# S6 Table. Top list of significant DEGs in the three samples

## Top 50 DGEs con:wat6-up

| Gene_ID | Reads1 | RPKM1 | Reads2 | RPKM2 | Log2 | Pvalue | FDR | NR ref | Description |
|---|---|---|---|---|---|---|---|---|---|
| Vr39448_c0_seq1 | 0 | 0.00 | 973 | 53.6 | NA | 0 | 0 | XP_004500339.1 | cationic peroxidase 1-like [Cicer arietinum] |
| Vr44006_c0_seq1 | 0 | 0.00 | 489 | 9.79 | NA | 0 | 0 | BAJ22384.1 | terminal flower 1a [Vigna unguiculata] |
| Vr58732_c0_seq1 | 0 | 0.00 | 370 | 6.08 | NA | 0 | 0 | XP_003551178.1 | cationic peroxidase 1-like [Glycine max] |
| Vr69119_c0_seq1 | 0 | 0.00 | 335 | 5.16 | NA | 0 | 0 | XP_003520006.1 | probable pectinesterase 29-like [Glycine max] |
| Vr43029_c0_seq1 | 0 | 0.00 | 197 | 6.19 | NA | 0 | 0 | XP_003529031.1 | patatin group A-3-like [Glycine max] |
| Vr37067_c0_seq4 | 0 | 0.00 | 128 | 1.2 | NA | 0 | 0 | XP_003548678.1 | G-type lectin S-receptor-like serine/threonine-protein kinase |
| Vr35851_c0_seq1 | 825 | 11.60 | 43774 | 752 | -6.02 | 0 | 0 | NP_001237786.1 | Kunitz trypsin protease inhibitor precursor [Glycine max] |
| Vr38231_c0_seq1 | 1125 | 17.01 | 29772 | 550 | -5.02 | 0 | 0 | NP_001235010.1 | uncharacterized protein LOC100500484 precursor [Glycine max] |
| Vr35207_c0_seq2 | 668 | 7.68 | 18340 | 258 | -5.07 | 1.6E-11 | 1.1E-10 | XP_003537598.1 | isoflavone reductase-like [Glycine max] |
| Vr38993_c0_seq1 | 509 | 3.90 | 15083 | 141 | -5.18 | 9.5E-12 | 6.4E-11 | NP_001240000.1 | isoflavone 2'-hydroxylase-like [Glycine max] |
| Vr31128_c0_seq2 | 366 | 4.20 | 12075 | 169 | -5.33 | 4.7E-12 | 3.3E-11 | XP_003547616.1 | cationic peroxidase 2-like [Glycine max] |
| Vr39039_c0_seq1 | 52 | 0.82 | 10890 | 210 | -8.00 | 6.2E-14 | 4.9E-13 | ADX66343.1 | pathogenesis-related protein [Glycine max] |
| Vr36526_c0_seq1 | 174.5 | 6.49 | 10690 | 486 | -6.23 | 5.8E-13 | 4.4E-12 | ABS70717.1 | pathogen-related protein [Vigna angularis] |
| Vr40472_c0_seq1 | 109 | 1.22 | 7732 | 106 | -6.44 | 0 | 0 | CAA61279.1 | basic chitinase class 3 [Vigna unguiculata] |
| Vr22610_c0_seq1 | 13 | 0.19 | 7681 | 140 | -9.50 | 0 | 0 | XP_003544327.1 | cationic peroxidase 1-like [Glycine max] |
| Vr39180_c0_seq1 | 2 | 0.04 | 6952 | 155 | -12.05 | 1.6E-15 | 1.3E-14 | XP_003538325.1 | cationic peroxidase 1-like [Glycine max] |
| Vr34333_c0_seq1 | 170 | 2.00 | 6546 | 94.3 | -5.56 | 6.2E-13 | 4.7E-12 | NP_001236116.1 | uncharacterized protein LOC100500048 precursor [Glycine max] |
| Vr39339_c0_seq1 | 227 | 2.28 | 6519 | 80.2 | -5.13 | 7.2E-13 | 5.4E-12 | NP_001236520.1 | vestitone reductase [Glycine max] |
| Vr35930_c0_seq1 | 165 | 2.51 | 6102 | 114 | -5.50 | 7.6E-13 | 5.7E-12 | NP_001236934.1 | uncharacterized protein LOC100500621 precursor [Glycine max] |
| Vr39225_c0_seq1 | 133 | 2.02 | 5616 | 104 | -5.69 | 6.4E-13 | 4.9E-12 | XP_003534655.1 | cationic peroxidase 1-like [Glycine max] |
| Vr36176_c0_seq1 | 95 | 0.90 | 5444 | 63.3 | -6.13 | 0 | 0 | XP_003529158.1 | leucoanthocyanidin dioxygenase-like [Glycine max] |
| Vr39450_c0_seq1 | 136 | 2.21 | 5138 | 102 | -5.53 | 6.9E-13 | 5.2E-12 | XP_003533952.1 | 21 kDa protein-like [Glycine max] |
| Vr13687_c0_seq1 | 77 | 0.47 | 4326 | 32.1 | -6.10 | 0 | 0 | XP_003531311.1 | low affinity cationic amino acid transporter 2-like [Glycine max] |
| Vr42500_c0_seq1 | 156 | 1.32 | 4293 | 44.5 | -5.07 | 1.3E-12 | 9.8E-12 | XP_003547675.1 | lysine histidine transporter 1-like [Glycine max] |
| Vr41972_c0_seq1 | 93 | 1.04 | 3151 | 43.1 | -5.37 | 0 | 0 | XP_003536550.1 | thiazole biosynthetic enzyme, chloroplastic-like [Glycine max] |
| Vr42108_c0_seq1 | 6 | 0.11 | 3129 | 69.2 | -9.32 | 0 | 0 | NP_001238339.1 | uncharacterized protein LOC100527589 [Glycine max] |
| Vr41271_c0_seq1 | 66 | 0.83 | 2487 | 38.4 | -5.53 | 0 | 0 | ACM89628.1 | TIR-NBS-LRR type disease resistance protein [Glycine max] |
| Vr41725_c0_seq1 | 45 | 0.59 | 1929 | 31 | -5.71 | 6.3E-14 | 5E-13 | NP_001241518.1 | uncharacterized protein LOC100788713 [Glycine max] |
| Vr36323_c0_seq1 | 35 | 0.31 | 1573 | 17 | -5.78 | 4.5E-14 | 3.6E-13 | XP_003552581.1 | anthocyanin 5-aromatic acyltransferase-like [Glycine max] |
| Vr49784_c0_seq1 | 18 | 0.33 | 1553 | 35.1 | -6.72 | 1.3E-14 | 1.1E-13 | XP_003543377.1 | cysteine-rich repeat secretory protein 38 [Glycine max] |

