Unknow | | | | | 6.82 | 113.09 | Vr05 | Unknow |
| g35122.t1 | Phospholipid-transporting ATPase-like protein [Medicagotruncatula] | KEH20221.1 | 97% | 0 | 86% | 5.90 | 0.80 | Vr07 | Enzyme |
| g8776.t1 | Auxin-induced protein 22D [Vignaradiata var. radiata] | O24542.1 | 99% | 1.00E-136 | 99% | 5.90 | 7.08 | Vr08 | Hormone response |
| g28381.t1 | Cytochrome P450 71A26 [Glycine soja] | KHM99155.1 | 99% | 0 | 76% | 5.72 | 4.50 | Vr01 | P450 family |
| g27539.t1 | Proline rich protein [Medicagotruncatula] | XP_003608742.1 | 66% | 8.00E-22 | 92% | 5.59 | 113.69 | Vr07 | Other |

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|---|---|---|---|---|---|---|---|---|---|
| g17147.t1 | Unknow | | | | | 5.56 | 37.98 | Vr07 | Unknow |
| g432.t1 | Heavy metal-associated domain protein [Medicagotruncatula] | KEH17134.1 | 72% | 7.00E-52 | 56% | 5.27 | 2.97 | Vr03 | Transporter |
| g14164.t1 | Trihelix transcription factor GT-3a [Glycine soja] | KHN34752.1 | 88% | 4.00E-76 | 73% | 5.27 | 4.23 | Vr04 | Gene expression and regulation |
| g8208.t1 | Cytochrome P450 82A4 [Glycine soja] | KHN13272.1 | 99% | 0 | 74% | 5.22 | 4.42 | Vr01 | P450 family |
| g5284.t1 | BAG family molecular chaperone regulator 5, mitochondrial [Glycine soja] | KHN13853.1 | 99% | 2.00E-83 | 56% | 5.18 | 129.62 | Vr04 | Chaperone |
| g10095.t1 | 17.9 kDa class II heat shock protein [Glycine soja] | KHN04254.1 | 99% | 1.00E-75 | 85% | 5.13 | 352.86 | Vr06 | Small HSP |
| g19550.t1 | Beta-1,4-N-acetylglucosaminyltransferase-like protein [Medicagotruncatula] | KEH20776.1 | 99% | 0 | 79% | 5.07 | 4.47 | Vr02 | Enzyme |
| g1737.t1 | Multiprotein-bridging factor 1c [Morusnotabilis] | XP_010088841.1 | 99% | 1.00E-75 | 81% | 5.06 | 269.13 | Vr01 | Gene expression and regulation |
| g17423.t1 | Receptor-like protein kinase HSL1 [Glycine soja] | KHN40380.1 | 95% | 0 | 86% | 4.88 | 1.08 | Vr01 | Signal transduction |
| g19825.t1 | Vacuolar iron transporter-like protein [Medicagotruncatula] | KEH28141.1 | 88% | 1.00E-162 | 44% | 4.78 | 1.36 | Vr06 | Transporter |
| g10677.t1 | Protein pns1 [Glycine soja] | KHN34641.1 | 92% | 0 | 66% | 4.71 | 2.30 | Vr01 | Transporter |
| g11655.t1 | Putative protein TPRXL-like [Glycine max] | XP_003546585.1 | 98% | 2.00E-52 | 58% | 4.57 | 13.27 | Vr05 | Unknow |
| g21562.t1 | Amino acid transporter [Medicagotruncatula] | XP_003616739.1 | 91% | 1.00E-144 | 74% | 4.37 | 16.44 | Vr06 | Transporter |
| g37446.t1 | Small heat shock protein, chloroplastic [Glycine soja] | KHN23313.1 | 86% | 6.00E-115 | 86% | 4.31 | 513.65 | scaffold_106 | Small HSP |
| g32232.t1 | Heat shock protein 83 [Glycine soja] | KHN09298.1 | 97% | 0 | 98% | 4.29 | 361.13 | Vr01 | Chaperone |
| g19590.t1 | Glyceraldehyde 3-phosphate dehydrogenase [Medicagotruncatula] | XP_003601828.1 | 99% | 0 | 95% | 4.24 | 476.54 | Vr02 | Enzyme |
| g11576.t1 | Lysine-specific demethylase 5A [Medicagotruncatula] | XP_003591723.1 | 98% | 0 | 68% | 4.15 | 1.22 | Vr05 | Enzyme |
| g15435.t1 | Cytochrome P450 81D1 [Medicagotruncatula] | XP_003611660.1 | 99% | 0 | 67% | 4.14 | 11.10 | Vr11 | P450 family |
| g4095.t1 | Protein ROOT PRIMORDIUM DEFECTIVE 1-like isoform X1 [Glycine max] | XP_003531312.1 | 99% | 0 | 86% | 4.00 | 2.56 | Vr07 | Development |
| g5283.t2 | BAG family molecular chaperone regulator 5, mitochondrial [Glycine soja] | KHN13855.1 | 48% | 6.00E-13 | 60% | 3.93 | 44.88 | Vr04 | Chaperone |
| g5283.t1 | BAG family molecular chaperone regulator 5, | KHN13853.1 | 79% | 1.00E-63 | 75% | 3.93 | 105.18 | Vr04 | Chaperone |

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|---|---|---|---|---|---|---|---|---|---|
| | mitochondrial [Glycine soja] | | | | | | | | |
| g13228.t1 | 22.7 kDa class IV heat shock protein [Medicagotruncatula] | XP_003622351.1 | 90% | 2.00E-80 | 74% | 3.93 | 291.55 | Vr01 | Small HSP |
| g980.t1 | polyubiquitin (ubq10) [Arabidopsis thaliana] | CAB81074.1 | 96% | 0 | 99% | 3.91 | 546.81 | Vr07 | Protein synthesis and digestion |
| g28393.t1 | Heat shock transcription factor HSFB2a [Glycine max] | AFQ93677.1 | 98% | 2.00E-144 | 78% | 3.90 | 180.28 | Vr01 | Chaperone |
| g3997.t1 | Heat shock transcription factor [Cicer arietinum] | ACN76855.1 | 87% | 2.00E-122 | 68% | 3.83 | 220.18 | Vr08 | Chaperone |
| g26346.t3 | ADP-ribosylation factor GTPase-activating protein AGD4 [Glycine soja] | KHN05422.1 | 99% | 0 | 81% | 3.79 | 1.44 | Vr02 | Other |
| g17881.t1 | Glucan endo-1,3-beta-glucosidase [Medicagotruncatula] | XP_003622030.1 | 95% | 0 | 77% | 3.76 | 7.41 | Vr04 | Enzyme |
| g18728.t1 | Heat stress transcription factor A3 [Solanum lycopersicum] | NP_001234854.1 | 88% | 1.00E-68 | 39% | 3.75 | 12.97 | Vr08 | Chaperone |
| g38384.t1 | Pentatricopeptide repeat-containing protein [Medicagotruncatula] | XP_003609638.1 | 99% | 0 | 72% | 3.69 | 2.98 | Vr07 | Gene expression and regulation |
| g32177.t1 | Indole-3-acetic acid-amidosynthetase GH3.6 [Glycine soja] | KHN27995.1 | 99% | 0 | 91% | 3.68 | 8.46 | scaffold_216 | Hormone response |
| g9246.t2 | Agglutinin-like protein ALA1, putative isoform 1 [Theobroma cacao] | XP_007011118.1 | 98% | 0 | 51% | 3.63 | 1.69 | Vr05 | Defense-related protein |
| g5283.t3 | BAG family molecular chaperone regulator 5, mitochondrial [Glycine soja] | KHN13855.1 | 49% | 5.00E-13 | 60% | 3.59 | 39.67 | Vr04 | Chaperone |
| g2273.t1 | Mitochondrion heat shock 22 kDa protein [Phaseolus vulgaris] | AHA84250.1 | 90% | 1.00E-79 | 91% | 3.59 | 1291.42 | Vr02 | Small HSP |
| g19674.t1 | Cytochrome P450 monooxygenase CYP704G9 [Medicagotruncatula] | XP_003592376.1 | 99% | 3.00E-113 | 57% | 3.57 | 5.02 | Vr08 | P450 family |
| g1978.t1 | Heat stress transcription factor B-2b [Medicagotruncatula] | XP_003611134.1 | 96% | 1.00E-74 | 79% | 3.55 | 45.65 | Vr11 | Chaperone |
| g28487.t1 | Dof zinc finger protein DOF2.1 [Glycine soja] | KHN22036.1 | 99% | 2.00E-129 | 81% | 3.51 | 3.63 | Vr02 | Gene expression and regulation |
| g5446.t1 | Isoflavonoidmalonyl transferase | XP_003621460.1 | 66% | 6.00E-87 | 54% | 3.47 | 6.47 | Vr04 | Enzyme |

