# Drought Stress Triggers the Proteomic Changes Involved in Lignins, Flavonoids and Fatty Acids in Tea Plants

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## Supplementary Table S2. Protein annotation

| Protein accession | Protein description | MW [kDa] | Score | Coverage [%] | Peptides | PSMs | Unique peptides | CK1 | CK2 | CK3 | DT1 | DT2 | DT3 | DT/CK Ratio | DT/CK P value |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL102Contig1_m.19364 | PREDICTED: elongation factor 1-alpha [Juglans regia] | 49.307 | 98.797 | 40 | 20 | 83 | 14 | 0.987 | 0.966 | 0.967 | 1.004 | 1.016 | 1.028 | 1.044 | 1.18E-02 |
| cds.CL1030Contig1_m.1728 | PREDICTED: myosin-11 [Jatropha curcas] | 121.45 | 7.0306 | 3.7 | 4 | 4 | 4 | 1.026 | 1.075 | 1.026 | 0.93 | 0.953 | 0.984 | 0.917 | 1.83E-02 |
| cds.CL1053Contig1_m.23076 |  | 46.32 | 10.38 | 13.5 | 5 | 5 | 5 | 0.985 | 0.956 | 0.974 | 1.037 | 1.022 | 1.068 | 1.073 | 1.09E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL106Contig2_m.1683 | PREDICTED: serine/arginine-rich splicing factor SC35-like [Ipomoea nil] | 31.737 | 2.4863 | 4.4 | 1 | 1 | 1 | 1.041 | 0.996 | 0.975 | 1.009 | 1.019 | 0.966 | 0.994 | 8.28E-01 |
| cds.CL1156Contig1_m.12309 | PREDICTED: probable aminopyrimidine aminohydrolase, mitochondrial isoform X2 [Pyrus x bretschnei | 44.766 | 8.0998 | 8.6 | 4 | 5 | 3 | 0.972 | 0.95 | 1.004 | 1.042 | 1.014 | 1.12 | 1.085 | 7.33E-02 |
| cds.CL1156Contig1_m.12310 | PREDICTED: probable aminopyrimidine aminohydrolase, mitochondrial isoform X2 [Vitis | 26.967 | 7.3566 | 8.8 | 2 | 3 | 1 | 1.019 | 0.892 | 0.973 | 1.004 | 1.087 | 1.041 | 1.086 | 1.39E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL116Contig1_m.2773 | PREDICTED: alanine--tRNA ligase, chloroplastic/mitochondrial [Vitis vinifera] | 39.694 | 13.502 | 16.5 | 6 | 6 | 4 | 1.018 | 1.095 | 0.974 | 1.013 | 0.991 | 0.918 | 0.947 | 2.95E-01 |
| cds.CL116Contig1_m.2777 | PREDICTED: probable alanine--tRNA ligase, chloroplastic [Jatropha curcas] | 12.511 | 27.73 | 27 | 3 | 3 | 3 | 0.942 | 1.037 | 1.044 | 0.978 | 1.027 | 0.987 | 0.99 | 8.08E-01 |
| cds.CL1177Contig1_m.9340 | PREDICTED: ubiquitin carboxyl-terminal hydrolase MINDY-2 isoform X1 [Vitis vinifera] | 62.451 | 6.3082 | 7.4 | 4 | 4 | 3 | 0.992 | 1.008 | 1.024 | 1.015 | 1.014 | 0.968 | 0.991 | 6.41E-01 |
| cds.CL117Contig1_m.44135 | PREDICTED: actin-7-like [Fragaria vesca subsp. vesca] | 24.496 | 8.0323 | 48 | 10 | 83 | 0 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL1185Contig1_m.11093 | PREDICTED: factor of DNA methylation 1 isoform X2 [Vitis vinifera] | 73.837 | 2.2803 | 2.1 | 1 | 1 | 1 | 1.067 | 1.101 | 1.142 | 0.956 | 0.858 | 0.858 | 0.807 | 6.34E-03 |
| cds.CL1210Contig1_m.9829 | PREDICTED: serine protease SPPA, chloroplastic [Vitis vinifera] | 77.864 | 82.858 | 26 | 18 | 24 | 18 | 1.023 | 1.064 | 1.026 | 0.942 | 0.934 | 0.995 | 0.922 | 2.60E-02 |
| cds.CL1253Contig1_m.16152 | PREDICTED: acidic leucine-rich nuclear phosphoprotein 32-related protein [Vitis vinifera] | 52.56 | 9.4981 | 3.4 | 1 | 1 | 1 | | | | | | | | |
| cds.CL1254Contig1_m.23559 | PREDICTED: serine carboxypeptidase-like 51 [Sesamum indicum] | 27.468 | 8.0864 | 16.5 | 5 | 6 | 5 | 0.942 | 0.954 | 0.947 | 1.077 | 1.035 | 1.004 | 1.096 | 1.15E-02 |
| cds.CL127Contig1_m.47294 | PREDICTED: cullin-1-like isoform X4 [Nicotiana tabacum] | 26.008 | 1.6763 | 9 | 2 | 2 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL1290Contig1_m.20447 | PREDICTED: phospholipase SGR2-like [Nicotiana tabacum] | 22.067 | 9.9686 | 9.5 | 1 | 1 | 1 | | | | | | | | |
| cds.CL1310Contig1_m.8622 | Myc2 bHLH protein [Vitis vinifera] | 68.241 | 1.1529 | 1.8 | 1 | 2 | 1 | 0.901 | 0.962 | 0.958 | 1.126 | 1.026 | 1.064 | 1.14 | 1.90E-02 |
| cds.CL131Contig2_m.19755 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 11, chloroplastic/mitochondrial isoform X1 [Sesamum indicum] | 57.774 | 11.676 | 9.1 | 4 | 4 | 4 | | | | | | | | |
| cds.CL1334Contig1_m.16732 | PREDICTED: AP-1 complex subunit mu-2 [Nelumbo nucifera] | 45.632 | 5.5313 | 6.5 | 3 | 4 | 3 | 0.96 | 1.021 | 1.044 | 1.017 | 0.972 | 0.944 | 0.97 | 4.06E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL1340Contig1_m.43986 | PREDICTED: crocetin glucosyltransferase, chloroplastic-like [Nelumbo nucifera] | 26.525 | 5.3964 | 13.2 | 3 | 3 | 3 | 0.943 | 1.056 | 0.978 | 0.986 | 1.025 | 1.027 | 1.02 | 5.86E-01 |
| cds.CL1357Contig1_m.25269 | PREDICTED: heparanase-like protein 3 [Ziziphus jujuba] | 22.003 | 10.872 | 11.9 | 2 | 2 | 2 | 1.097 | 1.037 | 1.069 | 0.921 | 0.967 | 0.894 | 0.869 | 7.34E-03 |
| cds.CL1367Contig1_m.12959 | PREDICTED: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic [Vitis vinifera] | 85.391 | 198.51 | 29.1 | 20 | 40 | 20 | 1.02 | 1.081 | 1.026 | 0.934 | 0.941 | 0.963 | 0.908 | 9.38E-03 |
| cds.CL1371Contig1_m.20317 | PREDICTED: UDP-glycosyltransferase 708A6-like [Ziziphus jujuba] | 55.498 | 1.9449 | 3.4 | 2 | 2 | 2 | 1.291 | 1.277 | 1.364 | 0.711 | 0.649 | 0.62 | 0.504 | 1.04E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL1397Contig1_m.17638 | PREDICTED: cytochrome P450 CYP72A219-like [Nicotiana tabacum] | 60.644 | 8.7646 | 7 | 4 | 4 | 3 | 0.952 | 0.959 | 0.956 | 1.102 | 1.085 | 0.975 | 1.103 | 1.29E-01 |
| cds.CL1408Contig1_m.16271 | PREDICTED: ectonucleotide pyrophosphatase/phosphodiesterase family member 3-like [Nicotiana tomentosiformis] | 54.985 | 1.5956 | 4.3 | 2 | 3 | 1 | 1.049 | 0.964 | 1.081 | 1.045 | 0.944 | 0.92 | 0.94 | 2.98E-01 |
| cds.CL1412Contig1_m.34245 | PREDICTED: alpha-soluble NSF attachment protein-like [Erythranthe guttata] | 34.165 | 54.64 | 30.8 | 7 | 9 | 6 | 0.971 | 0.951 | 0.944 | 1.05 | 1.054 | 1.049 | 1.1 | 3.64E-04 |
| cds.CL1426Contig1_m.12123 | PREDICTED: glycerol kinase [Theobroma cacao] | 36.076 | 65.239 | 18.3 | 6 | 11 | 6 | 0.919 | 0.906 | 0.91 | 1.108 | 1.112 | 1.047 | 1.195 | 8.82E-04 |

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| cds.CL1426Contig1_m.12124 | PREDICTED: glycerol kinase-like [Sesamum indicum] | 13.942 | 2.8054 | 14.1 | 2 | 3 | 2 | 0.878 | 0.905 | 0.922 | 1.037 | 1.067 | 1.109 | 1.188 | 2.04E-03 |
| cds.CL1435Contig1_m.3955 | PREDICTED: phagocyte signaling-impaired protein isoform X1 [Vitis vinifera] | 69.451 | 3.0933 | 2.6 | 2 | 2 | 2 | 0.934 | 0.92 | 0.982 | 1.046 | 1.1 | 1.048 | 1.126 | 9.78E-03 |
| cds.CL1435Contig1_m.3956 | PREDICTED: phagocyte signaling-impaired protein isoform X3 [Cucumis melo] | 27.59 | 3.7463 | 4.5 | 1 | 1 | 1 | 0.986 | 0.968 | 1.057 | 1.047 | 0.977 | 0.979 | 0.997 | 9.48E-01 |
| cds.CL1436Contig1_m.4483 | acetyltransferase-related family protein [Populus trichocarpa] | 80.427 | 17.449 | 12.8 | 9 | 10 | 9 | 1.119 | 1.161 | 1.124 | 0.893 | 0.84 | 0.884 | 0.769 | 2.95E-04 |
| cds.CL1444Contig1_m.12503 | PREDICTED: pyruvate decarboxylase 1 [Erythranthe guttata] | 69.705 | 6.991 | 7.3 | 5 | 7 | 3 | 0.976 | 0.928 | 0.997 | 1.087 | 1.001 | 1.008 | 1.067 | 1.28E-01 |

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| cds.CL1451Contig1_m.46213 | transferring glycosyl group transferase [Medicago truncatula] | 19.324 | 3.9875 | 7.3 | 1 | 2 | 1 | 0.985 | 1.043 | 0.991 | 0.988 | 1.04 | 0.964 | 0.991 | 7.66E-01 |
| cds.CL1472Contig1_m.15003 | PREDICTED: carboxyl-terminal-processing peptidase 2, chloroplastic-like isoform X2 [Juglans regia] | 37.106 | 72.742 | 35.9 | 11 | 15 | 10 | 1.007 | 1.021 | 0.968 | 1.017 | 0.951 | 1.003 | 0.992 | 7.59E-01 |
| cds.CL1488Contig1_m.8339 | PREDICTED: conserved oligomeric Golgi complex subunit 2 [Ricinus communis] | 83.986 | 3.4794 | 2.5 | 2 | 2 | 2 | 0.93 | 1.126 | 1.024 | 0.976 | 0.986 | 0.968 | 0.951 | 4.87E-01 |
| cds.CL1496Contig1_m.28002 | PREDICTED: cinnamoyl-CoA reductase 1 [Ipomoea nil] | 40.663 | 18.225 | 17.8 | 7 | 14 | 7 | 0.947 | 0.967 | 0.958 | 1.035 | 1.043 | 1.024 | 1.08 | 6.64E-04 |

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| cds.CL1507Contig1_m.34653 | PREDICTED: elongation factor 1-delta-like [Daucus carota subsp. sativus] | 25.236 | 56.763 | 46.4 | 9 | 27 | 7 | 0.95 | 0.957 | 0.961 | 1.045 | 1.075 | 1.049 | 1.105 | 4.61E-04 |
| cds.CL1528Contig1_m.12829 | PREDICTED: uridine-cytidine kinase C isoform X1 [Jatropha curcas] | 74.6 | 19.08 | 11.7 | 7 | 8 | 7 | 0.998 | 1.011 | 0.985 | 1.024 | 0.988 | 0.985 | 1.001 | 9.54E-01 |
| cds.CL1535Contig1_m.21159 | PREDICTED: 5'-nucleotidase SurE-like [Prunus mume] | 32.59 | 4.3828 | 2.9 | 1 | 1 | 1 | 1.008 | 0.937 | 0.999 | 0.985 | 0.979 | 1.101 | 1.041 | 4.27E-01 |
| cds.CL1559Contig1_m.17467 | 2-phosphoglycerate kinase [Medicago truncatula] | 50.321 | 9.5714 | 2.2 | 1 | 1 | 1 | 0.909 | 1.027 | 1.061 | 0.951 | 1.044 | 1.024 | 1.007 | 8.82E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL1561Contig1_m.17435 | PREDICTED: palmitoyl-protein thioesterase 1 isoform X1 [Theobroma cacao] | 41.191 | 2.4941 | 4.3 | 2 | 2 | 2 | 1.039 | 1.101 | 1.046 | 0.942 | 0.948 | 0.915 | 0.88 | 3.96E-03 |
| cds.CL1573Contig1_m.5993 | PREDICTED: coatomer subunit gamma-2 [Jatropha curcas] | 103.23 | 98.108 | 21.5 | 17 | 22 | 17 | 1.007 | 0.99 | 1.025 | 0.989 | 1.012 | 1.01 | 0.996 | 7.87E-01 |
| cds.CL1574Contig1_m.10547 | PREDICTED: leucine--tRNA ligase, cytoplasmic-like [Solanum pennellii] | 87.197 | 44.376 | 20.2 | 13 | 15 | 8 | 0.947 | 0.99 | 0.973 | 0.993 | 1.053 | 1.018 | 1.053 | 7.36E-02 |
| cds.CL1593Contig1_m.10476 | PREDICTED: dnaJ homolog subfamily C member 16 [Jatropha curcas] | 74.663 | 6.9919 | 3.6 | 2 | 2 | 2 | 0.904 | 1.105 | 1.147 | 0.941 | 1.011 | 0.902 | 0.904 | 3.00E-01 |

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| cds.CL1609Contig1_m.16739 | PREDICTED: calcium-dependent protein kinase 1-like [Nelumbo nucifera] | 57.202 | 39.498 | 21.6 | 9 | 10 | 5 | 0.876 | 0.994 | 0.935 | 1.11 | 1.012 | 1.035 | 1.125 | 6.08E-02 |
| cds.CL1635Contig1_m.8106 | PREDICTED: transketolase, chloroplastic-like [Gossypium hirsutum] | 41.639 | 159.07 | 26.8 | 8 | 31 | 8 | 0.973 | 0.956 | 0.959 | 1.022 | 1.048 | 1.027 | 1.072 | 1.76E-03 |
| cds.CL1635Contig1_m.8107 | PREDICTED: transketolase, chloroplastic-like, partial [Juglans regia] | 29.958 | 137.79 | 40.9 | 11 | 48 | 8 | 0.973 | 0.963 | 0.982 | 1.05 | 1.029 | 1.023 | 1.063 | 3.24E-03 |
| cds.CL1645Contig1_m.49449 | PREDICTED: exosome component 10 isoform X2 [Prunus | 17.508 | 1.302 | 8.3 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL164Contig1_m.696 | PREDICTED: plasma membrane ATPase 4 isoform X1 [Theobroma cacao] | 105.14 | 131.71 | 35.3 | 31 | 66 | 12 | 1.021 | 0.977 | 1.032 | 0.986 | 1.011 | 0.998 | 0.988 | 5.66E-01 |
| cds.CL164Contig1_m.698 | PREDICTED: photosynthetic NDH subunit of lumenal location 5, chloroplastic [Ziziphus jujuba] | 28.353 | 99.231 | 36 | 11 | 39 | 9 | 1.044 | 1.022 | 1.043 | 0.986 | 0.96 | 0.976 | 0.94 | 4.02E-03 |
| cds.CL1670Contig1_m.28637 | PREDICTED: CBS domain-containing protein CBSX1, chloroplastic-like isoform X3 [Nicotiana attenuata] | 30.077 | 18.033 | 13.4 | 5 | 9 | 4 | 1.037 | 1.014 | 1.041 | 0.996 | 1 | 0.963 | 0.957 | 3.85E-02 |

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| cds.CL1675Contig1_m.13474 | PREDICTED: multiprotein-bridging factor 1b [Vigna radiata var. radiata] | 15.516 | 21.061 | 27.5 | 6 | 8 | 6 | 1.069 | 1.089 | 1.065 | 0.905 | 0.884 | 0.958 | 0.852 | 2.96E-03 |
| cds.CL168Contig1_m.5686 | PREDICTED: ribonuclease J isoform X1 [Theobroma cacao] | 93.003 | 3.7114 | 4 | 4 | 5 | 3 | 1.215 | 1.183 | 1.09 | 0.843 | 0.809 | 0.809 | 0.706 | 6.01E-04 |
| cds.CL1715Contig1_m.18765 | PREDICTED: serine carboxypeptidase-like 20 [Citrus sinensis] | 55.629 | 14.729 | 6 | 3 | 5 | 3 | 1.133 | 1.081 | 1.074 | 0.893 | 0.905 | 0.888 | 0.817 | 3.41E-04 |
| cds.CL1729Contig1_m.14968 | PREDICTED: regulator of nonsense transcripts 1 homolog isoform X1 [Malus domestica] | 70.475 | 43.035 | 9.1 | 5 | 5 | 5 | 0.995 | 0.986 | 0.95 | 1.022 | 1.06 | 1.012 | 1.056 | 5.36E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL1797Contig1_m.33392 | PREDICTED: proteasome subunit beta type-4-like [Juglans regia] | 27.608 | 71.281 | 23.2 | 5 | 12 | 5 | 0.94 | 0.96 | 0.973 | 1.005 | 1.07 | 1.051 | 1.088 | 1.65E-02 |
| cds.CL1865Contig1_m.42192 | PREDICTED: 50S ribosomal protein L18, chloroplastic [Prunus mume] | 18.583 | 6.2433 | 11.4 | 3 | 3 | 3 | 1.106 | 1.154 | 1.201 | 0.866 | 0.828 | 0.814 | 0.725 | 4.37E-04 |
| cds.CL1876Contig1_m.33456 | PREDICTED: protein TIC 22-like, chloroplastic [Pyrus x bretschneideri] | 26.913 | 62.791 | 27.5 | 5 | 10 | 5 | 0.957 | 0.974 | 1.041 | 1.019 | 0.911 | 0.994 | 0.984 | 7.14E-01 |
| cds.CL1906Contig1_m.9375 | PREDICTED: U-box domain-containing protein 14 [Sesamum indicum] | 68.421 | 1.9885 | 1.4 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL1933Contig1_m.27314 | PREDICTED: double-stranded RNA-binding protein 4 isoform X3 [Vitis vinifera] | 38.172 | 2.1287 | 9.2 | 4 | 4 | 2 | 1.068 | 1.09 | 1.037 | 0.881 | 1.058 | 0.853 | 0.874 | 1.12E-01 |
| cds.CL194Contig1_m.32217 | PREDICTED: ATPase 4, plasma membrane-type [Cicer | 44.994 | 23.253 | 49 | 18 | 41 | 5 | 0.959 | 0.991 | 0.994 | 0.982 | 1.096 | 1.008 | 1.048 | 2.59E-01 |
| cds.CL1995Contig1_m.25635 | PREDICTED: GDSL esterase/lipase At5g33370 [Vitis vinifera] | 40.32 | 1.5601 | 2.7 | 1 | 1 | 1 | | | | | | | | |
| cds.CL2003Contig1_m.12351 | PREDICTED: glycine--tRNA ligase, mitochondrial 1-like [Nicotiana attenuata] | 79.364 | 80.449 | 22.3 | 15 | 30 | 6 | 0.96 | 0.981 | 0.922 | 1.058 | 1.065 | 1.044 | 1.106 | 6.08E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL2126Contig1_m.4592 | PREDICTED: muscle M-line assembly protein unc-89 [Citrus sinensis] | 101.96 | 31.676 | 10 | 8 | 10 | 8 | 1.069 | 1.055 | 1.046 | 0.94 | 0.948 | 0.947 | 0.894 | 8.18E-05 |
| cds.CL2137Contig1_m.26096 | PREDICTED: putative 12-oxophytodienoate reductase 11 [Ipomoea nil] | 42.45 | 4.5057 | 7.9 | 3 | 6 | 2 | 1.037 | 0.986 | 0.983 | 1.011 | 0.966 | 1.001 | 0.991 | 6.98E-01 |
| cds.CL2147Contig1_m.5684 | PREDICTED: alpha-mannosidase 2 [Vitis vinifera] | 105.17 | 8.7406 | 6 | 6 | 8 | 6 | 1.058 | 1.141 | 1.086 | 0.93 | 0.865 | 0.881 | 0.815 | 2.72E-03 |
| cds.CL228Contig2_m.587 | PREDICTED: titin homolog [Ziziphus jujuba] | 89.665 | 2.1739 | 2.3 | 2 | 3 | 2 | 0.993 | 0.89 | 0.925 | 1.081 | 1.07 | 1.067 | 1.146 | 5.12E-02 |
| cds.CL230Contig1_m.8625 | PREDICTED: 3-dehydroquinate synthase, chloroplastic-like [Juglans regia] | 48.666 | 27.352 | 20.7 | 10 | 17 | 10 | 1.154 | 1.112 | 1.148 | 0.839 | 0.86 | 0.854 | 0.748 | 2.47E-05 |

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| cds.CL230Contig1_m.8626 | PREDICTED: glycolipid transfer protein 1-like [Nelumbo nucifera] | 22.569 | 7.0458 | 12.4 | 2 | 2 | 2 | 0.978 | 0.985 | 1.088 | 0.969 | 0.93 | 1.055 | 0.968 | 5.56E-01 |
| cds.CL2331Contig1_m.13695 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 6 [Vitis vinifera] | 54.732 | 28.128 | 13.8 | 6 | 7 | 6 | 1.007 | 0.982 | 1.013 | 0.982 | 0.983 | 1.04 | 1.001 | 9.74E-01 |
| cds.CL2340Contig1_m.9723 | PREDICTED: regulator of nonsense transcripts 1 homolog isoform X2 [Vitis vinifera] | 69.374 | 6.555 | 3.3 | 2 | 2 | 2 | 0.958 | 0.967 | 0.92 | 1.032 | 1.005 | 1.138 | 1.116 | 5.63E-02 |
| cds.CL2367Contig1_m.9697 | PREDICTED: flagellar radial spoke protein 5 [Ziziphus jujuba] | 43.671 | 26.89 | 18.6 | 6 | 11 | 6 | 0.895 | 1.004 | 1.034 | 0.995 | 0.988 | 0.999 | 1.017 | 7.16E-01 |

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| cds.CL2386Contig1_m.14397 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP62 [Vitis vinifera] | 62.425 | -2 | 21.6 | 14 | 20 | 1 | | | | | | | | |
| cds.CL238Contig1_m.244 | PREDICTED: E3 ubiquitin-protein ligase UPL2 [Vitis vinifera] | 338.38 | 73.196 | 4.8 | 14 | 18 | 12 | 1.05 | 1.12 | 1.062 | 0.926 | 0.93 | 0.907 | 0.855 | 1.84E-03 |
| cds.CL238Contig1_m.245 | PREDICTED: E3 ubiquitin-protein ligase UPL2 [Vitis vinifera] | 70.383 | 6.4925 | 1.7 | 1 | 1 | 1 | 0.833 | 1.086 | 1.174 | 1.109 | 0.949 | 0.881 | 0.95 | 7.34E-01 |
| cds.CL2400Contig1_m.14899 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP62 [Vitis vinifera] | 63.76 | 45.213 | 21.3 | 14 | 20 | 1 | | | | | | | | |

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| cds.CL2405Contig1_m.22784 | PREDICTED: rab9 effector protein with kelch motifs [Vitis vinifera] | 58.895 | 49.316 | 9.7 | 3 | 3 | 3 | 1.023 | 0.926 | 0.805 | 1.062 | 1.039 | 1.164 | 1.186 | 8.91E-02 |
| cds.CL245Contig1_m.18020 | PREDICTED: protein transport protein Sec61 subunit alpha-like [Juglans regia] | 52.133 | 21.068 | 12.6 | 6 | 11 | 1 | 1.013 | 0.909 | 0.849 | 1.161 | 1.081 | 1.019 | 1.177 | 6.18E-02 |
| cds.CL245Contig2_m.19427 | PREDICTED: protein transport protein Sec61 subunit alpha-like [Daucus carota subsp. sativus] | 51.988 | -2 | 12.6 | 6 | 10 | 1 | 0.873 | 0.983 | 0.998 | 0.979 | 1.192 | 1.008 | 1.114 | 2.29E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL247Contig1_m.30180 | PREDICTED: serine/threonine-protein phosphatase PP2A catalytic subunit [Eucalyptus grandis] | 35.03 | 39.466 | 34.6 | 8 | 11 | 6 | 0.931 | 0.973 | 0.968 | 1.029 | 1.03 | 1.054 | 1.084 | 7.24E-03 |
| cds.CL256Contig2_m.600 | PREDICTED: helicase protein MOM1 isoform X1 [Vitis vinifera] | 253.86 | 1.9074 | 0.4 | 1 | 4 | 1 | 0.951 | 0.937 | 0.968 | 1.036 | 1.041 | 1.084 | 1.107 | 4.12E-03 |
| cds.CL2604Contig1_m.30733 | PREDICTED: subtilisin-like protease SBT1.7 [Citrus sinensis] | 41.299 | 23.066 | 7.6 | 2 | 4 | 2 | 0.967 | 0.975 | 0.976 | 1.027 | 1.053 | 1.073 | 1.081 | 4.04E-03 |
| cds.CL2607Contig1_m.32294 | PREDICTED: eukaryotic translation initiation factor 2 subunit beta [Sesamum indicum] | 34.869 | 2.6801 | 8.1 | 2 | 2 | 2 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL260Contig1_m.2359 | PREDICTED: golgin subfamily B member 1 isoform X4 [Vitis vinifera] | 151.06 | 20.876 | 4.2 | 5 | 5 | 5 | 1.054 | 1.102 | 1.072 | 0.917 | 0.958 | 0.884 | 0.855 | 4.10E-03 |
| cds.CL2654Contig1_m.34567 | PREDICTED: myosin-11-like [Juglans regia] | 43.435 | 9.8454 | 13.6 | 4 | 4 | 4 | 0.933 | 1.049 | 0.941 | 1.03 | 1.053 | 1.016 | 1.06 | 2.01E-01 |
| cds.CL2675Contig1_m.36719 | PREDICTED: proline synthase co-transcribed bacterial homolog protein isoform X2 [Vitis vinifera] | 29.441 | 2.2478 | 10.1 | 3 | 5 | 2 | | | | | | | | |
| cds.CL2682Contig1_m.23652 | PREDICTED: arogenate dehydratase/prephenate dehydratase 2, chloroplastic [Sesamum indicum] | 46.301 | 9.521 | 7.9 | 4 | 5 | 3 | 0.939 | 0.912 | 0.963 | 1.057 | 1.095 | 1.042 | 1.135 | 4.18E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL2709Contig1_m.35266 | PREDICTED: proteasome subunit alpha type-4 [Daucus carota subsp. sativus] | 27.283 | 115.11 | 38.6 | 11 | 23 | 11 | 0.963 | 0.944 | 1.003 | 1.026 | 1.025 | 1.068 | 1.072 | 3.61E-02 |
| cds.CL271Contig1_m.26532 | PREDICTED: tobamovirus multiplication protein 2A-like [Gossypium hirsutum] | 31.186 | 19.5 | 19.7 | 3 | 7 | 3 | 0.927 | 0.926 | 0.934 | 0.999 | 1.079 | 1.114 | 1.145 | 5.35E-02 |
| cds.CL2759Contig1_m.27804 | PREDICTED: reticulon-4-interacting protein 1, mitochondrial [Nicotiana tabacum] | 16.774 | 51.014 | 21.3 | 3 | 5 | 3 | 0.959 | 0.993 | 1.001 | 1.024 | 1.059 | 1.013 | 1.048 | 6.53E-02 |
| cds.CL2759Contig1_m.27806 | PREDICTED: reticulon-4-interacting protein 1, mitochondrial [Ziziphus jujuba] | 12.937 | 48.968 | 18.3 | 2 | 2 | 2 | 0.942 | 0.944 | 0.981 | 1.121 | 1.046 | 0.997 | 1.104 | 5.56E-02 |

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| cds.CL27Contig1_m.26912 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 13-like isoform X1 [Nelumbo nucifera] | 36.84 | 42.511 | 16.6 | 7 | 7 | 6 | 0.997 | 0.976 | 1.01 | 1.03 | 0.996 | 1.01 | 1.018 | 2.75E-01 |
| cds.CL2817Contig1_m.45088 | PREDICTED: maf-like protein DDB_G0281937 [Ziziphus jujuba] | 11.916 | 2.7867 | 20 | 2 | 2 | 2 | 0.757 | 1.404 | 0.972 | 0.948 | 0.933 | 1.002 | 0.92 | 8.04E-01 |
| cds.CL2818Contig1_m.52277 | PREDICTED: solanesyl diphosphate synthase 3, chloroplastic/mitochondrial isoform X5 [Citrus sinensis] | 18.125 | 2.7812 | 6.1 | 1 | 1 | 1 | | | | | | | | |

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| cds.CL2855Contig1_m.13226 | PREDICTED: T-complex protein 1 subunit zeta-like isoform X2 [Nicotiana sylvestris] | 59.14 | 116.37 | 40.9 | 17 | 27 | 17 | 0.939 | 0.936 | 0.932 | 1.078 | 1.083 | 1.036 | 1.139 | 1.18E-02 |
| cds.CL2864Contig1_m.31320 | PREDICTED: dihydrolipoyl dehydrogenase 2, chloroplastic [Vitis vinifera] | 45.824 | 74.859 | 28.2 | 11 | 14 | 7 | 0.998 | 1.043 | 1.003 | 1.008 | 0.999 | 0.996 | 0.987 | 4.05E-01 |
| cds.CL2872Contig1_m.26765 | PREDICTED: mitotic checkpoint protein BUB3.1 isoform X2 [Nicotiana attenuata] | 37.703 | 42.021 | 15 | 5 | 5 | 5 | 0.948 | 1.009 | 0.986 | 1.043 | 1.042 | 1.026 | 1.057 | 4.23E-02 |
| cds.CL2893Contig1_m.49322 | PREDICTED: cytochrome c oxidase assembly factor 6 isoform X2 [Erythranthe guttata] | 12.615 | 1.1576 | 7.3 | 1 | 1 | 1 | | | | | | | | |

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| cds.CL2899Contig1_m.9257 | PREDICTED: probable polygalacturonase [Malus domestica] | 33.787 | 3.5492 | 5.7 | 2 | 2 | 2 | 1.068 | 0.988 | 1.038 | 0.928 | 1.003 | 0.968 | 0.937 | 1.11E-01 |
| cds.CL28Contig1_m.10182 | PREDICTED: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase [Vitis | 55.994 | 7.6735 | 13.4 | 7 | 9 | 3 | 1.077 | 1.012 | 1.023 | 0.982 | 1.012 | 0.971 | 0.953 | 1.02E-01 |
| cds.CL28Contig4_m.11804 | PREDICTED: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase [Vitis | 61.645 | 57.006 | 17.9 | 9 | 11 | 4 | 0.979 | 1.038 | 1.029 | 1 | 1.01 | 0.955 | 0.973 | 3.44E-01 |
| cds.CL2924Contig1_m.35673 | PREDICTED: thaumatin-like protein [Theobroma cacao] | 31.726 | 1.9529 | 3.4 | 1 | 1 | 1 | | | | | | | | |
| cds.CL300Contig2_m.5020 | PREDICTED: AP-1 complex subunit gamma-2-like [Citrus sinensis] | 44.087 | 85.051 | 13 | 4 | 6 | 4 | 0.952 | 0.949 | 0.961 | 0.989 | 1.062 | 1.093 | 1.099 | 8.98E-02 |

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| cds.CL3034Contig1_m.23283 | PREDICTED: spermidine hydroxycinnamoyl transferase-like [Vitis vinifera] | 53.446 | 5.4276 | 7.2 | 3 | 3 | 3 | 1.088 | 1.049 | 1.136 | 1.032 | 0.923 | 0.907 | 0.874 | 4.38E-02 |
| cds.CL3080Contig1_m.32184 | PREDICTED: carboxylesterase 1-like [Juglans regia] | 37.081 | 7.4766 | 7.7 | 2 | 3 | 2 | 0.908 | 0.955 | 0.985 | 1.051 | 1.078 | 1.055 | 1.118 | 1.10E-02 |
| cds.CL3085Contig1_m.12532 | PREDICTED: endonuclease 4-like [Juglans regia] | 12.539 | 2.1971 | 12.4 | 2 | 2 | 2 | 1.041 | 0.982 | 1.081 | 0.955 | 0.95 | 0.988 | 0.932 | 8.43E-02 |
| cds.CL3102Contig1_m.6260 | PREDICTED: UDP-D-apiose/UDP-D-xylose synthase 2-like [Nelumbo nucifera] | 43.689 | 15.068 | 14.7 | 5 | 7 | 5 | 0.98 | 1.062 | 1.111 | 0.986 | 0.928 | 0.956 | 0.91 | 8.40E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL3102Contig1_m.6261 | PREDICTED: polyadenylate-binding protein-interacting protein 12-like [Sesamum | 36.614 | 2.4509 | 3.9 | 1 | 1 | 1 | | | | | | | | |
| cds.CL3107Contig1_m.13113 | PREDICTED: protein ACCUMULATION AND REPLICATION OF CHLOROPLASTS 6, chloroplastic [Vitis vinifera] | 52.03 | 4.6955 | 3.8 | 2 | 2 | 2 | 1.036 | 1.054 | 1.128 | 0.928 | 0.981 | 0.866 | 0.862 | 2.87E-02 |
| cds.CL310Contig1_m.6128 | PREDICTED: centrosomal protein of 164 kDa isoform X3 [Arachis | 76.57 | 18.812 | 5.7 | 4 | 4 | 2 | 0.983 | 1.05 | 1.013 | 0.945 | 1.01 | 1.003 | 0.971 | 3.60E-01 |

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| cds.CL310Contig1_m.6129 | PREDICTED: serine/threonine-protein kinase dst2-like isoform X7 [Lupinus angustifolius] | 27.829 | 3.6606 | 3.5 | 1 | 1 | 1 | 1.052 | 1.012 | 0.903 | 1.031 | 1.005 | 1.003 | 1.024 | 6.08E-01 |
| cds.CL3123Contig1_m.26192 | PREDICTED: 2-dehydro-3-deoxyphosphooctonate aldolase 1 [Capsicum annuum] | 31.744 | 16.186 | 24.1 | 5 | 6 | 5 | 1.074 | 1.056 | 1.055 | 0.959 | 0.936 | 0.953 | 0.894 | 2.77E-04 |
| cds.CL3128Contig1_m.6449 | Bifunctional aspartokinase/homoserine dehydrogenase [Morus notabilis] | 100.28 | 284.78 | 32 | 23 | 43 | 13 | 0.975 | 1.015 | 0.961 | 1.055 | 1.027 | 1.023 | 1.052 | 5.49E-02 |