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|---|---|---|---|---|---|---|---|---|---|
| Vr31555_c0_seq1 | 48 | 0.38 | 1542 | 14.9 | -5.30 | 9.5E-14 | 7.5E-13 | XP_003521608.1 | sex determination protein tasselseed-2-like [Glycine max] |
| Vr13838_c0_seq1 | 11 | 0.08 | 1386 | 12.5 | -7.27 | 0 | 0 | XP_003518665.1 | polygalacturonase At1g48100-like [Glycine max] |
| Vr41762_c0_seq1 | 1 | 0.01 | 1370 | 16.4 | -10.71 | 2.2E-16 | 2E-15 | XP_003556683.1 | polygalacturonase-like [Glycine max] |
| Vr50416_c0_seq1 | 12 | 0.10 | 1313 | 13.3 | -7.06 | 0 | 0 | XP_003548705.1 | D-inositol-3-phosphate glycosyltransferase-like [Glycine max] |
| Vr46027_c0_seq1 | 6 | 0.11 | 1094 | 24.4 | -7.80 | 0 | 0 | NP_001235010.1 | uncharacterized protein LOC100500484 precursor [Glycine max] |
| Vr21159_c0_seq1 | 28 | 0.32 | 1088 | 15.1 | -5.57 | 5.9E-14 | 4.7E-13 | ABN08535.1 | Auxin Efflux Carrier [Medicago truncatula] |
| Vr28474_c0_seq3 | 32 | 0.21 | 1074 | 8.72 | -5.36 | 4.9E-14 | 3.9E-13 | XP_003543367.1 | equilibrative nucleoside transporter 3-like [Glycine max] |
| Vr49226_c0_seq1 | 3 | 0.03 | 1028 | 11.5 | -8.71 | 0 | 0 | XP_003525322.1 | cytochrome P450 716B2-like [Glycine max] |
| Vr46582_c0_seq1 | 8 | 0.14 | 941 | 19.4 | -7.17 | 0 | 0 | NP_001241331.1 | uncharacterized protein LOC100811719 precursor [Glycine max] |
| Vr34208_c0_seq1 | 9 | 0.23 | 889.5 | 27.4 | -6.92 | 1.1E-15 | 9.6E-15 | XP_003537598.1 | isoflavone reductase-like [Glycine max] |
| Vr39778_c0_seq1 | 19 | 0.93 | 802 | 47.8 | -5.69 | 1.8E-14 | 1.5E-13 | XP_003552297.1 | cationic peroxidase 1-like [Glycine max] |
| Vr35894_c0_seq1 | 18 | 0.15 | 699 | 7.02 | -5.57 | 1.3E-14 | 1.1E-13 | XP_003520743.1 | probable pectinesterase/pectinesterase inhibitor 7-like [Glycine max] |
| Vr53527_c0_seq1 | 17 | 0.21 | 658 | 9.91 | -5.56 | 5.6E-15 | 4.7E-14 | XP_003538484.1 | abscisic acid receptor PYL6-like [Glycine max] |
| Vr48273_c0_seq1 | 2.5 | 0.07 | 624 | 21.5 | -8.25 | 1.6E-15 | 1.3E-14 | BAA92940.1 | yieldin precursor [Vigna unguiculata] |
| Vr45385_c0_seq1 | 14 | 0.11 | 617 | 5.71 | -5.75 | 0 | 0 | BAA19161.1 | 1-aminocyclopropane-1-carboxylate synthase [Vigna radiata var. radiata] |
| Vr45777_c0_seq1 | 22 | 0.31 | 609 | 10.4 | -5.08 | 3.4E-14 | 2.7E-13 | XP_003548263.1 | 4,5-DOPA dioxygenase extradiol-like protein-like [Glycine max] |
| Vr45152_c0_seq1 | 22 | 0.39 | 607 | 13.1 | -5.08 | 3.4E-14 | 2.7E-13 | XP_003527180.1 | blue copper protein-like [Glycine max] |
| Vr44274_c0_seq1 | 12 | 0.58 | 605 | 35.6 | -5.95 | 0 | 0 | AAM12529.1 | chalcone reductase [Pueraria montana var. lobata] |
| Vr50284_c0_seq1 | 4 | 0.05 | 534 | 8.41 | -7.35 | 2.2E-16 | 2E-15 | XP_003524361.1 | expansin-like B1-like [Glycine max] |
| Vr59439_c0_seq1 | 2 | 0.02 | 522 | 6.85 | -8.32 | 1.6E-15 | 1.3E-14 | XP_003546286.1 | reticuline oxidase-like protein-like [Glycine max] |
| Vr34971_c0_seq1 | 6195 | 96.16 | 1E+05 | 2679 | -4.80 | 2.8E-10 | 1.6E-09 | XP_003548287.1 | trypsin inhibitor A-like [Glycine max] |
| Vr38156_c0_seq1 | 4981 | 36.71 | 91843 | 827 | -4.49 | 3E-11 | 1.9E-10 | ACC77194.1 | isoflavone synthase 1 [Vigna unguiculata] |
| Vr36280_c0_seq2 | 4779 | 38.56 | 83481 | 823 | -4.42 | 0 | 0 | XP_003539343.1 | anthocyanin 3'-O-beta-glucosyltransferase-like [Glycine max] |

## Top 50 DGEs con:wat6-down

| Gene_ID | Reads1 -con | RPKM1 | Reads2 -wat6 | RPKM2 | Log2 | Pvalue | FDR | NR references | description |
|---|---|---|---|---|---|---|---|---|---|
| Vr22942_c0_seq1 | 209 | 2.20 | 0 | 0.00 | NA | 6.05E-55 | 9.57E-54 | XP_003520521.1 | polygalacturonase-like [Glycine max] |
| Vr175308_c0_seq1 | 197 | 7.32 | 0 | 0.00 | NA | 7.89E-52 | 1.22E-50 | XP_003526623.1 | auxin-induced protein 5NG4-like [Glycine max] |
| Vr108548_c0_seq1 | 176 | 11.43 | 0 | 0.00 | NA | 2.23E-46 | 3.27E-45 | ABG56534.1\| | polyprotein precursor [Bean common mosaic virus] |
| Vr123225_c0_seq1 | 167 | 11.23 | 0 | 0.00 | NA | 8.81E-44 | 1.25E-42 | AGS41513.1 | HC-Pro, partial [Bean common mosaic virus strain peanut stripe] |
| Vr754819_c0_seq1 | 107 | 1.17 | 0 | 0.00 | NA | 1.83E-28 | 2.11E-27 | XP_003548659.1 | transcription factor bHLH91-like [Glycine max] |

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|---|---|---|---|---|---|---|---|---|---|
| Vr30105_c0_seq1 | 103 | 6.01 | 0 | 0.00 | NA | 2E-27 | 2.25E-26 | XP_003541676.1 | serine carboxypeptidase-like 12-like [Glycine max] |
| Vr39799_c0_seq1 | 21964 | 249.38 | 377 | 5.23 | 5.57 | 0 | 0 | ABH02878.1 | MYB transcription factor MYB134 [Glycine max] |
| Vr41217_c0_seq1 | 16245 | 142.63 | 474 | 5.09 | 4.81 | 0 | 0 | ACJ61246.1 | serine glyoxylate aminotransferase 2 [Glycine max] |
| Vr40489_c0_seq1 | 13321 | 223.86 | 200 | 4.11 | 5.77 | 0 | 0 | NP_001236400.1\| | MYB transcription factor MYB114 [Glycine max] |
| Vr38043_c0_seq1 | 12585 | 19.59 | 8 | 0.02 | 10.33 | 0 | 0 | ACE95704.1 | polyprotein precursor [Bean common mosaic virus] |
| Vr15096_c0_seq1 | 10976 | 70.99 | 364 | 2.88 | 4.62 | 0 | 0 | XP_003544189.1 | probable E3 ubiquitin-protein ligase HERC1-like [Glycine max] |
| Vr33063_c0_seq2 | 8706 | 28.73 | 270 | 1.09 | 4.72 | 0 | 0 | XP_004512150.1 | histidine kinase 1-like isoform X2 [Cicer arietinum] |
| Vr40796_c0_seq1 | 5243 | 57.69 | 153 | 2.06 | 4.81 | | 0 | XP_003549537.1 | heat shock 70 kDa protein-like [Glycine max] |
| Vr50534_c0_seq1 | 4847 | 28.21 | 226 | 1.61 | 4.13 | 0 | 0 | XP_003519092.1 | ABC transporter G family member 22-like [Glycine max] |
| Vr13836_c0_seq2 | 4622 | 75.72 | 84 | 1.68 | 5.49 | 0 | 0 | ABH02918.1 | MYB transcription factor MYB114 [Glycine max] |
| Vr48206_c0_seq1 | 3644 | 65.60 | 153 | 3.37 | 4.28 | 0 | 0 | XP_003523924.1 | auxin-induced protein 5NG4-like [Glycine max] |
| Vr55469_c0_seq1 | 3578 | 27.63 | 74 | 0.70 | 5.31 | 0 | 0 | XP_003537193.1 | auxin-induced protein 5NG4-like isoform 1 [Glycine max] |
| Vr56588_c0_seq1 | 2173 | 16.46 | 72 | 0.67 | 4.63 | 0 | 0 | AAO83155.1 | putative organic cation transport protein [Phaseolus vulgaris] |
| Vr55489_c0_seq1 | 2101 | 23.85 | 97 | 1.35 | 4.15 | 0 | 0 | XP_003529644.1 | S-type anion channel SLAH1-like [Glycine max] |
| Vr24590_c0_seq1 | 2030 | 13.88 | 28 | 0.23 | 5.89 | 0 | 0 | XP_003535586.1 | S-type anion channel SLAH3-like [Glycine max] |
| Vr28255_c0_seq1 | 1388 | 11.09 | 39 | 0.38 | 4.86 | 4.8E-298 | 1.6E-296 | XP_003539445.1 | lysosomal Pro-X carboxypeptidase-like [Glycine max] |
| Vr14132_c0_seq1 | 1308 | 14.39 | 59 | 0.79 | 4.18 | 2.3E-256 | 7.2E-255 | XP_002304053.1 | predicted protein [Populus trichocarpa] |
| Vr42894_c0_seq1 | 1211 | 19.88 | 48 | 0.96 | 4.37 | 2.2E-244 | 6.9E-243 | XP_003549537.1 | heat shock 70 kDa protein-like [Glycine max] |
| Vr54849_c0_seq1 | 902 | 18.45 | 36 | 0.90 | 4.36 | 3.6E-182 | 9.8E-181 | XP_003523141.1 | calcium-binding protein CML38-like [Glycine max] |
| Vr37145_c0_seq1 | 808 | 7.32 | 24 | 0.27 | 4.78 | 1.3E-172 | 3.5E-171 | NP_001236165.1 | cytochrome P450 71D10 [Glycine max] |
| Vr27182_c0_seq1 | 806 | 6.18 | 21 | 0.20 | 4.97 | 9.6E-176 | 2.6E-174 | XP_003529007.1 | protein WAX2-like [Glycine max] |
| Vr112545_c0_seq1 | 753 | 12.39 | 14 | 0.28 | 5.46 | 1.3E-171 | 3.4E-170 | XP_003529396.1 | ethylene-responsive transcription factor ERF109-like [Glycine max] |
| Vr35442_c0_seq1 | 730 | 16.72 | 14 | 0.39 | 5.41 | 7.8E-166 | 2.1E-164 | AAF81194.1 | LEA-18 [Phaseolus vulgaris] |
| Vr50845_c0_seq1 | 726 | 16.18 | 15 | 0.41 | 5.31 | 1.8E-163 | 4.6E-162 | XP_003531926.1 | 3-ketoacyl-CoA synthase 6-like [Glycine max] |
| Vr77281_c0_seq1 | 709 | 19.03 | 26 | 0.85 | 4.48 | 5.2E-146 | 1.3E-144 | XP_003538774.1 | nitrate transporter 1.5-like [Glycine max] |
| Vr51893_c0_seq1 | 694 | 19.39 | 25 | 0.85 | 4.51 | 1.9E-143 | 4.7E-142 | ACZ51240.1 | 3-ketoacyl-CoA synthase [Arachis hypogaea] |
| Vr71314_c0_seq1 | 673 | 13.19 | 25 | 0.60 | 4.46 | 2.5E-138 | 6.2E-137 | XP_003538534.1 | cysteine proteinase inhibitor 2 [Glycine max] |
| Vr46055_c0_seq1 | 672 | 8.55 | 31 | 0.48 | 4.15 | 8.3E-132 | 2E-130 | XP_003538574.1 | small heat shock protein, chloroplastic-like [Glycine max] |
| Vr22084_c0_seq1 | 645 | 8.78 | 4 | 0.07 | 7.04 | 1.2E-159 | 3.1E-158 | XP_003516973.1 | UPF0098 protein MTH_273-like [Glycine max] |
| Vr15106_c0_seq1 | 602 | 15.34 | 30 | 0.93 | 4.04 | 4.9E-116 | 1.1E-114 | NP_001241449.1 | uncharacterized protein LOC100775900 [Glycine max] |
| Vr72294_c0_seq1 | 529 | 11.23 | 15 | 0.39 | 4.85 | 2.3E-114 | 5.2E-113 | XP_003538774.1\| | nitrate transporter 1.5-like [Glycine max] |
| Vr10403_c0_seq1 | 506 | 8.13 | 25 | 0.49 | 4.05 | 5.5E-98 | 1.15E-96 | XP_003522798.1 | sugar transport protein 5-like [Glycine max] |
| Vr32314_c0_seq1 | 146470 | 1096.47 | 9745 | 89.17 | 3.62 | 0 | 0 | CAX94843.1 | myo-inositol 1-phosphate synthase [Phaseolus vulgaris] |