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|---|---|---|---|---|---|---|---|---|---|
| | [Medicagotruncatula] | | | | | | | | |
| g16484.t1 | Activator of 90 kDa heat shock protein ATPase like 1 [Glycine soja] | KHN07444.1 | 99% | 0 | 77% | 3.44 | 92.60 | Vr03 | Chaperone |
| g3028.t1 | 18.5 kDa class I heat shock protein [Glycine soja] | KHN09977.1 | 86% | 5.00E-78 | 91% | 3.43 | 2627.24 | Vr07 | Small HSP |
| g982.t1 | Polyubiquitin (ubq10) [Arabidopsis thaliana] | CAB81074.1 | 99% | 0 | 99% | 3.40 | 371.74 | Vr07 | Protein synthesis and digestion |
| g14748.t1 | 2-aminoethanethiol dioxygenase [Glycine soja] | KHN13236.1 | 86% | 1.00E-166 | 93% | 3.36 | 23.38 | Vr01 | Enzyme |
| g40324.t1 | Chitinase class 1 [Vignaunguiculata] | CAA61278.1 | 99% | 0 | 92% | 3.34 | 6.38 | Vr05 | Defense-related protein |
| g5551.t1 | Aspartic proteinase [Vignaunguiculata] | AAB03843.2 | 99% | 0 | 94% | 3.32 | 1019.85 | Vr07 | Enzyme |
| g25302.t1 | GDP-fucose O-fucosyltransferase-like protein [Medicagotruncatula] | KEH25156.1 | 98% | 0 | 85% | 3.30 | 5.19 | scaffold_190 | Enzyme |
| g25933.t1 | Rpp4 candidate R5 [Glycine max] | AEB06128.1 | 98% | 0 | 69% | 3.30 | 2.18 | Vr04 | Defense-related protein |
| g33331.t1 | Thermosensitive gluconokinase [Medicagotruncatula] | XP_003628688.1 | 94% | 1.00E-62 | 77% | 3.29 | 59.17 | scaffold_73 | Enzyme |
| g40635.t1 | Epidermis-specific secreted glycoprotein EP1-like protein [Phaseolus vulgaris] | AFY98639.1 | 98% | 0 | 72% | 3.29 | 34.43 | scaffold_214 | Transporter |
| g9258.t3 | F-box protein [Glycine soja] | KHN21309.1 | 99% | 0 | 86% | 3.27 | 1.16 | Vr05 | Signal transduction |
| g8905.t2 | Protein TIME FOR COFFEE [Glycine soja] | KHN18877.1 | 99% | 0 | 50% | 3.25 | 1.22 | Vr03 | Development |
| g3022.t1 | 18.5 kDa class I heat shock protein [Glycine soja] | KHN09977.1 | 86% | 2.00E-76 | 88% | 3.24 | 3051.81 | Vr07 | Small HSP |
| g22971.t1 | Polyubiquitin (ubq10) [Arabidopsis thaliana] | CAB81074.1 | 96% | 0 | 99% | 3.23 | 189.16 | Vr07 | Protein synthesis and digestion |
| g4663.t1 | DUF668 family protein [Medicagotruncatula] | KEH35646.1 | 85% | 5.00E-177 | 65% | 3.21 | 2.25 | scaffold_201 | Other |
| g5591.t1 | Scarecrow-like protein 13 [Glycine soja] | KHN03530.1 | 99% | 0 | 81% | 3.19 | 15.69 | Vr07 | Development |
| g15029.t1 | Oxidative stress 3 [Theobroma cacao] | XP_007012998.1 | 30% | 1.00E-16 | 65% | 3.18 | 8.70 | Vr10 | Stress-related |
| g5654.t1 | Stem-specific TSJT1 [Gossypiumarboreum] | KHG02917.1 | 99% | 8.00E-144 | 84% | 3.16 | 18.96 | Vr07 | Development |
| g25435.t1 | NAC domain-containing protein 78 [Glycine soja] | KHN19577.1 | 99% | 0 | 75% | 3.16 | 2.14 | scaffold_106 | Gene expression and regulation |
| g5774.t1 | 70 kDa heat shock cognate protein 1 [Vignaradiata] | AAS57912.1 | 99% | 0 | 100% | 3.14 | 139.65 | Vr02 | Chaperone |
| g9714.t1 | Ein3-binding f-box protein 4 [Theobroma cacao] | XP_007013466.1 | 86% | 0 | 55% | 3.14 | 9.73 | Vr05 | Hormone response |
| g1891.t2 | Pentatricopeptide repeat-containing protein [Glycine soja] | KHN45826.1 | 76% | 0 | 86% | 3.14 | 3.12 | Vr01 | Gene expression and regulation |
| g27722.t1 | Tetraspanin family protein [Medicagotruncatula] | KEH32585.1 | 99% | 2.00E-116 | 71% | 3.12 | 104.55 | Vr07 | Signal transduction |
| g17354.t1 | Plant/F27B13-30 protein [Medicagotruncatula] | KEH37496.1 | 99% | 0 | 71% | 3.07 | 1.43 | Vr05 | Unknow |

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|---|---|---|---|---|---|---|---|---|---|
| g34949.t1 | Scarecrow-like protein 5 [Glycine soja] | KHN43816.1 | 99% | 0 | 88% | 3.07 | 2.95 | Vr10 | Development |
| g43035.t1 | Remorin family protein [Theobroma cacao] | XP_007028802.1 | 78% | 2.00E-75 | 71% | 3.05 | 13.31 | Vr03 | Gene expression and regulation |
| g18063.t1 | 17.4 kDa class III heat shock protein [Medicagotruncatula] | XP_003627410.1 | 99% | 2.00E-71 | 73% | 3.04 | 458.61 | Vr09 | Small HSP |
| g16334.t1 | O-acyltransferase WSD1-like [Glycine max] | NP_001276179.1 | 48% | 0 | 83% | 3.03 | 44.70 | Vr11 | Enzyme |
| g1986.t1 | Myosin heavy chain-like protein [Medicagotruncatula] | KEH21046.1 | 99% | 0 | 62% | 2.99 | 1.71 | Vr11 | Unknow |
| g12863.t1 | Malate synthase, glyoxysomal [Glycine soja] | KHN14088.1 | 99% | 0 | 90% | 2.99 | 3.81 | Vr07 | Enzyme |
| g914.t1 | WRKY transcription factor [Medicagotruncatula] | XP_003594714.1 | 94% | 4.00E-57 | 48% | 2.98 | 10.02 | Vr07 | Gene expression and regulation |
| g33013.t1 | Retrotransposon protein, putative, unclassified [Oryza sativa Japonica Group] | ABA99612.1 | 96% | 8.00E-169 | 33% | 2.96 | 1.35 | Vr09 | Other |
| g5606.t1 | Nudix hydrolase superfamily protein [Medicagotruncatula] | KEH32689.1 | 92% | 8.00E-159 | 79% | 2.96 | 12.03 | Vr07 | Enzyme |
| g39062.t1 | G-type lectin S-receptor-like serine/threonine-protein kinase [Glycine soja] | KHN15347.1 | 88% | 3.00E-177 | 79% | 2.94 | 10.40 | scaffold_264 | Signal transduction |
| g3316.t1 | F-box/kelch-repeat protein [Medicagotruncatula] | XP_003597790.1 | 98% | 6.00E-134 | 59% | 2.89 | 11.00 | Vr09 | Signal transduction |
| g29687.t1 | Ribulose bisphosphate carboxylase/oxygenase activase 1 [Phaseolus vulgaris] | AGZ15382.1 | 99% | 0 | 95% | 2.87 | 17.82 | Vr09 | Enzyme |
| g1081.t1 | Nuclear transcription factor Y subunit A-3-like isoform 2 [Phaseolus vulgaris] | AGV54765.1 | 99% | 2.00E-140 | 90% | 2.87 | 10.24 | Vr07 | Gene expression and regulation |
| g21392.t1 | Polyubiquitin (ubq10) [Arabidopsis thaliana] | CAB81074.1 | 96% | 0 | 99% | 2.87 | 386.19 | scaffold_167 | Protein synthesis and digestion |
| g7278.t1 | TPR repeat protein [Medicagotruncatula] | KEH36103.1 | 99% | 0 | 78% | 2.86 | 1.50 | Vr05 | Other |
| g27723.t1 | Auxin-induced protein 5NG4 [Glycine soja] | KHN17537.1 | 99% | 0 | 89% | 2.86 | 42.51 | Vr07 | Hormone response |
| g34197.t1 | NAC transcription factor [Glycine max] | AGO14648.1 | 97% | 6.00E-158 | 81% | 2.85 | 13.09 | scaffold_51 | Gene expression and regulation |
| g5349.t1 | Protein NSP-INTERACTING KINASE 1 [Glycine soja] | KHN14464.1 | 99% | 0 | 95% | 2.84 | 7.07 | Vr04 | Signal transduction |
| g27225.t1 | DEAD-box ATP-dependent RNA helicase ISE2 [Medicagotruncatula] | AES96395.2 | 94% | 0 | 81% | 2.84 | 1.67 | Vr05 | Enzyme |
| g21194.t1 | Protein MKS1 [Glycine soja] | KHN44242.1 | 90% | 3.00E-24 | 42% | 2.81 | 20.71 | Vr01 | Defense-related protein |

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|---|---|---|---|---|---|---|---|---|---|
| g27184.t1 | WD repeat-containing protein 76 [Glycine soja] | KHN18586.1 | 99% | 0 | 81% | 2.78 | 7.18 | Vr07 | Development |
| g10700.t1 | Lamin-like protein [Glycine soja] | KHN07162.1 | 80% | 1.00E-84 | 92% | 2.76 | 12.43 | Vr01 | Cell skeleton |
| g6477.t1 | Phospholipase D alpha 1 [Medicagotruncatula] | AES95217.2 | 99% | 0 | 80% | 2.76 | 1.92 | Vr11 | Enzyme |
| g24152.t1 | Protein Hikeshi-like [Glycine max] | XP_003544973.1 | 95% | 2.00E-130 | 96% | 2.75 | 68.37 | Vr06 | Stress-related |
| g6634.t1 | Zinc finger protein [Medicagotruncatula] | XP_003612571.1 | 98% | 4.00E-36 | 90% | 2.74 | 139.12 | Vr11 | Other |
| g6697.t1 | KH domain-containing protein [Glycine soja] | KHN23351.1 | 90% | 0 | 90% | 2.73 | 2.76 | Vr10 | Unknow |
| g8280.t1 | Peptidyl-prolyl cis-trans isomerase [Arachishypogaea] | AGL08211.1 | 83% | 8.00E-70 | 93% | 2.72 | 158.22 | Vr03 | Enzyme |
| g27195.t1 | Alpha/beta-Hydrolases superfamily protein [Theobroma cacao] | XP_007011984.1 | 89% | 2.00E-176 | 86% | 2.72 | 7.94 | Vr07 | Enzyme |
| g27192.t1 | Cysteine-rich RLK (receptor-like kinase) protein [Medicagotruncatula] | KEH32180.1 | 99% | 1.00E-89 | 79% | 2.71 | 27.51 | Vr07 | Signal transduction |
| g9508.t1 | DUF581 family protein [Medicagotruncatula] | KEH39801.1 | 91% | 1.00E-113 | 57% | 2.70 | 6.18 | Vr06 | Other |
| g15465.t1 | Formin-like protein [Medicagotruncatula] | XP_003611598.1 | 95% | 0 | 71% | 2.69 | 7.05 | Vr11 | Cell skeleton |
| g39574.t3 | Cytochrome P450 704C1 [Glycine soja] | KHN04574.1 | 99% | 0 | 81% | 2.69 | 2.95 | scaffold_298 | P450 family |
| g11770.t1 | Cellulose synthase-like protein D3 [Glycine soja] | KHN04843.1 | 97% | 0 | 84% | 2.69 | 2.76 | Vr11 | Enzyme |
| g11873.t1 | Probable folate-biopterin transporter 9 [Arabidopsis thaliana] | O22780.2 | 97% | 8.00E-112 | 47% | 2.68 | 39.32 | Vr05 | Transporter |
| g9258.t1 | F-box protein [Glycine soja] | KHN21309.1 | 99% | 0 | 83% | 2.66 | 1.08 | Vr05 | Signal transduction |
| g13669.t1 | Receptor-like kinase [Medicagotruncatula] | KEH35517.1 | 99% | 0 | 80% | 2.65 | 5.42 | Vr05 | Signal transduction |
| g17348.t1 | Chaperone protein ClpB1 [Glycine soja] | KHN17811.1 | 96% | 1.00E-175 | 49% | 2.65 | 4.96 | Vr05 | Chaperone |
| g40215.t1 | Ferritin 3 chloroplastic-like protein [Phaseolus vulgaris] | AGV54763.1 | 70% | 9.00E-34 | 96% | 2.65 | 85.40 | Vr08 | Other |
| g34226.t1 | Chitin-inducible gibberellin-responsive protein 1 [Glycine soja] | KHN20452.1 | 76% | 0 | 89% | 2.64 | 11.70 | Vr02 | Hormone response |
| g43056.t1 | Elongation factor Tu GTP-binding domain-containing protein 1 [Glycine soja] | KHN29587.1 | 14% | 8.00E-06 | 68% | 2.63 | 5.91 | scaffold_538 | Gene expression and regulation |
| g8462.t1 | Mutator-like transposase isoform 1 [Theobroma cacao] | XP_007030505.1 | 99% | 0 | 87% | 2.62 | 9.18 | Vr08 | Enzyme |