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| cds.CL3154Contig1_m.20832 | PREDICTED: 2-oxoisovalerate dehydrogenase subunit alpha 1, mitochondrial-like isoform X1 [Nelumbo nucifera] | 54.758 | 23.689 | 20.2 | 9 | 12 | 9 | 0.966 | 1.015 | 0.993 | 1.038 | 0.999 | 0.999 | 1.021 | 3.42E-01 |
| cds.CL3164Contig1_m.13657 | PREDICTED: probable inactive purple acid phosphatase 2 [Citrus sinensis] | 73.307 | 27.801 | 16 | 9 | 12 | 9 | 1.054 | 1 | 1.015 | 0.971 | 0.946 | 0.99 | 0.947 | 5.71E-02 |
| cds.CL3176Contig1_m.24113 | PREDICTED: sulfite oxidase [Capsicum annuum] | 37.417 | 3.9321 | 7.4 | 3 | 3 | 3 | 0.949 | 1.067 | 0.947 | 0.957 | 1.026 | 0.967 | 0.996 | 9.45E-01 |
| cds.CL3183Contig1_m.34717 | PREDICTED: 50S ribosomal protein L21, chloroplastic [Sesamum indicum] | 20.722 | 2.9491 | 8.6 | 2 | 3 | 2 | 1.142 | 1.099 | 1.096 | 0.868 | 0.874 | 0.887 | 0.788 | 8.27E-05 |

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| cds.CL318Contig1_m.48735 | PREDICTED: (+)-neomenthol dehydrogenase-like [Ziziphus jujuba] | 14.599 | 67.431 | 57.7 | 7 | 20 | 7 | 0.965 | 0.951 | 0.967 | 1.068 | 1.052 | 1.019 | 1.089 | 4.58E-03 |
| cds.CL3233Contig1_m.1855 | PREDICTED: translocase of chloroplast 120, chloroplastic-like isoform X1 [Glycine max] | 92.542 | 23.24 | 10.8 | 8 | 11 | 8 | 1.049 | 1.065 | 1.087 | 0.911 | 0.935 | 0.942 | 0.871 | 6.76E-04 |
| cds.CL3233Contig1_m.1856 | PREDICTED: translocase of chloroplast 120, chloroplastic isoform X1 [Vitis vinifera] | 44.644 | 1.3694 | 1.9 | 1 | 1 | 1 | 1.097 | 1.138 | 1.116 | 0.922 | 0.844 | 0.858 | 0.783 | 1.10E-03 |
| cds.CL323Contig1_m.7000 | PREDICTED: vacuolar protein sorting-associated protein 35A [Theobroma cacao] | 63.014 | 8.1278 | 8.2 | 5 | 5 | 5 | 0.926 | 0.975 | 1.027 | 1.04 | 0.991 | 1.056 | 1.054 | 2.07E-01 |

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| cds.CL323Contig1_m.7001 | PREDICTED: vacuolar protein sorting-associated protein 35A-like [Malus domestica] | 23.016 | 5.1691 | 13.1 | 3 | 3 | 3 | 0.932 | 1.065 | 0.945 | 1.139 | 1.003 | 0.944 | 1.049 | 5.41E-01 |
| cds.CL3251Contig1_m.45324 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 12-like [Malus domestica] | 28.091 | 5.2496 | 7.3 | 2 | 2 | 2 | | | | | | | | |
| cds.CL3258Contig1_m.25630 | PREDICTED: cell division control protein 2 homolog A-like [Solanum tuberosum | 33.865 | -2 | 5.8 | 2 | 3 | 1 | 1.081 | 1.111 | 1.048 | 0.905 | 0.924 | 0.912 | 0.846 | 7.39E-04 |
| cds.CL3259Contig1_m.25268 | calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] | 20.49 | 1.353 | 11.5 | 2 | 2 | 2 | 0.965 | 1.03 | 0.906 | 1.067 | 1.042 | 1.011 | 1.075 | 1.40E-01 |

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| cds.CL3262Contig1_m.34763 | PREDICTED: protein EARLY RESPONSIVE TO DEHYDRATION 15-like [Daucus carota subsp. sativus] | 24.665 | 15.181 | 7.1 | 1 | 2 | 1 | 0.853 | 0.957 | 0.976 | 1.14 | 1.037 | 1.083 | 1.17 | 3.44E-02 |
| cds.CL3284Contig1_m.30235 | PREDICTED: cytochrome P450 89A2-like [Nicotiana tabacum] | 44.755 | 11.535 | 14.8 | 6 | 8 | 3 | 0.875 | 0.969 | 0.979 | 1.174 | 1.006 | 1.033 | 1.138 | 9.78E-02 |
| cds.CL3299Contig1_m.20125 | PREDICTED: 7-deoxyloganetin glucosyltransferase [Vitis vinifera] | 40.612 | 2.9666 | 5.1 | 2 | 3 | 1 | | | | | | | | |
| cds.CL3323Contig1_m.32482 | PREDICTED: thioredoxin-like 4, chloroplastic isoform X1 [Vitis vinifera] | 21.703 | 1.2624 | 3.7 | 1 | 1 | 1 | 1.068 | 0.989 | 1.051 | 0.919 | 0.993 | 0.972 | 0.928 | 8.53E-02 |

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| cds.CL3325Contig1_m.15610 | PREDICTED: luminal-binding protein 4-like [Nelumbo nucifera] | 77.071 | 7.6128 | 13.1 | 9 | 16 | 3 | 1.177 | 1.137 | 1.128 | 0.887 | 0.88 | 0.763 | 0.735 | 3.60E-03 |
| cds.CL3327Contig1_m.35996 | PREDICTED: putative UDP-glucose flavonoid 3-O-glucosyltransferase 3 [Fragaria vesca subsp. vesca] | 40.281 | 40.817 | 12.7 | 4 | 12 | 4 | 0.971 | 0.97 | 1.066 | 0.985 | 1.011 | 1.028 | 1.006 | 8.57E-01 |
| cds.CL3334Contig1_m.18342 | PREDICTED: protein HGV2 isoform X2 [Vitis vinifera] | 50.412 | 5.8536 | 6.3 | 3 | 3 | 3 | 1.142 | 1.065 | 1.238 | 0.847 | 0.809 | 0.861 | 0.731 | 2.74E-03 |
| cds.CL3362Contig1_m.38227 | PREDICTED: REF/SRPP-like protein At3g05500 [Juglans regia] | 31.545 | 21.731 | 16.6 | 4 | 7 | 4 | 0.905 | 0.955 | 0.998 | 1.059 | 1.075 | 1.034 | 1.108 | 2.72E-02 |

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| cds.CL337Contig1_m.34411 | PREDICTED: uncharacterized isomerase BH0283-like isoform X1 [Citrus sinensis] | 32.115 | 9.7744 | 7.5 | 2 | 4 | 2 | 0.962 | 0.857 | 1.003 | 1.045 | 1.049 | 1.11 | 1.135 | 6.48E-02 |
| cds.CL3387Contig1_m.17553 | PREDICTED: polyadenylate-binding protein RBP47 [Sesamum | 47.629 | 20.274 | 2.1 | 1 | 1 | 1 | 0.979 | 0.997 | 0.947 | 1.064 | 1.037 | 0.996 | 1.06 | 7.75E-02 |
| cds.CL3404Contig1_m.20723 | PREDICTED: probable membrane metalloprotease ARASP2, chloroplastic [Vitis vinifera] | 48.816 | 4.1136 | 7.5 | 3 | 5 | 3 | 0.985 | 0.94 | 1.115 | 0.942 | 1.013 | 1.013 | 0.976 | 7.17E-01 |
| cds.CL3427Contig1_m.23699 | PREDICTED: putative disease resistance protein At1g50180 isoform X2 [Vitis vinifera] | 51.693 | 2.1801 | 2 | 1 | 1 | 1 | | | | | | | | |

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| cds.CL3440Contig1_m.18521 | PREDICTED: dol-P-Man:Man(6)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase [Nicotiana tomentosiformis] | 25.787 | 34.245 | 7.8 | 1 | 1 | 1 | | | | | | | | |
| cds.CL3443Contig1_m.6184 | PREDICTED: linoleate 13S-lipoxygenase 2-1, chloroplastic-like [Ziziphus jujuba] | 105.36 | 11.229 | 36.8 | 37 | 96 | 1 | 0.909 | 0.939 | 0.97 | 1.153 | 1.007 | 1.096 | 1.155 | 3.06E-02 |
| cds.CL3460Contig1_m.13358 | PREDICTED: protein CASP isoform X1 [Vitis vinifera] | 79.134 | 2.6519 | 2.2 | 2 | 2 | 2 | 1.041 | 1.008 | 1.048 | 0.966 | 0.962 | 0.973 | 0.937 | 6.36E-03 |
| cds.CL3471Contig1_m.24104 | PREDICTED: alpha-galactosidase 3 [Malus domestica] | 46.934 | 2.5192 | 10.6 | 5 | 13 | 1 | 0.973 | 0.956 | 0.949 | 1.02 | 1.039 | 1.082 | 1.091 | 1.00E-02 |

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| cds.CL3474Contig1_m.38487 | PREDICTED: acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha, chloroplastic-like [Nicotiana tabacum] | 26.019 | 2.1233 | 3.5 | 1 | 1 | 1 | 1.012 | 1.206 | 1.127 | 0.974 | 0.858 | 0.81 | 0.79 | 3.40E-02 |
| cds.CL3478Contig1_m.24459 | PREDICTED: protein SGT1 homolog B [Theobroma cacao] | 40.61 | 30.532 | 21.8 | 9 | 15 | 8 | 1.04 | 0.986 | 0.973 | 1.004 | 1.038 | 1.006 | 1.016 | 5.13E-01 |
| cds.CL3510Contig1_m.34721 | PREDICTED: dnaJ protein homolog 2-like [Nelumbo nucifera] | 39.427 | 1.8909 | 5.9 | 2 | 2 | 1 | 1.165 | 1.153 | 1.124 | 0.868 | 0.793 | 0.855 | 0.731 | 4.63E-04 |
| cds.CL3522Contig1_m.48014 | late embryogenesis abundant protein Lea5 [Citrus sinensis] | 13.474 | 5.6271 | 13.7 | 2 | 2 | 2 | 1.092 | 1.116 | 1.143 | 0.855 | 0.868 | 0.898 | 0.782 | 2.37E-04 |

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| cds.CL3528Contig1_m.20155 | plant/F10M23-360 protein [Medicago truncatula] | 60.031 | 16.251 | 8.2 | 5 | 6 | 5 | 1.039 | 1.052 | 1.065 | 0.959 | 0.959 | 0.935 | 0.904 | 7.99E-04 |
| cds.CL353Contig1_m.27496 | PREDICTED: UDP-glycosyltransferase 87A1 [Vitis vinifera] | 52.028 | 4.2687 | 6.9 | 2 | 2 | 2 | 0.554 | | 1.451 | 1.283 | 0.7 | 1.117 | 1.031 | 8.14E-01 |
| cds.CL3548Contig1_m.10891 | PREDICTED: KH domain-containing protein At4g18375 [Vitis vinifera] | 51.606 | 3.4907 | 2.8 | 1 | 1 | 1 | 1.087 | 1.152 | 1.143 | 0.864 | 0.838 | 0.885 | 0.765 | 3.76E-04 |
| cds.CL3554Contig1_m.16489 | PREDICTED: coatomer subunit delta [Vitis vinifera] | 58.46 | 63.359 | 22.1 | 11 | 20 | 9 | 1.03 | 1.019 | 1.036 | 0.973 | 0.964 | 0.965 | 0.941 | 4.20E-04 |
| cds.CL357Contig1_m.20184 | PREDICTED: serine hydroxymethyltransferase, mitochondrial [Nicotiana attenuata] | 57.213 | 181.09 | 41.6 | 18 | 71 | 14 | 1.01 | 1.016 | 1.011 | 0.977 | 0.996 | 0.981 | 0.973 | 1.07E-02 |

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| cds.CL36Contig2_m.31756 | PREDICTED: ras-related protein RABE1a-like [Tarenaya hassleriana] | 24.068 | 71.755 | 43.8 | 10 | 22 | 3 | 0.974 | 0.937 | 0.939 | 1.12 | 1.031 | 1.05 | 1.123 | 1.46E-02 |
| cds.CL379Contig1_m.39933 | PREDICTED: alpha-glucosidase 2 [Prunus | 22.427 | 13.567 | 14.2 | 2 | 3 | 2 | 1.006 | 1.033 | 0.948 | 1.068 | 0.977 | 0.979 | 1.012 | 7.71E-01 |
| cds.CL389Contig1_m.20104 | PREDICTED: autophagy-related protein 18a isoform X1 [Nelumbo nucifera] | 42.791 | 2.5172 | 2.6 | 1 | 1 | 1 | | | | | | | | |
| cds.CL38Contig5_m.23750 | PREDICTED: aspartate--tRNA ligase, chloroplastic/mitochondrial [Vitis vinifera] | 27.953 | 27.166 | 24 | 5 | 6 | 5 | 0.961 | 0.925 | 0.961 | 1.067 | 1.087 | 1.069 | 1.132 | 9.00E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL423Contig1_m.10274 | PREDICTED: heat shock 70 kDa protein 6, chloroplastic [Gossypium arboreum] | 75.705 | 323.31 | 54.5 | 39 | 128 | 22 | 1.053 | 1.011 | 1.022 | 0.963 | 0.958 | 0.971 | 0.937 | 7.14E-03 |
| cds.CL42Contig3_m.9636 | PREDICTED: protein RAE1 [Ricinus communis] | 46.158 | 10.582 | 11.3 | 4 | 4 | 4 | 1.025 | 0.971 | 0.954 | 0.984 | 1.037 | 1.059 | 1.044 | 2.33E-01 |
| cds.CL449Contig1_m.2878 | PREDICTED: topless-related protein 4-like [Nicotiana tabacum] | 68.994 | 2.0319 | 4.9 | 3 | 4 | 1 | 1.009 | 0.962 | 1.008 | 0.978 | 1.079 | 0.976 | 1.018 | 6.65E-01 |
| cds.CL449Contig1_m.2879 | PREDICTED: topless-related protein 4 isoform X1 [Solanum tuberosum | 59.834 | 13.964 | 9.9 | 4 | 4 | 3 | 1.026 | 0.99 | 1.011 | 1.029 | 0.951 | 0.999 | 0.984 | 5.51E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL45Contig1_m.14786 | PREDICTED: DEAD-box ATP-dependent RNA helicase 56-like isoform X2 [Jatropha curcas] | 39.04 | 39.163 | 30.2 | 10 | 21 | 1 | 1.105 | 1.044 | 1.051 | 0.923 | 0.918 | 0.941 | 0.869 | 1.98E-03 |
| cds.CL45Contig3_m.16586 | PREDICTED: DEAD-box ATP-dependent RNA helicase 56-like isoform X2 [Jatropha curcas] | 39.081 | -2 | 30.2 | 10 | 21 | 1 | 1.102 | 1.044 | 1.026 | 0.901 | 0.951 | 0.958 | 0.886 | 1.39E-02 |
| cds.CL471Contig1_m.7053 | PREDICTED: U-box domain-containing protein 44-like [Daucus carota subsp. sativus] | 13.256 | 1.7795 | 7.8 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL488Contig1_m.3995 | PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Vitis vinifera] | 116.63 | 187.78 | 21.9 | 20 | 34 | 17 | 1.028 | 1.034 | 1.027 | 0.947 | 0.992 | 0.96 | 0.938 | 4.47E-02 |
| cds.CL494Contig1_m.6764 | PREDICTED: GBF-interacting protein 1-like isoform X1 [Vitis vinifera] | 83.811 | 1.3491 | 1 | 1 | 1 | 1 | 1.09 | 1.129 | 1.162 | 0.857 | 0.862 | 0.87 | 0.766 | 1.45E-04 |
| cds.CL500Contig1_m.7530 | PREDICTED: glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform [Citrus sinensis] | 59.16 | 90.935 | 33.1 | 16 | 31 | 15 | 0.992 | 1.004 | 0.971 | 1.04 | 0.991 | 0.993 | 1.019 | 3.66E-01 |
| cds.CL503Contig1_m.27374 | PREDICTED: cellulose synthase-like protein G3 [Sesamum indicum] | 51.484 | 1.3148 | 2.6 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL504Contig1_m.33268 | PREDICTED: putative quinone-oxidoreductase homolog, chloroplastic [Populus euphratica] | 34.622 | 24.52 | 29.2 | 9 | 21 | 9 | 0.892 | 0.942 | 0.98 | 1.058 | 1.066 | 1.055 | 1.13 | 4.66E-02 |
| cds.CL520Contig1_m.30441 | PREDICTED: ATPase GET3 [Sesamum indicum] | 38.279 | 26.525 | 10 | 3 | 6 | 3 | 0.995 | 0.99 | 1.022 | 1.019 | 0.986 | 1.03 | 1.009 | 6.06E-01 |
| cds.CL52Contig2_m.22591 | PREDICTED: E3 ubiquitin-protein ligase RGLG2 [Vitis vinifera] | 27.973 | 8.8601 | 8.7 | 1 | 1 | 1 | 1.061 | 1.129 | 0.819 | 1.055 | 1.04 | 0.9 | 0.995 | 9.85E-01 |
| cds.CL539Contig1_m.56311 | PREDICTED: universal stress protein A-like protein [Ziziphus jujuba] | 13.724 | 13.932 | 37.6 | 3 | 5 | 3 | 0.91 | 0.897 | 0.856 | 1.058 | 1.084 | 1.146 | 1.235 | 2.16E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL546Contig1_m.8418 | PREDICTED: cell division cycle protein 48 homolog [Jatropha curcas] | 91.241 | 298.93 | 49.5 | 34 | 84 | 6 | 1.051 | 1.056 | 1.075 | 0.927 | 0.934 | 0.938 | 0.88 | 7.79E-05 |
| cds.CL546Contig2_m.7929 | PREDICTED: cell division cycle protein 48 homolog [Gossypium hirsutum] | 89.542 | 84.355 | 43.1 | 30 | 70 | 2 | 1.061 | 1.119 | 1.115 | 1.063 | 0.922 | 0.838 | 0.857 | 8.91E-02 |
| cds.CL563Contig1_m.8180 | PREDICTED: probable cytosolic oligopeptidase A [Nicotiana attenuata] | 91.055 | 82.411 | 26.3 | 21 | 32 | 21 | 0.96 | 0.969 | 0.975 | 1.063 | 1.054 | 1.026 | 1.082 | 2.42E-03 |
| cds.CL568Contig1_m.38094 | PREDICTED: ADP,ATP carrier protein 1, mitochondrial-like [Musa acuminata subsp. malaccensis] | 24.335 | 14.379 | 27.2 | 6 | 28 | 2 | 1.045 | 1.066 | 1.02 | 0.915 | 0.904 | 1.039 | 0.913 | 1.15E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL624Contig1_m.19144 | PREDICTED: glyceraldehyde-3-phosphate dehydrogenase GAPCP2, chloroplastic-like [Nelumbo nucifera] | 44.8 | 21.881 | 15.3 | 6 | 15 | 4 | 1.128 | 1.053 | 1.063 | 0.916 | 0.916 | 0.929 | 0.851 | 1.88E-03 |
| cds.CL627Contig1_m.6284 | PREDICTED: probable inactive ATP-dependent zinc metalloprotease FTSHI 4, chloroplastic [Gossypium hirsutum] | 96.864 | 11.934 | 7.1 | 7 | 8 | 7 | 0.985 | 0.997 | 1.025 | 1.02 | 0.997 | 0.989 | 1 | 9.86E-01 |
| cds.CL646Contig1_m.14438 | PREDICTED: WD-40 repeat-containing protein MSI1 [Sesamum indicum] | 48.38 | 31.607 | 13.7 | 5 | 7 | 5 | 0.926 | 1.044 | 0.967 | 1.042 | 0.98 | 1.062 | 1.05 | 3.10E-01 |
| cds.CL663Contig1_m.36704 | PREDICTED: nigrin b-like [Malus domestica] | 33.44 | 4.5206 | 9.4 | 3 | 3 | 3 | 0.987 | 0.959 | 0.942 | 1.031 | 1.048 | 1.052 | 1.084 | 5.62E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL670Contig1_m.41479 | PREDICTED: 1-aminocyclopropane-1-carboxylate oxidase homolog 1 [Vitis vinifera] | 28.5 | 35.266 | 18.9 | 3 | 6 | 3 | 1.032 | 1.029 | 1.123 | 0.927 | 1.024 | 0.982 | 0.921 | 1.14E-01 |
| cds.CL677Contig1_m.26553 | PREDICTED: FAM10 family protein At4g22670-like [Nicotiana tabacum] | 42.365 | 19.308 | 17.9 | 8 | 8 | 8 | 1.096 | 1.048 | 0.987 | 0.883 | 0.914 | 0.983 | 0.888 | 5.33E-02 |
| cds.CL680Contig1_m.5310 | PLAC8 family protein [Medicago truncatula] | 28.559 | 2.2328 | 6.6 | 2 | 2 | 2 | 0.874 | 0.889 | 0.862 | 1.16 | 1.095 | 1.172 | 1.306 | 3.18E-04 |
| cds.CL685Contig1_m.9727 | PREDICTED: probable serine/threonine-protein kinase At5g41260 [Ipomoea | 57.737 | 6.8604 | 7.6 | 5 | 5 | 3 | 0.897 | 0.924 | 0.901 | 1.196 | 1.01 | 1.117 | 1.221 | 1.69E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL686Contig1_m.20439 | PREDICTED: putative RNA-binding protein Luc7-like 2 isoform X5 [Nelumbo nucifera] | 33.344 | 6.3235 | 8.6 | 3 | 3 | 3 | 1.103 | 1.049 | 1.05 | 0.936 | 0.908 | 0.92 | 0.863 | 1.44E-03 |
| cds.CL6Contig1_m.11214 | PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 [Vitis vinifera] | 91.978 | 2.7721 | 1.3 | 1 | 1 | 1 | 0.995 | 0.987 | 0.947 | 0.981 | 1.102 | 1.002 | 1.053 | 2.61E-01 |
| cds.CL708Contig1_m.16547 | PREDICTED: apoptosis inhibitor 5 [Sesamum indicum] | 34.799 | 9.9676 | 20.4 | 7 | 8 | 7 | 1.013 | 1.007 | 0.991 | 1.006 | 1.001 | 0.992 | 0.996 | 6.35E-01 |
| cds.CL708Contig1_m.16548 | PREDICTED: apoptosis inhibitor 5-like protein API5 isoform X1 [Vitis vinifera] | 31.314 | 37.299 | 28.3 | 7 | 9 | 7 | 1.037 | 1.02 | 0.984 | 0.974 | 0.963 | 0.99 | 0.963 | 9.47E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL709Contig1_m.3289 | PREDICTED: probable alpha-mannosidase At5g13980 isoform X1 [Nicotiana attenuata] | 115.27 | 254.14 | 28 | 27 | 70 | 25 | 0.973 | 0.987 | 0.993 | 1.024 | 1.012 | 1.009 | 1.031 | 1.51E-02 |
| cds.CL740Contig1_m.21417 | PREDICTED: acyl-coenzyme A oxidase 4, peroxisomal isoform X2 [Vitis vinifera] | 53.939 | 6.8311 | 22.8 | 11 | 15 | 2 | | | | | | | | |
| cds.CL74Contig3_m.5858 | PREDICTED: K(+) efflux antiporter 2, chloroplastic [Malus domestica] | 42.401 | 13.099 | 11.2 | 5 | 7 | 5 | 1.089 | 1.023 | 1.11 | 0.918 | 0.92 | 0.911 | 0.853 | 2.38E-02 |
| cds.CL763Contig1_m.5271 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 4, mitochondrial [Vitis vinifera] | 45.041 | 11.704 | 10.2 | 4 | 4 | 2 | 0.999 | 0.996 | 0.981 | 1.06 | 0.971 | 1.006 | 1.02 | 4.93E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL772Contig1_m.15228 | PREDICTED: glutamate-1-semialdehyde 2,1-aminomutase 2, chloroplastic [Citrus sinensis] | 50.993 | 137.82 | 37.5 | 16 | 39 | 16 | 1.069 | 1.05 | 1.057 | 0.909 | 0.949 | 0.947 | 0.883 | 1.14E-03 |
| cds.CL776Contig1_m.41420 | PREDICTED: glycerophosphodiester phosphodiesterase GDPD1, chloroplastic-like [Pyrus x bretschneideri] | 18.072 | 11.28 | 29.8 | 5 | 8 | 5 | 1.104 | 1.06 | 1.117 | 0.876 | 0.901 | 0.911 | 0.819 | 5.39E-04 |
| cds.CL782Contig1_m.4507 | PREDICTED: importin subunit beta-1 [Vitis vinifera] | 96.404 | 15.599 | 9.6 | 6 | 10 | 3 | 0.985 | 1.032 | 1.026 | 1.014 | 0.939 | 1.01 | 0.974 | 4.03E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL798 Contig1_m .5776 | PREDICTED: ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic-like [Nicotiana tabacum] | 104.65 | 323.31 | 46.7 | 43 | 138 | 42 | 1.024 | 1.021 | 1.017 | 0.98 | 0.987 | 0.977 | 0.961 | 4.02E-04 |
| cds.CL817 Contig1_m .5545 | PREDICTED: cytosolic Fe-S cluster assembly factor NBP35-like [Sesamum indicum] | 37.852 | 4.2373 | 4.5 | 2 | 2 | 2 | 0.964 | 1.003 | 0.959 | 0.977 | 0.992 | 1.117 | 1.055 | 3.12E-01 |
| cds.CL83 Contig1_m .15259 | PREDICTED: tubulin alpha chain [Ziziphus jujuba] | 49.677 | 103.8 | 32 | 12 | 24 | 2 | 1.164 | 1.213 | 1.213 | 0.788 | 0.835 | 0.757 | 0.663 | 2.00E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL883Contig1_m.18608 | PREDICTED: sphingosine kinase 2-like isoform X3 [Juglans regia] | 22.618 | 1.7371 | 6.4 | 1 | 2 | 1 | 0.901 | 0.964 | 0.955 | 1.053 | 1.101 | 1.059 | 1.139 | 6.72E-03 |
| cds.CL883Contig1_m.18609 | PREDICTED: sphingosine kinase 1 isoform X4 [Jatropha curcas] | 20.216 | 4.4335 | 8.1 | 1 | 1 | 1 | 1.007 | 0.937 | 1.067 | 1.069 | 0.958 | 0.975 | 0.997 | 9.59E-01 |
| cds.CL89Contig1_m.16639 | PREDICTED: phosphoenolpyruvate carboxylase [Theobroma cacao] | 47.931 | 55.278 | 47.5 | 22 | 47 | 5 | 1.048 | 1.056 | 1.052 | 0.963 | 0.892 | 0.914 | 0.877 | 2.86E-02 |
| cds.CL89Contig1_m.16640 | PREDICTED: phosphoenolpyruvate carboxylase, housekeeping isozyme [Juglans | 21.338 | 14.112 | 37.9 | 7 | 15 | 2 | 0.907 | 1.147 | 1.223 | 0.962 | 0.761 | 0.997 | 0.83 | 2.10E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.CL905Contig1_m.52008 | NAD(P)-binding Rossmann-fold superfamily protein [Arabidopsis thaliana] | 13.125 | 9.1757 | 27.6 | 3 | 3 | 3 | 1.086 | 1.043 | 0.975 | 0.938 | 0.914 | 1.012 | 0.923 | 1.41E-01 |
| cds.CL976Contig1_m.11581 | PREDICTED: apoptotic chromatin condensation inducer in the nucleus isoform X2 [Vitis vinifera] | 65.388 | 52.01 | 24.6 | 12 | 14 | 12 | 1.104 | 1.085 | 1.119 | 0.877 | 0.879 | 0.881 | 0.797 | 1.58E-03 |
| cds.CL977Contig1_m.7693 | PREDICTED: LETM1 and EF-hand domain-containing protein 1, mitochondrial isoform X1 [Theobrom | 85.465 | 30.62 | 11.9 | 8 | 10 | 8 | 1.128 | 1.056 | 1.129 | 0.848 | 0.909 | 0.936 | 0.813 | 4.82E-03 |

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| cds.CL988Contig1_m.34155 | PREDICTED: non-functional NADPH-dependent codeinone reductase 2-like [Jatropha curcas] | 42.05 | 5.5254 | 6.2 | 2 | 4 | 2 | 0.975 | 1.074 | 1.065 | 1.005 | 0.946 | 0.958 | 0.934 | 1.34E-01 |
| cds.CL99Contig2_m.1015 | PREDICTED: glutamate synthase 1 [NADH], chloroplastic isoform X1 [Vitis vinifera] | 122.3 | 4.3976 | 5.1 | 5 | 5 | 2 | 0.864 | 1.014 | 0.914 | 0.98 | 1.165 | 1.096 | 1.161 | 9.73E-02 |
| cds.Camellia_sinensis.comp10002_c0_seq1_m.13184 | PREDICTED: histone deacetylase 5 [Theobroma cacao] | 56.377 | 10.34 | 5.4 | 2 | 2 | 2 | 1.051 | 1.029 | 1.025 | 1.018 | 0.936 | 0.94 | 0.932 | 6.66E-02 |
| cds.Camellia_sinensis.comp10009_c0_seq1_m.34659 | PREDICTED: UPF0587 protein C1orf123 homolog [Vitis vinifera] | 21.445 | 9.3395 | 22 | 4 | 4 | 4 | 0.907 | 0.937 | 0.868 | 1.046 | 1.156 | 1.123 | 1.226 | 5.37E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp10027_c0_seq1_m.52968 | PREDICTED: pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic isoform X1 [Citrus sinensis] | 17.263 | 1.8233 | 8.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp10031_c0_seq1_m.34320 | PREDICTED: probable pyridoxal 5'-phosphate synthase subunit PDX2 isoform X1 [Pyrus x bretschneideri] | 27.039 | 52.302 | 21.4 | 3 | 3 | 3 | 0.956 | 1.012 | 1.136 | 0.922 | 1.012 | 0.967 | 0.935 | 3.16E-01 |
| cds.Camellia_sinensis.comp10045_c0_seq1_m.58892 | PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Daucus carota subsp. sativus] | 11.199 | 6.5161 | 31.1 | 3 | 4 | 2 | 0.966 | 0.947 | 0.985 | 1.028 | 1.043 | 1.051 | 1.077 | 4.68E-03 |

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| cds.Camellia_sinensis.comp10076_c0_seq1_m.41904 | PREDICTED: mitochondrial import inner membrane translocase subunit tim16 [Nelumbo nucifera] | 12.913 | 6.0369 | 24.8 | 2 | 2 | 2 | 0.83 | 0.963 | 1.007 | 1.094 | 1.085 | 1.066 | 1.159 | 1.25E-01 |
| cds.Camellia_sinensis.comp10119_c0_seq1_m.18571 | PREDICTED: alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial [Nelumbo | 50.652 | 6.5426 | 7.5 | 3 | 3 | 3 | 1.011 | 1.102 | 1.095 | 0.878 | 0.921 | 0.982 | 0.867 | 2.84E-02 |
| cds.Camellia_sinensis.comp10251_c0_seq1_m.35387 | PREDICTED: ras-related protein Rab7-like [Juglans regia] | 23.156 | 69.963 | 55.8 | 9 | 19 | 4 | 0.995 | 0.998 | 0.957 | 1.024 | 1.011 | 1.052 | 1.046 | 6.39E-02 |
| cds.Camellia_sinensis.comp10277_c0_seq2_m.42068 | PREDICTED: thioredoxin-like 3-2, chloroplastic isoform X1 [Ziziphus jujuba] | 21.499 | 3.4925 | 10.5 | 2 | 3 | 1 | 0.984 | 0.968 | 0.951 | 1.017 | 1.042 | 1.055 | 1.073 | 8.62E-03 |

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| cds.Camellia_sinensis.comp103677_c0_seq1_m.50947 | PREDICTED: E3 ubiquitin-protein ligase RGLG2 [Prunus mume] | 20.388 | 1.4193 | 3.9 | 1 | 1 | 1 | 0.895 | 1.345 | 0.937 | 0.965 | 0.945 | 0.918 | 0.89 | 5.23E-01 |
| cds.Camellia_sinensis.comp103776_c0_seq1_m.58345 | PREDICTED: chitotriosidase-1 [Theobroma cacao] | 11.646 | 21.655 | 15 | 1 | 2 | 1 | 0.882 | 0.868 | 0.809 | 1.12 | 1.157 | 1.215 | 1.365 | 9.41E-04 |
| cds.Camellia_sinensis.comp104279_c0_seq1_m.44387 | PREDICTED: flavin-dependent oxidoreductase FOX3 [Eucalyptus grandis] | 27.511 | 5.1642 | 12.1 | 4 | 8 | 4 | 0.914 | 0.922 | 0.869 | 1.099 | 1.119 | 1.118 | 1.233 | 4.15E-04 |
| cds.Camellia_sinensis.comp10428_c0_seq1_m.47545 | PREDICTED: guanylate-binding protein 4-like [Daucus carota subsp. sativus] | 25.314 | 5.9305 | 29.7 | 6 | 8 | 3 | 0.839 | 1.184 | 0.925 | 1.031 | 1.028 | 1.02 | 1.044 | 6.50E-01 |
| cds.Camellia_sinensis.comp10437_c0_seq1_m.48501 | PREDICTED: antifungal protein ginkbilobin-2-like [Juglans regia] | 14.951 | 2.4097 | 13.1 | 2 | 2 | 2 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp10466_c0_seq1_m.43937 | PREDICTED: non-specific lipid-transfer protein-like 1 isoform X1 [Vitis vinifera] | 13.756 | 10.589 | 41.1 | 6 | 10 | 6 | 1.038 | 1.041 | 1.047 | 0.934 | 0.938 | 0.948 | 0.902 | 3.77E-05 |
| cds.Camellia_sinensis.comp105256_c0_seq1_m.46391 | PREDICTED: beta-glucosidase 24-like isoform X2 [Erythranthe guttata] | 20.853 | 5.1094 | 13 | 2 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp10550_c0_seq1_m.39041 | PREDICTED: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ-like [Nicotiana tabacum] | 25.576 | 62.654 | 30 | 6 | 16 | 6 | 0.993 | 1.004 | 1.018 | 0.985 | 1.005 | 1.023 | 0.999 | 9.58E-01 |
| cds.Camellia_sinensis.comp10577_c0_seq1_m.58057 | PREDICTED: mitochondrial dicarboxylate/tricarboxylate transporter DTC-like [Sesamum indicum] | 12.213 | 6.2969 | 11.8 | 1 | 2 | 1 | 1.062 | 1.038 | 1.03 | 0.903 | 0.958 | 0.997 | 0.913 | 3.86E-02 |

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| cds.Camellia_sinensis.comp10582_c0_seq1_m.24052 | PREDICTED: pyruvate dehydrogenase E1 component subunit alpha, mitochondrial [Malus domestica] | 48.512 | 80.594 | 34.9 | 19 | 40 | 19 | 1.016 | 1.001 | 0.996 | 0.985 | 0.994 | 0.986 | 0.984 | 7.28E-02 |
| cds.Camellia_sinensis.comp10602_c0_seq1_m.38915 | PREDICTED: AT-hook motif nuclear-localized protein 10 [Prunus mume] | 14.394 | 10.531 | 8.8 | 1 | 3 | 1 | 1.057 | 0.935 | 1.022 | 0.956 | 1.026 | 1.005 | 0.991 | 8.57E-01 |
| cds.Camellia_sinensis.comp10604_c0_seq1_m.33368 | PREDICTED: phosphoglycolate phosphatase-like [Prunus mume] | 30.956 | 17.021 | 14.2 | 3 | 4 | 3 | 0.974 | 0.945 | 0.885 | 1.042 | 1.076 | 1.087 | 1.143 | 1.24E-02 |
| cds.Camellia_sinensis.comp10649_c0_seq1_m.43648 | PREDICTED: phosphoenolpyruvate carboxykinase [ATP] [Ziziphus jujuba] | 24.519 | 4.0395 | 8.9 | 2 | 2 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp10650_c0_seq1_m.12647 | PREDICTED: phosphomethylpyrimidine synthase, chloroplastic-like isoform X3 [Daucus carota subsp. sativus] | 71.575 | 19.171 | 12.4 | 7 | 8 | 7 | 0.947 | 0.934 | 0.985 | 1.074 | 1.019 | 1.09 | 1.111 | 1.56E-02 |
| cds.Camellia_sinensis.comp10670_c0_seq1_m.13958 | PREDICTED: phytoene synthase 2, chloroplastic [Vitis vinifera] | 47.654 | 10.005 | 8.5 | 3 | 3 | 3 | 0.84 | 1.058 | 0.978 | 1.051 | 1.168 | 0.944 | 1.1 | 3.54E-01 |
| cds.Camellia_sinensis.comp10679_c0_seq1_m.20913 | PREDICTED: hsp70-binding protein 1 [Solanum lycopersicum] | 43.71 | 50.961 | 16.8 | 7 | 13 | 7 | 0.974 | 0.939 | 0.951 | 1.072 | 1.047 | 1.058 | 1.109 | 1.22E-03 |
| cds.Camellia_sinensis.comp10702_c0_seq1_m.27407 | PREDICTED: UBP1-associated protein 2A [Daucus carota subsp. sativus] | 41.879 | 1.7058 | 3.8 | 2 | 2 | 2 | 1.154 | 1.093 | 1.082 | 0.9 | 0.894 | 0.846 | 0.793 | 1.16E-03 |