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|---|---|---|---|---|---|---|---|---|---|
| Vr28874_c0_seq9 | 73259 | 300.52 | 3932 | 19.72 | 3.93 | 0 | 0 | XP_003528756.1 | protein LHY [Glycine max] |
| Vr39139_c0_seq1 | 45984 | 283.81 | 3680 | 27.76 | 3.35 | 0 | 0 | XP_003523384.1\| | subtilisin-like protease-like [Glycine max] |
| Vr14424_c0_seq1 | 15783 | 88.89 | 1373 | 9.45 | 3.23 | 0 | 0 | XP_003549515.1 | protein WAX2-like [Glycine max] |
| Vr13806_c0_seq1 | 11403 | 74.71 | 1115 | 8.93 | 3.06 | 0 | 0 | XP_003548314.1 | uncharacterized protein LOC778089 [Glycine max] |
| Vr39861_c0_seq1 | 10124 | 242.94 | 1026 | 30.09 | 3.01 | 0 | 0 | XP_003541070.1 | 21 kDa protein-like [Glycine max] |
| Vr43985_c0_seq1 | 9228 | 76.96 | 904 | 9.22 | 3.06 | 0 | 0 | XP_003549204.1 | putative nuclease HARBI1-like [Glycine max] |
| Vr43431_c0_seq1 | 8805 | 72.74 | 825 | 8.33 | 3.13 | 0 | 0 | NP_001238594.1 | syringolide-induced protein 13-1-1 [Glycine max] |
| Vr36823_c0_seq4 | 7049 | 41.46 | 702 | 5.05 | 3.04 | 0 | 0 | XP_004492929.1 | subtilisin-like protease-like isoform X1 [Cicer arietinum] |
| Vr29009_c0_seq6 | 6073 | 56.56 | 464 | 5.28 | 3.42 | 0 | 0 | XP_003540767.1 | uncharacterized protein LOC100797817 [Glycine max] |
| Vr38900_c0_seq1 | 5313 | 99.19 | 417 | 9.51 | 3.38 | 0 | 0 | XP_003542731.1 | 18.5 kDa class I heat shock protein-like [Glycine max] |
| Vr32665_c0_seq2 | 5083 | 25.15 | 293 | 1.77 | 3.83 | 0 | 0 | XP_003519894.1 | phosphate transporter PHO1-like [Glycine max] |
| Vr36885_c0_seq1 | 4234 | 37.79 | 317 | 3.46 | 3.45 | 0 | 0 | XP_003548043.1 | isoflavone 2'-hydroxylase-like [Glycine max] |
| Vr47011_c0_seq1 | 4080 | 40.82 | 363 | 4.44 | 3.20 | 0 | 0 | XP_003524651.1 | transcription factor HEC1-like [Glycine max] |
| Vr50091_c0_seq1 | 3891 | 55.39 | 304 | 5.29 | 3.39 | 0 | 0 | XP_003533795.1 | ethylene-responsive transcription factor ERF017-like [Glycine max] |
| Vr22806_c0_seq1 | 3879 | 36.92 | 334 | 3.89 | 3.25 | 0 | 0 | XP_003534929.1 | putative nuclease HARBI1-like [Glycine max] |
| Vr44946_c0_seq1 | 3251 | 32.73 | 328 | 4.04 | 3.02 | 0 | 0 | XP_003544508.1 | homeobox-leucine zipper protein HOX19-like [Glycine max] |
| Vr17354_c0_seq1 | 2317 | 22.31 | 232 | 2.73 | 3.03 | 0 | 0 | XP_003545292.1 | phytoene synthase, chloroplastic-like [Glycine max] |

## Top 50 DGEs wat24:wat6-Down

| Gene_ID | Reads1-wat6 | RPKM1 | Reads 2-wat 24 | RPKM2 | Log2 | P-value | FDR | NR | |
|---|---|---|---|---|---|---|---|---|---|
| Vr41972_c0_seq1 | 3151 | 43.11 | 10 | 0.14 | 8.30 | 0 | 0 | XP_003536550.1 | thiazole biosynthetic enzyme, chloroplastic-like [Glycine max] |
| Vr13298_c0_seq1 | 2934 | 61.12 | 83 | 1.73 | 5.14 | 0 | 0 | XP_003594345.1 | hypothetical protein MTR_2g027550 [Medicago truncatula] |
| Vr49846_c0_seq1 | 2439 | 19.96 | 74 | 0.61 | 5.04 | 0 | 0 | NP_001235886.1 | circadian clock-associated FKF1 [Glycine max] |
| Vr34247_c0_seq1 | 1056 | 23.76 | 30 | 0.68 | 5.14 | 5.3E-269 | 1.7E-267 | NP_001239781.1 | uncharacterized protein LOC100782877 [Glycine max] |
| Vr45385_c0_seq1 | 617 | 5.71 | 6 | 0.06 | 6.68 | 2.8E-174 | 8.5E-173 | BAA19161.1 | 1-aminocyclopropane-1-carboxylate synthase [Vigna radiata var. radiata] |
| Vr21502_c0_seq1 | 561 | 9.02 | 6 | 0.10 | 6.55 | 1.1E-157 | 3.4E-156 | XP_003536475.1 | uncharacterized protein LOC100792832 [Glycine max] |
| Vr13406_c0_seq1 | 101800 | 1268.32 | 4898 | 61.06 | 4.38 | 0 | 0 | ACZ74696.1 | formate dehydrogenase [Phaseolus vulgaris] |
| Vr22757_c0_seq3 | 11699 | 187.39 | 620 | 9.94 | 4.24 | 0 | 0 | NP_001235540.1 | uncharacterized protein LOC100305960 [Glycine max] |
| Vr38378_c0_seq1 | 9249 | 205.20 | 375 | 8.33 | 4.62 | 0 | 0 | AAY51975.1 | GIR1 [Vigna radiata] |
| Vr40132_c0_seq1 | 7291 | 157.37 | 334 | 7.21 | 4.45 | 0 | 0 | XP_003551324.1 | uncharacterized protein LOC100811254 [Glycine max] |
| Vr41355_c0_seq1 | 6670 | 66.93 | 302 | 3.03 | 4.46 | 0 | 0 | XP_003547247.1 | beta-glucosidase 47-like [Glycine max] |