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|---|---|---|---|---|---|---|---|---|---|
| g970.t1 | Cytosolic purine 5'-nucleotidase [Glycine soja] | KHN03225.1 | 99% | 0 | 89% | 2.60 | 4.25 | Vr07 | Enzyme |
| g23234.t1 | Indole-3-acetic acid-amidosynthetase [Medicagotruncatula] | KEH19704.1 | 99% | 0 | 92% | 2.60 | 3.63 | Vr02 | Hormone response |
| g24466.t1 | DnaJ like subfamily B member 13 [Glycine soja] | KHN18947.1 | 88% | 3.00E-168 | 77% | 2.58 | 77.74 | Vr07 | Chaperone |
| g17723.t1 | Midasin [Glycine soja] | KHN28086.1 | 90% | 2.00E-165 | 69% | 2.58 | 3.28 | Vr05 | Chaperone |
| g2522.t2 | Unknow | | | | | 2.57 | 9.17 | Vr05 | Unknow |
| g5593.t3 | Cytosolic Fe-S cluster assembly factor NARFL [Glycine soja] | KHN42277.1 | 66% | 0 | 89% | 2.56 | 4.23 | Vr07 | Other |
| g31995.t1 | Brassinosteroid receptor [Glycine max] | ACM89522.1 | 88% | 0 | 88% | 2.56 | 3.99 | scaffold_43 | Hormone response |
| g43236.t1 | Protein BPS1, chloroplastic [Glycine soja] | KHN29323.1 | 99% | 0 | 81% | 2.55 | 7.38 | Vr04 | Development |
| g43081.t1 | Putative retrotransposon polyprotein [Ipomoea batatas] | AAV88076.1 | 52% | 4.00E-132 | 54% | 2.55 | 2.14 | scaffold_510 | Other |
| g7074.t1 | Bidirectional sugar transporter SWEET17 [Glycine soja] | KHN26542.1 | 97% | 8.00E-117 | 86% | 2.54 | 9.44 | Vr05 | Transporter |
| g40083.t1 | Brassinosteroid-regulated protein BRU1 [Glycine soja] | KHN44468.1 | 99% | 0 | 89% | 2.52 | 67.34 | scaffold_246 | Hormone response |
| g21096.t1 | Receptor like protein kinase S.2 [Glycine soja] | KHN01845.1 | 99% | 0 | 89% | 2.51 | 20.37 | scaffold_282 | Signal transduction |
| g29651.t1 | NADH glutamate synthase precursor [Phaseolus vulgaris] | AAL26865.2 | 99% | 0 | 95% | 2.50 | 1.36 | Vr06 | Enzyme |
| g6441.t1 | Phosphatase [Phaseolus vulgaris] | AGV54261.1 | 99% | 3.00E-170 | 90% | 2.50 | 31.47 | scaffold_315 | Enzyme |
| g14782.t1 | Prolyl 4-hydroxylase subunit alpha-2 [Medicagotruncatula] | XP_003618430.1 | 99% | 4.00E-178 | 79% | 2.50 | 25.27 | Vr01 | Enzyme |
| g33965.t1 | Phospholipase A1 [Medicagotruncatula] | XP_003624211.1 | 99% | 0 | 80% | 2.50 | 16.12 | scaffold_363 | Enzyme |
| g33684.t1 | Unknow | | | | | 2.49 | 257.59 | Vr01 | Unknow |
| g31373.t1 | WAS/WASL-interacting protein family member 2, putative isoform 1 [Theobroma cacao] | XP_007009141.1 | 98% | 3.00E-62 | 43% | 2.49 | 19.34 | Vr03 | Cell skeleton |
| g22634.t1 | RING/U-box protein, putative [Medicagotruncatula] | KEH38899.1 | 90% | 2.00E-164 | 71% | 2.48 | 8.65 | Vr02 | Protein synthesis and digestion |
| g936.t1 | Protein phosphatase 2C-like protein [Medicagotruncatula] | KEH32373.1 | 98% | 0 | 81% | 2.47 | 43.39 | Vr07 | Enzyme |

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|---|---|---|---|---|---|---|---|---|---|
| g21814.t2 | Phospholipase C [Vignaradiata] | AAQ95730.1 | 99% | 0 | 99% | 2.47 | 1.46 | Vr03 | Enzyme |
| g20971.t1 | Myb family transcription factor APL [Glycine soja] | KHN28253.1 | 98% | 2.00E-174 | 82% | 2.46 | 5.51 | Vr07 | Gene expression and regulation |
| g20863.t3 | Transcriptional corepressor SEUSS [Glycine soja] | KHN44265.1 | 99% | 2.00E-96 | 74% | 2.46 | 14.00 | scaffold_184 | Gene expression and regulation |
| g3682.t2 | SH3 domain protein [Medicagotruncatula] | KEH21301.1 | 78% | 0 | 89% | 2.45 | 4.65 | Vr07 | Signal transduction |
| g24963.t1 | ABC transporter B family member 15 [Glycine soja] | KHN10916.1 | 99% | 0 | 85% | 2.45 | 2.02 | scaffold_259 | Transporter |
| g9317.t1 | Unknow | | | | | 2.44 | 12.42 | Vr05 | Unknow |
| g5660.t1 | Neurogenic protein mastermind-like [Glycine max] | XP_003529611.1 | 44% | 3.00E-37 | 94% | 2.44 | 3.29 | Vr07 | Unknow |
| g2340.t1 | ABC transporter G family member 15 [Glycine soja] | KHN20635.1 | 98% | 0 | 85% | 2.42 | 3.38 | Vr02 | Transporter |
| g30663.t1 | RING/U-box protein [Medicagotruncatula] | KEH34255.1 | 99% | 1.00E-107 | 78% | 2.42 | 114.88 | Vr10 | Protein synthesis and digestion |
| g16175.t1 | Squalene monooxygenase [Glycine soja] | KHN36995.1 | 99% | 0 | 92% | 2.41 | 5.83 | Vr06 | Enzyme |
| g43474.t1 | Polyprotein [Glycine max] | AAO23078.1 | 95% | 2.00E-180 | 42% | 2.39 | 2.70 | scaffold_534 | Other |
| g25007.t1 | Serine/threonine-protein kinase ATM [Glycine soja] | KHN30902.1 | 86% | 0 | 95% | 2.38 | 3.41 | Vr05 | Signal transduction |
| g38814.t1 | Aluminum-activated malate transporter 9 [Glycine soja] | KHN21560.1 | 97% | 0 | 78% | 2.38 | 9.92 | Vr07 | Transporter |
| g29584.t1 | Pyruvate kinase [Glycine max] | NP_001236056.1 | 99% | 0 | 97% | 2.38 | 142.40 | Vr01 | Enzyme |
| g5222.t2 | Endochitinase [Glycine soja] | KHN00426.1 | 90% | 2.00E-142 | 77% | 2.37 | 32.57 | Vr07 | Defense-related protein |
| g35123.t1 | EF hand calcium-binding family protein [Medicagotruncatula] | KEH20220.1 | 99% | 4.00E-95 | 86% | 2.36 | 70.39 | Vr07 | Signal transduction |
| g8581.t1 | Unknow | | | | | 2.36 | 19.55 | Vr05 | Unknow |
| g31380.t1 | Putative sugar phosphate/phosphate translocator [Glycine soja] | KHN17860.1 | 99% | 0 | 86% | 2.36 | 7.33 | Vr03 | Transporter |
| g30105.t1 | AN1-type zinc finger protein [Medicagotruncatula] | XP_003596791.1 | 99% | 2.00E-61 | 65% | 2.35 | 367.44 | Vr04 | Stress-related |
| g16297.t1 | Serine/threonine-protein kinase TOR [Glycine soja] | KHN30445.1 | 99% | 0 | 99% | 2.35 | 10.81 | Vr11 | Signal transduction |
| g15067.t1 | Coiled-coil domain-containing protein 109A [Medicagotruncatula] | XP_003616093.1 | 99% | 3.00E-141 | 67% | 2.34 | 26.61 | Vr10 | Transporter |
| g30770.t1 | UNE1-like protein [Medicagotruncatula] | KEH19456.1 | 86% | 1.00E-174 | 63% | 2.34 | 9.34 | Vr02 | Unknow |
| g16844.t2 | PotyviralVPg interacting protein 2 [Phaseolus vulgaris] | ACQ59165.1 | 97% | 0 | 91% | 2.34 | 6.62 | Vr06 | Unknow |
| g18337.t1 | Ethylene-responsive transcription factor ERF112 | KHN41295.1 | 87% | 7.00E-106 | 70% | 2.33 | 15.66 | Vr01 | Hormone response |