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| cds.Camellia_sinensis.comp10716_c0_seq1_m.30794 | PREDICTED: lon protease 2-like [Ziziphus jujuba] | 32.11 | 32.236 | 9.5 | 2 | 3 | 2 | 0.955 | 0.916 | 0.95 | 1.137 | 1.058 | 1.017 | 1.139 | 2.15E-02 |
| cds.Camellia_sinensis.comp10740_c0_seq1_m.6969 | PREDICTED: uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic [Jatropha curcas] | 86.068 | 53.07 | 16.7 | 12 | 19 | 11 | 0.989 | 0.976 | 0.96 | 1.037 | 1.065 | 1.026 | 1.069 | 8.80E-03 |
| cds.Camellia_sinensis.comp107685_c0_seq1_m.5269 | | 18.556 | 2.2212 | 5.6 | 1 | 2 | 1 | 0.978 | 1.006 | 1.029 | 1.013 | 0.984 | 1.001 | 0.995 | 7.89E-01 |
| cds.Camellia_sinensis.comp10794_c0_seq1_m.22161 | PREDICTED: BAG family molecular chaperone regulator 7 [Nicotiana sylvestris] | 30.069 | 6.3271 | 10.6 | 3 | 4 | 3 | 0.989 | 1.058 | 1.07 | 1.035 | 0.947 | 0.909 | 0.927 | 1.70E-01 |

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| cds.Camellia_sinensis.comp10794_c0_seq1_m.22162 | PREDICTED: BAG family molecular chaperone regulator 7-like [Juglans regia] | 15.821 | 12.688 | 10.8 | 1 | 1 | 1 | 0.925 | 0.94 | 1.249 | 1.002 | 0.832 | 1.063 | 0.93 | 6.09E-01 |
| cds.Camellia_sinensis.comp10805_c0_seq1_m.49876 | PREDICTED: glycine-rich RNA-binding protein RZ1A-like [Gossypium hirsutum] | 17.868 | 12.882 | 21.3 | 3 | 5 | 3 | 1.145 | 1.153 | 1.244 | 0.744 | 0.842 | 0.799 | 0.673 | 8.95E-04 |
| cds.Camellia_sinensis.comp10829_c0_seq1_m.25743 | PREDICTED: AT-hook motif nuclear-localized protein 14 [Vitis vinifera] | 39.991 | 164.91 | 33 | 9 | 11 | 9 | 1.024 | 0.977 | 0.978 | 0.98 | 1.041 | 1.003 | 1.015 | 5.59E-01 |
| cds.Camellia_sinensis.comp10859_c0_seq2_m.23812 | PREDICTED: COP9 signalosome complex subunit 3 [Nicotiana | 48.594 | 37.069 | 18.9 | 7 | 9 | 7 | 0.982 | 0.945 | 1.015 | 1.018 | 1.056 | 1.059 | 1.065 | 5.97E-02 |
| cds.Camellia_sinensis.comp10873_c0_seq1_m.42113 | PREDICTED: 14-3-3-like protein B [Cicer arietinum] | 22.119 | 34.154 | 40.7 | 7 | 20 | 5 | 1.001 | 0.976 | 0.974 | 0.973 | 1.025 | 1.027 | 1.025 | 2.82E-01 |

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| cds.Camellia_sinensis.comp10899_c0_seq1_m.41027 | PREDICTED: transmembrane protein 205 [Vigna radiata var. radiata] | 24.758 | 5.8363 | 5.5 | 1 | 4 | 1 | 0.991 | 0.976 | 1.056 | 1.038 | 0.985 | 0.999 | 1 | 1.00E+00 |
| cds.Camellia_sinensis.comp10922_c0_seq1_m.28802 | PREDICTED: succinyl-CoA ligase [ADP-forming] subunit alpha-1, mitochondrial [Solanum tuberosum | 36.392 | 31.068 | 20.6 | 6 | 14 | 6 | 1.02 | 0.968 | 1.05 | 0.981 | 0.994 | 0.983 | 0.974 | 3.40E-01 |
| cds.Camellia_sinensis.comp10926_c0_seq1_m.45554 | PREDICTED: acyl carrier protein 1, mitochondrial [Sesamum indicum] | 18.28 | 2.3596 | 5.5 | 1 | 2 | 1 | 1.066 | 1.02 | 1.07 | 0.905 | 0.979 | 0.949 | 0.898 | 1.71E-02 |
| cds.Camellia_sinensis.comp10929_c0_seq1_m.22775 | PREDICTED: phosphoserine aminotransferase 2, chloroplastic [Vitis vinifera] | 47.171 | 111.85 | 38.5 | 13 | 28 | 13 | 0.993 | 1.043 | 1.023 | 1.023 | 0.962 | 0.97 | 0.966 | 2.21E-01 |

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| cds.Camellia_sinensis.comp10930_c0_seq1_m.21645 | PREDICTED: glucan endo-1,3-beta-glucosidase [Erythrant | 50.098 | 5.7764 | 3.9 | 2 | 2 | 2 | 0.999 | 1.023 | 1.061 | 1.018 | 0.979 | 0.927 | 0.948 | 1.74E-01 |
| cds.Camellia_sinensis.comp10937_c0_seq2_m.44764 | PREDICTED: photosystem II D1 precursor processing protein PSB27-H2, chloroplastic [Ipomoea nil] | 15.999 | 31.45 | 40.6 | 6 | 7 | 6 | 1.071 | 1.075 | 1.093 | 0.884 | 0.932 | 0.91 | 0.842 | 4.77E-04 |
| cds.Camellia_sinensis.comp10941_c0_seq1_m.18623 | PREDICTED: aldehyde dehydrogenase family 3 member F1-like [Daucus carota subsp. sativus] | 25.483 | 3.5866 | 4.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp10943_c0_seq1_m.42550 | PREDICTED: glutaredoxin-C4 [Populus euphratica] | 16.37 | 22.511 | 15.4 | 2 | 2 | 2 | 1.098 | 1.028 | 0.843 | 0.976 | 1.003 | 1.048 | 1.02 | 7.75E-01 |

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| cds.Camellia_sinensis.comp11072_c0_seq1_m.44776 | PREDICTED: succinate dehydrogenase subunit 6, mitochondrial-like [Solanum tuberosum | 19.945 | 11.896 | 29.4 | 4 | 5 | 4 | 1.013 | 0.982 | 1.002 | 1.052 | 1.058 | 0.992 | 1.035 | 2.04E-01 |
| cds.Camellia_sinensis.comp11086_c0_seq1_m.29628 | PREDICTED: calcium sensing receptor, chloroplastic [Citrus sinensis] | 43.539 | 156.22 | 42.3 | 16 | 36 | 16 | 0.984 | 0.992 | 0.981 | 1.014 | 1.018 | 1.004 | 1.027 | 7.60E-03 |
| cds.Camellia_sinensis.comp11136_c0_seq1_m.33507 | Proliferating cell nuclear antigen [Morus notabilis] | 33.406 | 14.977 | 19.1 | 5 | 7 | 5 | 0.978 | 0.98 | 1.008 | 1.011 | 1.046 | 1.02 | 1.037 | 5.98E-02 |
| cds.Camellia_sinensis.comp11149_c0_seq1_m.18881 | PREDICTED: ammonium transporter 3 member 1-like [Jatropha | 52.367 | 2.0667 | 3.5 | 2 | 2 | 2 | 1.166 | 1.133 | 1.051 | 0.91 | 0.831 | 0.874 | 0.781 | 3.66E-03 |

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| cds.Camellia_sinensis.comp11151_c0_seq1_m.35921 | PREDICTED: pleiotropic drug resistance protein 2-like, partial [Erythranthe guttata] | 40.419 | 9.4332 | 13.5 | 5 | 6 | 3 | 0.931 | 0.995 | 0.906 | 1.079 | 1.064 | 1.023 | 1.118 | 2.51E-02 |
| cds.Camellia_sinensis.comp11161_c0_seq1_m.44788 | PREDICTED: 60S ribosomal protein L4 [Ziziphus jujuba] | 28.225 | 18.139 | 35.5 | 8 | 11 | 3 | 1.114 | 1.147 | 1.114 | 0.822 | 0.84 | 0.926 | 0.767 | 2.14E-03 |
| cds.Camellia_sinensis.comp11194_c0_seq1_m.50433 | PREDICTED: disease resistance protein RPM1 [Vitis vinifera] | 21.26 | 1.2005 | 5.9 | 1 | 1 | 1 | 0.73 | 1.04 | 1.353 | 1.193 | 0.899 | 0.835 | 0.937 | 8.38E-01 |
| cds.Camellia_sinensis.comp11219_c0_seq1_m.30122 | PREDICTED: peroxisomal 2,4-dienoyl-CoA reductase [Vitis vinifera] | 31.846 | 1.3712 | 6.1 | 2 | 2 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp11229_c0_seq2_m.47116 | PREDICTED: phosphomannomutase/phosphoglucomutase [Prunus mume] | 24.123 | 16.236 | 20.6 | 4 | 6 | 4 | 0.999 | 0.978 | 0.978 | 0.99 | 1.017 | 1.005 | 1.019 | 1.44E-01 |
| cds.Camellia_sinensis.comp11267_c0_seq1_m.29394 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 7 homolog A [Nicotiana | 34.835 | 46.161 | 17.7 | 5 | 9 | 5 | 1.012 | 0.97 | 0.962 | 1 | 1.028 | 1.047 | 1.044 | 1.02E-01 |
| cds.Camellia_sinensis.comp11318_c0_seq1_m.52741 | PREDICTED: ferredoxin--NADP reductase, leaf isozyme, chloroplastic [Glycine max] | 11.816 | 20.431 | 70.7 | 8 | 29 | 4 | 0.978 | 0.947 | 0.959 | 1.021 | 1.067 | 1.037 | 1.084 | 7.34E-03 |
| cds.Camellia_sinensis.comp11344_c0_seq1_m.52995 | PREDICTED: STS14 protein [Vitis vinifera] | 16.43 | 4.0858 | 13.2 | 2 | 2 | 2 | 0.995 | 1.062 | 1.048 | 1.073 | 0.876 | 0.953 | 0.935 | 3.19E-01 |

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| cds.Camellia_sinensis.comp11350_c0_seq1_m.32544 | PREDICTED: uncharacterized oxidoreductase At4g09670-like [Nicotiana attenuata] | 41.58 | 16.216 | 9.6 | 3 | 6 | 3 | 0.958 | 1.014 | 1.066 | 0.942 | 1.028 | 1.01 | 0.981 | 6.65E-01 |
| cds.Camellia_sinensis.comp11374_c0_seq1_m.28394 | PREDICTED: WD-40 repeat-containing protein MSI3 [Vitis vinifera] | 46.422 | 3.9703 | 6.1 | 3 | 3 | 3 | 0.872 | 1.135 | 0.927 | 1.111 | 0.968 | 1.017 | 1.055 | 5.48E-01 |
| cds.Camellia_sinensis.comp11379_c0_seq1_m.29727 | PREDICTED: acetylglutamate kinase, chloroplastic [Vitis vinifera] | 41.239 | 15.931 | 14.3 | 4 | 5 | 4 | 1.075 | 1.016 | 1.002 | 0.954 | 0.998 | 0.916 | 0.927 | 8.23E-02 |
| cds.Camellia_sinensis.comp11391_c0_seq1_m.35926 | PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial [Ipomoea nil] | 26.285 | 66.654 | 35.5 | 9 | 18 | 9 | 1.02 | 0.984 | 1.048 | 0.98 | 0.969 | 0.983 | 0.961 | 1.01E-01 |

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| cds.Camellia_sinensis.comp11398_c0_seq1_m.34837 | PREDICTED: glyoxylate/succinic semialdehyde reductase 1 [Vitis vinifera] | 32.042 | 91.026 | 44.8 | 10 | 26 | 10 | 0.995 | 0.992 | 1.003 | 1.017 | 1.01 | 1.027 | 1.021 | 2.24E-02 |
| cds.Camellia_sinensis.comp11416_c0_seq1_m.21653 | PREDICTED: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic-like [Daucus carota subsp.sativus] | 51.808 | 77.835 | 40.7 | 19 | 34 | 19 | 0.991 | 1.039 | 1.01 | 0.997 | 0.978 | 0.993 | 0.976 | 1.86E-01 |
| cds.Camellia_sinensis.comp11449_c0_seq1_m.31170 | PREDICTED: phosphoglycolate phosphatase 1B, chloroplastic [Cucumis sativus] | 35.737 | 145.09 | 41.5 | 12 | 33 | 12 | 1.016 | 1.014 | 1.016 | 0.982 | 0.985 | 0.972 | 0.965 | 9.22E-04 |

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| cds.Camellia_sinensis.comp11457_c0_seq1_m.35713 | PREDICTED: structural maintenance of chromosomes protein 1A [Sesamum indicum] | 19.921 | 14.027 | 43 | 9 | 10 | 9 | 1 | 0.977 | 0.991 | 1.008 | 1.01 | 1.01 | 1.02 | 9.84E-02 |
| cds.Camellia_sinensis.comp11498_c0_seq1_m.44271 | PREDICTED: glucan endo-1,3-beta-glucosidase 12-like [Glycine | 27.773 | 27.131 | 8.9 | 2 | 2 | 2 | 0.942 | 0.927 | 0.942 | 1.047 | 1.084 | 1.086 | 1.144 | 4.97E-04 |
| cds.Camellia_sinensis.comp11527_c0_seq1_m.47902 | PREDICTED: molybdopterin synthase sulfur carrier subunit [Ipomoea nil] | 11.663 | 3.8458 | 9.4 | 1 | 1 | 1 | 0.978 | 0.897 | 0.898 | 1.065 | 1.081 | 1.109 | 1.174 | 6.54E-03 |
| cds.Camellia_sinensis.comp11529_c0_seq2_m.48725 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP12 [Fragaria vesca subsp. vesca] | 11.929 | 44.809 | 30.4 | 3 | 13 | 3 | 0.995 | 0.987 | 1.011 | 1 | 1.011 | 1.018 | 1.012 | 2.43E-01 |

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| cds.Camellia_sinensis.comp11557_c0_seq1_m.4291 | PREDICTED: probable glutamyl endopeptidase, chloroplastic isoform X2 [Vitis vinifera] | 110.49 | 119.62 | 22.3 | 16 | 29 | 16 | 1.003 | 1.041 | 1.014 | 0.967 | 0.961 | 0.992 | 0.955 | 3.49E-02 |
| cds.Camellia_sinensis.comp11579_c0_seq1_m.31962 | PREDICTED: 3-hydroxybutyryl-CoA dehydrogenase [Prunus mume] | 31.825 | 26.559 | 9.8 | 3 | 3 | 3 | 0.929 | 0.941 | 0.979 | 1.043 | 1.044 | 1.09 | 1.115 | 7.08E-03 |
| cds.Camellia_sinensis.comp11588_c0_seq1_m.34643 | PREDICTED: peptide methionine sulfoxide reductase B1, chloroplastic [Ziziphus jujuba] | 21.568 | 15.256 | 14.9 | 3 | 3 | 3 | 1.03 | 0.963 | 1.013 | 0.97 | 1.009 | 1.019 | 0.997 | 9.26E-01 |
| cds.Camellia_sinensis.comp11591_c0_seq1_m.53844 | PREDICTED: catalase isozyme 1 [Vitis vinifera] | 17.178 | 35.749 | 40.9 | 5 | 20 | 1 | 0.931 | 0.982 | 0.865 | 0.961 | 1.093 | 1.13 | 1.146 | 9.29E-02 |

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| cds.Camellia_sinensis.comp11597_c0_seq1_m.23792 | PREDICTED: putative MO25-like protein At5g47540 [Vitis vinifera] | 39.236 | 9.8383 | 18.8 | 7 | 13 | 7 | 0.927 | 0.952 | 0.966 | 1.056 | 1.052 | 1.021 | 1.1 | 4.10E-03 |
| cds.Camellia_sinensis.comp11628_c0_seq1_m.34499 | PREDICTED: vacuolar protein sorting-associated protein 28 homolog 1 [Populus euphratica] | 23.354 | 3.7567 | 12 | 2 | 2 | 2 | 0.853 | 1.064 | 1.016 | 1.151 | 1.022 | 0.933 | 1.059 | 5.57E-01 |
| cds.Camellia_sinensis.comp11639_c0_seq1_m.49146 | PREDICTED: probable plastid-lipid-associated protein 4, chloroplastic isoform X2 [Vitis vinifera] | 19.698 | 4.8786 | 9.1 | 2 | 6 | 2 | 1.043 | 1.022 | 0.971 | 0.928 | 1.059 | 0.931 | 0.961 | 4.44E-01 |
| cds.Camellia_sinensis.comp11661_c0_seq2_m.16778 | PREDICTED: protochlorophyllide-dependent translocon component 52, chloroplastic [Vitis vinifera] | 66.107 | 9.7587 | 9.8 | 7 | 8 | 6 | 1.02 | 1.015 | 1.002 | 1.033 | 0.982 | 0.953 | 0.977 | 3.85E-01 |

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| cds.Camellia_sinensis.comp11716_c0_seq1_m.37295 | PREDICTED: 40S ribosomal protein S7 [Nelumbo nucifera] | 26.673 | 10.971 | 19.4 | 5 | 8 | 5 | 1.188 | 1.23 | 1.177 | 0.751 | 0.773 | 0.773 | 0.639 | 1.55E-05 |
| cds.Camellia_sinensis.comp11738_c0_seq1_m.37320 | PREDICTED: outer envelope pore protein 16, chloroplastic [Nicotiana tomentosiformis] | 15.6 | 94.818 | 39 | 5 | 24 | 5 | 1.008 | 0.989 | 0.986 | 1.01 | 1.047 | 0.989 | 1.021 | 3.15E-01 |
| cds.Camellia_sinensis.comp117518_c0_seq1_m.43727 | PREDICTED: cytochrome P450 87A3-like [Juglans regia] | 26.7 | 1.7493 | 4.7 | 2 | 2 | 2 | 0.865 | 0.824 | 0.852 | 1.094 | 1.164 | 1.254 | 1.382 | 1.54E-03 |
| cds.Camellia_sinensis.comp11764_c1_seq1_m.32328 | PREDICTED: short-chain dehydrogenase TIC 32, chloroplastic [Vitis vinifera] | 33.759 | 159.67 | 55.8 | 13 | 40 | 13 | 1.03 | 1.011 | 1.031 | 0.975 | 0.99 | 0.966 | 0.954 | 8.02E-03 |
| cds.Camellia_sinensis.comp11800_c0_seq1_m.29878 | PREDICTED: glutathione S-transferase L3 [Vitis vinifera] | 31.872 | 156.82 | 47 | 15 | 64 | 14 | 0.949 | 0.908 | 0.925 | 1.062 | 1.106 | 1.085 | 1.169 | 8.40E-04 |

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| cds.Camellia_sinensis.comp11805_c0_seq1_m.42615 | profilin-1 [Jatropha curcas] | 14.199 | 2.6814 | 24.4 | 3 | 10 | 2 | 0.977 | 0.884 | 1.086 | 1.193 | 0.967 | 0.923 | 1.046 | 6.91E-01 |
| cds.Camellia_sinensis.comp11843_c0_seq1_m.25706 | PREDICTED: malate dehydrogenase, mitochondrial-like [Nelumbo nucifera] | 36.749 | 181.98 | 40.1 | 13 | 35 | 12 | 1.028 | 1.007 | 1.027 | 0.944 | 0.976 | 1.009 | 0.957 | 9.30E-02 |
| cds.Camellia_sinensis.comp11884_c0_seq1_m.37327 | PREDICTED: OTU domain-containing protein At3g57810 [Jatropha curcas] | 26.012 | 4.7359 | 4.3 | 1 | 1 | 1 | 1.148 | 1.042 | 1.194 | 0.805 | 0.911 | 0.865 | 0.763 | 7.48E-03 |
| cds.Camellia_sinensis.comp11900_c0_seq1_m.29683 | PREDICTED: peroxidase 4 [Citrus sinensis] | 35.543 | 92.403 | 36.8 | 9 | 22 | 8 | 1.125 | 1.091 | 1.049 | 0.908 | 0.876 | 0.901 | 0.822 | 1.06E-03 |
| cds.Camellia_sinensis.comp11934_c0_seq1_m.57022 | PREDICTED: heat shock cognate 70 kDa protein 2-like [Erythranthe guttata] | 12.911 | 8.5621 | 53.8 | 5 | 23 | 1 | 1.065 | 1.041 | 0.973 | 0.93 | 1.02 | 0.964 | 0.946 | 2.23E-01 |

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| cds.Camellia_sinensis.comp11945_c0_seq1_m.33686 | PREDICTED: stem-specific protein TSJT1-like [Sesamum indicum] | 25.441 | 18.713 | 14.4 | 3 | 7 | 3 | 0.924 | 0.963 | 0.886 | 1.078 | 1.104 | 1.105 | 1.185 | 2.56E-03 |
| cds.Camellia_sinensis.comp11995_c0_seq1_m.39460 | PREDICTED: small ubiquitin-related modifier 1-like [Fragaria vesca subsp. vesca] | 13.624 | 4.9855 | 29.4 | 4 | 9 | 1 | 1.017 | 0.921 | 1.125 | 0.943 | 1.032 | 0.968 | 0.961 | 5.89E-01 |
| cds.Camellia_sinensis.comp12026_c0_seq1_m.47397 | PREDICTED: photosystem I reaction center subunit psaK, chloroplastic [Vitis vinifera] | 13.451 | 2.7599 | 12.2 | 2 | 5 | 2 | 1.006 | 1.01 | 0.984 | 0.991 | 0.985 | 1.046 | 1.007 | 7.53E-01 |
| cds.Camellia_sinensis.comp12032_c0_seq1_m.38308 | PREDICTED: probable histone H2A.1 [Nicotiana attenuata] | 13.993 | 19.493 | 33.6 | 6 | 16 | 3 | 1.184 | 1.141 | 1.088 | 0.827 | 0.805 | 0.938 | 0.753 | 5.80E-03 |

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| cds.Camellia_sinensis.comp12035_c0_seq1_m.47225 | PREDICTED: photosystem I reaction center subunit V, chloroplastic [Vitis vinifera] | 15.891 | 12.339 | 17.8 | 3 | 4 | 3 | 0.928 | 0.99 | 0.985 | 1.007 | 1.065 | 0.998 | 1.058 | 1.27E-01 |
| cds.Camellia_sinensis.comp12046_c0_seq1_m.35841 | PREDICTED: HMG1/2-like protein isoform X2 [Vitis vinifera] | 24.621 | 4.1536 | 12.7 | 3 | 3 | 2 | 0.919 | 1.002 | 1.037 | 0.971 | 0.999 | 1.089 | 1.034 | 5.36E-01 |
| cds.Camellia_sinensis.comp12057_c0_seq1_m.27251 | cysteine protease RD19A-like [Cajanus cajan] | 45.032 | 16.485 | 14.4 | 6 | 12 | 4 | 1.053 | 1.02 | 1.001 | 0.928 | 1.001 | 0.981 | 0.947 | 1.11E-01 |
| cds.Camellia_sinensis.comp12070_c0_seq1_m.37627 | PREDICTED: protein CURVATURE THYLAKOID 1B, chloroplastic [Juglans regia] | 18.713 | 7.7143 | 13.6 | 4 | 10 | 4 | 1.046 | 1.002 | 1.046 | 0.984 | 0.985 | 0.964 | 0.948 | 2.88E-02 |

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| cds.Camellia_sinensis.comp12084_c0_seq1_m.30795 | PREDICTED: probable carboxylesterase 5 [Juglans regia] | 33.135 | 145.62 | 56.2 | 15 | 57 | 15 | 1.047 | 1.06 | 1.045 | 0.954 | 0.93 | 0.953 | 0.9 | 3.64E-04 |
| cds.Camellia_sinensis.comp12137_c0_seq1_m.17932 | PREDICTED: glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic [Nelumbo nucifera] | 43.261 | 323.31 | 49.1 | 19 | 127 | 16 | 0.995 | 1 | 1.002 | 1.003 | 0.989 | 1.004 | 1 | 9.50E-01 |
| cds.Camellia_sinensis.comp12164_c0_seq1_m.26995 | PREDICTED: leucoanthocyanidin reductase [Theobroma cacao] | 37.588 | 1.2298 | 4.1 | 2 | 2 | 2 | 1.429 | 1.296 | 1.581 | 0.591 | 0.449 | 0.524 | 0.363 | 4.95E-04 |
| cds.Camellia_sinensis.comp12185_c0_seq1_m.39884 | PREDICTED: stress-response A/B barrel domain-containing protein At5g22580 [Theobrom | 12.035 | 9.14 | 35.8 | 3 | 4 | 3 | 0.968 | 0.924 | 0.998 | 1.026 | 1.11 | 0.99 | 1.082 | 1.27E-01 |

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| cds.Camellia_sinensis.comp12192_c0_seq1_m.22171 | PREDICTED: fructose-bisphosphate aldolase 1, chloroplastic [Solanum pennellii] | 42.925 | 323.31 | 63.2 | 21 | 101 | 20 | 1.051 | 1.044 | 1.042 | 0.93 | 0.957 | 0.938 | 0.901 | 2.97E-04 |
| cds.Camellia_sinensis.comp12208_c0_seq1_m.38668 | PREDICTED: photosystem I reaction center subunit N, chloroplastic-like [Gossypium hirsutum] | 18.763 | 55.291 | 33.9 | 6 | 30 | 6 | 0.99 | 0.989 | 1.004 | 1.013 | 1.004 | 0.983 | 1.006 | 6.09E-01 |
| cds.Camellia_sinensis.comp12243_c0_seq1_m.43261 | PREDICTED: photosystem II repair protein PSB27-H1, chloroplastic [Solanum pennellii] | 21.983 | 80.639 | 23.3 | 6 | 28 | 6 | 1.021 | 1.019 | 0.988 | 1.004 | 1.007 | 0.998 | 0.994 | 6.03E-01 |

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| cds.Camellia_sinensis.comp12293_c0_seq1_m.10889 | RUBISCO SUBUNIT BINDING-protein ALPHA SUBUNIT [Populus trichocarpa] | 62.205 | 323.31 | 42.5 | 22 | 74 | 21 | 1.025 | 0.988 | 0.994 | 1.007 | 1.016 | 0.987 | 1.001 | 9.45E-01 |
| cds.Camellia_sinensis.comp12317_c0_seq1_m.25908 | PREDICTED: probable fructokinase-4 [Vitis vinifera] | 34.089 | 90.402 | 44.3 | 11 | 25 | 11 | 1.037 | 1.107 | 1.042 | 0.929 | 0.936 | 0.924 | 0.875 | 3.42E-03 |
| cds.Camellia_sinensis.comp12370_c1_seq10_c1_seq1_m.15160 | PREDICTED: patellin-3-like [Gossypium arboreum] | 64.688 | 110.89 | 43.4 | 21 | 36 | 20 | 0.871 | 0.863 | 0.889 | 1.115 | 1.153 | 1.163 | 1.308 | 6.31E-05 |
| cds.Camellia_sinensis.comp12396_c0_seq1_m.16096 | PREDICTED: T-complex protein 1 subunit beta [Ziziphus jujuba] | 57.154 | 181.76 | 45.9 | 21 | 40 | 21 | 0.941 | 0.969 | 0.922 | 1.057 | 1.048 | 1.064 | 1.119 | 1.72E-03 |

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| cds.Camellia_sinensis.comp12441_c0_seq1_m.14154 | PREDICTED: bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic [Vitis vinifera] | 58.235 | 113.88 | 32.7 | 17 | 30 | 16 | 1.237 | 1.275 | 1.282 | 0.707 | 0.716 | 0.69 | 0.557 | 1.48E-06 |
| cds.Camellia_sinensis.comp12442_c0_seq1_m.43097 | PREDICTED: probable xyloglucan endotransglucosylase/hydrolase protein 7 [Prunus mume] | 31.109 | 10.601 | 22.1 | 4 | 7 | 2 | 0.993 | 0.836 | 1.026 | 1.15 | 1.073 | 0.955 | 1.113 | 2.65E-01 |
| cds.Camellia_sinensis.comp12443_c0_seq1_m.27897 | PREDICTED: chloroplast stem-loop binding protein of 41 kDa a, chloroplastic-like [Populus euphratica] | 43.629 | 157.32 | 44.8 | 17 | 54 | 17 | 1.04 | 1.023 | 1.036 | 0.954 | 0.979 | 0.968 | 0.936 | 1.82E-03 |

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| cds.Camellia_sinensis.comp12477_c0_seq1_m.17378 | PREDICTED: glucan endo-1,3-beta-glucosidase 7-like [Jatropha | 28.881 | 3.5986 | 7.4 | 2 | 3 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp12500_c0_seq1_m.21591 | PREDICTED: serine carboxypeptidase-like 7 [Vitis vinifera] | 54.522 | 17.149 | 11.5 | 5 | 5 | 5 | 1.056 | 1.042 | 1.002 | 0.927 | 0.993 | 0.925 | 0.918 | 3.75E-02 |
| cds.Camellia_sinensis.comp12573_c0_seq1_m.29104 | PREDICTED: transcription factor VIP1 [Vitis vinifera] | 37.75 | 7.2577 | 7.9 | 3 | 6 | 3 | 1.038 | 1.032 | 1.055 | 0.978 | 0.941 | 0.989 | 0.931 | 1.18E-02 |
| cds.Camellia_sinensis.comp12605_c0_seq1_m.52149 | PREDICTED: coatomer subunit delta [Prunus mume] | 13.687 | 2.1048 | 17.6 | 2 | 2 | 1 | 1.079 | 0.987 | 1.028 | 0.9 | 0.983 | 1.012 | 0.936 | 2.00E-01 |
| cds.Camellia_sinensis.comp12611_c0_seq1_m.30871 | PREDICTED: protein BOLA4, chloroplastic/mitochondrial [Ricinus communis] | 20.032 | 29.401 | 17.2 | 2 | 3 | 2 | 1.015 | 1.083 | 0.97 | 0.987 | 0.953 | 0.985 | 0.953 | 2.40E-01 |

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| cds.Camellia_sinensis.comp12679_c0_seq1_m.35855 | PREDICTED: aquaporin TIP1-3 [Eucalyptus grandis] | 26.001 | 3.5046 | 6.3 | 2 | 3 | 2 | 0.853 | 0.798 | 0.853 | 1.104 | 1.169 | 1.278 | 1.418 | 1.92E-03 |
| cds.Camellia_sinensis.comp12682_c0_seq1_m.34284 | Rieske (2Fe-2S) domain protein [Medicago truncatula] | 31.181 | 224.77 | 48.3 | 11 | 44 | 11 | 1.026 | 1.037 | 1.043 | 0.971 | 0.963 | 0.964 | 0.933 | 2.22E-04 |
| cds.Camellia_sinensis.comp12697_c0_seq1_m.39056 | F1N21.17 [Arabidopsis lyrata subsp. lyrata] | 11.838 | 26.808 | 47.5 | 3 | 5 | 3 | 1.014 | 1.076 | 1.038 | 0.947 | 0.933 | 0.982 | 0.915 | 1.81E-02 |
| cds.Camellia_sinensis.comp12720_c0_seq1_m.56493 | PREDICTED: nitronate monooxygenase [Daucus carota subsp. sativus] | 12.511 | 7.9073 | 9.5 | 1 | 1 | 1 | 0.901 | 0.976 | 0.902 | 1.143 | 1.081 | 1.038 | 1.174 | 1.41E-02 |
| cds.Camellia_sinensis.comp12723_c0_seq1_m.32948 | PREDICTED: cytochrome c oxidase subunit 6b-1 [Sesamum indicum] | 19.951 | 8.4083 | 22.7 | 4 | 8 | 4 | 0.993 | 1.029 | 1.043 | 0.98 | 0.964 | 0.94 | 0.941 | 3.30E-02 |

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| cds.Camellia_sinensis.comp12739_c0_seq1_m.34624 | PREDICTED: 40S ribosomal protein S3-3-like [Nelumbo nucifera] | 21.394 | 39.616 | 73.4 | 12 | 20 | 7 | 0.99 | 0.995 | 0.983 | 1.043 | 1.047 | 1.002 | 1.042 | 4.82E-02 |
| cds.Camellia_sinensis.comp12750_c0_seq1_m.38253 | PREDICTED: transmembrane emp24 domain-containing protein p24delta3 [Vitis vinifera] | 24.849 | 4.1806 | 11.4 | 3 | 4 | 3 | 0.969 | 0.952 | 0.955 | 1.047 | 1.036 | 0.997 | 1.071 | 1.25E-02 |
| cds.Camellia_sinensis.comp12764_c0_seq1_m.17074 | PREDICTED: vegetative cell wall protein gp1 [Capsicum annuum] | 13.5 | 17.706 | 30.5 | 4 | 8 | 4 | 1.017 | 0.994 | 1.008 | 0.982 | 0.979 | 0.983 | 0.975 | 2.07E-02 |
| cds.Camellia_sinensis.comp12781_c0_seq1_m.25470 | PREDICTED: dihydroflavonol-4-reductase-like [Daucus carota subsp. sativus] | 38.694 | 20.965 | 19.6 | 9 | 16 | 9 | 1.433 | 1.386 | 1.417 | 0.53 | 0.54 | 0.534 | 0.379 | 5.31E-08 |

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| cds.Camellia_sinensis.comp12805_c0_seq1_m.26397 | PREDICTED: cathepsin B-like [Nelumbo nucifera] | 45.009 | 21.051 | 15 | 5 | 11 | 5 | 1.045 | 1.079 | 1.049 | 0.938 | 0.964 | 0.905 | 0.885 | 4.18E-03 |
| cds.Camellia_sinensis.comp12825_c0_seq1_m.44303 | PREDICTED: probable prefoldin subunit 5 [Theobroma cacao] | 20.62 | 3.3063 | 10.8 | 2 | 2 | 2 | 0.882 | 0.931 | 0.846 | 1.145 | 1.014 | 1.226 | 1.273 | 1.82E-02 |
| cds.Camellia_sinensis.comp12828_c1_seq1_m.58512 | 60S ribosomal protein L35a-3 [Morus notabilis] | 12.254 | 1.9256 | 13.2 | 2 | 2 | 2 | 1.098 | 1.204 | 1.164 | 0.907 | 0.783 | 0.811 | 0.722 | 3.22E-03 |
| cds.Camellia_sinensis.comp12830_c0_seq1_m.44966 | latex abundant protein 1 [Populus trichocarpa] | 17.592 | 183.19 | 71.2 | 10 | 24 | 10 | 1.134 | 1.077 | 1.012 | 0.896 | 0.94 | 0.931 | 0.859 | 1.36E-02 |
| cds.Camellia_sinensis.comp12874_c0_seq1_m.59108 | PREDICTED: probable methionine--tRNA ligase [Daucus carota subsp. sativus] | 11.747 | 1.1922 | 36.3 | 3 | 3 | 1 | 1.246 | 1.051 | 1.165 | 0.777 | 0.91 | 0.799 | 0.718 | 8.84E-03 |