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|---|---|---|---|---|---|---|---|---|---|
| Vr32306_c0_seq1 | 3766 | 51.45 | 160 | 2.19 | 4.56 | 0 | 0 | NP_001242314.1 | uncharacterized protein LOC100820588 [Glycine max] |
| Vr45510_c0_seq1 | 1515 | 18.91 | 54 | 0.67 | 4.81 | 0 | 0 | XP_003521784.1 | GDSL esterase/lipase At5g33370-like [Glycine max] |
| Vr42551_c0_seq1 | 1050 | 20.68 | 33 | 0.65 | 4.99 | 1.4E-263 | 4.4E-262 | NP_001238664.1 | uncharacterized protein LOC100500218 [Glycine max] |
| Vr67595_c0_seq1 | 868 | 6.95 | 52 | 0.42 | 4.06 | 6.2E-192 | 1.9E-190 | XP_003526280.1 | probable L-type lectin-domain containing receptor kinase VII.2-like [Glycine max] |
| Vr53207_c0_seq1 | 843 | 21.33 | 50 | 1.27 | 4.07 | 6.2E-187 | 1.9E-185 | XP_003546144.1 | 15.4 kDa class V heat shock protein-like [Glycine max] |
| Vr10963_c0_seq2 | 696 | 7.86 | 40 | 0.45 | 4.12 | 7.6E-156 | 2.2E-154 | XP_003531287.1 | UDP-glycosyltransferase 74F1-like [Glycine max] |
| Vr20800_c0_seq2 | 519 | 8.79 | 30 | 0.51 | 4.11 | 1.8E-116 | 5.3E-115 | XP_003548408.1 | uncharacterized protein LOC100791528 [Glycine max] |
| Vr34550_c0_seq2 | 29551 | 394.94 | 2952 | 39.48 | 3.32 | 0 | 0 | AAW27915.1 | xyloglucan endotransglucosylase/hydrolase precursor [Vigna radiata] |
| Vr23172_c0_seq1 | 21227 | 223.54 | 1912 | 20.15 | 3.47 | 0 | 0 | XP_003518844.1 | benzyl alcohol O-benzoyltransferase-like [Glycine max] |
| Vr37396_c0_seq1 | 18259 | 190.19 | 1665 | 17.35 | 3.45 | 0 | 0 | XP_003520588.1 | LOW QUALITY PROTEIN: cytochrome P450 94A1-like [Glycine max] |
| Vr36176_c0_seq1 | 5444 | 63.33 | 478 | 5.56 | 3.51 | 0 | 0 | XP_003529158.1 | leucoanthocyanidin dioxygenase-like [Glycine max] |
| Vr42461_c0_seq1 | 5259 | 73.63 | 531 | 7.44 | 3.31 | 0 | 0 | XP_003546057.1 | GDSL esterase/lipase At1g29670-like [Glycine max] |
| Vr22359_c0_seq1 | 4255 | 50.17 | 404 | 4.77 | 3.40 | 0 | 0 | XP_003531568.1 | auxin-induced protein 5NG4-like [Glycine max] |
| Vr36822_c0_seq1 | 3653 | 40.93 | 426 | 4.78 | 3.10 | 0 | 0 | AAA87182.1 | auxin-induced protein [Vigna radiata] |
| Vr22565_c0_seq2 | 3414 | 22.05 | 423 | 2.73 | 3.01 | 0 | 0 | ACU23356.1 | unknown [Glycine max] |
| Vr44347_c0_seq1 | 2886 | 40.20 | 301 | 4.20 | 3.26 | 0 | 0 | XP_003520449.1 | leucoanthocyanidin dioxygenase-like [Glycine max] |
| Vr40851_c0_seq1 | 2437 | 85.99 | 206 | 7.27 | 3.56 | 0 | 0 | XP_003522964.1 | uncharacterized protein LOC100500383 [Glycine max] |
| Vr46260_c0_seq1 | 2070 | 28.75 | 201 | 2.79 | 3.36 | 0 | 0 | XP_003534534.1 | 7-methylxanthosine synthase 1-like [Glycine max] |
| Vr42547_c0_seq1 | 1939 | 80.97 | 170 | 7.10 | 3.51 | 0 | 0 | AAK18751.1\| | patatin-like protein [Vigna unguiculata] |
| Vr45762_c0_seq1 | 1747 | 28.34 | 214 | 3.47 | 3.03 | 1E-298 | 3.3E-297 | NP_001240893.1 | uncharacterized protein LOC100790141 [Glycine max] |
| Vr52177_c0_seq1 | 1700 | 24.63 | 125 | 1.81 | 3.76 | 0 | 0 | NP_001248360.1 | expansin-B3-like precursor [Glycine max] |
| Vr41278_c0_seq1 | 1682 | 83.99 | 119 | 5.95 | 3.82 | 0 | 0 | NP_001237144.1 | uncharacterized protein LOC100305819 precursor [Glycine max] |
| Vr39198_c0_seq1 | 1659 | 43.77 | 181 | 4.78 | 3.20 | 6.3E-299 | 2E-297 | O24541.1 | Auxin-induced protein 22C; Aux22c [Vigna radiata] |
| Vr47043_c0_seq1 | 1597 | 39.72 | 106 | 2.64 | 3.91 | 0 | 0 | XP_003537630.1 | auxin-induced protein 15A-like [Glycine max] |
| Vr40704_c0_seq1 | 1571 | 64.61 | 160 | 6.58 | 3.29 | 2.3E-291 | 7.4E-290 | AAK18751.1 | patatin-like protein [Vigna unguiculata] |
| Vr39142_c0_seq1 | 1254 | 45.41 | 136 | 4.94 | 3.20 | 9.9E-227 | 3.1E-225 | O24541.1 | Auxin-induced protein 22C; AltName: Aux22c [Vigna radiata] |
| Vr30665_c0_seq1 | 1211 | 15.24 | 128 | 1.61 | 3.24 | 1.2E-221 | 3.7E-220 | XP_003518070.1 | uncharacterized protein LOC100809248 [Glycine max] |
| Vr42706_c0_seq1 | 1131 | 17.64 | 81 | 1.26 | 3.80 | 1.5E-237 | 4.7E-236 | XP_004494855.1 | uncharacterized protein LOC101493620 [Cicer arietinum] |
| Vr46027_c0_seq1 | 1094 | 24.41 | 80 | 1.79 | 3.77 | 2.1E-228 | 6.5E-227 | NP_001235010.1 | uncharacterized protein LOC100500484 precursor [Glycine max] |
| Vr20019_c0_seq1 | 1082 | 7.32 | 72 | 0.49 | 3.91 | 3.3E-232 | 1E-230 | XP_003528000.1 | two-Vronent response regulator-like PRR95-like [Glycine max] |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| Vr37789_c0_seq1 | 981 | 21.08 | 86 | 1.85 | 3.51 | 3.2E-193 | 9.9E-192 | XP_003534344.1 | auxin-induced protein 10A5-like [Glycine max] |
| Vr34208_c0_seq1 | 890 | 27.39 | 92 | 2.84 | 3.27 | 1.3E-164 | 3.9E-163 | XP_003537598.1 | isoflavone reductase-like [Glycine max] |
| Vr51018_c0_seq1 | 862 | 17.80 | 100 | 2.07 | 3.11 | 4.4E-152 | 1.3E-150 | XP_003528935.1 | uncharacterized protein LOC100795735 [Glycine max] |
| Vr36836_c0_seq3 | 829 | 19.60 | 82 | 1.95 | 3.33 | 2.1E-156 | 6.3E-155 | XP_003533487.1 | auxin-induced protein X10A-like [Glycine max] |
| Vr22989_c0_seq1 | 730 | 8.35 | 75 | 0.86 | 3.28 | 7E-136 | 2E-134 | XP_003517852.1 | UDP-glycosyltransferase 74B1-like [Glycine max] |
| Vr37739_c0_seq2 | 714 | 15.46 | 86 | 1.86 | 3.05 | 3.9E-124 | 1.1E-122 | ADI17229.1 | hypothetical protein [uncultured alpha proteobacterium HF0070_14E07] |
| Vr57190_c0_seq1 | 697 | 9.94 | 52 | 0.74 | 3.74 | 2.9E-145 | 8.5E-144 | XP_003544885.1 | uncharacterized protein LOC100793086 [Glycine max] |
| Vr22629_c0_seq1 | 658 | 12.22 | 64 | 1.19 | 3.36 | 2.6E-125 | 7.5E-124 | XP_003530613.1 | uncharacterized protein LOC100500563 [Glycine max]<br>gb\|ACU15678.1\| unknown [Glycine max] |
| Vr33294_c0_seq1 | 573 | 11.63 | 59 | 1.20 | 3.28 | 6.3E-107 | 1.7E-105 | XP_003535935.1 | calvin cycle protein CP12-like [Glycine max] |
| Vr44933_c0_seq1 | 513 | 10.01 | 40 | 0.78 | 3.68 | 6.8E-106 | 1.9E-104 | XP_003542633.1 | auxin-responsive protein IAA12-like [Glycine max] |
| Vr34844_c1_seq1 | 61856 | 154.98 | 14781 | 37.06 | 2.06 | 0 | 0 | XP_003637074.1 | Cell wall-associated hydrolase, partial [Medicago truncatula] |
| Vr38305_c0_seq1 | 32326 | 597.89 | 7981 | 147.71 | 2.02 | 0 | 0 | P14298.2 | Chalcone--flavonone isomerase; [Phaseolus vulgaris] |
| Vr38333_c0_seq1 | 31984 | 537.03 | 4339 | 72.90 | 2.88 | 0 | 0 | XP_003539812.1 | uncharacterized protein At5g22580-like [Glycine max] |
| Vr38231_c0_seq1 | 29772 | 550.12 | 5015 | 92.73 | 2.57 | 0 | 0 | NP_001235010.1 | uncharacterized protein LOC100500484 precursor [Glycine max] |
| Vr38502_c0_seq1 | 21672 | 302.31 | 4920 | 68.68 | 2.14 | 0 | 0 | XP_003549741.1 | uncharacterized protein LOC100801982 [Glycine max] |