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|---|---|---|---|---|---|---|---|---|---|
| | [Glycine soja] | | | | | | | | |
| g981.t1 | Polyubiquitin (ubq10) [Arabidopsis thaliana] | CAB81074.1 | 99% | 0 | 99% | 2.33 | 803.87 | Vr07 | Protein synthesis and digestion |
| g2376.t1 | L-ascorbate oxidase like [Glycine soja] | KHN05478.1 | 99% | 0 | 91% | 2.33 | 10.31 | Vr02 | Enzyme |
| g16844.t1 | PotyviralVPg interacting protein 2 [Phaseolus vulgaris] | ACQ59165.1 | 99% | 0 | 91% | 2.32 | 7.20 | Vr06 | Unknow |
| g10773.t1 | Vacuolar protein sorting-associated protein 13C, putative [Theobroma cacao] | XP_007047104.1 | 92% | 4.00E-138 | 74% | 2.31 | 11.22 | Vr07 | Vacuolar protein |
| g31270.t1 | ATP-dependent zinc metalloprotease FTSH 2, chloroplastic [Glycine soja] | KHN28946.1 | 98% | 0 | 94% | 2.30 | 3.35 | Vr07 | Enzyme |
| g22120.t1 | F-box protein [Medicagotruncatula] | XP_003602822.1 | 84% | 0 | 74% | 2.30 | 3.61 | Vr05 | Signal transduction |
| g31510.t2 | Alternative NAD(P)H-ubiquinone oxidoreductase C1 [Arabidopsis thaliana] | Q8GXR9.2 | 97% | 0 | 62% | 2.30 | 5.16 | Vr07 | Enzyme |
| g3682.t1 | SH3 domain protein [Medicagotruncatula] | KEH21301.1 | 78% | 0 | 91% | 2.29 | 5.14 | Vr07 | Signal transduction |
| g42465.t1 | Inactive rhomboid protein 1 [Glycine soja] | KHM99144.1 | 99% | 5.00E-150 | 90% | 2.29 | 12.41 | Vr01 | Protein synthesis and digestion |
| g993.t1 | RHOMBOID-like protein 14 isoform 1 [Theobroma cacao] | XP_007019736.1 | 91% | 3.00E-107 | 63% | 2.27 | 45.89 | Vr07 | Stress-related |
| g16966.t1 | Pentatricopeptide repeat (PPR-like) superfamily protein isoform 1 [Theobroma cacao] | XP_007024106.1 | 98% | 0 | 75% | 2.27 | 3.77 | Vr05 | Gene expression and regulation |
| g29346.t1 | Myb transcription factor [Medicagotruncatula] | KEH26846.1 | 99% | 0 | 69% | 2.26 | 39.28 | Vr01 | Gene expression and regulation |
| g7930.t1 | SAC domain protein [Medicagotruncatula] | XP_003608091.1 | 99% | 0 | 82% | 2.25 | 3.65 | Vr07 | Enzyme |
| g7871.t1 | Calmodulin-like protein 1 [Glycine soja] | KHN31070.1 | 98% | 3.00E-106 | 91% | 2.25 | 18.09 | Vr07 | Signal transduction |
| g6640.t1 | Alpha-glucosidase 2 [Glycine soja] | KHN42870.1 | 27% | 0 | 82% | 2.24 | 2.68 | Vr11 | Enzyme |
| g164.t1 | Arginine-glutamic acid dipeptide repeats [Gossypiumarboreum] | KHF99977.1 | 90% | 8.00E-158 | 48% | 2.24 | 7.31 | Vr03 | Gene expression and regulation |
| g3032.t1 | Polyubiquitin (ubq10) [Arabidopsis thaliana] | CAB81074.1 | 99% | 0 | 99% | 2.24 | 376.83 | Vr07 | Protein synthesis and digestion |
| g5222.t1 | Endochitinase [Glycine soja] | KHN00426.1 | 90% | 1.00E-143 | 77% | 2.23 | 31.79 | Vr07 | Defense-related protein |
| g9359.t1 | Pentatricopeptide repeat-containing protein, mitochondrial [Glycine soja] | KHN36632.1 | 95% | 0 | 68% | 2.22 | 59.15 | scaffold_86 | Gene expression and regulation |
| g4634.t1 | Poly(A) RNA polymerase cid14 [Glycine soja] | KHN25822.1 | 71% | 0 | 66% | 2.22 | 4.47 | scaffold_43 | Enzyme |

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|---|---|---|---|---|---|---|---|---|---|
| g7059.t2 | ABC transporter C family member 4 [Glycine soja] | KHN14620.1 | 98% | 0 | 82% | 2.21 | 3.30 | Vr05 | Transporter |
| g4310.t1 | Senescence-associated family protein [Populustrichocarpa] | XP_006385394.1 | 91% | 7.00E-58 | 65% | 2.21 | 49.09 | Vr07 | Senescence |
| g26379.t1 | Mitochondrial chaperone BCS1 [Medicagotruncatula] | XP_003596412.1 | 99% | 0 | 67% | 2.19 | 4.94 | Vr05 | Chaperone |
| g12192.t1 | DUF863 family protein [Medicagotruncatula] | AES96945.2 | 99% | 0 | 63% | 2.19 | 5.82 | scaffold_100 | Other |
| g25251.t1 | Mannitol dehydrogenase [Medicagotruncatula] | XP_003612978.1 | 99% | 0 | 82% | 2.18 | 312.03 | Vr11 | Enzyme |
| g17557.t1 | Histone-lysine N-methyltransferase SUVR5 [Glycine soja] | KHN42030.1 | 96% | 0 | 88% | 2.18 | 2.32 | Vr11 | Enzyme |
| g16571.t1 | UHRF1-binding protein 1-like [Glycine soja] | KHN36730.1 | 62% | 0 | 91% | 2.17 | 3.42 | scaffold_23 | Gene expression and regulation |
| g11973.t1 | MLO-like protein 8 [Glycine soja] | KHN12501.1 | 99% | 0 | 88% | 2.17 | 4.80 | Vr07 | Defense-related protein |
| g21023.t1 | 3'-5' exonuclease domain protein [Medicagotruncatula] | AES88131.2 | 99% | 0 | 72% | 2.17 | 11.05 | Vr02 | Gene expression and regulation |
| g9393.t1 | Putative E3 ubiquitin-protein ligase RING1a [Glycine soja] | KHN36653.1 | 52% | 5.00E-151 | 88% | 2.17 | 5.02 | scaffold_86 | Enzyme |
| g24017.t1 | Serine/threonine-protein kinase MHK [Glycine soja] | KHN15505.1 | 97% | 0 | 91% | 2.15 | 10.50 | Vr09 | Signal transduction |
| g25619.t1 | Alpha amylase domain protein [Medicagotruncatula] | AES59822.2 | 95% | 0 | 84% | 2.15 | 8.46 | Vr06 | Enzyme |
| g25526.t1 | GTPase-activating protein gyp7 [Glycine soja] | KHN19532.1 | 86% | 0 | 94% | 2.14 | 9.13 | Vr10 | Signal transduction |
| g10148.t1 | ATPase 11, plasma membrane-type [Glycine soja] | KHN19372.1 | 99% | 0 | 95% | 2.14 | 2.30 | Vr07 | Enzyme |
| g993.t2 | Rhomboid protein Ilepu_RBL14 [Ilex purpurea] | AIY60667.1 | 79% | 3.00E-90 | 73% | 2.13 | 18.12 | Vr07 | Enzyme |
| g18412.t1 | Ent-kaur-16-ene synthase, chloroplastic [Glycine soja] | KHN21375.1 | 97% | 0 | 85% | 2.12 | 4.53 | Vr05 | Enzyme |
| g15550.t1 | Protein BPS1, chloroplastic [Glycine soja] | KHN29323.1 | 99% | 0 | 82% | 2.12 | 10.39 | Vr04 | Development |
| g4990.t1 | RRP12-like protein [Medicagotruncatula] | KEH41642.1 | 99% | 0 | 67% | 2.12 | 5.55 | Vr08 | Gene expression and regulation |
| g32697.t1 | Serine/threonine-protein kinase WNK1 [Glycine soja] | KHN43209.1 | 91% | 0 | 79% | 2.11 | 3.85 | Vr10 | Signal transduction |
| g16899.t1 | Heat shock protein 90-2 [Glycine max] | NP_001236599.1 | 99% | 0 | 96% | 2.10 | 116.77 | Vr06 | Chaperone |
| g21338.t1 | Cysteine-rich TM module stress tolerance protein [Medicagotruncatula] | KEH41015.1 | 98% | 1.00E-13 | 68% | 2.10 | 1096.20 | Vr05 | Stress-related |

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|---|---|---|---|---|---|---|---|---|---|
| g40121.t1 | WD repeat-containing protein 36 [Glycine soja] | KHN24981.1 | 98% | 0 | 92% | 2.09 | 6.27 | Vr01 | Development |
| g16841.t1 | Histidine kinase 2 [Glycine soja] | KHN43950.1 | 99% | 0 | 77% | 2.09 | 3.67 | Vr06 | Signal transduction |
| g21370.t1 | NAC domain-containing protein 21/22 [Glycine soja] | KHN26800.1 | 99% | 0 | 92% | 2.08 | 14.06 | Vr05 | Gene expression and regulation |
| g10545.t1 | Translational activator GCN1 [Glycine soja] | KHN43147.1 | 98% | 0 | 95% | 2.08 | 12.69 | scaffold_83 | Protein synthesis and digestion |
| g2522.t1 | Elongation factor G [Gossypiumarboreum] | KHG18253.1 | 99% | 0 | 56% | 2.08 | 10.04 | Vr05 | Gene expression and regulation |
| g40994.t1 | Zinc finger HIT domain-containing protein 2 [Glycine soja] | KHN44976.1 | 99% | 0 | 83% | 2.08 | 26.92 | scaffold_239 | Other |
| g17261.t1 | Chaperone protein ClpB1 [Glycine soja] | KHN17811.1 | 98% | 0 | 93% | 2.08 | 98.22 | Vr03 | Chaperone |
| g30259.t1 | 5-oxoprolinase [Glycine soja] | KHN46268.1 | 99% | 0 | 95% | 2.07 | 18.43 | Vr10 | Enzyme |
| g21451.t1 | Phytochrome B-2 [Glycine max] | ACE79199.2 | 99% | 0 | 92% | 2.07 | 4.57 | scaffold_83 | Development |
| g11770.t2 | Cellulose synthase-like protein D3 [Glycine soja] | KHN04843.1 | 98% | 0 | 89% | 2.07 | 3.38 | Vr11 | Enzyme |
| g16300.t1 | Probable zinc metalloprotease EGY3, chloroplastic; AltName: Full=Protein ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN 3; Flags: Precursor [Oryza sativa Indica Group] | A2XLM6.1 | 66% | 0 | 74% | 2.06 | 18.88 | Vr11 | Development |
| g24024.t1 | 70 kDa peptidyl-prolyl isomerase [Medicagotruncatula] | XP_003626943.1 | 99% | 0 | 86% | 2.06 | 175.27 | Vr09 | Enzyme |
| g37809.t1 | Bromodomain-containing protein 9 [Glycine soja] | KHN02850.1 | 84% | 0 | 79% | 2.06 | 10.03 | scaffold_373 | Gene expression and regulation |
| g39296.t1 | Indole-3-acetic acid-induced protein ARG2 [Vignaradiata var. radiata] | P32292.1 | 99% | 8.00E-43 | 96% | 2.06 | 141.40 | Vr08 | Hormone response |
| g1324.t1 | Stress-related protein [Glycine soja] | KHN08531.1 | 99% | 2.00E-127 | 90% | 2.06 | 380.77 | Vr10 | Stress-related |
| g11255.t1 | Receptor-like cytosolic serine/threonine-protein kinase RBK2 [Glycine soja] | KHN05157.1 | 97% | 0 | 86% | 2.05 | 8.34 | Vr06 | Signal transduction |
| g29556.t1 | Sucrose synthase [Phaseolus vulgaris] | ACP17902.1 | 99% | 0 | 97% | 2.05 | 19.80 | Vr05 | Enzyme |
| g35094.t1 | Cysteine-rich RLK (receptor-like kinase) protein [Medicagotruncatula] | KEH32181.1 | 49% | 1.00E-92 | 66% | 2.04 | 5.67 | scaffold_207 | Signal transduction |
| g16377.t2 | Protein IQ-DOMAIN 14 [Glycine soja] | KHN15893.1 | 99% | 0 | 89% | 2.04 | 4.99 | scaffold_179 | Gene expression and regulation |
| g28505.t1 | Nucleolar complex protein 3 like [Glycine soja] | KHN02736.1 | 93% | 0 | 90% | 2.03 | 6.09 | Vr02 | Gene expression and regulation |