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| cds.Camellia_sinensis.comp12954_c0_seq1_m.32734 | PREDICTED: histone H1-like isoform X1 [Ipomoea nil] | 29.007 | 11.118 | 23.9 | 7 | 10 | 7 | 1.05 | 1.019 | 1.07 | 0.943 | 0.927 | 0.966 | 0.903 | 5.46E-03 |
| cds.Camellia_sinensis.comp13022_c0_seq1_m.21360 | PREDICTED: rhodanese-like domain-containing protein 4, chloroplastic [Prunus mume] | 47.668 | 172.77 | 34.7 | 16 | 47 | 16 | 1.003 | 0.996 | 1.008 | 0.981 | 1.019 | 0.999 | 0.997 | 8.22E-01 |
| cds.Camellia_sinensis.comp13036_c0_seq1_m.55058 | PREDICTED: pectinesterase [Ricinus communis] | 14.909 | 7.6807 | 16.8 | 2 | 3 | 2 | 0.999 | 0.994 | 0.963 | 0.996 | 0.996 | 1.048 | 1.028 | 2.45E-01 |
| cds.Camellia_sinensis.comp13044_c0_seq1_m.53290 | PREDICTED: putative cytochrome c oxidase subunit 5b-like [Nicotiana tabacum] | 13.886 | 31.738 | 35.2 | 4 | 8 | 4 | 1.003 | 1.09 | 1.027 | 1.025 | 0.947 | 0.907 | 0.923 | 1.36E-01 |

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| cds.Camellia_sinensis.comp13050_c0_seq1_m.35139 | PREDICTED: methyl-CpG-binding domain-containing protein 11 [Theobroma cacao] | 32.049 | 57.584 | 35.1 | 9 | 17 | 7 | 1.174 | 1.121 | 1.111 | 0.804 | 0.822 | 0.82 | 0.718 | 5.85E-05 |
| cds.Camellia_sinensis.comp13073_c0_seq1_m.39800 | PREDICTED: asparagine synthetase [glutamine-hydrolyzing] [Nicotiana tomentosiformis] | 26.758 | 1.7498 | 6.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp13077_c0_seq1_m.36053 | PREDICTED: disease resistance protein At4g27190-like isoform X3 [Ziziphus jujuba] | 41.085 | -2 | 3.3 | 1 | 1 | 1 | 0.983 | 0.89 | 0.939 | 1.119 | 1.125 | 0.976 | 1.145 | 7.00E-02 |

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| cds.Camellia_sinensis.comp13115_c0_seq1_m.35237 | PREDICTED: eukaryotic translation initiation factor NCBP-like [Nelumbo nucifera] | 26.529 | 11.516 | 21.7 | 3 | 3 | 3 | 0.661 | 1.136 | 0.969 | 1.3 | 0.987 | 1.019 | 1.195 | 3.45E-01 |
| cds.Camellia_sinensis.comp13136_c0_seq1_m.26302 | PREDICTED: protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB1, chloroplastic [Citrus sinensis] | 35.525 | 21.397 | 17.4 | 5 | 8 | 5 | 1.055 | 1.016 | 1.019 | 0.956 | 0.992 | 0.99 | 0.951 | 4.15E-02 |
| cds.Camellia_sinensis.comp13142_c0_seq1_m.52933 | PREDICTED: alcohol dehydrogenase-like, partial [Arachis ipaensis] | 16.871 | 2.0232 | 7 | 1 | 1 | 1 | 0.932 | 1.116 | 1.089 | 1.081 | 0.893 | 0.902 | 0.917 | 3.55E-01 |

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| cds.Camellia_sinensis.comp13259_c0_seq1_m.37930 | PREDICTED: outer envelope pore protein 24A, chloroplastic-like [Nelumbo nucifera] | 28.734 | 3.8169 | 3.1 | 1 | 1 | 1 | 1.01 | 1.005 | 0.909 | 0.986 | 1.024 | 1.076 | 1.055 | 2.71E-01 |
| cds.Camellia_sinensis.comp13300_c0_seq1_m.40162 | PREDICTED: glucan endo-1,3-beta-glucosidase 12 [Vitis | 24.224 | 2.2618 | 4.7 | 1 | 1 | 1 | 0.845 | 0.928 | 0.913 | 1.148 | 1.16 | 1.06 | 1.254 | 5.06E-03 |
| cds.Camellia_sinensis.comp133106_c0_seq1_m.54569 | PREDICTED: dammarenediol II synthase-like [Sesamum indicum] | 14.114 | 3.3692 | 15.2 | 2 | 2 | 2 | 1.409 | 1.282 | 1.25 | 0.624 | 0.618 | 0.707 | 0.495 | 2.40E-04 |
| cds.Camellia_sinensis.comp13328_c0_seq1_m.30564 | PREDICTED: prohibitin-1, mitochondrial-like [Nicotiana tomentosiformis] | 31.89 | 53.102 | 37.8 | 8 | 14 | 8 | 0.991 | 0.996 | 0.989 | 0.98 | 1.018 | 1.011 | 1.011 | 4.11E-01 |

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| cds.Camellia_sinensis.comp13338_c0_seq1_m.40775 | PREDICTED: protein SPA, chloroplastic [Prunus mume] | 22.737 | 52.392 | 11.2 | 1 | 1 | 1 | 0.88 | 1.133 | 1.07 | 1.045 | 0.703 | 1.177 | 0.949 | 7.07E-01 |
| cds.Camellia_sinensis.comp13351_c0_seq1_m.35324 | PREDICTED: putative glucose-6-phosphate 1-epimerase isoform X2 [Vitis vinifera] | 37.453 | 92.128 | 52 | 13 | 20 | 8 | 0.94 | 0.915 | 1 | 1.087 | 1.099 | 1.051 | 1.134 | 1.29E-02 |
| cds.Camellia_sinensis.comp13361_c0_seq1_m.13837 | PREDICTED: polyadenylate-binding protein-interacting protein 4 isoform X1 [Vitis | 69.81 | 17.606 | 6.6 | 5 | 6 | 5 | 1.081 | 1.096 | 1.01 | 0.868 | 0.913 | 1.012 | 0.876 | 6.15E-02 |
| cds.Camellia_sinensis.comp13400_c0_seq1_m.38479 | 3-demethylubiquinone-9 3-methyltransferase domain protein [Medicago truncatula] | 16.924 | 78.972 | 65.6 | 8 | 22 | 8 | 0.912 | 0.911 | 0.906 | 1.111 | 1.043 | 1.115 | 1.198 | 1.43E-02 |

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| cds.Camellia_sinensis.comp13434_c0_seq1_m.32107 | PREDICTED: probable signal peptidase complex subunit 2 [Ricinus communis] | 26.467 | 14.892 | 24.2 | 5 | 7 | 5 | 0.983 | 0.939 | 0.969 | 1.017 | 1.062 | 1.014 | 1.07 | 2.86E-02 |
| cds.Camellia_sinensis.comp13435_c0_seq1_m.13067 | PREDICTED: asparagine synthetase [glutamine-hydrolyzing] 3 [Juglans regia] | 65.75 | 28.875 | 16.4 | 7 | 10 | 7 | 0.961 | 0.988 | 1.011 | 1.032 | 1.01 | 1.088 | 1.057 | 1.04E-01 |
| cds.Camellia_sinensis.comp13455_c0_seq1_m.37151 | ripening regulated protein DDTFR8 [Solanum lycopersicum] | 20.784 | 2.0867 | 9.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp13487_c0_seq1_m.27899 | PREDICTED: quinone oxidoreductase-like [Nicotiana tabacum] | 40.012 | 85.314 | 45.9 | 13 | 20 | 13 | 0.94 | 0.965 | 1.021 | 1.026 | 1.065 | 1.029 | 1.066 | 7.60E-02 |

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| cds.Camellia_sinensis.comp13488_c0_seq1_m.33920 | PREDICTED: protein CHAPERONE-LIKE PROTEIN OF POR1, chloroplastic [Vitis vinifera] | 37.877 | 15.687 | 11 | 3 | 4 | 3 | 1.044 | 0.946 | 1.024 | 0.926 | 0.978 | 1.079 | 0.99 | 8.42E-01 |
| cds.Camellia_sinensis.comp1349_c0_seq1_m.56647 | PREDICTED: NADH kinase isoform X1 [Ziziphus jujuba] | 13.873 | 1.6191 | 7.4 | 1 | 1 | 1 | 0.991 | 1.035 | 1.074 | 0.94 | 1.066 | 0.899 | 0.937 | 2.98E-01 |
| cds.Camellia_sinensis.comp13521_c0_seq1_m.24653 | PREDICTED: plasma membrane ATPase 1-like [Nicotiana tabacum] | 56.45 | -2 | 16.7 | 9 | 27 | 1 | 1.029 | 0.997 | 0.96 | 0.99 | 0.957 | 1.07 | 1.01 | 8.15E-01 |
| cds.Camellia_sinensis.comp135558_c0_seq1_m.58691 | PREDICTED: plasma membrane ATPase 4-like [Gossypium hirsutum] | 12.185 | 3.7779 | 42.9 | 4 | 6 | 2 |  |  |  |  |  |  |  |  |

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| cds.Camellia_sinensis.comp13598_c0_seq1_m.48857 | PREDICTED: glycine-rich RNA-binding protein 2, mitochondrial-like [Populus euphratica] | 15.038 | 74.468 | 27.7 | 3 | 5 | 3 | 1.014 | 0.987 | 0.995 | 0.971 | 1.004 | 1.017 | 0.999 | 9.31E-01 |
| cds.Camellia_sinensis.comp13601_c0_seq1_m.43173 | PREDICTED: probable prefoldin subunit 4 [Nelumbo nucifera] | 14.742 | 40.049 | 29.4 | 3 | 6 | 3 | 0.955 | 0.977 | 0.967 | 1.099 | 1.029 | 0.971 | 1.069 | 1.46E-01 |
| cds.Camellia_sinensis.comp13626_c0_seq1_m.14698 | PREDICTED: pentatricopeptide repeat-containing protein At3g49240 [Solanum | 64.039 | 32.252 | 18.1 | 10 | 17 | 10 | 0.979 | 1.024 | 0.967 | 1.008 | 1.011 | 0.992 | 1.014 | 4.89E-01 |
| cds.Camellia_sinensis.comp13654_c0_seq1_m.41269 | PREDICTED: glutaredoxin-like [Juglans regia] | 11.293 | 36.926 | 37.4 | 3 | 5 | 3 | 0.936 | 0.893 | 0.916 | 1.067 | 1.12 | 1.038 | 1.175 | 3.50E-03 |

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| cds.Camellia_sinensis.comp13714_c0_seq1_m.40317 | PREDICTED: acyl-coenzyme A thioesterase 13 [Jatropha curcas] | 18.83 | 3.3492 | 6.4 | 1 | 1 | 1 | 1.022 | 1.03 | 1.03 | 0.963 | 0.99 | 0.966 | 0.947 | 3.96E-03 |
| cds.Camellia_sinensis.comp13716_c0_seq1_m.40622 | | 16.969 | 6.2586 | 16.8 | 2 | 2 | 2 | 1.132 | 1.115 | 1.021 | 0.833 | 0.945 | 0.924 | 0.827 | 1.94E-02 |
| cds.Camellia_sinensis.comp13771_c0_seq1_m.36982 | transmembrane protein, putative [Medicago truncatula] | 30.502 | 9.6132 | 12.9 | 2 | 3 | 2 | 0.992 | 0.902 | 0.948 | 1.015 | 1.016 | 1.144 | 1.117 | 8.51E-02 |
| cds.Camellia_sinensis.comp13825_c0_seq1_m.4415 | PREDICTED: protein FAR1-RELATED SEQUENCE 3 [Vitis | 98.894 | 41.633 | 16.9 | 13 | 15 | 10 | 0.969 | 0.987 | 0.956 | 1.069 | 0.998 | 1.033 | 1.065 | 4.67E-02 |
| cds.Camellia_sinensis.comp13828_c0_seq1_m.31187 | PREDICTED: protein usf-like [Gossypium hirsutum] | 32.97 | 125.84 | 42.4 | 11 | 30 | 11 | 0.976 | 0.97 | 0.966 | 1.021 | 1.064 | 1.029 | 1.069 | 6.76E-03 |

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| cds.Camellia_sinensis.comp13829_c0_seq1_m.38050 | PREDICTED: nucleoside diphosphate kinase 2, chloroplastic isoform X2 [Vitis vinifera] | 26.49 | 35.449 | 27.8 | 6 | 14 | 6 | 0.993 | 1.001 | 1.009 | 0.971 | 0.976 | 0.988 | 0.977 | 2.95E-02 |
| cds.Camellia_sinensis.comp13875_c0_seq1_m.28867 | PREDICTED: galactinol synthase 1 [Vitis vinifera] | 45.691 | 119.14 | 28.5 | 10 | 38 | 10 | 1.008 | 0.994 | 0.992 | 0.99 | 1.013 | 0.992 | 1 | 9.74E-01 |
| cds.Camellia_sinensis.comp13898_c0_seq1_m.43751 | PREDICTED: auxin-binding protein ABP19a-like [Nelumbo nucifera] | 28.03 | 23.122 | 8.4 | 3 | 13 | 3 | 0.937 | 0.91 | 0.913 | 1.079 | 1.116 | 1.088 | 1.189 | 2.23E-04 |
| cds.Camellia_sinensis.comp13953_c0_seq1_m.37154 | SOUL heme-binding family protein [Medicago truncatula] | 22.706 | 12.149 | 22.4 | 4 | 4 | 4 | 0.993 | 0.954 | 0.986 | 1.008 | 0.983 | 1.052 | 1.038 | 1.92E-01 |

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| cds.Camellia_sinensis.comp13994_c0_seq1_m.19902 | PREDICTED: protein FATTY ACID EXPORT 3, chloroplastic-like isoform X1 [Nicotiana tabacum] | 35.682 | 42.138 | 25.4 | 10 | 18 | 10 | 1.039 | 0.973 | 0.959 | 0.974 | 1.027 | 1.013 | 1.014 | 6.42E-01 |
| cds.Camellia_sinensis.comp14014_c0_seq1_m.31949 | PREDICTED: protein argonaute 4A [Vitis vinifera] | 40.561 | 3.6431 | 14.2 | 6 | 8 | 2 | 1.039 | 1.018 | 1.074 | 0.964 | 0.947 | 0.955 | 0.915 | 5.80E-03 |
| cds.Camellia_sinensis.comp14021_c0_seq1_m.42083 | PREDICTED: protein LHCP TRANSLOCATION DEFECT [Fragaria vesca subsp. vesca] | 19.534 | 24.398 | 17.2 | 3 | 5 | 3 | 1.111 | 1.082 | 1.033 | 0.88 | 0.883 | 0.955 | 0.843 | 7.36E-03 |
| cds.Camellia_sinensis.comp14034_c0_seq1_m.41985 | PREDICTED: inorganic pyrophosphatase 2 [Theobroma cacao] | 30.709 | 1.8505 | 3.7 | 1 | 1 | 1 | 1.046 | 1.07 | 1.047 | 0.876 | 0.922 | 1.025 | 0.893 | 6.88E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp14043_c0_seq1_m.732 | PREDICTED: callose synthase 9 [Jatropha curcas] | 219.55 | 12.406 | 2.6 | 5 | 6 | 4 | 0.962 | 1.005 | 1.02 | 0.985 | 1.043 | 0.999 | 1.013 | 6.17E-01 |
| cds.Camellia_sinensis.comp14102_c0_seq1_m.37770 | PREDICTED: 50S ribosomal protein L6, chloroplastic-like [Malus domestica] | 24.949 | 17.897 | 40.7 | 9 | 12 | 9 | 1.123 | 1.114 | 1.143 | 0.835 | 0.862 | 0.826 | 0.746 | 3.98E-05 |
| cds.Camellia_sinensis.comp14106_c0_seq1_m.25350 | PREDICTED: D-amino-acid transaminase, chloroplastic [Vitis vinifera] | 43.381 | 3.1102 | 2.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp14113_c0_seq1_m.25364 | PREDICTED: pheophytinase, chloroplastic [Ziziphus jujuba] | 41.845 | 2.6148 | 4.5 | 2 | 2 | 2 | 1.088 | 1.012 | 1.018 | 0.891 | 0.973 | 1.003 | 0.919 | 1.17E-01 |

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| cds.Camellia_sinensis.comp14132_c0_seq2_m.40264 | PREDICTED: ATP-dependent Clp protease proteolytic subunit 2, mitochondrial-like [Nicotiana tabacum] | 28.391 | 15.948 | 26.7 | 6 | 9 | 6 | 1.041 | 1.027 | 0.957 | 0.976 | 1.025 | 1.007 | 0.994 | 8.71E-01 |
| cds.Camellia_sinensis.comp14159_c0_seq1_m.5231 | PREDICTED: protein argonaute 5 [Vitis vinifera] | 109.24 | 39.289 | 13 | 13 | 17 | 13 | 0.997 | 1.003 | 1.05 | 1.008 | 0.96 | 0.989 | 0.97 | 2.27E-01 |
| cds.Camellia_sinensis.comp14167_c0_seq1_m.35045 | PREDICTED: glutathione S-transferase U17 [Eucalyptus grandis] | 25.834 | 33.405 | 19.5 | 5 | 8 | 5 | 1.064 | 1.078 | 1.037 | 0.963 | 0.884 | 0.967 | 0.885 | 1.74E-02 |
| cds.Camellia_sinensis.comp14201_c0_seq1_m.20780 | PREDICTED: hydroquinone glucosyltransferase-like [Nicotiana sylvestris] | 58.009 | 4.1695 | 6.1 | 4 | 4 | 3 | 1.061 | 1.119 | 1.038 | 0.944 | 0.917 | 0.886 | 0.854 | 5.42E-03 |

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| cds.Camellia_sinensis.comp14270_c0_seq1_m.33370 | PREDICTED: enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic [Nelumbo nucifera] | 31.24 | 6.3352 | 31.4 | 9 | 25 | 3 | 1.012 | 1.036 | 0.98 | 1.055 | 1.018 | 0.935 | 0.993 | 8.55E-01 |
| cds.Camellia_sinensis.comp14278_c0_seq1_m.18955 | PREDICTED: zinc finger CCCH domain-containing protein 37 isoform X1 [Nelumbo nucifera] | 58.591 | 68.879 | 12.9 | 6 | 8 | 6 | 0.979 | 1.021 | 0.981 | 1.005 | 0.992 | 0.994 | 1.003 | 8.17E-01 |
| cds.Camellia_sinensis.comp14306_c0_seq1_m.53197 | centrosomal protein [Arabidopsis thaliana] | 17.68 | 1.8398 | 12.5 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp14308_c0_seq1_m.56539 | | 12.959 | 49.047 | 26 | 3 | 5 | 3 | 1.149 | 1.123 | 1.164 | 0.844 | 0.808 | 0.854 | 0.729 | 9.55E-05 |

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| cds.Camellia_sinensis.comp14350_c0_seq1_m.44674 | PREDICTED: CAP-Gly domain-containing linker protein 1 isoform X1 [Sesamum indicum] | 16.367 | 75.071 | 25.3 | 3 | 5 | 3 | 0.956 | 1.008 | 0.999 | 1.077 | 0.973 | 1.031 | 1.04 | 3.17E-01 |
| cds.Camellia_sinensis.comp14364_c0_seq1_m.35071 | chromosome-associated kinesin [Arabidopsis thaliana] | 28.048 | 52.699 | 30 | 7 | 8 | 7 | 1.009 | 0.974 | 1.036 | 0.97 | 0.974 | 1.013 | 0.979 | 4.13E-01 |
| cds.Camellia_sinensis.comp14428_c0_seq1_m.32371 | PREDICTED: protein-L-isoaspartate O-methyltransferase 1 isoform X2 [Sesamum indicum] | 33.385 | 12.93 | 17.6 | 5 | 5 | 5 | 0.96 | 0.959 | 0.99 | 1.083 | 0.981 | 1.025 | 1.062 | 1.23E-01 |
| cds.Camellia_sinensis.comp14487_c0_seq1_m.36591 | triosephosphate isomerase, cytosolic [Capsicum annuum] | 27.853 | 219.05 | 53.5 | 11 | 43 | 11 | 1.024 | 1.003 | 0.995 | 1 | 0.997 | 0.985 | 0.987 | 2.44E-01 |
| cds.Camellia_sinensis.comp14530_c0_seq1_m.42158 | Thioredoxin-like protein 4A [Morus notabilis] | 16.561 | 1.899 | 9.9 | 1 | 1 | 1 | 0.845 | 1.177 | 0.822 | 1.08 | 1.038 | 1.07 | 1.121 | 3.85E-01 |

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| cds.Camellia_sinensis.comp145391_c0_seq1_m.34585 | PREDICTED: alpha-amylase-like isoform X1 [Solanum tuberosum | 42.66 | 9.2585 | 11 | 3 | 5 | 3 | 0.963 | 0.945 | 0.984 | 1.1 | 1.069 | 0.993 | 1.093 | 5.35E-02 |
| cds.Camellia_sinensis.comp14542_c0_seq2_m.28332 | PREDICTED: aldehyde dehydrogenase family 2 member B7, mitochondrial-like [Nelumbo nucifera] | 42.468 | 43.081 | 24.3 | 10 | 28 | 4 | 0.949 | 0.934 | 0.954 | 1.165 | 1.069 | 0.985 | 1.135 | 1.26E-01 |
| cds.Camellia_sinensis.comp14546_c0_seq1_m.32603 | PREDICTED: derlin-1-like [Nicotiana tabacum] | 27.492 | 4.7639 | 9.2 | 2 | 2 | 2 | 1.019 | 0.976 | 1.016 | 1.046 | 0.947 | 1.006 | 0.996 | 8.92E-01 |
| cds.Camellia_sinensis.comp14563_c0_seq1_m.17079 | PREDICTED: glycerol-3-phosphate 2-O-acyltransferase 4 [Capsicum annuum] | 57.936 | 4.0159 | 5.2 | 3 | 3 | 3 | | | | | | | | |

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| cds.Camellia_sinensis.comp14596_c0_seq1_m.39671 | PREDICTED: 1-aminocyclopropane-1-carboxylate oxidase homolog 1-like [Prunus mume] | 27.748 | 11.908 | 22.7 | 5 | 7 | 5 | 0.984 | 0.922 | 0.982 | 1.003 | 1.07 | 1.003 | 1.065 | 1.06E-01 |
| cds.Camellia_sinensis.comp14651_c0_seq1_m.44151 | anthocyanidin reductase [Vitis vinifera] | 13.547 | 15.52 | 37.4 | 3 | 5 | 3 | 1.259 | 1.307 | 1.22 | 0.707 | 0.747 | 0.665 | 0.56 | 1.19E-04 |
| cds.Camellia_sinensis.comp14653_c0_seq2_m.41836 | PREDICTED: peptide methionine sulfoxide reductase B5-like [Pyrus x bretschneideri] | 23.11 | 82.647 | 34.3 | 5 | 11 | 4 | 0.995 | 0.928 | 0.917 | 1.034 | 1.069 | 1.045 | 1.108 | 1.92E-02 |
| cds.Camellia_sinensis.comp14661_c0_seq1_m.38530 | PREDICTED: thioredoxin H9 [Erythranthe guttata] | 15.55 | 2.905 | 9.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp14664_c0_seq1_m.4137 | PREDICTED: histone H1 [Vitis vinifera] | 46.714 | 6.9213 | 5.9 | 3 | 4 | 3 | | | | | | | | |

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| cds.Camellia_sinensis.comp14674_c0_seq2_m.51551 | PREDICTED: peroxidase 4-like [Vitis vinifera] | 17.319 | 42.14 | 44.8 | 6 | 10 | 4 | 0.979 | 1.025 | 1.084 | 0.919 | 0.946 | 1.042 | 0.941 | 2.73E-01 |
| cds.Camellia_sinensis.comp14680_c0_seq1_m.21638 | Chaperone protein DnaJ [Morus notabilis] | 57.761 | 11.501 | 13 | 7 | 8 | 7 | 1.112 | 1.034 | 1.129 | 0.936 | 0.859 | 0.902 | 0.824 | 6.20E-03 |
| cds.Camellia_sinensis.comp14695_c0_seq1_m.52872 | myosin-G heavy chain-like protein [Arabidopsis thaliana] | 16.92 | 1.4243 | 9.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp14706_c0_seq1_m.41134 | PREDICTED: hydroquinone glucosyltransferase-like [Nicotiana sylvestris] | 32.264 | 6.2764 | 11.6 | 4 | 5 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp14707_c0_seq1_m.20162 | Sugar transport protein 5 [Morus notabilis] | 43.697 | 4.1782 | 3.6 | 1 | 1 | 1 | 1.047 | 1.061 | 1.036 | 0.957 | 0.945 | 0.947 | 0.906 | 2.41E-04 |
| cds.Camellia_sinensis.comp14709_c0_seq1_m.42842 | PREDICTED: 60S ribosomal protein L26-1-like [Nicotiana tabacum] | 20.09 | 8.8667 | 22.5 | 4 | 9 | 4 | 1.053 | 1.059 | 1.01 | 0.96 | 0.943 | 0.922 | 0.905 | 6.22E-03 |

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| cds.Camellia_sinensis.comp14741_c0_seq1_m.57407 | PREDICTED: proteasome subunit alpha type-3-like [Populus euphratica] | 12.794 | 4.354 | 43.5 | 5 | 9 | 2 | 0.876 | 0.844 | 1.141 | 1.109 | 1.201 | 0.877 | 1.114 | 4.63E-01 |
| cds.Camellia_sinensis.comp14760_c0_seq1_m.25844 | PREDICTED: mitochondrial import inner membrane translocase subunit TIM50-like [Solanum tuberosum | 41.721 | 2.1041 | 2.5 | 1 | 1 | 1 | 0.994 | 0.971 | 0.989 | 0.973 | 1.055 | 1.029 | 1.035 | 2.48E-01 |
| cds.Camellia_sinensis.comp14761_c0_seq1_m.43823 | PREDICTED: pyruvate kinase isozyme G, chloroplastic [Theobrom | 21.999 | 9.8489 | 9.5 | 2 | 2 | 2 | 0.969 | 0.997 | 0.99 | 0.99 | 1.033 | 1.035 | 1.035 | 1.15E-01 |
| cds.Camellia_sinensis.comp14771_c0_seq1_m.16671 | PREDICTED: NADP-dependent glyceraldehyde-3-phosphate dehydrogenase [Sesamum indicum] | 57.801 | 286.17 | 49.7 | 21 | 62 | 21 | 0.997 | 1.033 | 1.013 | 1.006 | 0.972 | 1.005 | 0.98 | 2.61E-01 |

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| cds.Camellia_sinensis.comp14778_c0_seq1_m.21986 | PREDICTED: phytochrome-associated serine/threonine-protein phosphatase [Ipomoea | 34.961 | 32.52 | 9.5 | 3 | 5 | 3 | 0.94 | 0.962 | 0.999 | 1.037 | 1.048 | 1.023 | 1.071 | 2.22E-02 |
| cds.Camellia_sinensis.comp14779_c0_seq1_m.55154 | PREDICTED: AAA-ATPase At5g57480-like [Juglans regia] | 13.848 | 1.7459 | 8.2 | 1 | 1 | 1 | 1.079 | 1.108 | 1.064 | 1.036 | 0.748 | 0.949 | 0.841 | 2.03E-01 |
| cds.Camellia_sinensis.comp14794_c0_seq1_m.31056 | PREDICTED: glutathionyl-hydroquinone reductase YqjG [Ricinus communis] | 42.705 | 127.24 | 21.7 | 7 | 18 | 7 | 0.935 | 0.958 | 0.963 | 1.076 | 1.061 | 1.026 | 1.107 | 3.72E-03 |
| cds.Camellia_sinensis.comp14803_c0_seq2_m.38105 | PREDICTED: ubiquitin thioesterase OTU1 isoform X1 [Nicotiana attenuata] | 23.159 | 21.482 | 18.4 | 3 | 5 | 3 | 0.958 | 0.97 | 0.929 | 1.079 | 0.993 | 1.096 | 1.109 | 3.66E-02 |

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| cds.Camellia_sinensis.comp14827_c0_seq1_m.33282 | PREDICTED: chlorophyll a-b binding protein 6A, chloroplastic [Nicotiana attenuata] | 26.332 | 36.237 | 21.2 | 9 | 29 | 9 | 0.947 | 0.896 | 0.882 | 1.09 | 1.122 | 1.103 | 1.217 | 1.06E-03 |
| cds.Camellia_sinensis.comp14849_c0_seq1_m.54978 | PREDICTED: HMG-Y-related protein A [Theobroma cacao] | 14.829 | 3.189 | 10.9 | 1 | 1 | 1 | 0.962 | 1.355 | 1.214 | 0.823 | 0.859 | 0.761 | 0.692 | 2.83E-02 |
| cds.Camellia_sinensis.comp14856_c0_seq1_m.31110 | PREDICTED: BAHD acyltransferase DCR [Ricinus communis] | 48.112 | 1.166 | 3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp14866_c0_seq1_m.29987 | PREDICTED: chlorophyll a-b binding protein 7, chloroplastic [Solanum tuberosum | 33.769 | 72.027 | 23.7 | 4 | 14 | 4 | 0.97 | 0.943 | 0.979 | 0.994 | 1.018 | 1.031 | 1.052 | 3.07E-02 |

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| cds.Camellia_sinensis.comp14868_c0_seq1_m.51576 | PREDICTED: heavy metal-associated isoprenylated plant protein 26-like [Sesamum indicum] | 15.323 | 1.323 | 5.1 | 1 | 1 | 1 | 1.373 | 1.289 | 1.244 | 0.632 | 0.668 | 0.691 | 0.51 | 6.24E-05 |
| cds.Camellia_sinensis.comp14885_c0_seq1_m.20656 | serine carboxypeptidase S10 family protein [Populus trichocarpa] | 51.194 | 15.302 | 6.3 | 3 | 4 | 3 | 1.039 | 1.043 | 1.045 | 0.946 | 0.96 | 0.99 | 0.926 | 2.95E-02 |
| cds.Camellia_sinensis.comp14900_c0_seq1_m.9568 | PREDICTED: glutamine-dependent NAD(+) synthetase [Sesamum indicum] | 89.256 | 5.7361 | 3.1 | 3 | 4 | 3 | 0.972 | 1.023 | 1.019 | 1.006 | 0.988 | 0.976 | 0.985 | 4.80E-01 |
| cds.Camellia_sinensis.comp14948_c0_seq1_m.21121 | PREDICTED: 26S protease regulatory subunit 7 [Gossypium hirsutum] | 47.654 | 165.82 | 55.9 | 22 | 48 | 21 | 1.004 | 1.018 | 1.019 | 1.008 | 0.986 | 1.007 | 0.987 | 2.00E-01 |

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| cds.Camellia_sinensis.comp14952_c0_seq1_m.34818 | PREDICTED: probable carboxylesterase 8 [Theobroma cacao] | 37.333 | 2.5966 | 4.7 | 1 | 2 | 1 | 1.029 | 0.979 | 1.107 | 1.054 | 0.789 | 1.042 | 0.926 | 4.53E-01 |
| cds.Camellia_sinensis.comp14985_c0_seq1_m.42840 | PREDICTED: thioredoxin X, chloroplastic [Prunus mume] | 21.136 | 21.583 | 15.4 | 3 | 6 | 3 | 0.957 | 1.042 | 0.996 | 0.967 | 1.04 | 0.956 | 0.989 | 7.79E-01 |
| cds.Camellia_sinensis.comp14986_c0_seq1_m.37943 | PREDICTED: ribulose bisphosphate carboxylase small chain, chloroplastic-like [Juglans regia] | 19.795 | 23.148 | 40.3 | 10 | 96 | 6 | 0.997 | 1.029 | 1.061 | 0.982 | 0.979 | 0.969 | 0.949 | 4.79E-02 |
| cds.Camellia_sinensis.comp15033_c0_seq1_m.11003 | PREDICTED: nudix hydrolase 26, chloroplastic-like isoform X2 [Nicotiana attenuata] | 20.647 | 2.9544 | 11.6 | 1 | 1 | 1 | 1.255 | 0.954 | 1.01 | 0.974 | 0.774 | 0.998 | 0.853 | 2.46E-01 |

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| cds.Camellia_sinensis.comp15033_c0_seq1_m.11004 | PREDICTED: photosystem II 10 kDa polypeptide, chloroplastic [Juglans regia] | 14.263 | 26.492 | 23.2 | 3 | 13 | 3 | 1.13 | 1.056 | 1.106 | 0.885 | 0.916 | 0.884 | 0.816 | 9.21E-04 |
| cds.Camellia_sinensis.comp15037_c0_seq1_m.35395 | PREDICTED: thylakoid membrane protein slr0575 [Solanum tuberosum | 31.624 | 89.845 | 34.1 | 9 | 17 | 9 | 0.981 | 1.035 | 1.009 | 1.006 | 1.024 | 0.972 | 0.992 | 7.44E-01 |
| cds.Camellia_sinensis.comp15078_c0_seq1_m.40747 | PREDICTED: putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2 [Nicotiana attenuata] | 17.8 | 23.837 | 37.3 | 6 | 8 | 5 | 1.008 | 1 | 1.001 | 0.982 | 0.969 | 1.005 | 0.982 | 1.78E-01 |
| cds.Camellia_sinensis.comp15079_c0_seq1_m.27628 | PREDICTED: bifunctional protein FolD 4, chloroplastic isoform X2 [Citrus sinensis] | 38.976 | 37.062 | 22 | 9 | 15 | 9 | 1 | 1.046 | 1.009 | 0.951 | 0.972 | 0.977 | 0.949 | 3.17E-02 |

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| cds.Camellia_sinensis.comp15085_c0_seq1_m.32666 | PREDICTED: non-functional NADPH-dependent codeinone reductase 2-like [Nicotiana tabacum] | 35.677 | 11.693 | 14.4 | 6 | 11 | 4 | 0.924 | 0.889 | 0.857 | 1.116 | 1.156 | 1.103 | 1.264 | 8.22E-04 |
| cds.Camellia_sinensis.comp15105_c0_seq1_m.45326 | PREDICTED: galactokinase-like, partial [Ziziphus jujuba] | 22.37 | 55.949 | 46.6 | 7 | 10 | 5 | 0.98 | 0.99 | 1.033 | 0.972 | 1.018 | 0.99 | 0.992 | 7.35E-01 |
| cds.Camellia_sinensis.comp15118_c0_seq1_m.21662 | PREDICTED: chromatin modification-related protein eaf-1-like isoform X2 [Pyrus x bretschneideri] | 53.075 | 20.007 | 23.8 | 9 | 10 | 8 | 0.995 | 1.027 | 0.995 | 0.986 | 1.013 | 1.018 | 1 | 9.99E-01 |
| cds.Camellia_sinensis.comp15125_c0_seq1_m.36668 | PREDICTED: oxygen-evolving enhancer protein 2, chloroplastic-like [Nelumbo nucifera] | 28.472 | 234.15 | 45.3 | 12 | 82 | 12 | 1.017 | 1.002 | 0.994 | 1.014 | 0.977 | 0.985 | 0.988 | 3.97E-01 |

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| cds.Camellia_sinensis.comp15130_c0_seq1_m.33712 | PREDICTED: 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplastic [Ipomoea nil] | 27.806 | 45.091 | 28.2 | 6 | 9 | 6 | 1.036 | 1.035 | 0.951 | 1.052 | 1.047 | 0.916 | 0.998 | 9.50E-01 |
| cds.Camellia_sinensis.comp15131_c0_seq1_m.44648 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP17-1, chloroplastic-like isoform X1 [Nicotiana tabacum] | 24.294 | 1.4097 | 4.5 | 1 | 1 | 1 | 0.971 | 1.092 | 0.867 | 1.076 | 1.04 | 0.973 | 1.054 | 4.82E-01 |
| cds.Camellia_sinensis.comp15138_c0_seq1_m.58116 | PREDICTED: LOW QUALITY PROTEIN: hydroquinone glucosyltransferase [Ricinus communis] | 11.945 | 27.267 | 19.3 | 1 | 2 | 1 | 0.93 | 1.038 | 0.971 | 1.106 | 0.939 | 1.04 | 1.05 | 4.57E-01 |