# Top 50 DGEs Wat24:Wat6-Up

| Gene_ID | Reads 1-wat 6 | RPKM1 | Reads2-wat24 | RPKM2 | Log2 | P-value | FDR | NR | Description |
|---|---|---|---|---|---|---|---|---|---|
| Vr68124_c0_seq1 | 0 | 0.00 | 988 | 22.01 | NA | 0 | 0 | P0DI41.1 | VIGUN Casparian strip membrane protein 3 |
| Vr68249_c0_seq1 | 0 | 0.00 | 705 | 18.66 | NA | 0 | 0 | AFK36631.1 | unknown [Medicago truncatula] |
| Vr41572_c0_seq1 | 0 | 0.00 | 438 | 5.81 | NA | 0 | 0 | XP_003554607.1 | auxin-induced protein 5NG4-like [Glycine max] |
| Vr51177_c0_seq1 | 0 | 0.00 | 244 | 4.99 | NA | 0 | 0 | XP_003528524.1 | auxin-binding protein ABP19a-like [Glycine max] |
| Vr19710_c0_seq1 | 0 | 0.00 | 205 | 3.07 | NA | 0 | 0 | CBJ28620.1 | Ribosomal protein L3 [Ectocarpus siliculosus] |
| Vr36832_c0_seq1 | 0 | 0.00 | 188 | 3.01 | NA | 0 | 0 | CBJ31444.1 | Cathepsin L-like proteinase [Ectocarpus siliculosus] |
| Vr17981_c0_seq1 | 0 | 0.00 | 177 | 4.02 | NA | 0 | 0 | NP_001236648.1 | CASP-like protein 1 [Glycine max] |
| Vr118414_c0_seq | 0 | 0.00 | 175 | 2.90 | NA | 0 | 0 | XP_003528650.1 | ethylene-responsive transcription factor ERF086-like [Glycine max] |
| Vr404398_c0_seq | 0 | 0.00 | 141 | 2.81 | NA | 0 | 0 | NP_001239790.1 | uncharacterized protein LOC100778526 precursor [Glycine max] |
| Vr44673_c0_seq1 | 15 | 0.28 | 3255 | 61.19 | -7.76 | 2.66E-15 | 4.34E-14 | XP_003539771.1 | vignain-like [Glycine max] |
| Vr22850_c0_seq1 | 14 | 0.16 | 2822 | 32.99 | -7.66 | 0 | 0 | NP_001241330.1 | uncharacterized protein LOC100808391 [Glycine max] |
| Vr34411_c0_seq1 | 20 | 0.21 | 2782 | 28.56 | -7.12 | 2.35E-14 | 3.69E-13 | XP_003521576.1 | endoglucanase 17-like [Glycine max] |

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|---|---|---|---|---|---|---|---|---|---|
| Vr35020_c0_seq1 | 7 | 0.11 | 1955 | 31.52 | -8.13 | 0 | 0 | XP_003539707.1 | uncharacterized protein LOC100784571 [Glycine max] |
| Vr59584_c0_seq1 | 7 | 0.12 | 1296 | 21.83 | -7.53 | 0 | 0 | XP_003543376.1 | early nodulin-like protein 1-like [Glycine max] |
| Vr36698_c0_seq1 | 4 | 0.09 | 1294 | 29.64 | -8.34 | 0 | 0 | P0DI40.1 | VIGUNCasparian strip membrane protein 2 |
| Vr22476_c0_seq1 | 15 | 0.16 | 1023 | 10.96 | -6.09 | 2.66E-15 | 4.34E-14 | XP_003556105.1 | low-temperature-induced 65 kDa protein-like [Glycine max] |
| Vr35419_c0_seq1 | 20 | 0.26 | 972 | 12.57 | -5.60 | 2.35E-14 | 3.69E-13 | AAU94657. | ef1a [Stramenopile sp. ex Nuclearia delicatula CCAP1552/1] |
| Vr58105_c0_seq1 | 2 | 0.04 | 951 | 16.99 | -8.89 | 0 | 0 | XP_003555719.1 | uncharacterized protein LOC100810925 [Glycine max] |
| Vr35442_c0_seq1 | 14 | 0.39 | 868 | 24.32 | -5.96 | 0 | 0 | AAF81194.1 | LEA-18 [Phaseolus vulgaris] |
| Vr100707_c0_seq | 4 | 0.02 | 511 | 2.29 | -7.00 | 0 | 0 | XP_003524132.1 | LRR receptor-like serine/threonine-protein kinase GSO1-like [Glycine max] |
| Vr22680_c0_seq1 | 1892 | 23.45 | 34863 | 432.38 | -4.20 | 0 | 0 | XP_003529031.1 | patatin group A-3-like [Glycine max] |
| Vr39095_c0_seq1 | 1149 | 14.01 | 25010 | 305.24 | -4.44 | 0 | 0 | XP_003554078.1 | metacaspase-9-like [Glycine max] |
| Vr39799_c0_seq1 | 377 | 5.23 | 8130 | 112.91 | -4.43 | 7.58E-12 | 9.08E-11 | ABH02878.1 | MYB transcription factor MYB134 [Glycine max] |
| Vr15096_c0_seq1 | 364 | 2.88 | 6605 | 52.25 | -4.18 | 7.32E-12 | 8.83E-11 | XP_003544189.1 | probable E3 ubiquitin-protein ligase HERC1-like [Glycine max] |
| Vr43029_c0_seq1 | 197 | 6.19 | 5100 | 160.26 | -4.70 | 2.64E-13 | 3.86E-12 | XP_003529031.1 | patatin group A-3-like [Glycine max] |
| Vr23696_c0_seq1 | 243 | 1.69 | 4951 | 34.48 | -4.35 | 1.6E-12 | 2.11E-11 | XP_003547234.1 | uncharacterized protein LOC100782145 [Glycine max] |
| Vr40489_c0_seq1 | 200 | 4.11 | 4616 | 94.88 | -4.53 | 6.08E-13 | 8.64E-12 | NP_001236400.1 | MYB transcription factor MYB114 [Glycine max] gb\|ABW87009.1\| late elongated hypocotyl and circadian clock associated-1-like protein 2 [Glycine max] |
| Vr40796_c0_seq1 | 153 | 2.06 | 4450 | 59.89 | -4.86 | 8.39E-13 | 1.16E-11 | XP_003549537.1 | heat shock 70 kDa protein-like [Glycine max] |
| Vr24999_c1_seq1 | 90 | 2.05 | 2396 | 54.52 | -4.74 | 0 | 0 | XP_003534948.1 | protein LURP-one-related 6-like [Glycine max] |
| Vr53159_c0_seq1 | 90 | 0.80 | 1914 | 16.95 | -4.41 | 0 | 0 | XP_003539873.1 | isocitrate lyase 2-like [Glycine max] |
| Vr42894_c0_seq1 | 48 | 0.96 | 1432 | 28.76 | -4.90 | 6.73E-14 | 1.01E-12 | XP_003549537.1 | heat shock 70 kDa protein-like [Glycine max] |
| Vr13836_c0_seq2 | 84 | 1.68 | 1369 | 27.43 | -4.03 | 0 | 0 | ABH02918.1 | MYB transcription factor MYB114 [Glycine max] |
| Vr51789_c0_seq1 | 65 | 1.11 | 1125 | 19.15 | -4.11 | 0 | 0 | XP_003540338.1 | protein THYLAKOID FORMATION1, chloroplastic-like [Glycine max] |
| Vr24590_c0_seq1 | 28 | 0.23 | 512 | 4.28 | -4.19 | 5.37E-14 | 8.15E-13 | XP_003535586.1 | S-type anion channel SLAH3-like [Glycine max] |
| Vr38255_c0_seq1 | 9577 | 64.00 | 85379 | 570.89 | -3.16 | 0 | 0 | AAA92063.1 | cysteinyl endopeptidase [Vigna radiata] |
| Vr38664_c0_seq1 | 3003 | 43.67 | 31249 | 454.75 | -3.38 | 1.01E-10 | 9.98E-10 | XP_003540200.1 | serine carboxypeptidase-like 48-like [Glycine max] |
| Vr36096_c0_seq1 | 2660 | 24.31 | 29102 | 266.09 | -3.45 | 0 | 0 | XP_003544396.1 | galactose oxidase-like [Glycine max] |
| Vr36446_c0_seq1 | 1372 | 7.64 | 15451 | 86.10 | -3.49 | 0 | 0 | XP_003516513.1 | subtilisin-like protease-like [Glycine max] |
| Vr14990_c0_seq1 | 1128 | 8.55 | 15322 | 116.17 | -3.76 | 0 | 0 | XP_003555206.1 | hippocampus abundant transcript 1 protein-like [Glycine max] |
| Vr39702_c0_seq1 | 1066 | 14.00 | 14742 | 193.76 | -3.79 | 0 | 0 | XP_003519813.1 | auxin-induced protein 5NG4-like [Glycine max] |
| Vr34889_c0_seq1 | 1143 | 19.33 | 13312 | 225.24 | -3.54 | 0 | 0 | P29024.1 | Acidic endochitinase; Flags: Precursor |
| Vr13808_c0_seq1 | 579 | 8.82 | 8271 | 126.02 | -3.84 | 1.81E-11 | 2E-10 | NP_001235325.1 | endonuclease [Glycine max] |
| Vr34289_c0_seq2 | 698 | 11.61 | 7644 | 127.20 | -3.45 | 3.47E-12 | 4.4E-11 | XP_002523505.1 | apolipoprotein d, putative [Ricinus communis] |