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|---|---|---|---|---|---|---|---|---|---|
| g31426.t1 | Transcription elongation factor Spt5-like protein, putative [Medicagotruncatula] | KEH44273.1 | 57% | 0 | 64% | 2.02 | 7.81 | Vr08 | Gene expression and regulation |
| g11760.t1 | Homeobox-leucine zipper protein ROC3 [Glycine soja] | KHN38952.1 | 68% | 0 | 91% | 2.02 | 3.08 | scaffold_259 | Development |
| g20863.t1 | Transcriptional corepressor SEUSS [Glycine soja] | KHN44265.1 | 90% | 0 | 84% | 2.02 | 8.42 | scaffold_184 | Gene expression and regulation |
| g12744.t1 | Protein MOR1 [Glycine soja] | KHN00874.1 | 99% | 0 | 92% | 2.01 | 6.14 | Vr08 | Cell skeleton |
| g8552.t1 | Acetyl-CoA carboxylase 1 [Glycine soja] | KHN45348.1 | 99% | 0 | 94% | 2.01 | 2.34 | Vr05 | Enzyme |
| g28505.t2 | Nucleolar complex protein 3 like [Glycine soja] | KHN02736.1 | 93% | 0 | 86% | 2.01 | 4.66 | Vr02 | Gene expression and regulation |
| g27259.t1 | Pentatricopeptide repeat-containing protein, mitochondrial [Glycine soja] | KHN06297.1 | 99% | 0 | 86% | 2.01 | 9.19 | Vr09 | Gene expression and regulation |
| g7816.t1 | Abscisic acid specific glucosyltransferase [Phaseolus vulgaris] | AJS11517.1 | 98% | 0 | 87% | 2.00 | 71.24 | Vr07 | Enzyme |
| g5920.t1 | Fructokinase [Medicagotruncatula] | XP_003597523.1 | 93% | 0 | 81% | 0.50 | 24.62 | Vr02 | Enzyme |
| g11741.t2 | RNA-binding region RNP-1 [Phaseolus vulgaris] | AHA84227.1 | 99% | 7.00E-172 | 87% | 0.50 | 14.89 | Vr11 | Gene expression and regulation |
| g19664.t1 | ATP sulfurylase 1, chloroplastic [Glycine soja] | KHN02762.1 | 99% | 0 | 94% | 0.50 | 69.30 | Vr08 | Enzyme |
| g20490.t1 | Cytochrome P450 86B1 [Glycine soja] | KHN45347.1 | 96% | 6.00E-174 | 76% | 0.50 | 8.52 | scaffold_134 | P450 family |
| g11741.t1 | RNA-binding region RNP-1 [Phaseolus vulgaris] | AHA84227.1 | 99% | 8.00E-170 | 87% | 0.50 | 21.43 | Vr11 | Gene expression and regulation |
| g5539.t1 | Lactoylglutathionelyase [Phaseolus vulgaris] | AGZ15371.1 | 99% | 0 | 96% | 0.50 | 6.90 | Vr07 | Enzyme |
| g16395.t2 | Cytochrome P450 78A3 [Glycine soja] | KHN15903.1 | 98% | 0 | 77% | 0.50 | 6.34 | scaffold_179 | P450 family |
| g40011.t1 | Protein transport SEC13-like protein [Phaseolus vulgaris] | AGV54445.1 | 99% | 0 | 97% | 0.50 | 6.33 | Vr08 | Transporter |
| g18121.t1 | AP2-like ethylene-responsive transcription factor AIL1 [Glycine soja] | KHN39632.1 | 99% | 0 | 75% | 0.50 | 33.81 | Vr09 | Hormone response |
| g10530.t1 | F-box protein PP2-B1 [Glycine soja] | KHN04971.1 | 90% | 2.00E-98 | 62% | 0.50 | 363.92 | scaffold_83 | Signal transduction |
| g2426.t1 | Spastin [Glycine soja] | KHN05442.1 | 92% | 0 | 85% | 0.49 | 2.71 | Vr02 | Protein synthesis and digestion |
| g1662.t2 | CHY zinc finger protein [Medicagotruncatula] | AES76656.2 | 99% | 0 | 79% | 0.49 | 1.29 | Vr01 | Unknow |
| g19635.t1 | Homocysteine S-methyltransferase 3 [Glycine soja] | KHN15741.1 | 98% | 9.00E-170 | 82% | 0.49 | 19.05 | Vr08 | Enzyme |
| g18900.t1 | Serine-rich protein-like protein [Arabidopsis thaliana] | NP_200409.1 | 37% | 2.00E-07 | 62% | 0.49 | 34.03 | scaffold_176 | Gene expression and regulation |
| g26265.t2 | Peroxisome biogenesis protein 22 [Glycine soja] | KHN25774.1 | 99% | 8.00E-150 | 84% | 0.49 | 13.56 | Vr05 | Stress-related |

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| g34269.t1 | Abscisic acid 8'-hydroxylase 2 [Glycine soja] | KHN29579.1 | 91% | 0 | 89% | 0.49 | 19.60 | scaffold_134 | Enzyme |
| g19288.t1 | Glutathione transferase [Phaseolus vulgaris] | AEX37999.1 | 99% | 6.00E-135 | 87% | 0.49 | 464.66 | Vr06 | Enzyme |
| g754.t1 | Rhodanese/cell cycle control phosphatase superfamily protein [Medicagotruncatula] | KEH35021.1 | 56% | 9.00E-151 | 82% | 0.49 | 3.68 | Vr05 | Enzyme |
| g1690.t1 | Unknow | | | | | 0.49 | 102.87 | Vr01 | Unknow |
| g8044.t1 | Sister chromatid cohesion 1 protein 3 [Morusnotabilis] | XP_010095386.1 | 99% | 1.00E-114 | 37% | 0.49 | 2.37 | Vr05 | Other |
| g5937.t1 | Peroxin 13 [Theobroma cacao] | XP_007049511.1 | 68% | 6.00E-58 | 79% | 0.48 | 11.98 | Vr02 | Stress-related |
| g23925.t1 | Protein phosphatase type 2C [Lotus japonicus] | AAD17805.1 | 73% | 4.00E-154 | 86% | 0.48 | 56.74 | Vr02 | Enzyme |
| g16906.t2 | Oligopeptide transporter OPT family protein [Medicagotruncatula] | AET00810.2 | 99% | 0 | 75% | 0.48 | 16.59 | Vr06 | Transporter |
| g16210.t1 | ATP binding protein, putative [Ricinuscommunis] | XP_002520054.1 | 91% | 0 | 69% | 0.48 | 4.99 | Vr11 | Other |
| g13745.t1 | SBP family protein, putative isoform 1 [Theobroma cacao] | XP_007024896.1 | 87% | 3.00E-81 | 54% | 0.48 | 6.18 | Vr07 | Gene expression and regulation |
| g19901.t2 | Lactoylglutathionelyase [Gossypiumhirsutum] | ACJ11750.1 | 95% | 0 | 84% | 0.48 | 10.26 | Vr10 | Enzyme |
| g8922.t1 | Unknow | | | | | 0.48 | 125.40 | Vr03 | Unknow |
| g8711.t1 | Sulfate transporter 3.1 [Glycine soja] | KHN03817.1 | 99% | 0 | 92% | 0.48 | 10.19 | Vr08 | Transporter |
| g26802.t1 | Plant/T7A14-6 protein [Medicagotruncatula] | KEH29717.1 | 99% | 1.00E-99 | 79% | 0.48 | 11.31 | Vr02 | Unknow |
| g1005.t1 | Vacuolar protein sorting-associated protein 27 [Glycine soja] | KHN45033.1 | 41% | 1.00E-53 | 87% | 0.48 | 8.78 | Vr07 | Vacuolar protein |
| g6667.t1 | RNA-binding protein with multiple splicing protein [Medicagotruncatula] | AES72538.2 | 99% | 5.00E-125 | 79% | 0.48 | 7.71 | Vr10 | Gene expression and regulation |
| g16906.t1 | Oligopeptide transporter OPT family protein [Medicagotruncatula] | AET00810.2 | 99% | 0 | 80% | 0.48 | 18.84 | Vr06 | Transporter |
| g41871.t1 | Taxadiene 5-alpha hydroxylase [Glycine soja] | KHN38311.1 | 99% | 0 | 87% | 0.47 | 4.88 | Vr06 | Enzyme |
| g30114.t1 | TGACG-sequence-specific DNA-binding protein TGA-2.1 [Glycine soja] | KHN32878.1 | 99% | 0 | 92% | 0.47 | 8.87 | Vr04 | Gene expression and regulation |
| g1598.t1 | Protein phosphatase 2c, putative [Ricinuscommunis] | XP_002520360.1 | 97% | 2.00E-133 | 67% | 0.47 | 3.90 | Vr01 | Enzyme |
| g6587.t2 | Auxin-induced protein 5NG4 [Glycine soja] | KHN41783.1 | 91% | 0 | 88% | 0.47 | 1.40 | Vr11 | Hormone response |