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| cds.Camellia_sinensis.comp15156_c0_seq2_m.19699 | PREDICTED: protease Do-like 8, chloroplastic isoform X1 [Juglans regia] | 53.255 | 61.765 | 22.8 | 11 | 23 | 11 | 0.99 | 0.976 | 0.978 | 1.016 | 1.028 | 1.023 | 1.042 | 1.86E-03 |
| cds.Camellia_sinensis.comp151911_c0_seq1_m.50408 | PREDICTED: EG45-like domain containing protein [Juglans regia] | 12.876 | 57.379 | 42.4 | 3 | 7 | 3 | 0.68 | 0.698 | 0.747 | 1.243 | 1.34 | 1.394 | 1.872 | 1.39E-04 |
| cds.Camellia_sinensis.comp15207_c0_seq1_m.26369 | PREDICTED: lipoyl synthase 2, mitochondrial-like [Nicotiana attenuata] | 44.761 | 7.6395 | 9 | 3 | 3 | 3 | 1.01 | 0.919 | 1.001 | 1.041 | 1.067 | 0.98 | 1.054 | 2.50E-01 |
| cds.Camellia_sinensis.comp15246_c0_seq1_m.45602 | PREDICTED: phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and protein-tyrosine-phosphatase PTEN2A[Vitis vinifera] | 14.7 | 1.9197 | 6.4 | 1 | 1 | 1 | 1.196 | 1.115 | 1.227 | 0.844 | 0.752 | 0.817 | 0.682 | 1.02E-03 |

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| cds.Camellia_sinensis.comp15287_c0_seq1_m.18815 | PREDICTED: 6-phosphogluconate dehydrogenase, decarboxylating 3 [Ziziphus jujuba] | 53.493 | 131.91 | 42.7 | 19 | 44 | 17 | 1.015 | 1.001 | 0.986 | 0.997 | 1.016 | 0.989 | 1 | 1.00E+00 |
| cds.Camellia_sinensis.comp15297_c0_seq1_m.4262 | ATP synthase CF1 alpha subunit (chloroplast) [Camellia pubicosta] | 55.468 | 323.31 | 38.7 | 18 | 112 | 16 | 0.987 | 0.976 | 0.992 | 1.008 | 1.017 | 1.02 | 1.03 | 7.38E-03 |
| cds.Camellia_sinensis.comp15298_c0_seq1_m.35004 | PREDICTED: psbP domain-containing protein 6, chloroplastic [Vitis vinifera] | 29.406 | 109.67 | 47.2 | 11 | 22 | 11 | 0.991 | 0.982 | 0.967 | 1.034 | 1.053 | 1.032 | 1.061 | 3.54E-03 |
| cds.Camellia_sinensis.comp15306_c0_seq1_m.24456 | PREDICTED: vacuolar protein sorting-associated protein 26B [Vitis vinifera] | 35.199 | 2.1279 | 10.6 | 3 | 3 | 2 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp15326_c0_seq1_m.35297 | PREDICTED: superoxide dismutase [Cu-Zn], chloroplastic [Daucus carota subsp. sativus] | 21.644 | 166.42 | 50.2 | 6 | 21 | 4 | 0.954 | 0.932 | 0.928 | 1.056 | 1.101 | 1.065 | 1.145 | 9.18E-04 |
| cds.Camellia_sinensis.comp15329_c0_seq1_m.14629 | PREDICTED: nucleobase-ascorbate transporter 3 [Solanum tuberosum | 60.284 | 2.4328 | 1.8 | 1 | 1 | 1 | 0.894 | 1.048 | 0.969 | 1.134 | 1.032 | 0.957 | 1.073 | 3.56E-01 |
| cds.Camellia_sinensis.comp15334_c0_seq1_m.36519 | PREDICTED: oxygen-evolving enhancer protein 3-2, chloroplastic [Pyrus x bretschneideri] | 24.704 | 144.61 | 42.5 | 12 | 86 | 12 | 1.003 | 1.003 | 0.989 | 1 | 1.003 | 0.993 | 1 | 9.53E-01 |
| cds.Camellia_sinensis.comp15342_c0_seq1_m.36209 | PREDICTED: protein ABHD11 [Vitis vinifera] | 20.277 | 1.8572 | 15.9 | 3 | 3 | 3 | 1.055 | 1.021 | 0.995 | 1.076 | 0.926 | 0.931 | 0.955 | 4.07E-01 |

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| cds.Camellia_sinensis.comp15342_c0_seq1_m.36210 | PREDICTED: alpha/beta hydrolase domain-containing protein 11 [Citrus sinensis] | 14.115 | 9.2371 | 36.8 | 5 | 5 | 5 | 0.947 | 0.956 | 1.055 | 1.044 | 1.031 | 0.989 | 1.036 | 3.98E-01 |
| cds.Camellia_sinensis.comp15355_c0_seq1_m.41637 | photosystem I reaction center subunit IV A [Medicago truncatula] | 16.886 | 88.761 | 50 | 6 | 41 | 6 | 1.071 | 1.014 | 1.012 | 0.93 | 0.986 | 0.958 | 0.928 | 4.09E-02 |
| cds.Camellia_sinensis.comp15359_c0_seq1_m.28895 | PREDICTED: cytochrome b-c1 complex subunit Rieske-4, mitochondrial-like [Sesamum indicum] | 29.243 | 104.76 | 20.9 | 5 | 12 | 5 | 0.991 | 1.019 | 1.017 | 0.99 | 1.02 | 1.003 | 0.995 | 7.29E-01 |
| cds.Camellia_sinensis.comp15364_c0_seq1_m.17207 | PREDICTED: GMP synthase [glutamine-hydrolyzing]-like [Daucus carota subsp. sativus] | 63.741 | 65.823 | 20.5 | 10 | 13 | 10 | 0.945 | 0.966 | 0.925 | 1.052 | 1.057 | 1.085 | 1.126 | 1.66E-03 |

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| cds.Camellia_sinensis.comp15365_c0_seq1_m.25957 | PREDICTED: psbP domain-containing protein 1, chloroplastic [Vitis vinifera] | 30.511 | 110.59 | 34.1 | 9 | 14 | 9 | 1.02 | 1.024 | 1.006 | 1.006 | 0.971 | 1.009 | 0.979 | 1.88E-01 |
| cds.Camellia_sinensis.comp15366_c0_seq1_m.9995 | PREDICTED: glutamate--tRNA ligase, cytoplasmic isoform X1 [Vitis vinifera] | 83.157 | 82.443 | 23.2 | 18 | 23 | 18 | 0.968 | 1.009 | 0.975 | 1.011 | 1.005 | 0.998 | 1.021 | 1.91E-01 |
| cds.Camellia_sinensis.comp15377_c0_seq1_m.51446 | PREDICTED: WD repeat-containing protein 20-like [Nicotiana tomentosiformis] | 11.18 | 5.3034 | 19.4 | 1 | 1 | 1 | 0.949 | 0.974 | 0.77 | 1.233 | 0.894 | 1.217 | 1.242 | 1.76E-01 |
| cds.Camellia_sinensis.comp15383_c0_seq2_m.37999 | transmembrane protein, putative [Medicago truncatula] | 26.885 | 21.071 | 9.6 | 2 | 3 | 2 | 0.95 | 1.023 | 1.09 | 0.934 | 1.033 | 0.952 | 0.953 | 3.98E-01 |

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| cds.Camellia_sinensis.comp15418_c0_seq1_m.38718 | PREDICTED: chlorophyll a-b binding protein, chloroplastic [Sesamum indicum] | 20.814 | 9.0459 | 5.8 | 1 | 3 | 1 | 0.771 | 1.127 | 1.133 | 1.001 | 0.941 | 1.057 | 0.989 | 9.79E-01 |
| cds.Camellia_sinensis.comp15473_c0_seq1_m.58569 | PREDICTED: DEAD-box ATP-dependent RNA helicase 31-like isoform X2 [Juglans regia] | 11.445 | 1.6649 | 12.3 | 1 | 1 | 1 | 0.854 | 0.882 | 1.116 | 1.063 | 0.941 | 1.179 | 1.116 | 3.49E-01 |
| cds.Camellia_sinensis.comp15485_c0_seq1_m.44167 | DUF1230 family protein [Medicago truncatula] | 23.827 | 3.3517 | 5.5 | 1 | 1 | 1 | 0.965 | 0.988 | 0.96 | 1.064 | 0.983 | 1.059 | 1.066 | 7.91E-02 |
| cds.Camellia_sinensis.comp15493_c0_seq1_m.30430 | PREDICTED: heat shock cognate 70 kDa protein 2-like [Solanum pennellii] | 48.561 | 213.42 | 56.1 | 23 | 92 | 6 | 1.051 | 1.025 | 1.028 | 0.959 | 0.953 | 0.976 | 0.93 | 2.48E-03 |

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| cds.Camellia_sinensis.comp15502_c0_seq1_m.12796 | PREDICTED: phosphoglucan phosphatase LSF1, chloroplastic isoform X1 [Vitis vinifera] | 55.465 | 4.08 | 3.2 | 2 | 2 | 2 | 0.97 | 0.964 | 0.972 | 1.113 | 1.087 | 0.92 | 1.074 | 3.77E-01 |
| cds.Camellia_sinensis.comp15502_c0_seq1_m.12797 | PREDICTED: phosphoglucan phosphatase LSF1, chloroplastic [Ipomoea nil] | 11.887 | 1.2785 | 6.4 | 1 | 1 | 1 | 1.034 | 0.899 | 1.017 | 1.027 | 1.005 | 1.029 | 1.038 | 4.35E-01 |
| cds.Camellia_sinensis.comp15518_c0_seq1_m.22248 | PREDICTED: dnaJ protein homolog 2 isoform X2 [Solanum pennellii] | 46.487 | 54.094 | 16.9 | 7 | 12 | 2 | 1.26 | 1.201 | 1.286 | 0.744 | 0.787 | 0.751 | 0.609 | 4.47E-05 |
| cds.Camellia_sinensis.comp15527_c0_seq1_m.24033 | DUF1995 domain protein, putative (DUF1995) [Arabidopsis thaliana] | 41.608 | 54.694 | 19.2 | 5 | 7 | 5 | 1.028 | 1.038 | 1.059 | 0.989 | 0.903 | 0.967 | 0.915 | 3.55E-02 |

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| cds.Camellia_sinensis.comp15528_c0_seq1_m.32944 | PREDICTED: protein GrpE [Ricinus communis] | 34.762 | 34.77 | 28.4 | 11 | 18 | 11 | 1.002 | 1.041 | 1.019 | 0.988 | 0.962 | 0.991 | 0.96 | 5.02E-02 |
| cds.Camellia_sinensis.comp15601_c0_seq1_m.41643 | PREDICTED: protochlorophyllide reductase, chloroplastic [Ricinus communis] | 30.961 | 2.1983 | 24.2 | 6 | 6 | 3 | 0.906 | 0.963 | 0.98 | 1.059 | 1.076 | 1.048 | 1.117 | 1.12E-02 |
| cds.Camellia_sinensis.comp15602_c0_seq1_m.26722 | PREDICTED: ABC transporter I family member 6, chloroplastic-like [Nicotiana tabacum] | 38.475 | 60.888 | 18.4 | 5 | 9 | 5 | 1.029 | 1.007 | 1.007 | 0.968 | 0.975 | 1.018 | 0.973 | 1.87E-01 |
| cds.Camellia_sinensis.comp15618_c0_seq1_m.27755 | PREDICTED: BRCA1-A complex subunit Abraxas [Jatropha curcas] | 39.021 | 5.8587 | 12.5 | 4 | 4 | 4 | 0.998 | 1.053 | 0.986 | 1.021 | 0.945 | 1.007 | 0.979 | 5.30E-01 |

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| cds.Camellia_sinensis.comp15666_c0_seq1_m.32513 | PREDICTED: vacuolar protein sorting-associated protein 20 homolog 2-like [Nicotiana tabacum] | 26.302 | 5.3656 | 12.8 | 3 | 3 | 3 | 1.069 | 1.098 | 1.08 | 0.905 | 0.898 | 0.933 | 0.843 | 2.59E-04 |
| cds.Camellia_sinensis.comp15676_c0_seq1_m.56970 | PREDICTED: photosystem II 22 kDa protein, chloroplastic [Vitis vinifera] | 12.716 | 57.07 | 35.3 | 3 | 7 | 1 | 1.06 | 1.032 | 1.081 | 0.936 | 0.992 | 0.947 | 0.906 | 1.14E-02 |
| cds.Camellia_sinensis.comp15677_c0_seq1_m.38526 | PREDICTED: metal-independent phosphoserine phosphatase [Gossypium arboreum] | 26.6 | 6.9332 | 13 | 2 | 2 | 2 | 1.08 | 0.851 | 0.919 | 1.238 | 1.015 | 0.925 | 1.115 | 3.92E-01 |
| cds.Camellia_sinensis.comp15686_c0_seq1_m.2101 | PREDICTED: protein NBR1 homolog isoform X2 [Citrus sinensis] | 92.885 | 4.9446 | 5.4 | 3 | 3 | 3 | | | | | | | | |

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| cds.Camellia_sinensis.comp15686_c0_seq1_m.2103 | PREDICTED: adenosine kinase 2 [Vitis vinifera] | 19.639 | 95.336 | 31.1 | 3 | 5 | 3 | 1.027 | 1.116 | 1.029 | 0.859 | 1.018 | 0.939 | 0.888 | 9.81E-02 |
| cds.Camellia_sinensis.comp15686_c0_seq1_m.2104 | PREDICTED: adenosine kinase 1-like [Gossypium hirsutum] | 16.822 | 97.817 | 48 | 5 | 18 | 5 | 1.042 | 1.045 | 0.999 | 0.982 | 0.942 | 0.982 | 0.942 | 4.04E-02 |
| cds.Camellia_sinensis.comp15711_c0_seq1_m.22211 | PREDICTED: fatty-acid-binding protein 1 [Vitis vinifera] | 11.424 | 3.8027 | 10.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp15716_c0_seq1_m.31680 | PREDICTED: putative glucose-6-phosphate 1-epimerase isoform X1 [Ricinus communis] | 34.406 | 29.71 | 19.1 | 5 | 11 | 5 | 1.066 | 1.021 | 1.032 | 0.932 | 0.943 | 0.949 | 0.905 | 2.10E-03 |
| cds.Camellia_sinensis.comp15718_c0_seq1_m.36938 | PREDICTED: peroxidase 73 [Vitis vinifera] | 34.324 | 129.59 | 39.7 | 10 | 20 | 8 | 1.022 | 0.986 | 1.024 | 0.983 | 0.992 | 0.981 | 0.975 | 1.19E-01 |

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| cds.Camellia_sinensis.comp15730_c0_seq1_m.27007 | PREDICTED: dihydrolipoyllysine-residue acetyltransferase component 1 of pyruvate dehydrogenase complex,mitochondrial-like isoform X7 [Gossypium hirsutum] | 40.459 | 16.019 | 18.8 | 7 | 8 | 6 | 0.941 | 1 | 0.969 | 1.018 | 1.049 | 1.044 | 1.069 | 2.80E-02 |
| cds.Camellia_sinensis.comp15731_c0_seq1_m.30644 | PREDICTED: clathrin heavy chain 1-like isoform X2 [Juglans regia] | 50.439 | 4.2616 | 21.9 | 9 | 19 | 2 | 0.945 | 1.162 | 1.025 | 0.959 | 0.869 | 1.04 | 0.916 | 3.35E-01 |
| cds.Camellia_sinensis.comp15748_c0_seq1_m.44277 | PREDICTED: glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic [Malus domestica] | 19.306 | 253.51 | 85.1 | 13 | 60 | 10 | 1.003 | 0.994 | 1.003 | 0.999 | 1.008 | 0.983 | 0.997 | 6.92E-01 |

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| cds.Camellia_sinensis.comp15756_c0_seq1_m.36168 | PREDICTED: UBP1-associated protein 2C isoform X2 [Theobroma cacao] | 36.561 | 1.4143 | 2.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp15767_c0_seq1_m.45369 | PREDICTED: myosin-11 isoform X2 [Citrus sinensis] | 13.944 | 11.937 | 34.1 | 5 | 6 | 5 | 0.986 | 0.972 | 0.924 | 1.011 | 1.034 | 1.109 | 1.094 | 5.81E-02 |
| cds.Camellia_sinensis.comp15790_c1_seq1_m.53352 | PREDICTED: SKP1-like protein 1B [Citrus sinensis] | 11.715 | 1.3124 | 39 | 6 | 6 | 2 | 0.92 | 0.907 | 0.892 | 1.157 | 1.077 | 1.089 | 1.222 | 1.12E-03 |
| cds.Camellia_sinensis.comp15819_c0_seq1_m.3488 | PREDICTED: nodal modulator 1 [Vitis vinifera] | 131.25 | 110 | 15.3 | 15 | 21 | 15 | 0.991 | 0.983 | 1.013 | 1.002 | 0.976 | 0.992 | 0.994 | 6.55E-01 |
| cds.Camellia_sinensis.comp15853_c0_seq1_m.14378 | PREDICTED: U1 small nuclear ribonucleoprotein A-like [Gossypium raimondii] | 36.069 | 40.859 | 28.3 | 8 | 9 | 8 | 0.93 | 0.943 | 0.999 | 1.062 | 1.13 | 1.036 | 1.124 | 2.62E-02 |

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| cds.Camellia_sinensis.comp15864_c0_seq1_m.58049 | PREDICTED: heat shock cognate 70 kDa protein 2 [Ricinus communis] | 12.663 | 18.529 | 51.8 | 8 | 34 | 4 | 1.081 | 0.992 | 0.997 | 0.947 | 0.99 | 0.995 | 0.955 | 2.28E-01 |
| cds.Camellia_sinensis.comp15872_c0_seq1_m.39633 | PREDICTED: probable U6 snRNA-associated Sm-like protein LSm4 [Ipomoea nil] | 16.096 | 1.7176 | 9.3 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp15888_c0_seq1_m.4259 | oxidoreductase/transition metal ion-binding protein, putative [Medicago truncatula] | 101.7 | 177.94 | 27.1 | 24 | 30 | 24 | 1.024 | 0.981 | 1.029 | 0.98 | 0.988 | 0.986 | 0.974 | 1.60E-01 |
| cds.Camellia_sinensis.comp15966_c0_seq1_m.15878 | PREDICTED: O-acyltransferase WSD1-like [Daucus carota subsp. sativus] | 60.034 | 90.549 | 26.2 | 14 | 32 | 14 | 1.114 | 1.1 | 1.11 | 0.874 | 0.876 | 0.885 | 0.793 | 8.60E-07 |

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| cds.Camellia_sinensis.comp15985_c0_seq1_m.20246 | stress up-regulated Nod 19 protein [Medicago truncatula] | 51.937 | 52.957 | 14.8 | 7 | 11 | 7 | 1.005 | 1.065 | 1.056 | 0.978 | 0.954 | 0.959 | 0.925 | 1.65E-02 |
| cds.Camellia_sinensis.comp15996_c0_seq1_m.35151 | electron carrier/oxidoreductase [Arabidopsis lyrata subsp. lyrata] | 32.317 | 23.083 | 27.6 | 6 | 8 | 6 | 0.992 | 1.073 | 1.012 | 0.936 | 0.954 | 0.968 | 0.929 | 4.51E-02 |
| cds.Camellia_sinensis.comp16016_c0_seq1_m.17394 | PREDICTED: WPP domain-interacting protein 1 [Theobroma cacao] | 65.063 | 9.7238 | 7.8 | 4 | 5 | 4 | 0.969 | 1.113 | 0.994 | 0.952 | 1.003 | 0.974 | 0.952 | 3.54E-01 |
| cds.Camellia_sinensis.comp16030_c0_seq1_m.20464 | PREDICTED: low-temperature-induced cysteine proteinase [Nelumbo nucifera] | 48.443 | 30.205 | 19.1 | 6 | 9 | 6 | 0.905 | 0.989 | 0.942 | 1.086 | 1.023 | 1.074 | 1.122 | 2.14E-02 |
| cds.Camellia_sinensis.comp16051_c0_seq1_m.15178 | PREDICTED: aspartic proteinase A1-like [Nelumbo nucifera] | 55.138 | 56.905 | 21.5 | 10 | 28 | 10 | 1.053 | 1.05 | 1.033 | 0.935 | 0.94 | 0.959 | 0.904 | 4.83E-04 |

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| cds.Camellia_sinensis.comp16063_c0_seq1_m.46848 | NtPRp27-like protein precursor [Solanum tuberosum | 25.568 | 14.293 | 9.3 | 2 | 5 | 1 | 0.932 | 0.867 | 0.836 | 1.12 | 1.183 | 1.106 | 1.294 | 2.46E-03 |
| cds.Camellia_sinensis.comp16098_c0_seq1_m.39069 | PREDICTED: rhodanese-like domain-containing protein 10 isoform X1 [Vitis vinifera] | 24.434 | 14.456 | 24.1 | 4 | 5 | 4 | 1.086 | 1.064 | 1.066 | 0.885 | 0.934 | 0.927 | 0.854 | 9.39E-04 |
| cds.Camellia_sinensis.comp16103_c0_seq1_m.15293 | PREDICTED: magnesium transporter MRS2-11, chloroplastic [Jatropha | 40.64 | 22.585 | 22 | 7 | 8 | 7 | 1.025 | 1.023 | 1.075 | 0.979 | 0.954 | 0.938 | 0.919 | 1.47E-02 |
| cds.Camellia_sinensis.comp16110_c0_seq1_m.43593 | PREDICTED: glycosyltransferase-like protein gnt13 [Nicotiana tomentosiformis] | 19.215 | 6.9989 | 10.7 | 2 | 7 | 2 | 0.991 | 0.948 | 0.917 | 1.002 | 1.093 | 1.015 | 1.089 | 7.32E-02 |

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| cds.Camellia_sinensis.comp16116_c0_seq1_m.38134 | PREDICTED: remorin [Daucus carota subsp. sativus] | 30.655 | 1.4493 | 3.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp16127_c0_seq1_m.46989 | PREDICTED: NAD(P)H-quinone oxidoreductase subunit L, chloroplastic [Vitis vinifera] | 23.33 | 3.1694 | 11 | 2 | 3 | 2 | 0.955 | 0.96 | 0.997 | 0.991 | 1.075 | 1.042 | 1.067 | 7.67E-02 |
| cds.Camellia_sinensis.comp16154_c0_seq1_m.42494 | PREDICTED: glycine-rich protein 2-like [Juglans regia] | 19.893 | 132.3 | 26.6 | 4 | 9 | 4 | 1.083 | 1.06 | 1.034 | 0.937 | 0.904 | 0.946 | 0.877 | 2.44E-03 |
| cds.Camellia_sinensis.comp16161_c0_seq1_m.34022 | PREDICTED: pleiotropic drug resistance protein 2-like [Fragaria vesca subsp. vesca] | 43.652 | 7.0768 | 4.4 | 1 | 1 | 1 | 0.813 | 1.007 | 0.971 | 1.097 | 1.084 | 1.074 | 1.166 | 1.40E-01 |

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| cds.Camellia_sinensis.comp16161_c0_seq2_m.41376 | PREDICTED: pleiotropic drug resistance protein 2-like isoform X3 [Nelumbo nucifera] | 33.68 | 4.0356 | 6.2 | 2 | 2 | 2 | 1.02 | 1.068 | 1.052 | 0.934 | 0.947 | 0.974 | 0.909 | 6.54E-03 |
| cds.Camellia_sinensis.comp16164_c0_seq1_m.43742 | PREDICTED: NAD(P)H-quinone oxidoreductase subunit O, chloroplastic [Citrus sinensis] | 21.496 | 2.7668 | 8.4 | 2 | 3 | 2 | 1.049 | 1.104 | 1.05 | 0.998 | 0.918 | 0.873 | 0.871 | 3.04E-02 |
| cds.Camellia_sinensis.comp16191_c0_seq1_m.18823 | DNA binding protein [Arabidopsis thaliana] | 47.717 | 9.9999 | 8.8 | 3 | 3 | 3 | 1.035 | 1.065 | 0.961 | 0.869 | 0.985 | 1.075 | 0.957 | 5.33E-01 |
| cds.Camellia_sinensis.comp16207_c0_seq1_m.48693 | PREDICTED: hypersensitive-induced response protein 2 [Erythranthe guttata] | 23.34 | 3.8695 | 11.7 | 3 | 6 | 1 | 1.008 | 0.983 | 0.853 | 1.111 | 0.939 | 1.124 | 1.116 | 2.34E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp16225_c0_seq2_m.40027 | TPR repeat protein [Medicago truncatula] | 26.525 | 1.3692 | 3.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp16250_c0_seq1_m.38511 | PREDICTED: profilin-1 [Vitis vinifera] | 14.145 | 13.6 | 29.8 | 3 | 3 | 2 | 0.936 | 1.015 | 1.124 | 1.111 | 0.903 | 0.93 | 0.957 | 6.19E-01 |
| cds.Camellia_sinensis.comp16265_c0_seq1_m.29040 | PREDICTED: exosome complex component RRP4 homolog [Vitis vinifera] | 37.256 | 7.6043 | 6.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp16285_c0_seq1_m.52727 | PREDICTED: 40S ribosomal protein S4-3-like [Pyrus x bretschneideri] | 18.551 | -2 | 26.7 | 5 | 11 | 1 | 1.184 | 1.142 | 1.179 | 0.822 | 0.83 | 0.796 | 0.698 | 2.49E-05 |
| cds.Camellia_sinensis.comp16348_c0_seq1_m.43055 | PREDICTED: 40S ribosomal protein S17-4-like [Daucus carota subsp. sativus] | 17.554 | 18.444 | 37.1 | 5 | 8 | 5 | 1.143 | 1.189 | 1.055 | 0.855 | 0.898 | 0.806 | 0.756 | 4.00E-03 |

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| cds.Camellia_sinensis.comp16373_c0_seq1_m.51330 | PREDICTED: chalcone synthase [Pyrus x bretschneideri] | 19.938 | 47.804 | 46.6 | 6 | 27 | 1 | 1.467 | 1.452 | 1.298 | 0.561 | 0.511 | 0.575 | 0.391 | 6.01E-05 |
| cds.Camellia_sinensis.comp16389_c0_seq1_m.25964 | CAAX amino terminal protease family protein [Medicago truncatula] | 20.84 | 1.3771 | 5.5 | 1 | 1 | 1 | 1.014 | 1.01 | 1.052 | 0.962 | 0.891 | 1.069 | 0.95 | 3.77E-01 |
| cds.Camellia_sinensis.comp16399_c0_seq1_m.26573 | PREDICTED: heterogeneous nuclear ribonucleoprotein 1-like [Sesamum indicum] | 40.377 | 2.6678 | 2.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp16436_c0_seq1_m.39676 | PREDICTED: importin subunit alpha-like [Sesamum indicum] | 31.172 | 13.912 | 37.9 | 10 | 11 | 4 | 0.998 | 1.063 | 0.993 | 0.834 | 1.094 | 1.015 | 0.964 | 6.35E-01 |

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| cds.Camellia_sinensis.comp16445_c0_seq1_m.37082 | PREDICTED: hydroxyacylglutathione hydrolase cytoplasmic [Nicotiana sylvestris] | 28.84 | 43.735 | 36.4 | 9 | 20 | 9 | 0.908 | 0.93 | 0.926 | 1.078 | 1.068 | 1.073 | 1.165 | 4.07E-05 |
| cds.Camellia_sinensis.comp16447_c0_seq1_m.16705 | PREDICTED: ribosome-recycling factor, chloroplastic-like [Gossypium hirsutum] | 19.694 | 95.317 | 61.8 | 12 | 36 | 12 | 1.018 | 1.013 | 1 | 1 | 0.984 | 0.995 | 0.983 | 7.26E-02 |
| cds.Camellia_sinensis.comp16470_c0_seq2_m.43636 | transmembrane protein, putative (DUF3464) [Arabidopsis thaliana] | 20.415 | 10.396 | 12.8 | 2 | 2 | 2 | 0.985 | 1.023 | 1.022 | 1.051 | 0.913 | 1.016 | 0.983 | 7.01E-01 |
| cds.Camellia_sinensis.comp165067_c0_seq1_m.53440 | PREDICTED: bark storage protein A [Vitis vinifera] | 16.928 | 5.69 | 16.4 | 2 | 2 | 2 | 0.924 | 0.985 | 1.037 | 1.201 | 0.908 | 0.979 | 1.048 | 6.72E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp16506_c0_seq1_m.29027 | PREDICTED: inactive protein RESTRICTED TEV MOVEMENT 2-like [Nicotiana sylvestris] | 46.902 | 28.374 | 20.1 | 7 | 7 | 7 | 1.058 | 1.102 | 1.119 | 0.938 | 0.899 | 0.903 | 0.836 | 1.12E-03 |
| cds.Camellia_sinensis.comp16515_c0_seq1_m.17608 | PREDICTED: plant UBX domain-containing protein 10 [Ipomoea nil] | 50.334 | 7.0513 | 6.7 | 3 | 4 | 3 | 0.952 | 1 | 0.995 | 0.996 | 1.027 | 1.026 | 1.035 | 1.40E-01 |
| cds.Camellia_sinensis.comp16538_c0_seq1_m.13562 | PREDICTED: dynamin-related protein 5A [Sesamum indicum] | 68.501 | 59.536 | 28.6 | 15 | 20 | 14 | 0.973 | 0.95 | 1.012 | 1.053 | 1.027 | 1.014 | 1.054 | 6.95E-02 |
| cds.Camellia_sinensis.comp16576_c0_seq1_m.36226 | PREDICTED: glutathione S-transferase-like [Nelumbo nucifera] | 15.216 | 42.262 | 42.1 | 5 | 15 | 5 | 1.019 | 0.983 | 0.985 | 1.014 | 0.995 | 1.046 | 1.023 | 2.96E-01 |
| cds.Camellia_sinensis.comp16577_c0_seq1_m.15298 | PREDICTED: UBP1-associated protein 2A [Vitis vinifera] | 54.081 | 9.8999 | 7.7 | 4 | 5 | 4 | 1.129 | 1.066 | 1.142 | 0.974 | 0.856 | 0.825 | 0.796 | 1.35E-02 |

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| cds.Camellia_sinensis.comp16582_c0_seq1_m.22277 | PREDICTED: rhodanese-like domain-containing protein 4A, chloroplastic [Vitis vinifera] | 42.729 | 1.6561 | 4.7 | 2 | 2 | 2 | 0.916 | 1.068 | 1.103 | 0.926 | 1.023 | 0.975 | 0.947 | 4.64E-01 |
| cds.Camellia_sinensis.comp16588_c0_seq1_m.38680 | PREDICTED: photosystem II reaction center PSB28 protein, chloroplastic [Prunus mume] | 21.185 | 7.5307 | 18.3 | 3 | 4 | 3 | 0.971 | 1.023 | 0.988 | 0.989 | 0.979 | 0.985 | 0.99 | 5.74E-01 |
| cds.Camellia_sinensis.comp16591_c0_seq1_m.34054 | PREDICTED: elongation factor 1-beta-like [Sesamum indicum] | 24.443 | 58.605 | 40 | 8 | 24 | 7 | 0.994 | 0.98 | 0.976 | 1.013 | 1.034 | 1.018 | 1.039 | 9.98E-03 |
| cds.Camellia_sinensis.comp16592_c0_seq1_m.51984 | PREDICTED: ADP-ribosylation factor-like protein 8B [Musa acuminata subsp. malaccensis] | 13.145 | 19.264 | 53.8 | 5 | 8 | 4 | 0.972 | 1.008 | 0.945 | 1.088 | 1.015 | 1.008 | 1.064 | 1.16E-01 |

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| cds.Camellia_sinensis.comp16595_c0_seq1_m.26718 | PREDICTED: DNA-directed RNA polymerase V subunit 1 [Vitis | 45.641 | 8.681 | 6.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp16607_c0_seq1_m.12090 | PREDICTED: mitotic spindle checkpoint protein MAD1 [Vitis vinifera] | 51.684 | 1.7796 | 2.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp16608_c0_seq1_m.28401 | PREDICTED: pleiotropic drug resistance protein 2-like [Sesamum indicum] | 50.888 | 1.8817 | 5.7 | 3 | 3 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp16608_c0_seq2_m.32924 | PREDICTED: pleiotropic drug resistance protein 2-like [Sesamum indicum] | 43.489 | 16.949 | 13.3 | 5 | 5 | 3 | 0.892 | 0.958 | 0.897 | 1.128 | 1.098 | 1.07 | 1.2 | 2.68E-03 |

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| cds.Camellia_sinensis.comp16615_c0_seq1_m.17318 | PREDICTED: aminomethyltransferase, mitochondrial [Nelumbo nucifera] | 37.162 | 131.88 | 46.4 | 15 | 56 | 15 | 1.045 | 1 | 1.016 | 0.979 | 0.993 | 0.984 | 0.966 | 6.20E-02 |
| cds.Camellia_sinensis.comp16620_c0_seq1_m.38325 | PREDICTED: peroxiredoxin-2B [Populus euphratica] | 17.412 | 44.896 | 30.9 | 4 | 13 | 4 | 1.057 | 1.016 | 1.059 | 0.944 | 0.987 | 0.952 | 0.92 | 1.25E-02 |
| cds.Camellia_sinensis.comp16662_c0_seq1_m.54393 | PREDICTED: beta-glucosidase BoGH3B-like [Prunus mume] | 13.029 | 15.962 | 37.8 | 4 | 5 | 4 | 1.012 | 1.03 | 1.052 | 0.981 | 0.97 | 0.995 | 0.952 | 2.18E-02 |
| cds.Camellia_sinensis.comp16665_c1_seq1_m.38592 | PREDICTED: kirola-like [Sesamum indicum] | 20.034 | 135.19 | 51.4 | 9 | 31 | 9 | 0.969 | 0.963 | 0.975 | 1.042 | 1.017 | 1.037 | 1.065 | 1.58E-03 |
| cds.Camellia_sinensis.comp16671_c0_seq1_m.25835 | PREDICTED: chaperonin CPN60-2, mitochondrial [Theobroma cacao] | 43.716 | 168.18 | 54.2 | 22 | 49 | 15 | 0.98 | 0.954 | 0.962 | 1.049 | 1.045 | 1.041 | 1.083 | 6.56E-04 |

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| cds.Camellia_sinensis.comp16680_c0_seq1_m.14842 | PREDICTED: pentatricopeptide repeat-containing protein At3g02490, mitochondrial [Vitis vinifera] | 73.699 | 4.7248 | 3.2 | 2 | 2 | 2 | 1.013 | 1.014 | 1.058 | 1.055 | 0.907 | 0.961 | 0.947 | 2.95E-01 |
| cds.Camellia_sinensis.comp16688_c0_seq1_m.25660 | PREDICTED: pyridoxal kinase [Nicotiana attenuata] | 37.385 | 20.742 | 19.8 | 7 | 10 | 7 | 1.04 | 0.934 | 0.976 | 1.014 | 1.032 | 1.022 | 1.04 | 2.73E-01 |
| cds.Camellia_sinensis.comp16722_c0_seq1_m.19086 | PREDICTED: BRO1 domain-containing protein BROX [Citrus sinensis] | 47.506 | 9.2122 | 13.1 | 4 | 5 | 4 | 1.047 | 0.989 | 0.964 | 0.985 | 1.046 | 0.973 | 1.001 | 9.68E-01 |
| cds.Camellia_sinensis.comp16730_c0_seq1_m.27278 | PREDICTED: annexin D1 [Populus | 35.899 | 127.46 | 47.2 | 16 | 37 | 16 | 0.96 | 0.961 | 0.937 | 1.053 | 1.068 | 1.061 | 1.113 | 3.05E-04 |
| cds.Camellia_sinensis.comp16741_c0_seq1_m.53860 | PREDICTED: CBS domain-containing protein CBSX3, mitochondrial [Citrus sinensis] | 11.542 | 11.159 | 15.1 | 1 | 2 | 1 | 0.886 | 0.875 | 0.923 | 1.111 | 1.12 | 1.129 | 1.252 | 1.80E-04 |