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|---|---|---|---|---|---|---|---|---|---|
| Vr41941_c0_seq1 | 591 | 6.27 | 4983 | 52.92 | -3.08 | 1.82E-11 | 2E-10 | XP_003533818.1 | CBL-interacting serine/threonine-protein kinase 1-like [Glycine max] |
| Vr41217_c0_seq1 | 474 | 5.09 | 4775 | 51.28 | -3.33 | 1.02E-11 | 1.18E-10 | ACJ61246.1 | serine glyoxylate aminotransferase 2 [Glycine max] |
| Vr35961_c0_seq6 | 295 | 1.18 | 4115 | 16.47 | -3.80 | 2.32E-12 | 2.99E-11 | XP_003527521.1 | probable nucleoredoxin 2-like isoform 2 [Glycine max] |
| Vr38900_c0_seq1 | 417 | 9.51 | 4064 | 92.80 | -3.29 | 7.17E-12 | 8.68E-11 | XP_003542731.1 | 18.5 kDa class I heat shock protein-like [Glycine max] |
| Vr39642_c0_seq1 | 446 | 17.81 | 3633 | 145.14 | -3.03 | 9.97E-12 | 1.15E-10 | XP_003540200.1 | serine carboxypeptidase-like 48-like [Glycine max] |
| Vr13830_c0_seq1 | 324 | 3.62 | 3295 | 36.83 | -3.35 | 4.18E-12 | 5.26E-11 | XP_003547855.1 | probable calcium-binding protein CML16-like [Glycine max] |
| Vr13152_c0_seq1 | 256 | 3.14 | 3028 | 37.17 | -3.57 | 2.32E-12 | 2.98E-11 | XP_003535208.1 | thaumatin-like protein 1a-like [Glycine max] |
| Vr46251_c0_seq1 | 266 | 2.62 | 2892 | 28.53 | -3.44 | 1.68E-12 | 2.21E-11 | XP_003517028.1 | pectinesterase 2-like [Glycine max] |
| Vr40741_c0_seq1 | 305 | 3.90 | 2650 | 33.94 | -3.12 | 4.1E-12 | 5.16E-11 | XP_003526939.1 | bidirectional sugar transporter SWEET12-like [Glycine max] |
| Vr35212_c0_seq3 | 191 | 1.28 | 2487 | 16.73 | -3.70 | 4.11E-13 | 5.94E-12 | XP_003552931.1 | laccase-3-like [Glycine max] |
| Vr46167_c0_seq1 | 165 | 2.05 | 2086 | 25.96 | -3.66 | 5.3E-13 | 7.57E-12 | XP_003541076.1 | UPF0496 protein At4g34320-like [Glycine max] |
| Vr13168_c0_seq1 | 131 | 2.33 | 2065 | 36.83 | -3.98 | 1.08E-12 | 1.48E-11 | BAB33036.1 | CPRD49 [Vigna unguiculata] |
| Vr44076_c0_seq1 | 161 | 2.35 | 1710 | 24.96 | -3.41 | 9.11E-13 | 1.26E-11 | XP_003546306.1 | desiccation-related protein PCC13-62-like [Glycine max] |

## Top 50 DGEs Con :Wat24 -Up

| Gene_ID | Reads1 | RPKM1 | Reads2 | RPKM2 | Log2 | P-value | FDR | NR | Description |
|---|---|---|---|---|---|---|---|---|---|
| Vr43029_c0_seq1 | 0 | 0 | 5100 | 160.26 | NA | 4.4E-16 | 4.4E-15 | XP_003529031.1 | patatin group A-3-like [Glycine max] |
| Vr39448_c0_seq1 | 0 | 0 | 4245 | 234.11 | NA | 4.4E-16 | 4.4E-15 | XP_004500339.1 | cationic peroxidase 1-like [Cicer arietinum] |
| Vr39419_c0_seq1 | 0 | 0 | 3670 | 79.1797 | NA | 4.4E-16 | 4.4E-15 | ACU24511.1 | unknown [Glycine max] |
| Vr44006_c0_seq1 | 0 | 0 | 2547 | 51.0384 | NA | 4.4E-16 | 4.4E-15 | BAJ22384.1 | terminal flower 1a [Vigna unguiculata] |
| Vr58791_c0_seq1 | 0 | 0 | 1221 | 15.6191 | NA | 4.4E-16 | 4.4E-15 | XP_003529031.1 | patatin group A-3-like [Glycine max] |
| Vr58732_c0_seq1 | 0 | 0 | 787 | 12.9499 | NA | 4.4E-16 | 4.4E-15 | XP_003551178.1 | cationic peroxidase 1-like [Glycine max] |
| Vr114032_c0_seq1 | 0 | 0 | 711 | 14.8541 | NA | 4.4E-16 | 4.4E-15 | gb\|ACG69488.1 | germin-like protein 12 [Glycine max] |
| Vr65533_c0_seq1 | 0 | 0 | 536 | 7.87212 | NA | 4.4E-16 | 4.4E-15 | XP_003518150.1 | ethylene-responsive transcription factor LEP-like [Glycine max] |
| Vr145400_c0_seq1 | 0 | 0 | 420 | 9.2919 | NA | 4.4E-16 | 4.4E-15 | ABP52096.1 | phosphate transporter [Phaseolus vulgaris] |
| Vr69119_c0_seq1 | 0 | 0 | 254 | 3.91682 | NA | 4.4E-16 | 4.4E-15 | XP_003520006.1 | probable pectinesterase 29-like [Glycine max] |
| Vr51177_c0_seq1 | 0 | 0 | 244 | 4.99401 | NA | 4.4E-16 | 4.4E-15 | XP_003528524.1 | auxin-binding protein ABP19a-like [Glycine max] |
| Vr185592_c0_seq1 | 0 | 0 | 237 | 8.84102 | NA | 4.4E-16 | 4.4E-15 | NP_001241164.1 | phosphate transporter 1-7-like [Glycine max] |
| Vr48482_c0_seq1 | 0 | 0 | 207 | 9.75698 | NA | 4.4E-16 | 4.4E-15 | XP_003551393.1 | probable LRR receptor-like serine/threonine-protein kinase At4g26540-like isoform 1 [Glycine max] |
| Vr37067_c0_seq4 | 0 | 0 | 168 | 1.56982 | NA | 4.4E-16 | 4.4E-15 | XP_003548678.1 | G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330-like [Glycine max] |
| Vr64026_c0_seq1 | 0 | 0 | 163 | 6.82563 | NA | 4.4E-16 | 4.4E-15 | XP_003551603.1\| | denine/guanine permease AZG1-like [Glycine max] |
| Vr12323_c0_seq1 | 0 | 0 | 144 | 2.91301 | NA | 4.4E-16 | 4.4E-15 | XP_003545985.1 | polygalacturonase-like [Glycine max] |
| Vr10342_c0_seq1 | 0 | 0 | 141 | 1.62646 | NA | 4.4E-16 | 4.4E-15 | XP_003519899.1\| | cytochrome P450 90B1-like [Glycine max] |