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| g4265.t1 | Ethylene-responsive transcription factor 5-like [Glycine max] | NP_001241150. | 99% | 1.00E-98 | 72% | 0.47 | 19.31 | Vr07 | Hormone response |
| g8134.t1 | Quinone oxidoreductase-like protein, chloroplastic [Glycine soja] | KHN23541.1 | 99% | 1.00E-173 | 86% | 0.47 | 192.93 | Vr01 | Enzyme |
| g6584.t1 | Pentatricopeptide repeat-containing protein [Medicagotruncatula] | XP_003612457.1 | 80% | 2.00E-178 | 73% | 0.47 | 3.22 | Vr11 | Gene expression and regulation |
| g8337.t1 | Nodulin-like protein [Medicagotruncatula] | XP_003597634.1 | 98% | 0 | 71% | 0.47 | 6.32 | Vr04 | Other |
| g634.t2 | Heavy metal-associated domain protein [Medicagotruncatula] | KEH21012.1 | 80% | 1.00E-66 | 58% | 0.47 | 13.08 | Vr05 | Transporter |
| g42753.t1 | Bidirectional sugar transporter [Medicagotruncatula] | KEH40468.1 | 90% | 1.00E-103 | 81% | 0.46 | 79.77 | Vr06 | Transporter |
| g29173.t1 | Plant/F18G18-200 protein [Medicagotruncatula] | AES58962.2 | 95% | 0 | 89% | 0.46 | 7.23 | Vr06 | Unknow |
| g3542.t1 | Glutathione peroxidase [Medicago sativa] | AFP99878.1 | 99% | 5.00E-103 | 88% | 0.46 | 329.49 | Vr07 | Enzyme |
| g5623.t1 | 6-phosphofructokinase [Medicagotruncatula] | XP_003637592.1 | 96% | 0 | 80% | 0.46 | 51.75 | Vr07 | Enzyme |
| g39123.t1 | Low affinity sulfate transporter 3 [Glycine soja] | KHN41503.1 | 93% | 0.00E+00 | 95% | 0.46 | 2.54 | Vr06 | Transporter |
| g8274.t1 | Expansin-A15 [Glycine soja] | KHN18562.1 | 89% | 8.00E-135 | 89% | 0.46 | 34.65 | Vr03 | Development |
| g16305.t1 | Thymocyte nuclear protein [Medicagotruncatula] | XP_003610642.1 | 81% | 5.00E-65 | 82% | 0.45 | 20.96 | Vr11 | Other |
| g2724.t1 | Aquaporin PIP2;4 [Gossypiumhirsutum] | ACB42441.1 | 99% | 0 | 92% | 0.45 | 53.97 | Vr05 | Transporter |
| g27343.t1 | E3 ubiquitin-protein ligase HERC2-like protein [Medicagotruncatula] | KEH36068.1 | 98% | 0 | 70% | 0.45 | 3.77 | Vr06 | Protein synthesis and digestion |
| g10472.t1 | DUF688 family protein [Medicagotruncatula] | KEH24687.1 | 97% | 5.00E-44 | 48% | 0.45 | 35.52 | scaffold_83 | Other |
| g782.t1 | UDP-glucose glucosyltransferase [Medicagotruncatula] | XP_003615827.1 | 95% | 7.00E-153 | 51% | 0.45 | 4.57 | Vr05 | Enzyme |
| g25765.t1 | 8S globulin beta isoform precursor [Vignaradiata] | ABG02262.1 | 99% | 0 | 86% | 0.45 | 15952.71 | Vr02 | Storage protein |
| g31401.t1 | Plasma membrane intrinsic protein 1;3 [Phaseolus vulgaris] | ABH85411.1 | 99% | 0 | 96% | 0.45 | 4.44 | Vr03 | Transporter |
| g20578.t1 | Ammonium transporter (AMT1.1) [Lotus japonicus] | CAC10555.1 | 98% | 0 | 84% | 0.45 | 19.12 | Vr08 | Transporter |
| g33691.t1 | Cytochrome P450 71A1 [Glycine soja] | KHN29102.1 | 92% | 0 | 79% | 0.45 | 49.49 | Vr01 | P450 family |
| g21325.t2 | 1-aminocyclopropane-1-carboxylate oxidase-like protein [Medicagotruncatula] | XP_003596176.1 | 99% | 0 | 72% | 0.45 | 14.03 | Vr05 | Enzyme |

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| g16930.t1 | Biotin carboxyl carrier protein of acetyl-CoA carboxylase [Glycine soja] | KHN44161.1 | 99% | 5.00E-130 | 83% | 0.45 | 6.61 | Vr05 | Enzyme |
| g8002.t2 | Cyclic pyranopterin monophosphate synthase, mitochondrial-like isoform X1 [Glycine max] | XP_003531456.1 | 99% | 0 | 81% | 0.44 | 2.98 | Vr05 | Enzyme |
| g26121.t1 | Unknow | | | | | 0.44 | 48.78 | Vr05 | Unknow |
| g3624.t1 | Trichome birefringence-like protein [Medicagotruncatula] | KEH21199.1 | 99% | 0 | 68% | 0.44 | 2.97 | Vr07 | Development |
| g40177.t1 | 8S globulin beta isoform precursor [Vignaradiata] | ABG02262.1 | 93% | 4.00E-113 | 75% | 0.44 | 455.26 | scaffold_374 | Storage protein |
| g6406.t1 | Polyubiquitin-A [Triticumurartu] | EMS54972.1 | 99% | 0 | 99% | 0.44 | 1848.35 | scaffold_450 | Protein synthesis and digestion |
| g16849.t1 | LHCII type II chlorophyll a/b-binding protein [Vignaradiata] | AAF89205.1 | 99% | 0 | 100% | 0.44 | 89.65 | Vr06 | Development |
| g22727.t1 | Ataxin-3 protein [Medicagotruncatula] | AES86776.2 | 82% | 7.00E-38 | 88% | 0.44 | 33.93 | scaffold_133 | Other |
| g16668.t1 | TCP family transcription factor [Medicagotruncatula] | KEH18996.1 | 99% | 2.00E-114 | 63% | 0.43 | 23.65 | scaffold_194 | Gene expression and regulation |
| g15412.t1 | Ethylene-responsive element binding factor 2 [Arachishypogaea] | AFU07644.1 | 97% | 1.00E-68 | 76% | 0.43 | 434.33 | Vr11 | Hormone response |
| g1105.t1 | Heat stress transcription factor A-2 [Glycine soja] | KHN17679.1 | 99% | 0 | 75% | 0.43 | 195.35 | Vr07 | Chaperone |
| g29615.t2 | COP9 signalosome complex subunit 7 [Glycine soja] | KHN27385.1 | 99% | 2.00E-156 | 96% | 0.43 | 9.85 | Vr08 | Protein synthesis and digestion |
| g30670.t1 | Peptidyl-prolyl cis-trans isomerase [Carica papaya] | AEK80448.1 | 89% | 1.00E-119 | 92% | 0.43 | 19.87 | Vr10 | Enzyme |
| g3437.t1 | Protein HOTHEAD [Glycine soja] | KHN39304.1 | 95% | 0 | 83% | 0.43 | 3.55 | Vr09 | Development |
| g4607.t2 | Auxin response factor [Medicagotruncatula] | XP_003597256.1 | 96% | 0 | 75% | 0.43 | 1.19 | Vr04 | Hormone response |
| g11573.t1 | Unknow | | | | | 0.42 | 129.63 | Vr05 | Unknow |
| g32284.t1 | DUF1262 family protein [Medicagotruncatula] | KEH27766.1 | 99% | 1.00E-154 | 61% | 0.42 | 2.51 | Vr11 | Other |
| g32711.t1 | Hydroxycinnamoyl-CoEnzyme A shikimate/quinatehydroxycinnamoyltransferase [Glycine soja] | KHN43198.1 | 98% | 0 | 72% | 0.42 | 9.09 | Vr10 | Enzyme |
| g22714.t1 | 8-amino-7-oxononanoate synthase [Theobroma cacao] | XP_007026789.1 | 99% | 1.00E-76 | 57% | 0.42 | 18.10 | scaffold_133 | Enzyme |
| g34711.t1 | Putative U6 snRNA-associated Sm-like protein LSm4 [Gossypiumarboreum] | KHG16578.1 | 79% | 1.00E-58 | 94% | 0.41 | 19.01 | Vr08 | Gene expression and regulation |

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| g12914.t1 | UDP-L-rhamnose synthase [Gossypiumhirsutum] | ADB24764.1 | 98% | 0 | 87% | 0.41 | 3.51 | Vr07 | Enzyme |
| g4546.t1 | Glutelin type-A 1 [Glycine soja] | KHN22001.1 | 99% | 0 | 88% | 0.41 | 7.22 | Vr04 | Storage protein |
| g37042.t1 | Mung bean seed albumin [Vignaradiata var. radiata] | CAA50008.1 | 97% | 9.00E-156 | 98% | 0.41 | 4387.34 | Vr08 | Storage protein |
| g2783.t1 | 3-ketoacyl-CoA synthase-like protein [Medicagotruncatula] | KEH42797.1 | 99% | 0 | 89% | 0.41 | 2.48 | Vr08 | Enzyme |
| g43361.t1 | Senescence-associated family protein [Populustrichocarpa] | XP_002302279.2 | 99% | 3.00E-42 | 56% | 0.41 | 11.60 | Vr06 | Senescence |
| g13663.t1 | Ubiquinol-cytochrome C reductase complex 6.7 kDa protein, putative [Medicagotruncatula] | KEH35528.1 | 98% | 2.00E-09 | 73% | 0.41 | 13.85 | Vr05 | Enzyme |
| g40178.t1 | 8S globulin alpha' isoform precursor [Vignaradiata] | ABG02261.1 | 97% | 0 | 96% | 0.41 | 1593.90 | scaffold_374 | Storage protein |
| g21211.t1 | Histone H3, expressed [Triticumaestivum] | CBH32561.1 | 99% | 6.00E-91 | 99% | 0.41 | 60.85 | Vr01 | Gene expression and regulation |
| g40195.t1 | Cysteine synthase [Glycine soja] | KHN15751.1 | 99% | 0 | 95% | 0.40 | 2.18 | scaffold_374 | Enzyme |
| g3564.t1 | BTB/POZ domain plant protein [Medicagotruncatula] | KEH21081.1 | 99% | 0 | 83% | 0.40 | 4.73 | Vr07 | Gene expression and regulation |
| g728.t1 | Cysteinyl endopeptidase [Vignaradiata] | AAA92063.1 | 99% | 0 | 99% | 0.40 | 2.65 | Vr05 | Enzyme |
| g7613.t1 | Ankyrin-3 [Glycine soja] | KHN34671.1 | 99% | 7.00E-97 | 77% | 0.39 | 2.66 | scaffold_7 | Defense-related protein |
| g11192.t1 | Flavonol synthase/flavanone 3-hydroxylase-like [Glycine max] | XP_003556632.1 | 98% | 0 | 84% | 0.39 | 17.25 | Vr11 | Defense-related protein |
| g8361.t1 | Alpha-N-acetylglucosaminidase [Glycine soja] | KHN19340.1 | 89% | 0 | 89% | 0.38 | 4.15 | Vr04 | Enzyme |
| g16395.t1 | Cytochrome P450 78A3 [Glycine soja] | KHN15903.1 | 98% | 0 | 80% | 0.38 | 6.69 | scaffold_179 | P450 family |
| g8290.t1 | Peptidyl-prolyl cis-trans isomerase [Arachishypogaea] | AGL08211.1 | 83% | 8.00E-70 | 93% | 0.38 | 78.27 | Vr03 | Enzyme |
| g30113.t2 | ABSCISIC ACID-INSENSITIVE 5-like protein 1 [Glycine soja] | KHN32879.1 | 99% | 9.00E-83 | 55% | 0.38 | 5.36 | Vr04 | Hormone response |
| g8859.t1 | Indole-3-glycerol phosphatelyase, chloroplastic [Glycine soja] | KHN02540.1 | 99% | 0 | 89% | 0.38 | 1.94 | Vr03 | Hormone response |
| g727.t1 | Peptide methionine sulfoxide reductase [Glycine soja] | KHN05803.1 | 85% | 3.00E-110 | 91% | 0.38 | 7.26 | Vr05 | Enzyme |
| g3618.t1 | Ethylene response factor protein 9 | AJK26929.1 | 97% | 7.00E-59 | 50% | 0.38 | 3.28 | Vr07 | Hormone response |