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| cds.Camellia_sinensis.comp16765_c0_seq1_m.35556 | PREDICTED: probable bifunctional TENA-E protein [Solanum tuberosum | 26.374 | 1.4183 | 6.5 | 2 | 2 | 2 | 0.986 | 0.959 | 0.987 | 0.991 | 1.057 | 1.035 | 1.052 | 7.80E-02 |
| cds.Camellia_sinensis.comp16766_c0_seq1_m.28858 | PREDICTED: FAD-dependent urate hydroxylase isoform X1 [Solanum pennellii] | 47.061 | 93.521 | 28.8 | 10 | 18 | 10 | 0.912 | 0.919 | 0.938 | 1.101 | 1.103 | 1.073 | 1.183 | 1.61E-04 |
| cds.Camellia_sinensis.comp16769_c0_seq1_m.31560 | PREDICTED: mediator of RNA polymerase II transcription subunit 36a-like [Daucus carota subsp. sativus] | 33.21 | 52.822 | 26.7 | 8 | 16 | 8 | 1.033 | 1.058 | 1.037 | 0.971 | 0.95 | 0.975 | 0.926 | 2.14E-03 |
| cds.Camellia_sinensis.comp16770_c0_seq1_m.38569 | PREDICTED: protein SPIRAL1-like 1 [Populus euphratica] | 11.306 | 72.789 | 46.1 | 3 | 7 | 3 | 1.12 | 1.016 | 1.052 | 0.922 | 0.948 | 0.917 | 0.874 | 1.16E-02 |

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| cds.Camellia_sinensis.comp16800_c0_seq1_m.15124 | PREDICTED: protein INVOLVED IN DE NOVO 2 [Solanum tuberosum | 73.091 | 4.6843 | 6.6 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp16821_c0_seq1_m.45046 | PREDICTED: peptidyl-prolyl cis-trans isomerase E [Nicotiana attenuata] | 20.846 | 25.661 | 32.8 | 5 | 5 | 5 | 1.041 | 0.967 | 1.014 | 1.028 | 0.956 | 1.016 | 0.993 | 8.25E-01 |
| cds.Camellia_sinensis.comp168375_c0_seq1_m.48819 | PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5 isoform X1 [Vitis vinifera] | 17.803 | 2.5583 | 6.9 | 1 | 1 | 1 | 0.965 | 0.992 | 1.072 | 0.993 | 1.041 | 0.95 | 0.985 | 7.39E-01 |
| cds.Camellia_sinensis.comp16853_c0_seq1_m.35026 | PREDICTED: mini-ribonuclease 3 [Capsicum annuum] | 26.541 | 1.8457 | 4.3 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp16868_c0_seq1_m.32972 | PREDICTED: nuclear transcription factor Y subunit C-1-like [Solanum pennellii] | 30.353 | 4.0613 | 10 | 3 | 3 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp16881_c0_seq1_m.43054 | PREDICTED: protein ALUMINUM SENSITIVE 3 [Juglans regia] | 21.705 | 4.3573 | 15.7 | 2 | 2 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp16928_c0_seq1_m.14871 | PREDICTED: external alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial-like [Juglans | 66.127 | 29.291 | 22.5 | 12 | 13 | 11 | 0.991 | 0.968 | 0.945 | 1.019 | 1.068 | 1.041 | 1.077 | 1.83E-02 |
| cds.Camellia_sinensis.comp16963_c0_seq1_m.38523 | PREDICTED: ycf3-interacting protein 1, chloroplastic [Nelumbo nucifera] | 30.199 | 57.802 | 17.5 | 4 | 9 | 4 | 1.225 | 1.268 | 1.168 | 0.741 | 0.855 | 0.751 | 0.641 | 9.77E-04 |

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| cds.Camellia_sinensis.comp16965_c1_seq1_m.43577 | PREDICTED: photosynthetic NDH subunit of lumenal location 2, chloroplastic [Vitis vinifera] | 18.219 | 41.309 | 39.5 | 5 | 6 | 5 | 0.999 | 1.003 | 1.045 | 0.985 | 1.012 | 0.951 | 0.968 | 2.24E-01 |
| cds.Camellia_sinensis.comp16976_c0_seq1_m.36981 | PREDICTED: heat shock cognate 70 kDa protein 2-like [Phoenix dactylifera] | 39.107 | 81.65 | 47.6 | 19 | 57 | 6 | 1.05 | 1.008 | 0.982 | 0.971 | 0.967 | 1.007 | 0.969 | 2.48E-01 |
| cds.Camellia_sinensis.comp16981_c0_seq1_m.10785 | PREDICTED: ABC transporter F family member 5 [Vitis vinifera] | 57.2 | 6.22 | 2 | 1 | 1 | 1 | 1.046 | 1.057 | 1.083 | 1.037 | 0.867 | 0.905 | 0.882 | 7.91E-02 |
| cds.Camellia_sinensis.comp16981_c0_seq1_m.10786 | PREDICTED: ABC transporter F family member 5 [Ziziphus jujuba] | 26.967 | 5.4578 | 14.9 | 3 | 4 | 3 | 1.024 | 1.017 | 0.976 | 1.081 | 0.908 | 1.001 | 0.991 | 8.41E-01 |

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| cds.Camellia_sinensis.comp17055_c0_seq1_m.38022 | PREDICTED: serine carboxypeptidase II-2 [Fragaria vesca subsp. vesca] | 32.13 | 7.1604 | 10.1 | 2 | 2 | 2 | 0.891 | 0.884 | 1.062 | 1.151 | 1.152 | 0.907 | 1.131 | 2.91E-01 |
| cds.Camellia_sinensis.comp17061_c0_seq1_m.30094 | pantothenate kinase [Medicago truncatula] | 42.208 | 44.734 | 20.3 | 10 | 12 | 10 | 0.961 | 0.996 | 0.961 | 1.033 | 1.023 | 1.024 | 1.056 | 1.17E-02 |
| cds.Camellia_sinensis.comp17087_c0_seq1_m.36448 | PREDICTED: vacuolar protein sorting-associated protein 29 [Setaria italica] | 11.371 | 2.7415 | 8.1 | 1 | 2 | 1 | 0.97 | 0.996 | 0.923 | 1.057 | 1.036 | 1.039 | 1.084 | 2.48E-02 |
| cds.Camellia_sinensis.comp17135_c0_seq1_m.34251 | PREDICTED: peroxidase 64 [Nelumbo nucifera] | 37.084 | 33.723 | 19.5 | 6 | 8 | 6 | 1.019 | 1.057 | 1.073 | 0.919 | 0.932 | 0.938 | 0.886 | 1.82E-03 |
| cds.Camellia_sinensis.comp17139_c0_seq1_m.20770 | PREDICTED: pinin [Sesamum indicum] | 32.316 | 2.0729 | 3.9 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp17147_c0_seq1_m.50824 | PREDICTED: BRISC and BRCA1-A complex member 1 [Cucumis | 14.116 | 1.6234 | 6.2 | 1 | 1 | 1 | 0.981 | 1.022 | 1.042 | 0.998 | 1.016 | 0.952 | 0.974 | 3.74E-01 |
| cds.Camellia_sinensis.comp17169_c0_seq1_m.46387 | PREDICTED: mannan endo-1,4-beta-mannosidase 7-like [Nelumbo nucifera] | 22.309 | 2.4031 | 9.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp17175_c0_seq1_m.36851 | PREDICTED: protein LOW PSII ACCUMULATION 1, chloroplastic [Nelumbo nucifera] | 38.066 | 17.386 | 9.3 | 3 | 5 | 3 | 1.008 | 0.984 | 0.979 | 1.05 | 0.984 | 1.028 | 1.031 | 2.30E-01 |
| cds.Camellia_sinensis.comp17237_c0_seq1_m.50048 | PREDICTED: protein SIEVE ELEMENT OCCLUSION B-like [Juglans regia] | 21.273 | 25.063 | 22 | 3 | 5 | 3 | 0.931 | 0.917 | 0.969 | 1.213 | 1.02 | 1.134 | 1.195 | 2.94E-02 |

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| cds.Camellia_sinensis.comp17242_c0_seq1_m.26782 | PREDICTED: PI-PLC X-box domain-containing protein DDB_G0293730 [Ziziphus jujuba] | 36.317 | 4.9145 | 8.5 | 3 | 5 | 3 | 1.012 | 1.033 | 1.001 | 0.972 | 1 | 0.991 | 0.973 | 9.10E-02 |
| cds.Camellia_sinensis.comp17285_c0_seq1_m.21253 | PREDICTED: aspartic proteinase-like protein 2 [Nelumbo nucifera] | 54.216 | 1.438 | 1.4 | 1 | 1 | 1 | 1.002 | 1.056 | 1.125 | 0.952 | 0.923 | 0.938 | 0.884 | 2.41E-02 |
| cds.Camellia_sinensis.comp17289_c0_seq1_m.33204 | PREDICTED: proteasome subunit alpha type-5 [Juglans regia] | 25.983 | 122.46 | 40.5 | 9 | 28 | 9 | 0.999 | 0.98 | 0.959 | 1.034 | 1.031 | 1.045 | 1.059 | 1.03E-02 |
| cds.Camellia_sinensis.comp17316_c0_seq1_m.34900 | PREDICTED: coatomer subunit beta-1 [Cucumis sativus] | 33.782 | 3.8181 | 3.4 | 1 | 2 | 1 | 1.024 | 1.035 | 1.042 | 0.938 | 0.945 | 1.013 | 0.934 | 5.10E-02 |
| cds.Camellia_sinensis.comp173194_c0_seq1_m.53015 | PREDICTED: peroxidase A2-like [Juglans regia] | 17.197 | 63.203 | 28.5 | 4 | 9 | 4 | 0.969 | 0.886 | 0.886 | 1.105 | 1.134 | 1.071 | 1.208 | 5.16E-03 |

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| cds.Camellia_sinensis.comp17320_c0_seq3_m.36333 | PREDICTED: DNA repair RAD52-like protein 2, chloroplastic [Ipomoea nil] | 28.007 | 42.357 | 25.7 | 6 | 14 | 6 | 0.95 | 0.982 | 1.024 | 1.009 | 1.036 | 1.016 | 1.036 | 2.01E-01 |
| cds.Camellia_sinensis.comp17327_c0_seq1_m.47678 | PREDICTED: triphosphate tunel metalloenzyme 3-like [Capsicum annuum] | 14.817 | 1.5128 | 6 | 1 | 1 | 1 | 0.953 | 1.053 | 0.964 | 1.034 | 1.019 | 0.995 | 1.026 | 4.68E-01 |
| cds.Camellia_sinensis.comp17330_c0_seq1_m.25747 | PREDICTED: transmembrane protein 184 homolog DDB_G0279555 [Ricinus communis] | 34.047 | 1.7759 | 2.7 | 1 | 2 | 1 | 0.917 | 1.029 | 1.017 | 0.993 | 1.033 | 1.03 | 1.031 | 4.55E-01 |
| cds.Camellia_sinensis.comp17389_c0_seq1_m.5176 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 2 homolog A [Prunus mume] | 97.952 | 237.79 | 32.4 | 24 | 37 | 24 | 1.001 | 1.014 | 1.024 | 1.003 | 0.983 | 1 | 0.983 | 1.25E-01 |

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| cds.Camellia_sinensis.comp17393_c0_seq1_m.55351 | PREDICTED: galactokinase isoform X2 [Gossypium raimondii] | 14.78 | 1.4127 | 17.2 | 3 | 3 | 2 | 0.97 | 0.981 | 0.96 | 0.964 | 1.027 | 1.111 | 1.066 | 2.75E-01 |
| cds.Camellia_sinensis.comp17394_c1_seq1_m.57350 | PREDICTED: thioredoxin H-type [Prunus mume] | 13.475 | 10.011 | 15.7 | 2 | 9 | 1 | 0.938 | 0.951 | 0.969 | 1.058 | 1.134 | 1.035 | 1.129 | 1.43E-02 |
| cds.Camellia_sinensis.comp17413_c0_seq1_m.32892 | PREDICTED: bark storage protein A [Vitis vinifera] | 40.465 | 11.414 | 3.8 | 1 | 1 | 1 | 1.034 | 0.89 | 0.911 | 0.908 | 1.083 | 1.182 | 1.119 | 2.95E-01 |
| cds.Camellia_sinensis.comp17414_c0_seq1_m.7290 | PREDICTED: subtilisin-like protease SBT1.4 [Nicotiana tabacum] | 96.47 | 70.889 | 14.4 | 11 | 25 | 11 | 1.036 | 1.068 | 1.037 | 0.965 | 0.956 | 0.943 | 0.912 | 1.54E-03 |
| cds.Camellia_sinensis.comp17446_c0_seq1_m.36742 | PREDICTED: probable methyltransferase PMT2 [Sesamum indicum] | 28.568 | 2.1685 | 3.1 | 1 | 1 | 1 | 1.239 | 1.309 | 1.203 | 0.721 | 0.729 | 0.723 | 0.579 | 2.08E-03 |

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| cds.Camellia_sinensis.comp17454_c0_seq1_m.52470 | PREDICTED: mitochondrial import inner membrane translocase subunit Tim9 [Erythranthe guttata] | 12.886 | 38.635 | 60.7 | 6 | 15 | 6 | 0.983 | 1.022 | 1.036 | 1.007 | 1.018 | 0.986 | 0.99 | 6.23E-01 |
| cds.Camellia_sinensis.comp17457_c0_seq1_m.39054 | PREDICTED: protein YLS3 [Vitis vinifera] | 20.165 | 1.9 | 7.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp17491_c0_seq1_m.52292 | PREDICTED: 28 kDa ribonucleoprotein, chloroplastic [Ziziphus jujuba] | 17.716 | 11.9 | 8.4 | 1 | 4 | 1 | 0.984 | 1.041 | 0.98 | 0.958 | 1.034 | 1.01 | 0.999 | 9.72E-01 |
| cds.Camellia_sinensis.comp17538_c0_seq2_m.4420 | PREDICTED: glycine--tRNA ligase, chloroplastic/mitochondrial 2 isoform X1 [Vitis vinifera] | 122.03 | 62.461 | 13.4 | 13 | 15 | 13 | 0.957 | 0.986 | 1.009 | 1.002 | 1.023 | 1.045 | 1.04 | 1.15E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp17559_c0_seq1_m.32084 | PREDICTED: dehydrogenase/reductase SDR family member 12 [Prunus mume] | 35.364 | 24.506 | 22.3 | 8 | 9 | 8 | 1.007 | 0.973 | 0.997 | 0.984 | 1.001 | 0.991 | 1 | 9.83E-01 |
| cds.Camellia_sinensis.comp17573_c0_seq1_m.30215 | PREDICTED: eukaryotic translation initiation factor 4B2-like [Juglans regia] | 37.334 | 12.135 | 17.4 | 5 | 5 | 3 | 1.357 | 1.197 | 1.342 | 0.656 | 0.678 | 0.675 | 0.516 | 9.51E-05 |
| cds.Camellia_sinensis.comp17573_c0_seq2_m.32838 | PREDICTED: eukaryotic translation initiation factor 4B2-like [Juglans regia] | 37.239 | 2.9224 | 11.9 | 4 | 4 | 2 | 1.211 | 1.176 | 1.074 | 0.822 | 0.809 | 0.857 | 0.719 | 1.20E-03 |
| cds.Camellia_sinensis.comp17619_c0_seq1_m.33696 | PREDICTED: protein EXORDIUM-like 2 [Nicotiana tomentosiformis] | 34.923 | 1.1819 | 3.1 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp176480_c0_seq1_m.50697 | PREDICTED: retrovirus-related Pol polyprotein from transposon TNT 1-94 isoform X7 [Daucus carota subsp.sativus] | 20.037 | 1.494 | 4.7 | 1 | 1 | 1 | 0.952 | 0.777 | 0.823 | 0.974 | 1.476 | 1.044 | 1.369 | 1.02E-01 |
| cds.Camellia_sinensis.comp17650_c0_seq1_m.41675 | FAM210B-like protein [Medicago truncatula] | 21.997 | 46.705 | 18.2 | 3 | 4 | 3 | 1.096 | 1.012 | 0.983 | 0.906 | 0.974 | 0.996 | 0.93 | 1.72E-01 |
| cds.Camellia_sinensis.comp17652_c0_seq1_m.47249 | PREDICTED: non-specific lipid-transfer protein 2-like [Nicotiana tabacum] | 16.696 | 11.88 | 23.9 | 3 | 3 | 3 | 1.04 | 1.041 | 1.067 | 1.008 | 0.888 | 0.953 | 0.905 | 5.48E-02 |
| cds.Camellia_sinensis.comp17723_c0_seq1_m.35916 | PREDICTED: mRNA-decapping enzyme-like protein [Daucus carota subsp. sativus] | 39.075 | 1.862 | 3.1 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp17725_c0_seq1_m.42198 | PREDICTED: protein argonaute 4A-like [Juglans regia] | 21.705 | 8.487 | 14.4 | 2 | 3 | 2 | 1.144 | 1.123 | 1.093 | 0.955 | 0.756 | 0.898 | 0.776 | 2.24E-02 |
| cds.Camellia_sinensis.comp17755_c0_seq1_m.43934 | PREDICTED: 14-3-3-like protein [Juglans regia] | 21.218 | 72.505 | 68.3 | 10 | 28 | 8 | 1.034 | 1.005 | 0.889 | 1.04 | 1.017 | 1.043 | 1.059 | 2.77E-01 |
| cds.Camellia_sinensis.comp17761_c0_seq1_m.35615 | PREDICTED: uncharacterized methyltransferase At1g78140, chloroplastic isoform X1 [Juglans regia] | 35.471 | 6.772 | 10.7 | 3 | 4 | 3 | 0.906 | 1.039 | 0.869 | 1.023 | 1.129 | 1.064 | 1.143 | 9.06E-02 |
| cds.Camellia_sinensis.comp17833_c0_seq1_m.45194 | DNA-binding family protein [Populus trichocarpa] | 17.9 | 68.535 | 27 | 4 | 6 | 3 | 0.969 | 1.002 | 0.959 | 1.042 | 1.004 | 1.046 | 1.055 | 4.44E-02 |

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| cds.Camellia_sinensis.comp17862_c0_seq1_m.51544 | PREDICTED: plasma membrane-associated cation-binding protein 1-like isoform X1 [Nicotiana tomentosiformis] | 14.382 | 74.525 | 39 | 6 | 17 | 6 | 0.972 | 0.913 | 0.941 | 1.051 | 1.07 | 1.057 | 1.125 | 3.34E-03 |
| cds.Camellia_sinensis.comp17865_c0_seq1_m.38533 | PREDICTED: caffeoyl-CoA O-methyltransferase isoform X1 [Ricinus communis] | 26.74 | 3.3912 | 7.2 | 2 | 3 | 2 | 0.981 | 0.943 | 0.942 | 1.031 | 1.095 | 1.024 | 1.099 | 2.00E-02 |
| cds.Camellia_sinensis.comp17870_c0_seq1_m.40532 | PREDICTED: psbP domain-containing protein 2, chloroplastic [Prunus mume] | 27.21 | 49.923 | 20 | 4 | 10 | 4 | 0.971 | 0.976 | 0.949 | 1.03 | 1.045 | 1.059 | 1.082 | 2.58E-03 |

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| cds.Camellia_sinensis.comp17872_c0_seq1_m.38423 | PREDICTED: peptidyl-prolyl cis-trans isomerase CYP18-2 [Vigna radiata var. radiata] | 18.195 | 15.309 | 29.3 | 4 | 4 | 4 | 1.004 | 1.011 | 0.985 | 0.982 | 1.026 | 1.001 | 1.003 | 8.55E-01 |
| cds.Camellia_sinensis.comp17904_c0_seq1_m.26470 | PREDICTED: aconitate hydratase, cytoplasmic [Sesamum indicum] | 37.957 | 95.837 | 45.2 | 16 | 40 | 8 | 0.968 | 0.993 | 0.919 | 1.044 | 1.052 | 1.048 | 1.092 | 6.12E-02 |
| cds.Camellia_sinensis.comp17913_c0_seq1_m.31582 | PREDICTED: probable choline kinase 1 [Sesamum indicum] | 25.128 | 3.1171 | 3.7 | 1 | 2 | 1 | 0.903 | 0.961 | 0.976 | 1.017 | 1.106 | 1.067 | 1.123 | 2.68E-02 |
| cds.Camellia_sinensis.comp17964_c0_seq1_m.38271 | PREDICTED: probable plastid-lipid-associated protein 13, chloroplastic [Juglans regia] | 36.09 | 110.56 | 41 | 11 | 28 | 11 | 0.985 | 0.955 | 0.963 | 1.03 | 1.042 | 1.05 | 1.075 | 2.52E-03 |

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| cds.Camellia_sinensis.comp17975_c0_seq1_m.28168 | PREDICTED: protein AIG1 [Jatropha curcas] | 38.3 | 12.175 | 9.4 | 3 | 3 | 3 | 0.91 | 0.965 | 0.949 | 1.107 | 1.021 | 1.081 | 1.136 | 1.27E-02 |
| cds.Camellia_sinensis.comp18017_c1_seq1_m.55054 | ATP synthase gamma chain 1 family protein [Populus trichocarpa] | 15.19 | 55.873 | 44.5 | 6 | 16 | 4 | 1.094 | 1.046 | 1.046 | 0.919 | 0.932 | 0.914 | 0.868 | 9.16E-04 |
| cds.Camellia_sinensis.comp18036_c0_seq1_m.53688 | ferritin-2, chloroplastic [Jatropha curcas] | 16.137 | 33.967 | 23.2 | 3 | 8 | 3 | 0.956 | 1.022 | 1.04 | 0.929 | 0.99 | 1.067 | 0.989 | 8.19E-01 |
| cds.Camellia_sinensis.comp18056_c0_seq1_m.41640 | PREDICTED: AP-4 complex subunit sigma [Ipomoea nil] | 17.976 | 8.4773 | 7.9 | 1 | 2 | 1 | 0.968 | 1.01 | 0.946 | 1.032 | 1.047 | 1.015 | 1.058 | 5.50E-02 |
| cds.Camellia_sinensis.comp18073_c0_seq1_m.53732 | PREDICTED: basic endochitinase [Eucalyptus grandis] | 16.084 | 60.577 | 34 | 3 | 9 | 3 | 0.893 | 0.904 | 0.931 | 1.138 | 1.107 | 1.092 | 1.223 | 3.16E-04 |
| cds.Camellia_sinensis.comp18087_c0_seq1_m.16587 | Transmembrane protein 87A [Morus notabilis] | 59.375 | 2.3081 | 3.2 | 2 | 2 | 2 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp18089_c0_seq1_m.28576 | PREDICTED: methylthioribose-1-phosphate isomerase [Populus euphratica] | 41.504 | 41.181 | 22 | 8 | 13 | 8 | 0.946 | 0.958 | 0.931 | 1.082 | 1.039 | 1.009 | 1.104 | 1.07E-02 |
| cds.Camellia_sinensis.comp181019_c0_seq1_m.53257 | PREDICTED: UDP-glycosyltransferase 73C2 [Vitis vinifera] | 17.497 | 1.9577 | 7.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp18152_c0_seq1_m.49380 | PREDICTED: hypersensitive-induced response protein 2 [Theobroma cacao] | 18.171 | 3.8593 | 30.7 | 5 | 5 | 4 | 0.911 | 0.953 | 0.938 | 1.068 | 1.063 | 1.095 | 1.151 | 9.38E-04 |
| cds.Camellia_sinensis.comp18157_c0_seq1_m.44976 | PREDICTED: cytochrome c [Arachis ipaensis] | 12.331 | 11.21 | 38.4 | 4 | 8 | 4 | 1.04 | 0.98 | 0.984 | 1.026 | 1.001 | 0.976 | 1 | 9.95E-01 |
| cds.Camellia_sinensis.comp18188_c0_seq1_m.33943 | PREDICTED: probable ribosome-binding factor A, chloroplastic [Theobroma cacao] | 25.487 | 3.8121 | 10.2 | 2 | 3 | 2 | 1.153 | 1.153 | 1.158 | 0.927 | 0.792 | 0.874 | 0.749 | 2.39E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp182174_c0_seq1_m.46675 | PREDICTED: D-3-phosphoglycerate dehydrogenase 3, chloroplastic [Vitis vinifera] | 20.892 | 4.3712 | 10.1 | 2 | 4 | 1 | 0.95 | 0.939 | 0.984 | 1.031 | 0.993 | 1.125 | 1.096 | 8.39E-02 |
| cds.Camellia_sinensis.comp18218_c0_seq1_m.53618 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 11, chloroplastic/mitochondrial-like [Nelumbo nucifera] | 16.927 | 8.9212 | 19.2 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp18252_c0_seq1_m.24814 | PREDICTED: protein tas-like [Nicotiana tabacum] | 48.881 | 71.7 | 29.9 | 12 | 24 | 12 | 0.965 | 0.939 | 0.96 | 1.059 | 1.059 | 1.027 | 1.098 | 2.10E-03 |
| cds.Camellia_sinensis.comp18262_c0_seq1_m.23547 | PREDICTED: rubisco accumulation factor 1, chloroplastic [Juglans regia] | 46.625 | 44.25 | 23.2 | 9 | 14 | 9 | 1.007 | 0.999 | 1.037 | 0.986 | 0.981 | 1.013 | 0.979 | 2.39E-01 |

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| cds.Camellia_sinensis.comp18275_c0_seq1_m.34006 | PREDICTED: ribulose-phosphate 3-epimerase, cytoplasmic isoform [Juglans regia] | 23.882 | 55.258 | 16.7 | 3 | 7 | 3 | 1.018 | 1.002 | 0.975 | 0.975 | 1.053 | 1.047 | 1.027 | 4.04E-01 |
| cds.Camellia_sinensis.comp18302_c0_seq1_m.26529 | PREDICTED: protein PTST, chloroplastic [Vitis vinifera] | 34.652 | 22.395 | 22.7 | 8 | 10 | 8 | 0.998 | 1.052 | 1.032 | 0.966 | 1.004 | 1.016 | 0.969 | 2.18E-01 |
| cds.Camellia_sinensis.comp18333_c0_seq1_m.25382 | PREDICTED: putative hydrolase YtaP [Theobroma cacao] | 39.856 | 31.934 | 29.7 | 9 | 12 | 9 | 1.055 | 1.036 | 1.024 | 0.943 | 0.963 | 0.935 | 0.912 | 1.72E-03 |
| cds.Camellia_sinensis.comp18340_c0_seq1_m.45325 | PREDICTED: nudC domain-containing protein 2 [Vitis vinifera] | 16.52 | 3.266 | 11.3 | 2 | 2 | 2 | 1.013 | 0.998 | 0.996 | 1.019 | 1.005 | 0.979 | 0.999 | 9.16E-01 |
| cds.Camellia_sinensis.comp18343_c0_seq1_m.1417 | photosystem II CP43 chlorophyll apoprotein (chloroplast) [Actinidia deliciosa] | 51.821 | 237.61 | 32.3 | 14 | 78 | 14 | 1.006 | 1.003 | 1.016 | 0.991 | 0.999 | 0.989 | 0.985 | 3.66E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp18343_c0_seq1_m.1418 | photosystem II protein D2 (chloroplast) [Erythranthe lutea] | 39.549 | 151.14 | 25.2 | 7 | 71 | 7 | 0.964 | 0.986 | 0.975 | 1.016 | 1.03 | 1.007 | 1.044 | 9.80E-03 |
| cds.Camellia_sinensis.comp18377_c0_seq1_m.650 | PREDICTED: nuclear-pore anchor isoform X1 [Vitis vinifera] | 235.5 | 21.868 | 6.1 | 13 | 13 | 13 | 1.082 | 1.093 | 1.149 | 0.897 | 0.84 | 0.852 | 0.779 | 7.82E-04 |
| cds.Camellia_sinensis.comp18428_c0_seq1_m.45049 | PREDICTED: protochlorophyllide reductase [Vitis vinifera] | 18.192 | 18.879 | 40 | 7 | 11 | 5 | 0.959 | 0.948 | 0.949 | 1.03 | 1.081 | 1.071 | 1.114 | 2.12E-03 |
| cds.Camellia_sinensis.comp18441_c0_seq1_m.49795 | PREDICTED: tubulin beta chain [Ricinus communis] | 14.998 | 4.0042 | 11.1 | 1 | 2 | 1 | 1.17 | 1.161 | 1.167 | 0.852 | 0.799 | 0.806 | 0.702 | 3.26E-03 |
| cds.Camellia_sinensis.comp18455_c0_seq1_m.34968 | transmembrane protein, putative [Medicago truncatula] | 26.104 | -2 | 7 | 2 | 2 | 2 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp18460_c0_seq1_m.14574 | PREDICTED: leukotriene A-4 hydrolase homolog isoform X1 [Nelumbo nucifera] | 68.846 | 52.409 | 22.5 | 12 | 18 | 12 | 0.962 | 0.955 | 0.94 | 1.062 | 1.029 | 1.064 | 1.104 | 1.50E-03 |
| cds.Camellia_sinensis.comp18462_c0_seq2_m.21658 | PREDICTED: CDK5RAP1-like protein [Ipomoea nil] | 39.829 | 1.7968 | 2.6 | 1 | 1 | 1 | 1.025 | 0.964 | 0.973 | 1.128 | 0.93 | 0.996 | 1.031 | 6.66E-01 |
| cds.Camellia_sinensis.comp18478_c0_seq1_m.19072 | plant inositol phosphorylceramide synthase [Medicago truncatula] | 54.099 | 1.3204 | 1.5 | 1 | 1 | 1 | 0.969 | 1.082 | 1.112 | 0.928 | 0.934 | 0.975 | 0.897 | 7.50E-02 |
| cds.Camellia_sinensis.comp18488_c0_seq1_m.48004 | PREDICTED: protein yippee-like At4g27745 [Sesamum indicum] | 12.123 | 8.056 | 23.6 | 2 | 3 | 2 | 1.037 | 0.952 | 1.056 | 0.997 | 0.993 | 0.97 | 0.972 | 4.55E-01 |
| cds.Camellia_sinensis.comp18510_c0_seq1_m.49141 | PREDICTED: dnaJ homolog 1, mitochondrial-like [Sesamum | 21.984 | 2.0803 | 19 | 3 | 4 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp18512_c0_seq1_m.27140 | PREDICTED: protein SLOW GREEN 1, chloroplastic [Cucumis sativus] | 35.31 | 18.754 | 15.8 | 6 | 8 | 6 | 1.013 | 1.048 | 1.06 | 0.976 | 0.951 | 0.914 | 0.91 | 1.59E-02 |
| cds.Camellia_sinensis.comp18556_c0_seq1_m.41305 | PREDICTED: probable glutathione S-transferase [Jatropha curcas] | 28.249 | 11.49 | 14.9 | 3 | 5 | 3 | 1.029 | 0.803 | 0.971 | 1.115 | 0.958 | 1.07 | 1.121 | 2.49E-01 |
| cds.Camellia_sinensis.comp18571_c0_seq1_m.11928 | PREDICTED: peroxisomal acyl-coenzyme A oxidase 1-like [Nelumbo nucifera] | 74.191 | 134.07 | 26.7 | 18 | 33 | 18 | 0.999 | 0.992 | 0.998 | 1.011 | 0.99 | 0.995 | 1.002 | 7.48E-01 |
| cds.Camellia_sinensis.comp18585_c0_seq1_m.48894 | PREDICTED: high mobility group B protein 1 [Vigna radiata var. radiata] | 13.703 | 3.5973 | 10.9 | 1 | 1 | 1 | 0.938 | 1.009 | 0.974 | 1.043 | 1.054 | 1.005 | 1.062 | 7.74E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp18602_c0_seq1_m.17410 | PREDICTED: aldehyde dehydrogenase family 3 member F1-like [Nicotiana sylvestris] | 54.591 | 21.556 | 12.7 | 6 | 7 | 5 | 1.152 | 1.168 | 1.139 | 0.856 | 0.831 | 0.792 | 0.717 | 1.45E-04 |
| cds.Camellia_sinensis.comp18626_c0_seq1_m.19241 | PREDICTED: LL-diaminopimelate aminotransferase, chloroplastic-like [Juglans regia] | 50.211 | 64.002 | 23.3 | 9 | 18 | 9 | 1.003 | 1 | 1.005 | 1.019 | 0.992 | 0.981 | 0.995 | 6.79E-01 |
| cds.Camellia_sinensis.comp18674_c0_seq1_m.44439 | PREDICTED: histone H1 [Jatropha curcas] | 22.575 | 6.4584 | 16.4 | 3 | 6 | 3 | 0.936 | 0.907 | 0.951 | 1.124 | 1.127 | 1.095 | 1.198 | 4.17E-04 |
| cds.Camellia_sinensis.comp18704_c0_seq1_m.42749 | PREDICTED: auxin-binding protein T85 [Juglans regia] | 23.213 | 1.3899 | 5.9 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp18707_c0_seq1_m.44851 | maternal effect embryo arrest protein, putative [Medicago truncatula] | 21.877 | 5.5153 | 9.9 | 2 | 3 | 2 | 1.001 | 0.962 | 0.976 | 1.002 | 0.994 | 0.993 | 1.017 | 2.28E-01 |

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| cds.Camellia_sinensis.comp18719_c0_seq1_m.23468 | PREDICTED: UBX domain-containing protein 4 [Vitis vinifera] | 46.727 | 33.359 | 22.1 | 8 | 13 | 8 | 1.061 | 1.061 | 1.045 | 0.953 | 0.931 | 0.955 | 0.896 | 3.39E-04 |
| cds.Camellia_sinensis.comp18724_c0_seq1_m.36095 | PREDICTED: DNA-damage-repair/toleration protein DRT111, chloroplastic [Vitis vinifera] | 22.122 | 2.7568 | 13.2 | 2 | 2 | 2 | 0.905 | 1.536 | 0.842 | 0.875 | 0.845 | 0.98 | 0.822 | 4.58E-01 |
| cds.Camellia_sinensis.comp18726_c0_seq1_m.54824 | PREDICTED: leucine aminopeptidase 2, chloroplastic-like [Erythranthe guttata] | 13.911 | 11.898 | 56.1 | 7 | 12 | 3 | 0.955 | 0.982 | 0.981 | 1.058 | 1.039 | 1.036 | 1.074 | 3.20E-03 |
| cds.Camellia_sinensis.comp18746_c0_seq2_m.39329 | PREDICTED: stem-specific protein TSJT1-like [Daucus carota subsp. sativus] | 27.702 | 10.723 | 16.3 | 3 | 4 | 3 | 0.823 | 0.992 | 0.811 | 1.265 | 1.082 | 1.143 | 1.329 | 2.25E-02 |

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| cds.Camellia_sinensis.comp18795_c0_seq1_m.49744 | PREDICTED: acyl-coenzyme A thioesterase 9, mitochondrial-like isoform X2 [Sesamum indicum] | 15.618 | 5.7794 | 8.1 | 1 | 2 | 1 | 0.956 | 1.029 | 1.02 | 0.956 | 1.029 | 1.022 | 1.001 | 9.85E-01 |
| cds.Camellia_sinensis.comp18839_c0_seq1_m.18683 | PREDICTED: 4-coumarate--CoA ligase-like 5 [Sesamum indicum] | 59.674 | 81.874 | 25.3 | 10 | 13 | 10 | 0.952 | 0.967 | 0.979 | 1.022 | 1.035 | 0.996 | 1.053 | 2.01E-02 |
| cds.Camellia_sinensis.comp18855_c0_seq1_m.21765 | isocitrate dehydrogenase family protein [Populus trichocarpa] | 47.749 | 319.14 | 48.8 | 22 | 63 | 19 | 0.987 | 0.971 | 0.958 | 1.027 | 1.04 | 1.028 | 1.061 | 3.32E-03 |
| cds.Camellia_sinensis.comp18859_c0_seq3_m.27103 | PREDICTED: protein LOW PSII ACCUMULATION 1, chloroplastic-like isoform X2 [Malus domestica] | 34.093 | 28.674 | 8.1 | 2 | 3 | 2 | 0.983 | 1.035 | 1.049 | 1.014 | 1.076 | 0.949 | 0.991 | 8.19E-01 |