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|---|---|---|---|---|---|---|---|---|---|
| Vr66297_c0_seq1 | 0 | 0 | 135 | 11.9054 | NA | 4.4E-16 | 4.4E-15 | P34952.1 | Chymotrypsin inhibitor ECI |
| Vr16293_c0_seq1 | 0 | 0 | 130 | 2.88943 | NA | 4.4E-16 | 4.4E-15 | NP_001242396.1 | uncharacterized protein LOC100812163 precursor [Glycine max] |
| Vr160743_c0_seq1 | 0 | 0 | 102 | 1.58438 | NA | 4.4E-16 | 4.4E-15 | XP_003541980.1 | transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR-like [Glycine max] |
| Vr34521_c0_seq2 | 2822 | 47.5 | 1E+05 | 2117.22 | -5.477 | 2.7E-11 | 1.8E-10 | AAA66288.1 | proline-rich protein [Glycine max] |
| Vr35851_c0_seq1 | 825 | 11.6 | 46041 | 791.627 | -6.093 | 0 | 0 | NP_001237786.1 | Kunitz trypsin protease inhibitor precursor [Glycine max] |
| Vr22610_c0_seq1 | 13 | 0.19 | 20516 | 372.845 | -10.91 | 0 | 0 | XP_003544327.1 | cationic peroxidase 1-like [Glycine max] |
| Vr31128_c0_seq2 | 366 | 4.2 | 16176 | 226.783 | -5.756 | 4.8E-12 | 3.6E-11 | XP_003547616.1 | cationic peroxidase 2-like [Glycine max] |
| Vr34889_c0_seq1 | 154 | 2.13 | 13312 | 225.243 | -6.724 | 1.4E-12 | 1.1E-11 | P29024.1 | Acidic endochitinase; Flags: Precursor |
| Vr39225_c0_seq1 | 133 | 2.02 | 12040 | 223.697 | -6.791 | 6.3E-13 | 5.2E-12 | XP_003534655.1 | cationic peroxidase 1-like [Glycine max] |
| Vr38890_c0_seq1 | 138 | 1.28 | 10070 | 114.164 | -6.48 | 7.6E-13 | 6.2E-12 | XP_003536300.1 | 7-ethoxycoumarin O-deethylase-like [Glycine max] |
| Vr39450_c0_seq1 | 136 | 2.21 | 8109 | 161.311 | -6.188 | 6.8E-13 | 5.6E-12 | XP_003533952.1 | 21 kDa protein-like [Glycine max] |
| Vr13838_c0_seq1 | 11 | 0.08 | 7752 | 70.0421 | -9.752 | 0 | 0 | XP_003518665.1 | polygalacturonase At1g48100-like [Glycine max] |
| Vr39180_c0_seq1 | 2 | 0.04 | 7480 | 166.842 | -12.16 | 4.4E-16 | 4.4E-15 | XP_003538325.1 | cationic peroxidase 1-like [Glycine max] |
| Vr34333_c0_seq1 | 170 | 2 | 7123 | 102.645 | -5.679 | 6E-13 | 5E-12 | NP_001236116.1 | uncharacterized protein LOC100500048 precursor [Glycine max] |
| Vr36526_c0_seq1 | 174.5 | 6.49 | 5962 | 270.993 | -5.385 | 5.6E-13 | 4.7E-12 | ABS70717.1 | pathogen-related protein [Vigna angularis] |
| Vr39755_c0_seq1 | 92 | 0.86 | 5637 | 64.1347 | -6.228 | 0 | 0 | NP_001238091.1 | polygalacturonase PG1 precursor [Glycine max] |
| Vr40472_c0_seq1 | 109 | 1.22 | 4060 | 55.656 | -5.51 | 0 | 0 | CAA61279.1 | basic chitinase class 3 [Vigna unguiculata] |
| Vr39039_c0_seq1 | 52 | 0.82 | 3989 | 76.9527 | -6.552 | 6.3E-14 | 5.5E-13 | ADX66343.1 | pathogenesis-related protein [Glycine max] |
| Vr44673_c0_seq1 | 82 | 1.26 | 3255 | 61.1892 | -5.601 | 0 | 0 | XP_003539771.1 | vignain-like [Glycine max] |
| Vr46251_c0_seq1 | 30 | 0.24 | 2892 | 28.5278 | -6.882 | 5.4E-14 | 4.8E-13 | XP_003517028.1 | pectinesterase 2-like [Glycine max] |
| Vr22850_c0_seq1 | 88 | 0.84 | 2822 | 32.9898 | -5.294 | 0 | 0 | NP_001241330.1 | uncharacterized protein LOC100808391 [Glycine max] |
| Vr34411_c0_seq1 | 6 | 0.05 | 2782 | 28.5616 | -9.148 | 0 | 0 | XP_003521576.1 | endoglucanase 17-like [Glycine max] |
| Vr41032_c0_seq1 | 51 | 0.79 | 2736 | 51.6866 | -6.036 | 8E-14 | 7E-13 | XP_003535070.1 | peroxidase C3-like isoform 2 [Glycine max] |
| Vr31555_c0_seq1 | 48 | 0.38 | 2186 | 21.0853 | -5.8 | 9.5E-14 | 8.2E-13 | XP_003521608.1 | sex determination protein tasselseed-2-like [Glycine max] |
| Vr40216_c0_seq1 | 47 | 1.2 | 2120 | 66.183 | -5.786 | 8.7E-14 | 7.6E-13 | XP_003535071.1 | peroxidase C3-like isoform 3 [Glycine max] |
| Vr42825_c0_seq1 | 47 | 0.68 | 2087 | 36.8778 | -5.763 | 8.7E-14 | 7.6E-13 | XP_003542895.1 | endo-1,3;1,4-beta-D-glucanase-like [Glycine max] |
| Vr35020_c0_seq1 | 50 | 0.66 | 1955 | 31.5186 | -5.58 | 1E-13 | 8.7E-13 | XP_003539707.1 | uncharacterized protein LOC100784571 [Glycine max] |
| Vr41271_c0_seq1 | 66 | 0.83 | 1918 | 29.6483 | -5.152 | 0 | 0 | ACM89628.1 | TIR-NBS-LRR type disease resistance protein [Glycine max] |
| Vr42199_c0_seq1 | 14 | 0.15 | 1858 | 23.72 | -7.343 | 0 | 0 | XP_003528650.1 | ethylene-responsive transcription factor ERF086-like [Glycine max] |
| Vr41762_c0_seq1 | 1 | 0.01 | 1669 | 20.0373 | -11 | 8.9E-16 | 8.6E-15 | XP_003556683.1 | polygalacturonase-like [Glycine max] |
| Vr45152_c0_seq1 | 22 | 0.39 | 1579 | 33.99 | -6.456 | 3.6E-14 | 3.3E-13 | XP_003527180.1 | blue copper protein-like [Glycine max] |
| Vr39778_c0_seq1 | 19 | 0.93 | 1532 | 91.3324 | -6.624 | 1.7E-14 | 1.6E-13 | XP_003552297.1 | cationic peroxidase 1-like [Glycine max] |

|  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|
| Vr46582_c0_seq1 | 8 | 0.14 | 1486 | 30.6768 | -7.828 | 0 | 0 | NP_001241331.1 | uncharacterized protein LOC100811719 precursor [Glycine max] |
| Vr59584_c0_seq1 | 43 | 0.59 | 1296 | 21.8322 | -5.204 | 7.3E-14 | 6.4E-13 | XP_003543376.1 | early nodulin-like protein 1-like [Glycine max] |
| Vr36698_c0_seq1 | 34 | 0.64 | 1294 | 29.645 | -5.54 | 4.6E-14 | 4.1E-13 | P0DI40.1 | Casparian strip membrane protein 2 |
| Vr50416_c0_seq1 | 12 | 0.1 | 1158 | 11.7687 | -6.883 | 0 | 0 | XP_003548705.1 | D-inositol-3-phosphate glycosyltransferase-like [Glycine max] |
| Vr18948_c0_seq1 | 18 | 0.11 | 1081 | 7.77121 | -6.199 | 1.1E-14 | 1E-13 | XP_003553810.1 | potassium transporter 5-like [Glycine max] |
| Vr44815_c0_seq1 | 37 | 0.24 | 1059 | 8.48303 | -5.13 | 5.1E-14 | 4.5E-13 | XP_003529133.1 | laccase-9-like [Glycine max] |