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| | [Betulaplatyphylla] | | | | | | | | |
| g38412.t1 | Quinone-oxidoreductase-like protein [Medicagotruncatula] | XP_003622874.1 | 99% | 0 | 82% | 0.38 | 1.77 | Vr04 | Enzyme |
| g40940.t1 | Glutelin type-A 1 [Glycine soja] | KHN22001.1 | 78% | 6.00E-52 | 85% | 0.37 | 28.08 | scaffold_518 | Storage protein |
| g9368.t1 | Pyrroline-5-carboxylate reductase 1 [Theobroma cacao] | XP_007043605.1 | 86% | 2.00E-46 | 73% | 0.37 | 8.97 | scaffold_86 | Enzyme |
| g5216.t1 | Unknow | | | | | 0.37 | 15.29 | Vr07 | Unknow |
| g22294.t1 | Phytochrome-associated serine/threonine protein phosphatase [Glycine soja] | KHN37342.1 | 99% | 0 | 99% | 0.37 | 7.18 | Vr08 | Enzyme |
| g38064.t1 | Aquaporin SIP1-2 [Glycine soja] | KHN08172.1 | 99% | 5.00E-92 | 69% | 0.37 | 3.99 | Vr01 | Transporter |
| g8361.t2 | Alpha-N-acetylglucosaminidase [Glycine soja] | KHN19340.1 | 87% | 0 | 89% | 0.37 | 4.08 | Vr04 | Enzyme |
| g33136.t1 | Non-specific lipid-transfer protein 1 [Vignaradiata var. radiata] | P83434.1 | 78% | 3.00E-56 | 99% | 0.37 | 3509.99 | scaffold_212 | Defense-related protein |
| g16342.t1 | UDP-galactose transporter 2 [Glycine soja] | KHN12124.1 | 98% | 8.00E-167 | 97% | 0.36 | 3.96 | Vr11 | Transporter |
| g20864.t1 | Thioredoxin M-type, chloroplastic [Glycine soja] | KHN44266.1 | 99% | 6.00E-82 | 88% | 0.36 | 5.99 | scaffold_184 | Stress-related |
| g21325.t1 | 1-aminocyclopropane-1-carboxylate oxidase-like protein 3 [Triticumurartu] | EMS57739.1 | 95% | 6.00E-58 | 44% | 0.35 | 5.54 | Vr05 | Enzyme |
| g26751.t1 | Cytochrome P450 monooxygenase CYP76E3 [Glycine max] | ABC68413.1 | 65% | 3.00E-175 | 72% | 0.35 | 1.04 | Vr07 | P450 family |
| g2636.t1 | Unknow | | | | | 0.35 | 15.13 | Vr05 | Unknow |
| g32786.t1 | Gibberellin 20 oxidase 1 [Glycine soja] | KHN32374.1 | 99% | 0 | 80% | 0.35 | 2.43 | Vr07 | Hormone response |
| g7516.t1 | Phosphatidylethanolamine-binding protein [Saussureainvolucrata] | AIT38248.1 | 98% | 2.00E-33 | 49% | 0.34 | 1451.76 | Vr08 | Signal transduction |
| g749.t1 | Putative galactinol--sucrose galactosyltransferase 2 [Glycine soja] | KHN30971.1 | 99% | 0 | 88% | 0.34 | 1.98 | Vr05 | Enzyme |
| g31434.t1 | Transcription factor MYB1R1 [Glycine soja] | KHN11452.1 | 98% | 4.00E-138 | 83% | 0.34 | 18.95 | Vr08 | Gene expression and regulation |
| g8346.t1 | 5-formyltetrahydrofolate cyclo-ligase [Glycine soja] | KHN19357.1 | 99% | 8.00E-121 | 87% | 0.34 | 4.37 | Vr04 | Enzyme |
| g19536.t1 | Histone H3.3 [Arabidopsis thaliana] | NP_001078516.1 | 99% | 1.00E-91 | 100% | 0.33 | 16.62 | Vr02 | Gene expression and regulation |
| g11999.t1 | HMG-1 [Canavaliagladiata] | BAA19156.1 | 74% | 1.00E-56 | 96% | 0.33 | 7.29 | Vr07 | Other |

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| g5635.t1 | Glutathione S-transferase GST 25 [Glycine max] | NP_001235036.1 | 99% | 2.00E-139 | 88% | 0.33 | 2.84 | Vr07 | Enzyme |
| g8336.t1 | Transducin/WD-like repeat-protein [Medicagotruncatula] | KEH32469.1 | 99% | 0 | 87% | 0.32 | 1.67 | Vr04 | Development |
| g10320.t1 | AT-hook DNA-binding protein [Catharanthusroseus] | ABL63119.1 | 62% | 7.00E-50 | 91% | 0.32 | 8.06 | Vr08 | Gene expression and regulation |
| g19899.t2 | 5'-adenylylsulfate reductase 1, chloroplastic-like [Glycine max] | XP_003546156.1 | 93% | 0 | 73% | 0.32 | 2.51 | Vr10 | Enzyme |
| g15187.t2 | Pentatricopeptide repeat-containing protein [Glycine soja] | KHN36495.1 | 99% | 0 | 86% | 0.32 | 1.20 | scaffold_234 | Gene expression and regulation |
| g39969.t1 | Sulfate transporter 1.3-like isoform X1 [Glycine max] | XP_003543770.2 | 99% | 0 | 94% | 0.31 | 0.86 | Vr06 | Transporter |
| g13576.t1 | DNA-directed RNA polymerases IV and V subunit 4-like [Glycine max] | XP_003534990.1 | 88% | 2.00E-69 | 74% | 0.31 | 1.93 | Vr10 | Enzyme |
| g5964.t1 | CASP-like protein Os03g0767900-like [Glycine max] | XP_003537907.1 | 85% | 4.00E-53 | 92% | 0.31 | 14.16 | Vr02 | Stress-related |
| g41841.t1 | Myosin heavy chain kinase B-like [Glycine max] | XP_003517744.1 | 85% | 0 | 74% | 0.31 | 4.95 | scaffold_207 | Cell skeleton |
| g4769.t1 | Vacuolar protein sorting-associated protein 20 like 2 [Glycine soja] | KHN09633.1 | 99% | 5.00E-104 | 96% | 0.30 | 11.00 | scaffold_160 | Vacuolar protein |
| g5469.t1 | Histone H3, expressed [Triticumaestivum] | CBH32561.1 | 99% | 6.00E-91 | 99% | 0.29 | 4.04 | Vr04 | Gene expression and regulation |
| g13625.t1 | Enzymatic polyprotein-like [Cicer arietinum] | XP_004499522.1 | 11% | 5.00E-09 | 45% | 0.29 | 0.70 | scaffold_1578 | Other |
| g7147.t1 | 3-ketoacyl-CoA synthase 1-like [Glycine max] | XP_003521822.1 | 99% | 0 | 88% | 0.29 | 22.71 | Vr05 | Enzyme |
| g8362.t1 | Alpha-N-acetylglucosaminidase [Glycine soja] | KHN19339.1 | 92% | 3.00E-173 | 88% | 0.29 | 3.30 | Vr04 | Enzyme |
| g11916.t1 | Glycosyltransferase family 92 protein [Medicagotruncatula] | KEH37330.1 | 98% | 0 | 69% | 0.28 | 0.64 | Vr07 | Enzyme |
| g3665.t1 | Bidirectional sugar transporter SWEET4-like [Glycine max] | XP_003530439.1 | 99% | 9.00E-101 | 72% | 0.27 | 2.47 | Vr07 | Transporter |
| g19899.t1 | 5'-adenylylsulfate reductase 1, chloroplastic-like [Glycine max] | XP_003546156.1 | 94% | 0 | 92% | 0.27 | 5.87 | Vr10 | Enzyme |
| g4750.t1 | Hypothetical protein PHAVU_002G169200g [Phaseolus vulgaris] | XP_007158634.1 | 25% | 0.35 | 74% | 0.24 | 1.97 | scaffold_160 | Unknow |