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| cds.Camellia_sinensis.comp18859_c0_seq3_m.27104 | PREDICTED: protein LOW PSII ACCUMULATION 1, chloroplastic isoform X2 [Ziziphus jujuba] | 25.304 | 36.274 | 31.4 | 7 | 13 | 7 | 1 | 0.997 | 1.006 | 1.003 | 1.001 | 0.96 | 0.987 | 4.13E-01 |
| cds.Camellia_sinensis.comp18882_c0_seq1_m.9549 | high chlorophyll fluorescence phenotype 173 [Arabidopsis thaliana] | 67.559 | 24.091 | 14.3 | 9 | 10 | 9 | 1.061 | 1.022 | 1.111 | 0.938 | 0.945 | 0.903 | 0.872 | 8.18E-03 |
| cds.Camellia_sinensis.comp18903_c0_seq1_m.19833 | Succinyl-CoA ligase [ADP-forming] subunit beta [Morus notabilis] | 45.919 | 208.93 | 48.9 | 20 | 50 | 20 | 1.017 | 1.012 | 0.989 | 0.977 | 1.004 | 0.987 | 0.983 | 2.27E-01 |
| cds.Camellia_sinensis.comp18909_c0_seq1_m.37086 | DUF1499 family protein [Medicago truncatula] | 24.841 | 19.971 | 16.4 | 3 | 5 | 3 | 0.974 | 0.944 | 0.979 | 1.005 | 1.002 | 1.088 | 1.068 | 8.88E-02 |

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| cds.Camellia_sinensis.comp18914_c0_seq1_m.37497 | PREDICTED: ER membrane protein complex subunit 8/9 homolog [Daucus carota subsp. sativus] | 28.247 | 40.867 | 27.5 | 6 | 8 | 6 | 1.003 | 0.95 | 0.968 | 1.034 | 1.054 | 1.027 | 1.066 | 2.19E-02 |
| cds.Camellia_sinensis.comp18919_c0_seq1_m.59329 | PREDICTED: 4-coumarate--CoA ligase-like 9 [Glycine max] | 10.726 | 19.238 | 28 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp18932_c0_seq1_m.32317 | PREDICTED: ATP synthase subunit gamma, mitochondrial-like [Pyrus x bretschneideri] | 35.44 | 121.97 | 42.4 | 13 | 37 | 13 | 1.071 | 1.05 | 1.01 | 0.943 | 0.963 | 0.955 | 0.914 | 7.92E-03 |
| cds.Camellia_sinensis.comp18936_c0_seq1_m.23704 | PREDICTED: malonyl-CoA-acyl carrier protein transacylase, mitochondrial [Sesamum indicum] | 44.298 | 39.715 | 24.9 | 9 | 17 | 9 | 1 | 1.009 | 1.056 | 0.965 | 0.976 | 0.965 | 0.948 | 3.74E-02 |

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| cds.Camellia_sinensis.comp18938_c0_seq1_m.40311 | Heat shock 70 kDa protein [Morus notabilis] | 32.963 | 7.7704 | 28.2 | 9 | 25 | 1 | 1.299 | 1.277 | 1.335 | 0.661 | 0.684 | 0.653 | 0.511 | 1.90E-06 |
| cds.Camellia_sinensis.comp18945_c0_seq1_m.40452 | PREDICTED: 50S ribosomal protein L27, chloroplastic [Nelumbo nucifera] | 20.981 | 3.3878 | 5.7 | 1 | 1 | 1 | 1.088 | 1.033 | 1.089 | 0.977 | 0.996 | 0.809 | 0.867 | 9.86E-02 |
| cds.Camellia_sinensis.comp18951_c0_seq1_m.49344 | PREDICTED: chaperonin CPN60-2, mitochondrial [Nelumbo nucifera] | 21.297 | 81.819 | 41.7 | 7 | 21 | 5 | 0.961 | 0.979 | 0.948 | 1.046 | 1.036 | 1.045 | 1.083 | 1.26E-03 |
| cds.Camellia_sinensis.comp18993_c0_seq1_m.44402 | PREDICTED: dCTP pyrophosphatase 1-like [Jatropha curcas] | 14.966 | 1.7745 | 7.5 | 1 | 1 | 1 | 0.922 | 0.986 | 0.96 | 1.151 | 0.951 | 1.062 | 1.103 | 1.79E-01 |
| cds.Camellia_sinensis.comp19039_c0_seq1_m.30178 | PREDICTED: glucuronokinase 1-like [Nelumbo nucifera] | 39.919 | 6.2353 | 6.9 | 2 | 2 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp19060_c0_seq1_m.4720 | PREDICTED: phosphoenolpyruvate carboxylase 2-like isoform X3 [Ziziphus jujuba] | 110.47 | 323.31 | 53.6 | 55 | 133 | 27 | 1.001 | 0.997 | 1.001 | 1.019 | 0.999 | 1.008 | 1.009 | 2.04E-01 |
| cds.Camellia_sinensis.comp19077_c0_seq1_m.41235 | PREDICTED: ubiquitin-fold modifier-conjugating enzyme 1 [Jatropha curcas] | 19.622 | 3.7751 | 17.8 | 3 | 4 | 3 | 1.011 | 1.007 | 0.924 | 1.077 | 0.956 | 1.039 | 1.044 | 4.03E-01 |
| cds.Camellia_sinensis.comp19093_c0_seq1_m.2096 | PREDICTED: protein RETICULATA-RELATED 4, chloroplastic-like [Nelumbo nucifera] | 30.657 | 31.311 | 28.4 | 8 | 24 | 8 | 0.983 | 0.981 | 0.974 | 1.003 | 1.024 | 1.025 | 1.039 | 7.50E-03 |
| cds.Camellia_sinensis.comp19098_c0_seq2_m.32157 | PREDICTED: eyes absent homolog 2 isoform X1 [Vitis vinifera] | 38.711 | 1.48 | 3.5 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp19099_c0_seq1_m.55604 | PREDICTED: pectinesterase 2.2-like [Juglans regia] | 14.265 | 17.85 | 29.8 | 3 | 5 | 3 | 1.037 | 1 | 0.985 | 0.977 | 1.006 | 0.949 | 0.97 | 2.54E-01 |
| cds.Camellia_sinensis.comp19106_c0_seq1_m.54673 | PREDICTED: TVP38/TMEM64 family membrane protein slr0305 [Solanum tuberosum | 15.644 | 10.132 | 17.7 | 4 | 6 | 4 | 1.031 | 1.049 | 1.045 | 0.946 | 0.922 | 0.976 | 0.91 | 5.44E-03 |
| cds.Camellia_sinensis.comp19124_c0_seq1_m.32589 | PREDICTED: zinc-finger homeodomain protein 1-like [Nelumbo nucifera] | 25.921 | 1.7656 | 4.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp19145_c0_seq1_m.46398 | PREDICTED: profilin-1 [Vitis vinifera] | 15.464 | 4.5685 | 22.7 | 3 | 9 | 1 | 1.156 | 1.047 | 1.031 | 0.901 | 0.927 | 0.911 | 0.847 | 1.10E-02 |
| cds.Camellia_sinensis.comp19170_c0_seq1_m.26266 | PREDICTED: COP9 signalosome complex subunit 2 [Sesamum | 51.367 | 2.4245 | 6.6 | 2 | 2 | 2 | 1.012 | 1.143 | 1.135 | 0.845 | 0.818 | 1.025 | 0.817 | 6.35E-02 |

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| cds.Camellia_sinensis.comp19187_c0_seq1_m.33599 | plant/F3H 11-7 protein [Medicago truncatula] | 37.918 | 5.0296 | 11.1 | 4 | 4 | 4 | | | | | | | | |
| cds.Camellia_sinensis.comp19201_c0_seq1_m.34376 | Myo28B1, putative [Medicago truncatula] | 33.259 | 1.2155 | 4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp1924_c0_seq1_m.51405 | PREDICTED: probable glutathione S-transferase [Populus euphratica] | 20.04 | 2.3827 | 10.3 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp19292_c0_seq1_m.44318 | PREDICTED: selenoprotein H [Vitis vinifera] | 18.474 | 11.985 | 20.1 | 4 | 7 | 4 | 1.185 | 1.132 | 1.144 | 0.781 | 0.844 | 0.818 | 0.706 | 1.96E-04 |
| cds.Camellia_sinensis.comp19327_c0_seq1_m.32266 | PREDICTED: plastid-lipid-associated protein, chloroplastic-like [Juglans regia] | 37.698 | 230.66 | 28.6 | 10 | 35 | 10 | 0.966 | 0.946 | 0.941 | 1.063 | 1.042 | 1.051 | 1.106 | 5.18E-04 |
| cds.Camellia_sinensis.comp19342_c0_seq1_m.8600 | transmembrane protein [Arabidopsis thaliana] | 91.748 | 12.705 | 5.8 | 5 | 5 | 5 | 1.075 | 1.036 | 1.096 | 0.948 | 0.912 | 0.92 | 0.867 | 2.14E-03 |

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| cds.Camellia_sinensis.comp19347_c0_seq1_m.29962 | PREDICTED: inositol oxygenase 1-like [Juglans regia] | 36.11 | 9.2103 | 3.9 | 1 | 1 | 1 | 1.258 | 1.238 | 1.051 | 0.813 | 0.773 | 0.806 | 0.674 | 2.78E-03 |
| cds.Camellia_sinensis.comp19413_c0_seq1_m.56055 | PREDICTED: mitochondrial import inner membrane translocase subunit TIM10-like [Juglans regia] | 14.691 | 5.7108 | 13.5 | 2 | 2 | 2 | 0.951 | 0.935 | 0.919 | 1.025 | 1.098 | 1.099 | 1.149 | 5.32E-03 |
| cds.Camellia_sinensis.comp19426_c0_seq1_m.51061 | PREDICTED: protein DCL, chloroplastic [Prunus mume] | 19.488 | 14.194 | 6.7 | 1 | 1 | 1 | 1.292 | 1.245 | 1.275 | 0.674 | 0.73 | 0.7 | 0.552 | 2.00E-05 |
| cds.Camellia_sinensis.comp19448_c0_seq2_m.39614 | PREDICTED: NAD(P)H-quinone oxidoreductase subunit T, chloroplastic [Theobroma cacao] | 33.63 | 11.637 | 14.8 | 3 | 3 | 3 |  |  |  |  |  |  |  |  |

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| cds.Camellia_sinensis.comp19456_c0_seq1_m.42200 | PREDICTED: subtilisin-like protease SBT1.7 [Solanum pennellii] | 28.352 | 4.9272 | 8.7 | 2 | 3 | 2 | 0.981 | 1.036 | 0.966 | 0.984 | 1.113 | 0.933 | 1.016 | 8.25E-01 |
| cds.Camellia_sinensis.comp19456_c1_seq1_m.50009 | PREDICTED: subtilisin-like protease SBT1.7 [Ricinus communis] | 17.152 | 13.568 | 14.4 | 2 | 4 | 2 | 0.97 | 0.98 | 0.979 | 1.035 | 1.042 | 1.013 | 1.055 | 4.22E-03 |
| cds.Camellia_sinensis.comp19463_c0_seq1_m.40348 | PREDICTED: serine hydroxymethyltransferase, mitochondrial [Nelumbo nucifera] | 34.043 | 18.047 | 30.2 | 6 | 20 | 2 | 1.1 | 1.11 | 1.048 | 0.935 | 0.88 | 0.949 | 0.848 | 4.86E-03 |
| cds.Camellia_sinensis.comp19503_c0_seq1_m.33408 | PREDICTED: ubiquitin-activating enzyme E1 1 isoform X2 [Vitis vinifera] | 45.411 | 7.1689 | 11.3 | 6 | 7 | 5 | 1.006 | 0.987 | 1.016 | 1.012 | 1.004 | 0.994 | 1 | 9.72E-01 |

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| cds.Camellia_sinensis.comp19518_c0_seq1_m.41879 | PREDICTED: glycine cleavage system H protein 2, mitochondrial-like isoform X2 [Daucus carota subsp. sativus] | 16.799 | 11.036 | 18.8 | 3 | 7 | 3 | 1.063 | 1.061 | 1.071 | 0.94 | 0.915 | 0.975 | 0.886 | 2.27E-02 |
| cds.Camellia_sinensis.comp19519_c0_seq1_m.29936 | PREDICTED: nuclear transcription factor Y subunit B-3 [Vitis vinifera] | 21.98 | 5.425 | 10.1 | 2 | 2 | 2 | 0.966 | 0.949 | 1.032 | 0.856 | 1.078 | 1.126 | 1.038 | 7.43E-01 |
| cds.Camellia_sinensis.comp19526_c0_seq1_m.10489 | PREDICTED: protein LUTEIN DEFICIENT 5, chloroplastic isoform X2 [Jatropha curcas] | 39.348 | 4.1567 | 12.2 | 3 | 3 | 3 | 0.999 | 1.057 | 1.003 | 0.992 | 0.921 | 1.03 | 0.962 | 3.53E-01 |

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| cds.Camellia_sinensis.comp19526_c0_seq1_m.10490 | PREDICTED: 1-aminocyclopropane-1-carboxylate oxidase [Juglans regia] | 36.206 | 33.361 | 31.2 | 9 | 18 | 9 | 1.05 | 1.051 | 1.094 | 0.909 | 0.936 | 0.934 | 0.87 | 1.08E-03 |
| cds.Camellia_sinensis.comp19532_c0_seq1_m.38865 | PREDICTED: guanine deaminase isoform X2 [Prunus | 24.129 | 6.119 | 9.8 | 2 | 2 | 2 | 1.037 | 1.176 | 0.992 | 0.958 | 0.846 | 0.978 | 0.868 | 1.08E-01 |
| cds.Camellia_sinensis.comp19546_c0_seq2_m.43914 | PREDICTED: ras-related protein RHN1-like isoform X3 [Ziziphus jujuba] | 20.218 | 2.5034 | 14.1 | 2 | 4 | 1 | 0.864 | 1.074 | 0.882 | 1.263 | 0.982 | 0.983 | 1.145 | 2.89E-01 |
| cds.Camellia_sinensis.comp19566_c0_seq1_m.28513 | PREDICTED: caffeoylshikimate esterase isoform X1 [Nicotiana attenuata] | 38.707 | 4.4981 | 7.3 | 2 | 2 | 2 | 1.002 | 1.103 | 0.974 | 0.91 | 0.982 | 1.026 | 0.948 | 3.57E-01 |

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| cds.Camellia_sinensis.comp19664_c1_seq1_m.22757 | PREDICTED: inner membrane protein PPF-1, chloroplastic isoform X2 [Nelumbo nucifera] | 43.585 | 25.629 | 15.1 | 5 | 8 | 5 | 1.136 | 1.121 | 1.084 | 0.837 | 0.825 | 0.888 | 0.763 | 5.19E-04 |
| cds.Camellia_sinensis.comp19683_c0_seq1_m.22038 | PREDICTED: LETM1 and EF-hand domain-containing protein 1, mitochondrial [Vitis vinifera] | 53.297 | 3.9721 | 4.9 | 2 | 2 | 2 | 1.068 | 1.053 | 0.996 | 1.041 | 0.891 | 0.948 | 0.924 | 1.82E-01 |
| cds.Camellia_sinensis.comp19699_c0_seq1_m.35253 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP18, chloroplastic [Sesamum indicum] | 24.57 | 10.477 | 16.7 | 4 | 6 | 4 | 1.043 | 1.073 | 1.04 | 0.922 | 0.985 | 0.943 | 0.903 | 9.38E-03 |

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| cds.Camellia_sinensis.comp19702_c0_seq1_m.40855 | PREDICTED: peptidyl-prolyl cis-trans isomerase CYP18-1 [Daucus carota subsp. sativus] | 21.608 | 29.916 | 19 | 3 | 4 | 3 | 0.952 | 0.933 | 0.98 | 0.969 | 1.084 | 1.078 | 1.093 | 8.89E-02 |
| cds.Camellia_sinensis.comp19715_c0_seq1_m.24588 | PREDICTED: BRCA1-A complex subunit BRE [Capsicum annuum] | 43.376 | 7.1822 | 11.1 | 4 | 4 | 4 | 0.94 | 0.975 | 0.988 | 1.085 | 1.134 | 0.909 | 1.078 | 3.67E-01 |
| cds.Camellia_sinensis.comp19728_c0_seq6_m.10243 | PREDICTED: DUF724 domain-containing protein 6 isoform X4 [Vitis vinifera] | 36.148 | 37.362 | 19.6 | 6 | 10 | 6 | 0.947 | 0.959 | 1.03 | 1.042 | 0.99 | 1.033 | 1.044 | 2.28E-01 |
| cds.Camellia_sinensis.comp19751_c0_seq1_m.30726 | PREDICTED: pyruvate kinase isozyme G, chloroplastic isoform X2 [Vitis | 40.765 | 20.58 | 25.7 | 8 | 15 | 8 | 1.031 | 1.005 | 0.997 | 0.962 | 1.016 | 1.011 | 0.985 | 5.03E-01 |

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| cds.Camellia_sinensis.comp19772_c0_seq1_m.47210 | PREDICTED: abscisic acid receptor PYL8 [Vitis vinifera] | 22.239 | 11.666 | 9.7 | 2 | 3 | 2 | 0.945 | 0.939 | 1.016 | 1.06 | 1.039 | 1.027 | 1.078 | 4.84E-02 |
| cds.Camellia_sinensis.comp19851_c0_seq1_m.25609 | PREDICTED: coproporphyrinogen-III oxidase 1, chloroplastic [Solanum tuberosum | 44.998 | 128.93 | 37.2 | 16 | 28 | 16 | 1.07 | 1.059 | 1.073 | 0.923 | 0.925 | 0.936 | 0.869 | 1.94E-05 |
| cds.Camellia_sinensis.comp19898_c0_seq1_m.41293 | PREDICTED: succinate dehydrogenase assembly factor 2, mitochondrial [Solanum lycopersicum] | 23.208 | 10.405 | 15.3 | 3 | 5 | 3 | 1.067 | 1.009 | 1.07 | 0.955 | 0.919 | 0.942 | 0.895 | 7.56E-03 |
| cds.Camellia_sinensis.comp19929_c0_seq1_m.31347 | PREDICTED: clathrin light chain 1-like [Capsicum annuum] | 37.317 | 14.334 | 9.5 | 3 | 3 | 2 | 1.269 | 1.241 | 1.205 | 0.735 | 0.758 | 0.719 | 0.595 | 1.87E-05 |

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| cds.Camellia_sinensis.comp19939_c0_seq1_m.14793 | PREDICTED: primary amine oxidase [Vitis vinifera] | 44.631 | 72.491 | 21 | 8 | 17 | 8 | 0.953 | 0.968 | 0.96 | 1.066 | 1.052 | 1.035 | 1.094 | 7.36E-04 |
| cds.Camellia_sinensis.comp19939_c0_seq1_m.14794 | PREDICTED: primary amine oxidase [Vitis vinifera] | 42.04 | 52.822 | 17.2 | 6 | 11 | 6 | 0.961 | 0.966 | 0.944 | 1.083 | 1.001 | 1.046 | 1.09 | 2.26E-02 |
| cds.Camellia_sinensis.comp19941_c0_seq1_m.6705 | PREDICTED: golgin candidate 6 isoform X2 [Jatropha curcas] | 101.47 | 29.054 | 7.6 | 6 | 8 | 6 | 1.037 | 1.035 | 0.99 | 0.982 | 0.926 | 1.006 | 0.952 | 1.59E-01 |
| cds.Camellia_sinensis.comp20002_c0_seq1_m.34779 | PREDICTED: zinc finger CCCH domain-containing protein 14-like [Ziziphus jujuba] | 31.895 | 60.409 | 35.2 | 8 | 18 | 6 | 0.944 | 0.98 | 1.032 | 0.986 | 1.009 | 1.034 | 1.025 | 4.43E-01 |

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| cds.Camellia_sinensis.comp20012_c0_seq1_m.22176 | PREDICTED: ATP-dependent Clp protease proteolytic subunit-related protein 1, chloroplastic-like [Juglans regia] | 43.231 | 58.739 | 29.7 | 9 | 15 | 9 | 1.017 | 1.028 | 1.013 | 0.984 | 0.946 | 0.981 | 0.952 | 2.10E-02 |
| cds.Camellia_sinensis.comp20019_c0_seq1_m.41433 | PREDICTED: chaperone protein DnaJ-like [Setaria italica] | 14.528 | 2.5125 | 8.7 | 1 | 1 | 1 | 1.009 | 1.006 | 1.066 | 0.936 | 0.965 | 1.018 | 0.947 | 1.54E-01 |
| cds.Camellia_sinensis.comp20043_c0_seq2_m.7680 | PREDICTED: spermatogenesis-associated protein 20 [Prunus mume] | 95.843 | 99.765 | 28 | 23 | 31 | 23 | 0.953 | 0.937 | 0.929 | 1.073 | 1.084 | 1.104 | 1.157 | 2.01E-04 |
| cds.Camellia_sinensis.comp20064_c0_seq1_m.24530 | PREDICTED: probable protein phosphatase 2C 9 [Sesamum indicum] | 30.483 | 61.517 | 54.3 | 12 | 18 | 12 | 0.94 | 0.992 | 0.934 | 1.089 | 1.032 | 1.079 | 1.117 | 1.21E-02 |

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| cds.Camellia_sinensis.comp20071_c0_seq1_m.17552 | PREDICTED: glucose-6-phosphate 1-dehydrogenase 1, chloroplastic [Ricinus communis] | 67.78 | 83.071 | 31 | 17 | 25 | 12 | 0.964 | 0.948 | 0.988 | 1.048 | 1.039 | 1.029 | 1.074 | 5.38E-03 |
| cds.Camellia_sinensis.comp20082_c1_seq1_m.14890 | PREDICTED: ketol-acid reductoisomerase, chloroplastic [Juglans regia] | 66.766 | 177.9 | 25.3 | 14 | 44 | 14 | 0.977 | 0.998 | 1.007 | 1.02 | 1.002 | 1.012 | 1.017 | 1.69E-01 |
| cds.Camellia_sinensis.comp20096_c0_seq1_m.15861 | PREDICTED: vacuolar fusion protein CCZ1 homolog isoform X2 [Theobroma cacao] | 55.404 | 20.741 | 15.4 | 8 | 10 | 8 | 0.887 | 0.938 | 0.937 | 1.117 | 1.073 | 1.083 | 1.185 | 1.54E-03 |
| cds.Camellia_sinensis.comp20121_c0_seq1_m.29155 | PREDICTED: trichohyalin-like [Malus domestica] | 19.675 | 1.2552 | 4.2 | 1 | 1 | 1 | 1.082 | 1.031 | 1.033 | 0.882 | 0.861 | 1.091 | 0.901 | 2.26E-01 |

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| cds.Camellia_sinensis.comp20127_c0_seq1_m.15233 | PREDICTED: phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic [Eucalyptus grandis] | 57.502 | 122.44 | 34.7 | 18 | 36 | 12 | 1.088 | 1.055 | 1.113 | 0.919 | 0.918 | 0.87 | 0.831 | 1.50E-03 |
| cds.Camellia_sinensis.comp20145_c0_seq1_m.31992 | PREDICTED: uncharacterized aarF domain-containing protein kinase At1g71810, chloroplastic isoform X1[Nelumbo nucifera] | 17.901 | 7.6004 | 14.6 | 2 | 2 | 2 | 0.906 | 0.977 | 0.942 | 0.99 | 1.019 | 1.191 | 1.133 | 1.18E-01 |

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| cds.Camellia_sinensis.comp20145_c1_seq1_m.40226 | PREDICTED: uncharacterized aarF domain-containing protein kinase At1g71810, chloroplastic-like isoform X3 [Nicotiana tabacum] | 29.818 | 3.4974 | 7.1 | 2 | 3 | 2 | 0.921 | 0.953 | 0.995 | 1.005 | 1.071 | 1.125 | 1.116 | 5.12E-02 |
| cds.Camellia_sinensis.comp20146_c0_seq1_m.59240 | | 10.949 | 1.5604 | 12.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp20165_c0_seq1_m.36124 | transmembrane protein, putative [Medicago truncatula] | 34.814 | 8.2128 | 6.3 | 2 | 3 | 2 | 0.938 | 0.908 | 0.919 | 1.116 | 1.124 | 1.033 | 1.184 | 4.22E-03 |
| cds.Camellia_sinensis.comp20176_c0_seq1_m.38992 | PREDICTED: myosin heavy chain, muscle [Nicotiana attenuata] | 19.655 | 33.817 | 17.3 | 3 | 4 | 3 | 1.028 | 0.985 | 0.928 | 0.997 | 1.025 | 1.04 | 1.041 | 2.71E-01 |

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| cds.Camellia_sinensis.comp20180_c0_seq1_m.9372 | PREDICTED: UTP--glucose-1-phosphate uridylyltransferase-like [Juglans regia] | 56.669 | 10.518 | 4.3 | 2 | 10 | 2 | 1.018 | 0.966 | 0.999 | 1.001 | 1.012 | 1.033 | 1.021 | 3.05E-01 |
| cds.Camellia_sinensis.comp20197_c0_seq1_m.39887 | PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 [Theobroma cacao] | 14.729 | 44.974 | 76.9 | 9 | 20 | 9 | 1.038 | 1.022 | 1.02 | 0.977 | 1.002 | 0.979 | 0.96 | 1.46E-02 |
| cds.Camellia_sinensis.comp20212_c0_seq1_m.13881 | PREDICTED: pentatricopeptide repeat-containing protein At1g02150 [Eucalyptu | 62.958 | 5.9796 | 6.9 | 4 | 5 | 4 | 0.92 | 1.023 | 1.043 | 1.058 | 1.008 | 0.996 | 1.025 | 5.75E-01 |
| cds.Camellia_sinensis.comp20228_c0_seq1_m.42581 | PREDICTED: V-type proton ATPase subunit G 1-like [Nelumbo | 12.309 | 33.272 | 39.1 | 5 | 10 | 5 | 0.907 | 0.92 | 0.837 | 1.103 | 1.033 | 1.106 | 1.217 | 5.98E-03 |

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| cds.Camellia_sinensis.comp20235_c0_seq1_m.17959 | PREDICTED: tryptophan synthase beta chain 1 [Populus euphratica] | 55.113 | 34.523 | 15.9 | 6 | 6 | 6 | 1.039 | 0.994 | 1.074 | 0.964 | 0.973 | 1.065 | 0.966 | 4.20E-01 |
| cds.Camellia_sinensis.comp20326_c0_seq2_m.55870 | PREDICTED: puromycin-sensitive aminopeptidase isoform X1 [Vitis vinifera] | 14.287 | 40.178 | 52.7 | 5 | 12 | 4 | 0.987 | 0.932 | 0.9 | 1.029 | 1.072 | 1.081 | 1.129 | 1.70E-02 |
| cds.Camellia_sinensis.comp20332_c0_seq1_m.49077 | PREDICTED: 60S ribosomal protein L19-3 [Ziziphus jujuba] | 11.977 | 2.2131 | 32.7 | 3 | 5 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp20339_c0_seq1_m.25394 | PREDICTED: eukaryotic translation initiation factor 4E-1-like [Arachis duranensis] | 26.025 | 3.4247 | 8.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp20339_c1_seq1_m.9048 | PREDICTED: phospholipase D alpha 1 [Sesamum indicum] | 92.214 | 249.4 | 35.8 | 23 | 57 | 21 | 0.923 | 0.912 | 0.914 | 1.095 | 1.114 | 1.067 | 1.192 | 1.79E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20344_c1_seq1_m.50331 | seed maturation protein PM35 [Glycine max] | 11.078 | 25.316 | 37.4 | 3 | 4 | 3 | 0.938 | 1.134 | 0.852 | 1.004 | 0.981 | 1.159 | 1.075 | 4.80E-01 |
| cds.Camellia_sinensis.comp20346_c0_seq1_m.45093 | PREDICTED: photosynthetic NDH subunit of subcomplex B 3, chloroplastic [Daucus carota subsp. sativus] | 21.322 | 20.289 | 21.1 | 3 | 5 | 3 | 1.043 | 1.062 | 1.058 | 0.923 | 0.939 | 0.99 | 0.902 | 8.84E-03 |
| cds.Camellia_sinensis.comp20347_c0_seq1_m.30439 | PREDICTED: cysteine protease RD19A [Ipomoea nil] | 40.173 | 6.8764 | 9 | 3 | 7 | 2 | 1.101 | 1.134 | 1.055 | 0.871 | 0.874 | 0.886 | 0.8 | 4.98E-04 |
| cds.Camellia_sinensis.comp20349_c0_seq1_m.22493 | PREDICTED: ferredoxin--NADP reductase, leaf isozyme, chloroplastic [Ricinus communis] | 40.573 | 293.46 | 56.9 | 20 | 103 | 7 | 1.043 | 1.018 | 0.971 | 0.982 | 0.984 | 0.989 | 0.975 | 3.54E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20349_c0_seq2_m.32225 | ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic [Capsicum annuum] | 29.897 | 17.759 | 49.5 | 11 | 56 | 2 | 1.016 | 1.156 | 1.074 | 0.903 | 0.861 | 1.054 | 0.868 | 1.15E-01 |
| cds.Camellia_sinensis.comp20350_c0_seq1_m.20984 | PREDICTED: enolase 1, chloroplastic [Jatropha curcas] | 52.778 | 38.528 | 8.9 | 4 | 6 | 4 | 1.068 | 1.052 | 1.08 | 0.976 | 0.913 | 0.881 | 0.866 | 9.40E-03 |
| cds.Camellia_sinensis.comp20356_c0_seq1_m.38217 | PREDICTED: photosynthetic NDH subunit of subcomplex B 5, chloroplastic [Nelumbo nucifera] | 25.565 | 5.5998 | 11.5 | 2 | 3 | 2 | 0.981 | 1.002 | 1.011 | 0.978 | 1.034 | 1.005 | 1.008 | 7.05E-01 |
| cds.Camellia_sinensis.comp20364_c0_seq1_m.41438 | heat shock cognate 70 kDa protein 2-like [Ananas comosus] | 27.816 | 33.941 | 59.8 | 13 | 71 | 2 | 1.012 | 0.988 | 0.988 | 0.977 | 1.044 | 1.003 | 1.012 | 6.06E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20367_c0_seq1_m.18869 | PREDICTED: flowering locus K homology domain isoform X1 [Ricinus communis] | 46.807 | 138.72 | 33.3 | 13 | 28 | 11 | 0.962 | 1.014 | 0.994 | 1.018 | 1.003 | 0.995 | 1.015 | 4.05E-01 |
| cds.Camellia_sinensis.comp20368_c0_seq2_m.30637 | PREDICTED: UPF0613 protein PB24D3.06c [Populus euphratica] | 27.726 | 26.399 | 4.8 | 1 | 1 | 1 | 1.015 | 0.934 | 0.995 | 0.943 | 1.134 | 0.99 | 1.042 | 5.60E-01 |
| cds.Camellia_sinensis.comp20369_c0_seq1_m.35674 | PREDICTED: thioredoxin-like protein CDSP32, chloroplastic [Nelumbo nucifera] | 33.819 | 205 | 43.9 | 13 | 41 | 13 | 1.063 | 1.04 | 1.039 | 0.96 | 0.928 | 0.959 | 0.906 | 1.82E-03 |
| cds.Camellia_sinensis.comp20371_c0_seq2_m.34391 | PREDICTED: probable trans-2-enoyl-CoA reductase, mitochondrial isoform X3 [Juglans | 38.069 | 4.0837 | 6.6 | 2 | 3 | 2 | 0.926 | 0.995 | 1.04 | 1.012 | 1.04 | 1.008 | 1.033 | 3.90E-01 |

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| cds.Camellia_sinensis.comp20380_c0_seq1_m.14804 | PREDICTED: probable carotenoid cleavage dioxygenase 4, chloroplastic [Nicotiana attenuata] | 47.042 | 65.941 | 18.3 | 8 | 13 | 8 | 1.005 | 1.005 | 1.021 | 1.011 | 0.968 | 0.965 | 0.971 | 1.39E-01 |
| cds.Camellia_sinensis.comp20382_c0_seq1_m.29159 | PREDICTED: trafficking protein particle complex subunit 12-like [Vitis | 40.524 | 1.272 | 2.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp20385_c0_seq1_m.15507 | PREDICTED: zeta-carotene desaturase, chloroplastic/chromoplastic [Vitis vinifera] | 64.292 | 12.08 | 9.3 | 5 | 6 | 5 | 1.057 | 1.056 | 0.933 | 0.9 | 0.896 | 0.987 | 0.914 | 1.60E-01 |
| cds.Camellia_sinensis.comp20387_c0_seq1_m.31718 | PREDICTED: flavonol synthase/flavanone 3-hydroxylase-like [Erythranthe guttata] | 38.417 | 15.974 | 6.2 | 2 | 2 | 2 | 0.95 | 1.008 | 0.948 | 1.026 | 1.046 | 1.043 | 1.072 | 2.92E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20390_c0_seq1_m.30556 | PREDICTED: protein SRC2 [Vitis vinifera] | 30.677 | 2.8683 | 3.5 | 1 | 1 | 1 | 0.976 | 0.976 | 0.982 | 1.036 | 1.031 | 1.019 | 1.052 | 6.84E-04 |
| cds.Camellia_sinensis.comp20401_c0_seq1_m.19860 | PREDICTED: kynurenine--oxoglutarate transaminase [Jatropha curcas] | 36.248 | 7.9103 | 14.9 | 5 | 6 | 5 | 0.976 | 0.977 | 1.076 | 0.971 | 0.997 | 0.99 | 0.977 | 5.32E-01 |
| cds.Camellia_sinensis.comp20401_c0_seq1_m.19861 | PREDICTED: probable N-succinyldiaminopimelate aminotransferase DapC [Gossypium hirsutum] | 22.039 | 29.962 | 32.8 | 5 | 7 | 5 | 1.031 | 0.971 | 1.011 | 1.011 | 0.95 | 1.021 | 0.99 | 7.32E-01 |
| cds.Camellia_sinensis.comp20402_c0_seq1_m.28705 | PREDICTED: titin-like [Fragaria vesca subsp. vesca] | 19.986 | 4.7872 | 15.1 | 3 | 5 | 3 | 1.118 | 1.203 | 1.17 | 0.851 | 0.85 | 0.771 | 0.708 | 9.00E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20403_c0_seq1_m.21322 | oligouridylate-binding protein 1B-like [Cajanus | 46.646 | 25.619 | 12.9 | 5 | 8 | 4 | 0.979 | 0.951 | 1.003 | 1.051 | 1.025 | 0.93 | 1.025 | 5.92E-01 |
| cds.Camellia_sinensis.comp20404_c0_seq1_m.31114 | PREDICTED: beta-carotene hydroxylase 2, chloroplastic [Vitis vinifera] | 39.932 | 9.2243 | 5.6 | 1 | 1 | 1 | 0.749 | 0.985 | 0.955 | 1.074 | 1.044 | 1.246 | 1.251 | 9.00E-02 |
| cds.Camellia_sinensis.comp20406_c0_seq2_m.22795 | PREDICTED: heterogeneous nuclear ribonucleoprotein R [Sesamum indicum] | 47.84 | 5.6169 | 5.7 | 2 | 2 | 2 | 0.949 | 0.988 | 1.108 | 1.032 | 0.924 | 1.013 | 0.975 | 6.95E-01 |
| cds.Camellia_sinensis.comp20407_c0_seq1_m.12567 | PREDICTED: ALBINO3-like protein 1, chloroplastic [Vitis vinifera] | 59.727 | 42.745 | 8.1 | 4 | 7 | 4 | 1.016 | 0.97 | 1.074 | 0.981 | 0.968 | 0.947 | 0.946 | 1.56E-01 |