## Top 50 DGEs Con :Wat24 -Down

| Gene_ID | Length | Reads1 | RPKM1 | Reads2 | RPKM2 | Log2 | P-value | FDR | NR | Description |
|---|---|---|---|---|---|---|---|---|---|---|
| Vr12598_c0_seq1 | 1156 | 506 | 6.85 | 0 | 0.00 | NA | 5.5E-132 | 1.6E-130 | XP_003517303.1 | transcription factor HEC1-like [Glycine max] |
| Vr108548_c0_seq1 | 241 | 176 | 11.43 | 0 | 0.00 | NA | 2.35E-46 | 4.2E-45 | ABG56534.1 | polyprotein precursor [Bean common mosaic virus] |
| Vr123225_c0_seq1 | 232 | 167 | 11.23 | 0 | 0.00 | NA | 9.25E-44 | 1.6E-42 | AGS41513.1 | HC-Pro, partial [Bean common mosaic virus strain peanut stripe] |
| Vr20601_c0_seq1 | 742 | 158 | 3.32 | 0 | 0.00 | NA | 2E-41 | 3.37E-40 | XP_004509731.1 | uncharacterized protein LOC101508712 [Cicer arietinum] |
| Vr34044_c0_seq3 | 587 | 116 | 3.09 | 0 | 0.00 | NA | 8.72E-31 | 1.26E-29 | XP_004492294.1 | uncharacterized protein LOC101515081 [Cicer arietinum] |
| Vr28706_c0_seq1 | 250 | 111 | 6.95 | 0 | 0.00 | NA | 1.73E-29 | 2.45E-28 | AAX82171.1 | polyprotein [Bean common mosaic virus strain peanut stripe] |
| Vr748356_c0_seq1 | 1589 | 105 | 1.03 | 0 | 0.00 | NA | 6.24E-28 | 8.6E-27 | XP_004510150.1 | protein ECERIFERUM 1-like [Cicer arietinum] |
| Vr30105_c0_seq1 | 268 | 103 | 6.01 | 0 | 0.00 | NA | 2.06E-27 | 2.81E-26 | XP_003541676.1 | serine carboxypeptidase-like 12-like [Glycine max] |
| Vr533222_c0_seq1 | 999 | 101 | 1.58 | 0 | 0.00 | NA | 6.81E-27 | 9.18E-26 | XP_003542039.1 | laccase-17-like [Glycine max] |
| Vr38043_c0_seq1 | 10052 | 12585 | 19.59 | 63 | 0.12 | 7.35 | 0 | 0 | ACE95704.1 | polyprotein precursor [Bean common mosaic virus] |
| Vr48206_c0_seq1 | 869 | 3644 | 65.60 | 70 | 1.54 | 5.41 | 0 | 0 | XP_003523924.1 | auxin-induced protein 5NG4-like [Glycine max] |
| Vr27182_c0_seq1 | 2039 | 806 | 6.18 | 8 | 0.08 | 6.36 | 6.2E-194 | 2E-192 | XP_003529007.1 | protein WAX2-like [Glycine max] |
| Vr72740_c0_seq1 | 1426 | 729 | 8.00 | 18 | 0.24 | 5.05 | 3E-160 | 9.1E-159 | XP_003535206.1 | peptide transporter PTR3-A-like [Glycine max] |
| Vr72751_c0_seq1 | 1496 | 699 | 7.31 | 17 | 0.22 | 5.07 | 4.8E-154 | 1.5E-152 | XP_003536954.1 | GDSL esterase/lipase At4g28780-like [Glycine max] |
| Vr22359_c0_seq1 | 1622 | 11841 | 114.22 | 404 | 4.77 | 4.58 | 0 | 0 | XP_003531568.1 | auxin-induced protein 5NG4-like [Glycine max] |
| Vr38378_c0_seq1 | 862 | 7422 | 134.71 | 375 | 8.33 | 4.02 | 0 | 0 | AAY51975.1 | GIR1 [Vigna radiata] |
| Vr13211_c1_seq1 | 1273 | 5205 | 63.97 | 244 | 3.67 | 4.12 | 0 | 0 | XP_003550171.1 | uncharacterized protein LOC100813910 [Glycine max] |
| Vr55469_c0_seq1 | 2026 | 3578 | 27.63 | 141 | 1.33 | 4.37 | 0 | 0 | XP_003537193.1 | auxin-induced protein 5NG4-like isoform 1 [Glycine max] |
| Vr45510_c0_seq1 | 1532 | 1959 | 20.01 | 54 | 0.67 | 4.89 | 0 | 0 | XP_003521784.1 | GDSL esterase/lipase At5g33370-like [Glycine max] |
| Vr101604_c0_seq1 | 1616 | 802 | 7.76 | 33 | 0.39 | 4.31 | 5.2E-161 | 1.6E-159 | XP_003554335.1 | probable pectate lyase 3-like [Glycine max] |
| Vr112545_c0_seq1 | 951 | 753 | 12.39 | 34 | 0.68 | 4.18 | 3.7E-148 | 1.1E-146 | XP_003529396.1 | ethylene-responsive transcription factor ERF109-like [Glycine max] |
| Vr57343_c0_seq1 | 405 | 673 | 26.00 | 33 | 1.56 | 4.06 | 5.5E-130 | 1.6E-128 | NP_001236386.1 | uncharacterized protein LOC100306533 [Glycine max] |
| Vr30607_c0_seq1 | 1539 | 639 | 6.50 | 26 | 0.32 | 4.33 | 6.6E-129 | 1.9E-127 | XP_003553275.1 | GDSL esterase/lipase At5g33370-like [Glycine max] |
| Vr72294_c0_seq1 | 737 | 529 | 11.23 | 23 | 0.60 | 4.23 | 1.9E-105 | 5E-104 | XP_003538774.1 | nitrate transporter 1.5-like [Glycine max] |
| Vr34550_c0_seq2 | 1431 | 40042 | 437.80 | 2952 | 39.48 | 3.47 | 0 | 0 | AAW27915.1 | xyloglucan endotransglucosylase/hydrolase precursor [Vigna radiata] |

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|---|---|---|---|---|---|---|---|---|---|---|
| Vr31512_c0_seq1 | 1405 | 8929 | 99.43 | 661 | 9.00 | 3.47 | 0 | 0 | XP_003533364.1 | transcription factor BEE 3-like [Glycine max] |
| Vr44566_c0_seq1 | 1467 | 6118 | 65.25 | 396 | 5.17 | 3.66 | 0 | 0 | NP_001241603.1 | uncharacterized protein LOC100812537 [Glycine max] |
| Vr36885_c0_seq1 | 1753 | 4234 | 37.79 | 421 | 4.60 | 3.04 | 0 | 0 | XP_003548043.1 | isoflavone 2'-hydroxylase-like [Glycine max] |
| Vr39383_c0_seq1 | 806 | 4139 | 80.34 | 401 | 9.52 | 3.08 | 0 | 0 | XP_003553069.1 | uncharacterized protein LOC100788078 [Glycine max] |
| Vr30665_c0_seq1 | 1520 | 1694 | 17.44 | 128 | 1.61 | 3.44 | 8E-285 | 2.9E-283 | XP_003518070.1 | uncharacterized protein LOC100809248 [Glycine max] |
| Vr44134_c0_seq1 | 1127 | 1520 | 21.10 | 132 | 2.24 | 3.23 | 2E-242 | 6.8E-241 | XP_003534342.1 | indole-3-acetic acid-induced protein ARG7-like [Glycine max] |
| Vr77281_c0_seq1 | 583 | 709 | 19.03 | 44 | 1.44 | 3.72 | 2.8E-128 | 8.1E-127 | XP_003538774.1 | nitrate transporter 1.5-like [Glycine max] |
| Vr14500_c0_seq1 | 1197 | 648 | 8.47 | 60 | 0.96 | 3.14 | 1.3E-101 | 3.5E-100 | XP_003553615.1 | uncharacterized protein LOC100785434 [Glycine max] |
| Vr30229_c0_seq3 | 2272 | 624 | 4.30 | 50 | 0.42 | 3.35 | 9.8E-104 | 2.5E-102 | XP_003525884.1 | transcription factor bHLH25-like [Glycine max] |
| Vr59002_c0_seq1 | 685 | 600 | 13.70 | 56 | 1.56 | 3.13 | 7.13E-94 | 1.78E-92 | ACU17538.1 | unknown [Glycine max] |
| Vr38010_c0_seq4 | 2806 | 503 | 2.80 | 45 | 0.31 | 3.19 | 3.75E-80 | 8.71E-79 | XP_003528365.1 | pleiotropic drug resistance protein 1-like [Glycine max] |
| Vr38147_c0_seq1 | 1608 | 191529 | 1863.56 | 39055 | 464.80 | 2.00 | 0 | 0 | NP_001237601.1 | cationic peroxidase 2 precursor [Glycine max] |
| Vr40878_c0_seq1 | 1582 | 18917 | 187.09 | 2801 | 33.88 | 2.47 | 0 | 0 | AAC49758.1 | gibberellin 20-oxidase [Phaseolus vulgaris] |
| Vr32702_c0_seq1 | 1886 | 14859 | 123.27 | 3015 | 30.59 | 2.01 | 0 | 0 | XP_003519380.1 | uncharacterized acetyltransferase At3g50280 [Glycine max] |
| Vr34855_c0_seq2 | 1659 | 14639 | 138.06 | 1577 | 18.19 | 2.92 | 0 | 0 | XP_003550831.1 | zinc finger Ran-binding domain-containing protein 2-like [Glycine max] |
| Vr13816_c0_seq1 | 3608 | 13084 | 56.74 | 2548 | 13.51 | 2.07 | 0 | 0 | XP_003555774.1 | transcription factor PIF3-like [Glycine max] |
| Vr39199_c0_seq1 | 794 | 12881 | 253.82 | 2396 | 57.75 | 2.14 | 0 | 0 | AFU81504.1 | LEA5-2.1, partial, late embryogenesis abundant [Vigna unguiculata] |
| Vr34116_c0_seq7 | 2268 | 9555 | 65.92 | 1469 | 12.40 | 2.41 | 0 | 0 | XP_003547999.1 | uncharacterized membrane protein YOL092W-like [Glycine max] |
| Vr43985_c0_seq1 | 1876 | 9228 | 76.96 | 1049 | 10.70 | 2.85 | 0 | 0 | XP_003549204.1 | putative nuclease HARBI1-like [Glycine max] |
| Vr28990_c0_seq3 | 3586 | 9216 | 40.21 | 1776 | 9.48 | 2.08 | 0 | 0 | XP_003526176.1 | chitin-inducible gibberellin-responsive protein 1-like [Glycine max] |
| Vr41680_c0_seq1 | 1842 | 8813 | 74.86 | 961 | 9.98 | 2.91 | 0 | 0 | XP_003542412.1 | cytochrome P450 94A2-like [Glycine max] |
| Vr33063_c0_seq2 | 4741 | 8706 | 28.73 | 1443 | 5.82 | 2.30 | 0 | 0 | XP_004512150.1 | histidine kinase 1-like isoform X2 [Cicer arietinum] |
| Vr13792_c0_seq1 | 2255 | 8402 | 58.30 | 1317 | 11.18 | 2.38 | 0 | 0 | XP_003553732.1 | uncharacterized protein LOC100811813 [Glycine max] |
| Vr41811_c0_seq1 | 1779 | 8207 | 72.18 | 1647 | 17.72 | 2.03 | 0 | 0 | XP_003553527.1 | auxin-induced protein 5NG4-like [Glycine max] |
| Vr33482_c1_seq4 | 2171 | 7035 | 50.70 | 1332 | 11.74 | 2.11 | 0 | 0 | NP_001242710.1 | uncharacterized protein LOC100805837 [Glycine max] |