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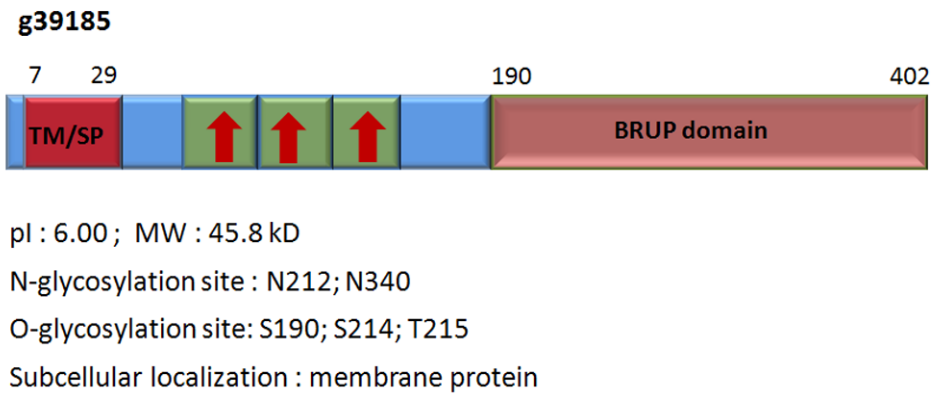
| g18443.t1 | Neoxanthin cleavage Enzyme [Vignaunguiculata] | BAB11932.1 | 99% | 0 | 93% | 0.24 | 0.61 | Vr05 | Enzyme |
| g23630.t1 | Glutelin type-A 1 [Glycine soja] | KHN22001.1 | 55% | 1.00E-34 | 89% | 0.22 | 9.14 | Vr08 | Storage protein |
| g14388.t1 | Male sterility MS5 family protein [Medicagotruncatula] | KEH22820.1 | 99% | 1.00E-169 | 85% | 0.22 | 47.51 | scaffold_324 | Development |
| g33804.t1 | Trihelix transcription factor GT-2-like [Nelumbonucifera] | XP_010249232.1 | 90% | 3.00E-59 | 41% | 0.22 | 1.44 | Vr07 | Gene expression and regulation |
| g8273.t1 | Chlorophyll a-b binding protein P4, chloroplastic [Glycine max] | XP_003527087.2 | 100% | 3.00E-171 | 97% | 0.17 | 1.28 | Vr03 | Development |
| g4498.t1 | Scarecrow-like protein 33 [Glycine soja] | KHN33372.1 | 99% | 0 | 78% | 0.17 | 1.21 | Vr04 | Development |
| g36630.t1 | RING-H2 finger protein ATL51 [Glycine soja] | KHN08798.1 | 99% | 4.00E-102 | 75% | 0.16 | 0.71 | Vr05 | Protein synthesis and digestion |
| g20065.t1 | LisH domain-containing protein C1711.05-like [Citrus sinensis] | XP_006483189.1 | 84% | 9.00E-18 | 42% | 0.15 | 4.64 | Vr07 | Development |
| g20813.t1 | Clathrin assembly protein, putative [Ricinuscommunis] | XP_002527535.1 | 94% | 1.00E-123 | 51% | 0.11 | 0.17 | Vr01 | Other |
| g32572.t1 | UDP-glycosyltransferase 79B6 [Glycine soja] | KHN36711.1 | 98% | 0 | 71% | 0.11 | 0.13 | scaffold_350 | Enzyme |
| g16648.t1 | Gibberellin 20-oxidase [Phaseoluscoccineus] | ACL11802.1 | 99% | 0 | 85% | 0.07 | 0.11 | scaffold_194 | Hormone response |
| g6305.t1 | Unknow | | | | | 0.03 | 0.31 | Vr08 | Unknow |
| g13470.t2 | Fatty acid 2-hydroxylase [Glycine soja] | KHN14310.1 | 65% | 2.00E-25 | 94% | 0.00 | 0.00 | Vr10 | Enzyme |

[a]differential expression genes (ID) were selected with condition of fold change > 5.2 or < 0.35 in Table S2.

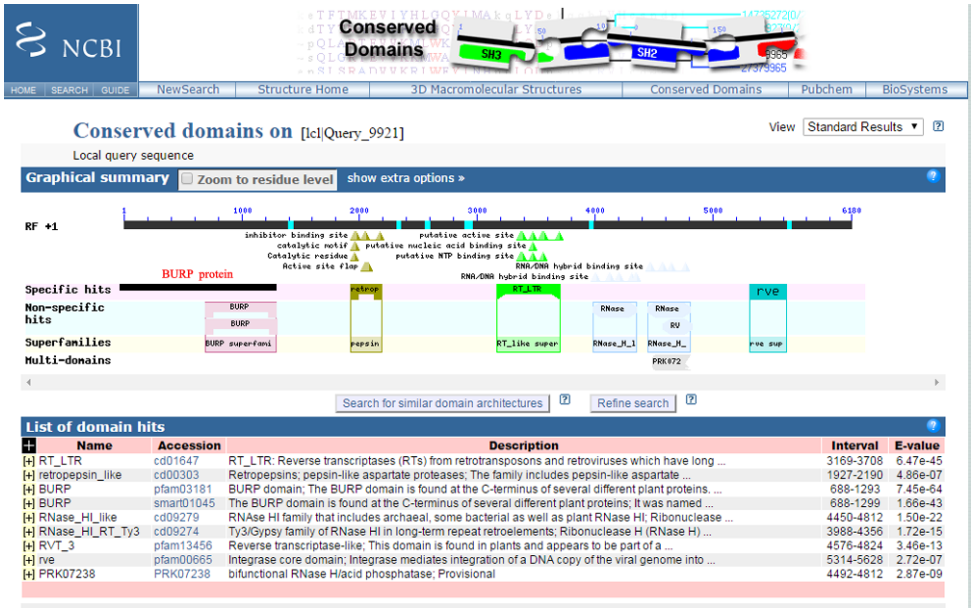
[b]Inf represented the genes expressed in VC6089A, but not in VC1973A.



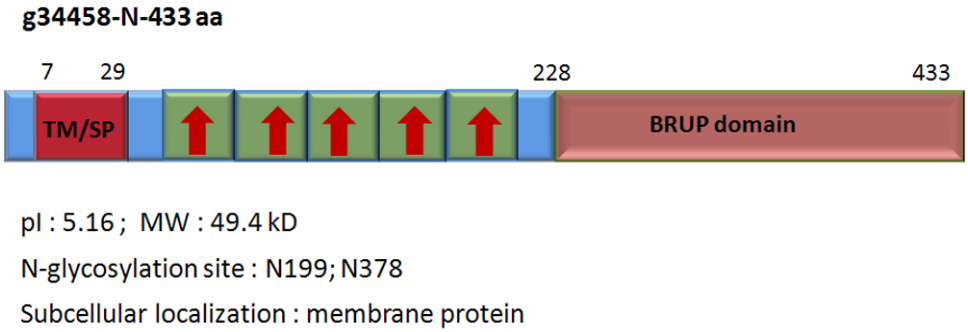

**Supplementary Figure S1. The predicted protein domain and glycosylation sites of resistant specific protein.**

The resistant specific protein contains an N-terminal transmembrane domain/signal peptide (TM/SP, 7-29 residues), near three hydrophilic repeats (red arrows) and C-terminal BURP domain (190-402 residues).

A




B




pI : 5.16 ; MW : 49.4 kD

N-glycosylation site : N199; N378

Subcellular localization : membrane protein

**Supplementary Figure S2. The predicted protein domain and N-glycosylation sites of polyprotein.**

(**A**)The predicted conserved domains of polyprotein (g34458) were analyzed by NCBI. The full length (1299 bases) of the BURP protein (433 residues) indicates with red color. (**B**) The N-terminal BURP protein of polyprotein (g34458) contains an N-terminal transmembrane domain/signal peptide (TM/SP, 7-29 residues), near five hydrophilic repeats (red arrows) and C-terminal BURP domain (228-433 residues).

```
g39815              MEFQCLALFFSLIVILMAAQAALPPEVYWERMLPNTPIPKVIRQFSELDGGQEIASKDEF
N-ter-BURP-g34458   MEFQCLALFFSLIVILMAAQASLPSEVYWERXLPNTPIPKVIRQFSKQDGGKDIASKDEF
                    ********************:** ****** **************: ***::*******

g39815              LLFGSGDKKNKDKLFHFGCGDKKNELQDDVKDISPEDENALLFYTKYANKKNELQDDVQD
N-ter-BURP-g34458   LLFGSGDKKNKDKLLRFGCGDKENKLQDDVQDISPEDENLLLIYDRYAK--NKLQDDLQD
                    **************::******:*:*****:******** **:* :**:  *:****:**

g39815              ISPEDENALLFYTKYANKKNELQDDVQDISPEDENALLLYTKYAN---------------
N-ter-BURP-g34458   ISPEDENFLLFYDRYAK--NKLQDDVQDISPEDENLLLFYDRYAKNKLQDNVQDISPEDE
                    ******* **** :**:  *:************** **:* :**:

g39815              ---------------------------KKNGVVLRRIGPIVNHHHHDHLKPSNFFSEERL
N-ter-BURP-g34458   NLLDYEKSKLQDDVQDISPEDENLSGYKKNGVVLRGIGPIANHHHHDHLKPSSYFSEEGL
                                                ******** ****.***********.:**** *

g39815              RRGAKLDVLFRKRNFSTPLLTREIAEHLPFSSEKINEILEILAVKPDSKDAKNVEETLNH
N-ter-BURP-g34458   RRGAKLVMLFHKRKFSTPLLTREIAEHLPFSSEKINEILEILAVKPDSKNAKNVEKTLNN
                    ****** :**:**:************************************:*****:***.

g39815              CEKPALKGEEKQCATSVESMVDFVTSKLGNNARVTSTELEIGSKFQKFIVKDGVKILAEE
N-ter-BURP-g34458   CEEPALKGEEKHCATSVESMVDFVTSKLGNNARVTSTELEIESKFQKFIVKDGVKILAEE
                    **:********:****************************** ******************

g39815              KIIACHPMSYPYVVFYCHKMANSTAHFLPLEGEDGTRVKAVAICHKDTSQWDPHHVAFQV
N-ter-BURP-g34458   EIIACHPMSYPYVVFYCHKMSNSTAHVVPLEGEDGTRVKAIVICHKDTSQWDPDHVAFQV
                    :********************:*****.:************:.***********.******

g39815              LKVKPGTSSACHFFPEGHLVWYAK
N-ter-BURP-g34458   LKVKPGTSPVCHFFPND-------
                    ******** .*****:
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**Supplementary Figure S3. Alignment of amino acid sequences of g39185 and N-terminal BURP protein of polyprotein (g34458).** Amino acid sequences of g39185 and N-terminal BURP protein of g34458 were aligned using the ClustalW program. The transmembrane domains/signal peptides are indicated by a red box. The blue line represents the BURP domain. The symbols “*”, “:”, and “.” represent identity, strong similarity, and weak similarity, respectively.