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| cds.Camellia_sinensis.comp20412_c0_seq1_m.33374 | PREDICTED: proteasome subunit alpha type-6 [Musa acuminata subsp. malaccensis] | 27.384 | 94.253 | 54.9 | 15 | 27 | 15 | 0.97 | 0.98 | 0.944 | 1.043 | 1.042 | 1.056 | 1.085 | 2.38E-03 |
| cds.Camellia_sinensis.comp20418_c0_seq1_m.35269 | PREDICTED: tropinone reductase homolog At5g06060-like isoform X1 [Nelumbo nucifera] | 29.741 | 8.531 | 12 | 4 | 11 | 2 | 0.972 | 0.94 | 0.981 | 1.064 | 1.003 | 1.062 | 1.082 | 2.84E-02 |
| cds.Camellia_sinensis.comp20423_c0_seq1_m.35425 | PREDICTED: rhodanese-like domain-containing protein 14, chloroplastic [Theobroma cacao] | 25.321 | 57.434 | 31.3 | 7 | 14 | 7 | 0.99 | 0.997 | 0.993 | 1.009 | 1.002 | 0.998 | 1.01 | 6.34E-02 |
| cds.Camellia_sinensis.comp20429_c0_seq1_m.24635 | PREDICTED: ultraviolet-B receptor UVR8 [Sesamum indicum] | 43.849 | 16.632 | 16.7 | 7 | 9 | 7 | 0.985 | 1 | 1.022 | 1.002 | 0.993 | 1.025 | 1.004 | 7.76E-01 |

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| cds.Camellia_sinensis.comp20430_c0_seq1_m.35205 | PREDICTED: 6,7-dimethyl-8-ribityllumazine synthase, chloroplastic [Ipomoea nil] | 27.433 | 9.152 | 10.2 | 4 | 6 | 4 | 0.986 | 0.93 | 0.951 | 1.071 | 1.056 | 1.037 | 1.104 | 7.06E-03 |
| cds.Camellia_sinensis.comp20433_c0_seq1_m.46290 | hydrogen peroxide induced protein, putative [Medicago truncatula] | 14.815 | 29.97 | 25.2 | 2 | 2 | 2 | 1.04 | 1.033 | 0.967 | 0.992 | 1.031 | 0.941 | 0.975 | 5.09E-01 |
| cds.Camellia_sinensis.comp20436_c0_seq1_m.16763 | PREDICTED: splicing factor SF3a60 homolog [Juglans regia] | 61.133 | 19.596 | 11.2 | 5 | 5 | 5 | 1.084 | 1.119 | 1.126 | 0.871 | 0.892 | 0.851 | 0.785 | 1.78E-04 |
| cds.Camellia_sinensis.comp20438_c0_seq1_m.37911 | PREDICTED: outer envelope pore protein 24A, chloroplastic-like [Nelumbo nucifera] | 25.464 | 14.584 | 28.3 | 7 | 9 | 7 | 1.036 | 0.996 | 1.014 | 1.006 | 0.983 | 0.985 | 0.976 | 1.54E-01 |

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| cds.Camellia_sinensis.comp20441_c0_seq3_m.33434 | RING-H2 zinc finger protein [Arabidopsis thaliana] | 31.331 | 4.4074 | 6.1 | 1 | 2 | 1 | 1.022 | 1.15 | 1.041 | 1.072 | 0.714 | 0.993 | 0.865 | 2.89E-01 |
| cds.Camellia_sinensis.comp20446_c0_seq1_m.28374 | PREDICTED: transcription factor DIVARICATA-like [Juglans regia] | 33.955 | 10.11 | 6 | 2 | 2 | 2 | 1.087 | 1.005 | 1.057 | 1.023 | 0.906 | 0.916 | 0.903 | 8.53E-02 |
| cds.Camellia_sinensis.comp20451_c0_seq1_m.36083 | PREDICTED: salicylic acid-binding protein 2 isoform X1 [Vitis vinifera] | 29.648 | 41.836 | 29.7 | 6 | 13 | 6 | 0.962 | 1.003 | 0.983 | 1.074 | 1.021 | 1.041 | 1.064 | 3.16E-02 |
| cds.Camellia_sinensis.comp20457_c0_seq1_m.38890 | PREDICTED: 22.0 kDa class IV heat shock protein-like [Solanum pennellii] | 21.783 | 12.871 | 23.4 | 5 | 5 | 5 | 1.14 | 1.035 | 1.042 | 0.906 | 0.956 | 0.899 | 0.858 | 1.42E-02 |
| cds.Camellia_sinensis.comp20458_c0_seq1_m.27298 | PREDICTED: SEC14 cytosolic factor [Jatropha curcas] | 14.124 | 2.8167 | 9.4 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp20463_c0_seq1_m.19640 | PREDICTED: probable serine protease EDA2 [Ziziphus jujuba] | 54.281 | 109.9 | 25.5 | 10 | 20 | 10 | 1.016 | 1.029 | 1.012 | 0.938 | 1.006 | 0.992 | 0.96 | 1.37E-01 |
| cds.Camellia_sinensis.comp20464_c0_seq1_m.30668 | PREDICTED: acyl-protein thioesterase 2 [Arachis duranensis] | 27.2 | 4.8794 | 11.4 | 4 | 5 | 4 | 1.084 | 0.983 | 1.03 | 0.95 | 0.967 | 0.988 | 0.938 | 1.06E-01 |
| cds.Camellia_sinensis.comp20467_c0_seq1_m.38457 | PREDICTED: probable N-acetyltransferase san [Juglans regia] | 19.308 | 1.8495 | 5.9 | 1 | 1 | 1 | 1.027 | 1.069 | 1.025 | 0.921 | 0.984 | 0.967 | 0.92 | 2.58E-02 |
| cds.Camellia_sinensis.comp20469_c0_seq1_m.23763 | PREDICTED: RAN GTPase-activating protein 1 [Vitis vinifera] | 50.407 | 26.233 | 13.4 | 5 | 6 | 5 | 1.136 | 1.092 | 1.042 | 0.905 | 0.932 | 0.905 | 0.839 | 2.82E-03 |
| cds.Camellia_sinensis.comp20474_c0_seq1_m.33064 | PREDICTED: GTP-binding nuclear protein Ran-3 [Camelina sativa] | 26.072 | 85.929 | 38.1 | 8 | 20 | 8 | 0.999 | 0.963 | 0.987 | 0.998 | 1.038 | 1.031 | 1.04 | 7.32E-02 |

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| cds.Camellia_sinensis.comp20478_c0_seq1_m.32271 | PREDICTED: reticulon-like protein B1 [Ricinus communis] | 33.99 | 15.592 | 17.9 | 6 | 8 | 6 | 0.991 | 0.982 | 1 | 0.974 | 1.042 | 1.026 | 1.023 | 3.45E-01 |
| cds.Camellia_sinensis.comp20486_c0_seq1_m.10822 | PREDICTED: glutamate--tRNA ligase, chloroplastic/mitochondrial [Ziziphus jujuba] | 44.706 | 15.758 | 17.9 | 7 | 11 | 7 | 1.046 | 0.99 | 1.041 | 1.001 | 0.973 | 0.965 | 0.955 | 9.30E-02 |
| cds.Camellia_sinensis.comp20486_c0_seq1_m.10823 | PREDICTED: glutamate--tRNA ligase, chloroplastic/mitochondrial [Ipomoea nil] | 32.179 | 7.6481 | 3.1 | 1 | 1 | 1 | 1.006 | 1.07 | 1.102 | 0.956 | 0.935 | 0.927 | 0.887 | 1.35E-02 |
| cds.Camellia_sinensis.comp20488_c0_seq1_m.22800 | PREDICTED: TOM1-like protein 2 [Vitis vinifera] | 44.052 | 62.16 | 40.1 | 16 | 22 | 16 | 0.972 | 0.987 | 0.981 | 1.026 | 1.031 | 1.014 | 1.045 | 2.80E-03 |

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| cds.Camellia_sinensis.comp20489_c0_seq1_m.16840 | PREDICTED: ribose-phosphate pyrophosphokinase 1 [Theobroma cacao] | 46.525 | 21.156 | 7.5 | 3 | 4 | 2 | 0.964 | 0.984 | 0.981 | 0.946 | 0.98 | 1.039 | 1.012 | 7.03E-01 |
| cds.Camellia_sinensis.comp20489_c0_seq2_m.22330 | PREDICTED: ribose-phosphate pyrophosphokinase 1 [Juglans regia] | 16.247 | 30.19 | 26 | 3 | 3 | 2 | 0.893 | 1.007 | 0.978 | 1.085 | 1.071 | 0.999 | 1.096 | 1.05E-01 |
| cds.Camellia_sinensis.comp20490_c0_seq1_m.37682 | PREDICTED: U2 small nuclear ribonucleoprotein B" [Ipomoea nil] | 29.103 | 1.5748 | 6.1 | 2 | 2 | 2 | 1.068 | 1.045 | 1.064 | 0.957 | 0.977 | 0.882 | 0.886 | 1.90E-02 |
| cds.Camellia_sinensis.comp20491_c0_seq1_m.30669 | PREDICTED: palmitoyl-protein thioesterase 1 [Prunus | 34.868 | 12.475 | 9.5 | 3 | 4 | 3 | 0.999 | 0.921 | 1.002 | 1.023 | 1.014 | 1.09 | 1.07 | 1.30E-01 |
| cds.Camellia_sinensis.comp20492_c0_seq1_m.1946 | putative serine/threonine-protein kinase dyrk2 [Morus notabilis] | 133.28 | 7.2607 | 1.5 | 1 | 1 | 1 | 1.264 | 1.312 | 1.033 | 0.733 | 0.772 | 0.812 | 0.642 | 5.38E-03 |

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| cds.Camellia_sinensis.comp20498_c0_seq1_m.16852 | PREDICTED: non-specific phospholipase C1 isoform X1 [Vitis vinifera] | 37.641 | 14.439 | 12.4 | 4 | 6 | 3 | 1.108 | 1.066 | 1.092 | 0.885 | 0.88 | 0.891 | 0.813 | 6.15E-05 |
| cds.Camellia_sinensis.comp20504_c0_seq1_m.22343 | PREDICTED: elongation factor Tu, chloroplastic [Juglans regia] | 54.717 | 323.31 | 52.8 | 23 | 115 | 21 | 1.033 | 1.017 | 1.001 | 0.986 | 0.975 | 0.976 | 0.963 | 1.76E-02 |
| cds.Camellia_sinensis.comp20504_c0_seq2_m.31348 | PREDICTED: ATP-dependent Clp protease proteolytic subunit-related protein 4, chloroplastic [Prunus mume] | 33.119 | 67.173 | 22.7 | 5 | 16 | 5 | 1.031 | 1.004 | 1.01 | 0.983 | 0.987 | 0.996 | 0.974 | 4.24E-02 |
| cds.Camellia_sinensis.comp20509_c0_seq1_m.40649 | tail fiber [Arabidopsis thaliana] | 24.764 | 1.7292 | 4 | 1 | 1 | 1 | 0.988 | 0.961 | 1.005 | 0.958 | 1.048 | 1.05 | 1.035 | 3.70E-01 |

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| cds.Camellia_sinensis.comp20515_c0_seq1_m.41744 | PREDICTED: pentatricopeptide repeat-containing protein At1g62350 [Beta vulgaris subsp. vulgaris] | 29.148 | 6.2141 | 8.2 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp20529_c0_seq1_m.34425 | PREDICTED: activating signal cointegrator 1-like [Nicotiana tabacum] | 28.621 | 2.825 | 7 | 2 | 2 | 2 | 0.944 | 0.978 | 1 | 1.058 | 1.036 | 1.007 | 1.061 | 5.41E-02 |
| cds.Camellia_sinensis.comp20534_c0_seq1_m.34889 | PREDICTED: stem-specific protein TSJT1 [Daucus carota subsp. sativus] | 27.284 | 11.146 | 24 | 7 | 10 | 7 | 0.981 | 0.979 | 0.984 | 1.038 | 1.049 | 1.002 | 1.049 | 7.53E-02 |
| cds.Camellia_sinensis.comp20535_c0_seq2_m.43958 | PREDICTED: nifU-like protein 3, chloroplastic [Nicotiana tomentosiformis] | 17.897 | 14.895 | 17.7 | 2 | 4 | 2 | 1.045 | 1.001 | 1.038 | 0.986 | 0.976 | 1.042 | 0.974 | 3.37E-01 |

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| cds.Camellia_sinensis.comp20538_c0_seq1_m.37612 | PREDICTED: small heat shock protein, chloroplastic-like [Juglans regia] | 32.824 | 43.486 | 23.8 | 7 | 16 | 7 | 1.078 | 1.071 | 1.037 | 0.951 | 0.941 | 0.915 | 0.881 | 1.60E-03 |
| cds.Camellia_sinensis.comp20539_c0_seq1_m.30179 | PREDICTED: ATP-dependent Clp protease proteolytic subunit 3, chloroplastic-like [Nicotiana tabacum] | 39.032 | 93.776 | 18.2 | 6 | 10 | 6 | 1.012 | 1.016 | 1.006 | 0.994 | 1.011 | 0.976 | 0.983 | 1.69E-01 |
| cds.Camellia_sinensis.comp20545_c0_seq1_m.27639 | PREDICTED: short-chain dehydrogenase reductase 2a [Theobroma cacao] | 41.456 | 1.597 | 3.1 | 1 | 1 | 1 | 0.872 | 1.16 | 1.051 | 0.98 | 0.965 | 0.986 | 0.951 | 6.54E-01 |
| cds.Camellia_sinensis.comp20551_c0_seq1_m.32591 | PREDICTED: photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic [Malus domestica] | 29.762 | 153.04 | 48.9 | 10 | 64 | 10 | 0.996 | 0.948 | 0.947 | 1.021 | 1.069 | 1.037 | 1.082 | 2.14E-02 |

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| cds.Camellia_sinensis.comp20552_c0_seq1_m.15501 | PREDICTED: ATP sulfurylase 2 [Vitis vinifera] | 44.513 | 33.222 | 26.1 | 10 | 18 | 9 | 0.994 | 0.984 | 0.979 | 1.029 | 0.985 | 1.018 | 1.025 | 1.47E-01 |
| cds.Camellia_sinensis.comp20559_c0_seq1_m.21086 | PREDICTED: protein bem46 [Vitis vinifera] | 35.166 | 9.5137 | 7.9 | 2 | 2 | 2 | 1.026 | 1.019 | 0.974 | 1.022 | 0.981 | 0.984 | 0.989 | 6.41E-01 |
| cds.Camellia_sinensis.comp20562_c0_seq1_m.18527 | UTP--glucose-1-phosphate uridylyltransferase [Ananas comosus] | 61.834 | 242.88 | 44.9 | 21 | 66 | 21 | 0.976 | 0.969 | 0.984 | 1.014 | 1.037 | 1.027 | 1.051 | 3.24E-03 |
| cds.Camellia_sinensis.comp20563_c0_seq1_m.32355 | PREDICTED: annexin D2-like [Jatropha curcas] | 25.672 | 5.4555 | 14.7 | 3 | 3 | 3 | 1.048 | 1.005 | 1.013 | 1.006 | 0.91 | 1.016 | 0.956 | 2.89E-01 |
| cds.Camellia_sinensis.comp20568_c0_seq1_m.47712 | PREDICTED: 60S ribosomal protein L35-like [Gossypium hirsutum] | 16.123 | 8.0699 | 24.8 | 5 | 5 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp20572_c0_seq1_m.45714 | PREDICTED: vesicle transport v-SNARE 12 [Prunus mume] | 18.709 | 5.5645 | 17.7 | 4 | 4 | 4 | 1.036 | 1.079 | 1.044 | 0.934 | 0.905 | 0.993 | 0.896 | 2.15E-02 |

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| cds.Camellia_sinensis.comp20590_c0_seq1_m.31254 | PREDICTED: pectinesterase 31 [Vitis vinifera] | 37.035 | 7.4034 | 11 | 3 | 3 | 3 | 0.956 | 0.998 | 0.948 | 0.985 | 1.043 | 1.088 | 1.074 | 9.87E-02 |
| cds.Camellia_sinensis.comp20591_c0_seq1_m.37440 | PREDICTED: single-stranded DNA-bindig protein WHY2, mitochondrial-like isoform X3 [Nicotiana tabacum] | 28.229 | 7.3975 | 11 | 3 | 4 | 3 | 0.951 | 0.96 | 1 | 0.958 | 1.012 | 1.092 | 1.052 | 2.95E-01 |
| cds.Camellia_sinensis.comp20592_c0_seq2_m.49303 | PREDICTED: 40S ribosomal protein S23 [Arachis ipaensis] | 14.037 | 5.4191 | 9.5 | 2 | 3 | 2 | 1.02 | 0.998 | 1.045 | 0.947 | 0.957 | 1.033 | 0.959 | 2.34E-01 |
| cds.Camellia_sinensis.comp20608_c0_seq1_m.16069 | PREDICTED: T-complex protein 1 subunit eta [Nelumbo nucifera] | 60.742 | 78.299 | 30.5 | 15 | 22 | 15 | 0.951 | 0.915 | 0.917 | 1.059 | 1.08 | 1.064 | 1.151 | 5.24E-04 |
| cds.Camellia_sinensis.comp20612_c0_seq1_m.52175 | PREDICTED: protein argonaute 4 [Vitis vinifera] | 18.614 | 3.692 | 42.5 | 6 | 9 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp20614_c0_seq1_m.31139 | PREDICTED: proline synthase co-transcribed bacterial homolog protein isoform X1 [Vitis vinifera] | 30.587 | 14.091 | 16.8 | 5 | 7 | 4 | 1.005 | 0.981 | 0.973 | 1.005 | 1.039 | 1.009 | 1.032 | 9.41E-02 |
| cds.Camellia_sinensis.comp20616_c0_seq1_m.32068 | PREDICTED: oxygen-evolving enhancer protein 1, chloroplastic [Ziziphus jujuba] | 35.011 | 323.31 | 52.7 | 21 | 149 | 21 | 1.019 | 0.965 | 0.982 | 0.997 | 1.015 | 1.014 | 1.02 | 3.01E-01 |
| cds.Camellia_sinensis.comp20617_c0_seq1_m.35166 | nucleic acid-binding, OB-fold-like protein [Medicago truncatula] | 17.371 | 3.8574 | 19.3 | 4 | 5 | 3 | 0.949 | 0.97 | 0.957 | 1.117 | 1.027 | 1.008 | 1.096 | 4.81E-02 |
| cds.Camellia_sinensis.comp20617_c0_seq2_m.40687 | nucleic acid-binding, OB-fold-like protein [Medicago truncatula] | 20.852 | 11.63 | 20.4 | 4 | 9 | 3 | 0.953 | 0.956 | 0.96 | 1.016 | 1.052 | 1.088 | 1.1 | 4.11E-02 |

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| cds.Camellia_sinensis.comp20618_c0_seq1_m.37751 | PREDICTED: ubiquitin-conjugating enzyme E2 27-like [Populus euphratica] | 21.23 | 8.4106 | 16 | 3 | 3 | 3 | 0.906 | 0.971 | 1.048 | 1.132 | 0.957 | 1.017 | 1.062 | 4.10E-01 |
| cds.Camellia_sinensis.comp20621_c0_seq1_m.25426 | PREDICTED: AT-hook motif nuclear-localized protein 8 isoform X1 [Vitis vinifera] | 36.627 | 16.336 | 3.9 | 1 | 1 | 1 | 1.063 | 1.015 | 1.043 | 0.985 | 0.969 | 0.921 | 0.921 | 2.75E-02 |
| cds.Camellia_sinensis.comp20622_c0_seq1_m.34048 | glycine-rich RNA-binding family protein [Populus trichocarpa] | 31.011 | 10.65 | 6.8 | 2 | 3 | 2 | 1.238 | 1.288 | 1.278 | 0.667 | 0.746 | 0.716 | 0.56 | 7.79E-05 |
| cds.Camellia_sinensis.comp20624_c0_seq1_m.11184 | vestitone reductase-related family protein [Populus trichocarpa] | 44.537 | 111.49 | 29.7 | 12 | 28 | 12 | 1.02 | 1.019 | 1.018 | 0.972 | 0.979 | 0.986 | 0.961 | 1.06E-02 |
| cds.Camellia_sinensis.comp20625_c0_seq1_m.16923 | PREDICTED: protein argonaute 4A [Vitis vinifera] | 62.952 | 41.399 | 15.8 | 8 | 14 | 8 | 1.062 | 1.08 | 1.083 | 0.911 | 0.935 | 0.905 | 0.853 | 1.64E-04 |

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| cds.Camellia_sinensis.comp20627_c0_seq1_m.29194 | PREDICTED: methionine aminopeptidase 1D, chloroplastic/mitochondrial isoform X1 [Vitis vinifera] | 39.177 | 8.288 | 10.1 | 4 | 5 | 4 | 1.028 | 0.993 | 1.065 | 0.946 | 0.993 | 0.956 | 0.938 | 6.35E-02 |
| cds.Camellia_sinensis.comp20631_c0_seq1_m.25567 | PREDICTED: heme-binding protein 2 [Pyrus x bretschneideri] | 25.013 | 71.351 | 46.5 | 8 | 22 | 8 | 0.992 | 1.021 | 0.967 | 1.037 | 0.991 | 0.998 | 1.015 | 5.07E-01 |
| cds.Camellia_sinensis.comp20633_c0_seq1_m.22719 | PREDICTED: ubiquitin receptor RAD23c-like isoform X2 [Gossypium raimondii] | 41.877 | 98.504 | 30.6 | 9 | 16 | 5 | 1.08 | 0.933 | 1.036 | 0.933 | 0.988 | 1.012 | 0.962 | 4.93E-01 |
| cds.Camellia_sinensis.comp20634_c0_seq1_m.34445 | PREDICTED: nitrogen regulatory protein P-II homolog isoform X2 [Theobroma cacao] | 21.593 | 16.839 | 27.9 | 6 | 9 | 6 | 0.978 | 0.984 | 1.001 | 1.011 | 1 | 1.024 | 1.024 | 6.98E-02 |

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| cds.Camellia_sinensis.comp20635_c0_seq1_m.28179 | PREDICTED: RNA-binding protein CP29B, chloroplastic [Prunus mume] | 29.591 | 186.76 | 47.8 | 11 | 38 | 11 | 1.001 | 0.998 | 0.994 | 0.995 | 0.998 | 1.014 | 1.005 | 4.97E-01 |
| cds.Camellia_sinensis.comp20635_c0_seq2_m.39693 | PREDICTED: 29 kDa ribonucleoprotein A, chloroplastic-like [Nelumbo nucifera] | 17.576 | 13.773 | 13 | 4 | 13 | 4 | 0.978 | 0.992 | 0.981 | 1.035 | 0.999 | 1.049 | 1.045 | 4.56E-02 |
| cds.Camellia_sinensis.comp20637_c0_seq1_m.49637 | PREDICTED: heterogeneous nuclear ribonucleoprotein 1 isoform X2 [Gossypium arboreum] | 10.588 | 2.6968 | 9.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp20648_c0_seq1_m.55086 | PREDICTED: 14-3-3-like protein D isoform X2 [Vitis vinifera] | 15.517 | 2.1677 | 10.9 | 2 | 4 | 2 | 1.002 | 0.984 | 1.016 | 1.006 | 0.995 | 1.006 | 1.002 | 8.70E-01 |

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| cds.Camellia_sinensis.comp20649_c0_seq1_m.31482 | PREDICTED: 2-keto-3-deoxy-L-rhamnonate aldolase-like [Solanum tuberosum | 38.631 | 7.8286 | 9.8 | 3 | 4 | 3 | 1.031 | 1.046 | 1.074 | 0.889 | 0.9 | 1.005 | 0.887 | 4.06E-02 |
| cds.Camellia_sinensis.comp20654_c0_seq1_m.39964 | PREDICTED: LDLR chaperone MESD [Vitis vinifera] | 28.854 | 14.722 | 18.9 | 5 | 9 | 5 | 1.093 | 1.116 | 1.05 | 0.934 | 0.9 | 0.885 | 0.834 | 1.64E-03 |
| cds.Camellia_sinensis.comp20665_c0_seq1_m.20922 | PREDICTED: enolase [Sesamum indicum] | 52.402 | 303.44 | 49.8 | 21 | 68 | 15 | 0.984 | 0.965 | 0.932 | 1.048 | 1.052 | 1.047 | 1.092 | 3.09E-02 |
| cds.Camellia_sinensis.comp20673_c0_seq1_m.13833 | PREDICTED: endoplasmin homolog [Ziziphus | 72.803 | 107.79 | 27.7 | 16 | 33 | 16 | 0.953 | 0.964 | 0.963 | 1.025 | 1.059 | 1.059 | 1.091 | 1.60E-03 |
| cds.Camellia_sinensis.comp20678_c0_seq1_m.44148 | alba DNA/RNA-binding protein [Medicago truncatula] | 22.119 | 6.4583 | 19.6 | 5 | 8 | 1 | 0.929 | 1.005 | 1.05 | 0.995 | 0.968 | 1.069 | 1.016 | 7.43E-01 |

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| cds.Camellia_sinensis.comp20681_c0_seq1_m.43982 | PREDICTED: NAD(P)H-quinone oxidoreductase subunit S, chloroplastic isoform X1 [Theobroma cacao] | 18.151 | 54.107 | 45.5 | 7 | 14 | 7 | 0.991 | 0.994 | 1.016 | 1.025 | 1.028 | 1.002 | 1.018 | 1.89E-01 |
| cds.Camellia_sinensis.comp20685_c0_seq2_m.34273 | PREDICTED: sec-independent protein translocase protein TATB, chloroplastic isoform X1 [Vitis vinifera] | 29.162 | 45.476 | 30.1 | 7 | 11 | 7 | 0.995 | 0.999 | 0.98 | 0.975 | 1.019 | 0.98 | 1 | 9.92E-01 |
| cds.Camellia_sinensis.comp20686_c0_seq1_m.38674 | PREDICTED: acyl carrier protein 1, chloroplastic [Vitis vinifera] | 16.625 | 4.9406 | 9.7 | 1 | 4 | 1 | 1.018 | 0.948 | 1.063 | 0.946 | 1.057 | 1.014 | 0.996 | 9.37E-01 |

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| cds.Camellia_sinensis.comp20687_c0_seq2_m.46943 | PREDICTED: flowering locus K homology domain-like isoform X1 [Nicotiana tabacum] | 20.68 | 9.5695 | 10.4 | 2 | 3 | 2 | 0.997 | 1.03 | 1.043 | 0.991 | 0.952 | 0.991 | 0.956 | 7.53E-02 |
| cds.Camellia_sinensis.comp20690_c0_seq2_m.20996 | PREDICTED: peptidyl-prolyl cis-trans isomerase, chloroplastic [Ziziphus jujuba] | 48.218 | 223.3 | 44.1 | 17 | 71 | 17 | 0.983 | 0.988 | 1.002 | 1.016 | 1.031 | 1.014 | 1.03 | 1.98E-02 |
| cds.Camellia_sinensis.comp20693_c0_seq1_m.16158 | PREDICTED: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Sesamum indicum] | 60.685 | 138.69 | 37.9 | 23 | 64 | 23 | 1.025 | 1.009 | 1.013 | 0.983 | 1.003 | 0.979 | 0.973 | 3.67E-02 |
| cds.Camellia_sinensis.comp20696_c0_seq1_m.14529 | PREDICTED: transmembrane protein 214 [Nelumbo nucifera] | 67.561 | 10.572 | 9.6 | 5 | 5 | 5 | 1.08 | 1.093 | 1.085 | 0.896 | 0.913 | 0.911 | 0.835 | 1.63E-05 |

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| cds.Camellia_sinensis.comp20697_c0_seq1_m.39788 | transmembrane protein, putative [Medicago truncatula] | 19.409 | 6.1872 | 9.2 | 2 | 2 | 2 | 0.839 | 0.926 | 0.893 | 1.129 | 1.139 | 1.127 | 1.277 | 1.37E-02 |
| cds.Camellia_sinensis.comp20698_c0_seq1_m.44790 | PREDICTED: universal stress protein PHOS32 [Theobroma cacao] | 17.911 | 29.132 | 34.8 | 6 | 7 | 5 | 1.01 | 0.986 | 0.989 | 1.052 | 0.941 | 1.036 | 1.015 | 7.25E-01 |
| cds.Camellia_sinensis.comp20699_c0_seq1_m.26825 | alpha/beta fold hydrolase [Medicago truncatula] | 43.135 | 2.959 | 7.6 | 2 | 2 | 2 | 1.096 | 0.949 | 1.053 | 0.949 | 1.071 | 0.878 | 0.935 | 3.97E-01 |
| cds.Camellia_sinensis.comp207013_c0_seq1_m.50709 | PREDICTED: vinorine synthase-like [Nicotiana tabacum] | 20.017 | 52.278 | 26.2 | 4 | 8 | 4 | 1.1 | 1.1 | 1.152 | 0.873 | 0.92 | 0.846 | 0.787 | 1.16E-03 |
| cds.Camellia_sinensis.comp20701_c0_seq1_m.31979 | PREDICTED: ABC transporter I family member 20 isoform X1 [Vitis vinifera] | 36.665 | 18.931 | 8.5 | 2 | 4 | 2 | 0.979 | 0.979 | 1.054 | 0.977 | 1.03 | 0.964 | 0.986 | 6.93E-01 |

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| cds.Camellia_sinensis.comp20705_c0_seq1_m.39969 | PREDICTED: inositol polyphosphate multikinase beta [Capsicum annuum] | 27.911 | 12.609 | 5.6 | 1 | 2 | 1 | 1.003 | 1.013 | 0.934 | 0.994 | 0.969 | 1.095 | 1.037 | 4.79E-01 |
| cds.Camellia_sinensis.comp20709_c0_seq1_m.51241 | DNA-binding family protein [Populus trichocarpa] | 17.137 | 42.84 | 45.2 | 9 | 19 | 8 | 0.927 | 0.911 | 0.886 | 1.087 | 1.082 | 1.125 | 1.209 | 4.59E-04 |
| cds.Camellia_sinensis.comp20711_c0_seq1_m.43518 | PREDICTED: thioredoxin H2-like [Cicer arietinum] | 15.388 | 24.333 | 28.5 | 3 | 6 | 3 | 0.969 | 1.032 | 0.932 | 1.067 | 0.989 | 0.995 | 1.04 | 3.59E-01 |
| cds.Camellia_sinensis.comp20712_c1_seq1_m.35145 | PREDICTED: coatomer subunit epsilon-1 [Ziziphus jujuba] | 33.522 | 2.0324 | 7.3 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp20714_c0_seq3_m.46434 | PREDICTED: protein FAM192A [Capsicum annuum] | 17.526 | 1.9464 | 11.1 | 1 | 1 | 1 | 0.936 | 1.159 | 1.003 | 0.968 | 0.987 | 0.954 | 0.939 | 4.52E-01 |

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| cds.Camellia_sinensis.comp20717_c0_seq1_m.12353 | heat shock cognate 70 kDa protein 2 [Gossypium hirsutum] | 71.179 | 323.31 | 54.3 | 36 | 156 | 11 | 1.051 | 1.029 | 1.008 | 0.973 | 0.973 | 0.965 | 0.943 | 8.90E-03 |
| cds.Camellia_sinensis.comp20726_c0_seq26_m.34782 | cyclin delta-3, putative [Medicago truncatula] | 38.31 | 7.057 | 12.5 | 5 | 6 | 5 | 0.967 | 1.003 | 1.044 | 1.008 | 0.945 | 1.002 | 0.98 | 5.50E-01 |
| cds.Camellia_sinensis.comp20737_c0_seq1_m.32462 | PREDICTED: UBP1-associated protein 2C [Nelumbo nucifera] | 36.101 | 49.378 | 19.4 | 7 | 11 | 6 | 1.001 | 0.963 | 1.023 | 0.975 | 1.012 | 1.023 | 1.008 | 7.51E-01 |
| cds.Camellia_sinensis.comp20738_c0_seq1_m.25402 | PREDICTED: probable plastid-lipid-associated protein 12, chloroplastic [Juglans regia] | 48.665 | 76.647 | 27.5 | 11 | 19 | 11 | 1.03 | 0.998 | 1.054 | 0.947 | 0.992 | 0.997 | 0.953 | 1.00E-01 |
| cds.Camellia_sinensis.comp20742_c0_seq1_m.46842 | PREDICTED: 40S ribosomal protein S10-1-like [Gossypium hirsutum] | 11.919 | 46.608 | 55.6 | 7 | 22 | 6 | 0.886 | 0.913 | 0.95 | 1.106 | 1.09 | 1.054 | 1.182 | 2.48E-03 |

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| cds.Camellia_sinensis.comp20748_c1_seq1_m.45323 | PREDICTED: protein bicaudal C homolog 1-like [Nicotiana attenuata] | 15.038 | 3.3975 | 8.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp20751_c0_seq1_m.43541 | PREDICTED: probable small nuclear ribonucleoprotein G [Ziziphus jujuba] | 12.136 | 7.049 | 35.8 | 4 | 6 | 4 | 0.985 | 0.941 | 0.946 | 1.063 | 1.01 | 1.035 | 1.082 | 1.87E-02 |
| cds.Camellia_sinensis.comp20756_c0_seq1_m.21710 | PREDICTED: SUN domain-containing protein 3-like [Jatropha curcas] | 50.359 | 40.23 | 29.8 | 12 | 15 | 12 | 1.02 | 1.037 | 1.012 | 0.962 | 1.013 | 0.975 | 0.961 | 8.04E-02 |
| cds.Camellia_sinensis.comp20758_c0_seq1_m.42404 | PREDICTED: nicotinamidase 2-like [Nelumbo nucifera] | 22.435 | 2.518 | 12.5 | 3 | 3 | 3 | 0.955 | 1.007 | 0.97 | 0.983 | 1.066 | 1.035 | 1.052 | 1.52E-01 |

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| cds.Camellia_sinensis.comp20763_c0_seq2_m.44518 | PREDICTED: DNA-directed RNA polymerases II, IV and V subunit 11 isoform X1 [Theobroma cacao] | 13.569 | 15.954 | 34.5 | 4 | 7 | 4 | 0.967 | 0.969 | 0.937 | 1.042 | 1.017 | 1.031 | 1.076 | 4.90E-03 |
| cds.Camellia_sinensis.comp20766_c0_seq1_m.23754 | PREDICTED: probable sugar phosphate/phosphate translocator At5g25400 [Nelumbo | 38.615 | 1.3266 | 3.2 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp20768_c0_seq1_m.35796 | PREDICTED: anthranilate synthase beta subunit 1, chloroplastic-like [Nicotiana tabacum] | 33.21 | 14.393 | 14 | 4 | 8 | 4 | 1.008 | 0.992 | 1.02 | 0.995 | 0.974 | 0.968 | 0.973 | 7.41E-02 |
| cds.Camellia_sinensis.comp20770_c0_seq1_m.3876 | elongation factor Ts (DUF810) [Arabidopsis thaliana] | 89.098 | 4.6025 | 2.1 | 2 | 2 | 2 | 1.042 | 1.075 | 1.025 | 0.907 | 0.979 | 0.963 | 0.907 | 2.22E-02 |

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| cds.Camellia_sinensis.comp20772_c0_seq1_m.32739 | PREDICTED: vestitone reductase-like [Vitis vinifera] | 36.6 | 6.3923 | 3.9 | 1 | 1 | 1 | 0.896 | 0.897 | 0.851 | 1.139 | 1.095 | 1.167 | 1.286 | 5.82E-04 |
| cds.Camellia_sinensis.comp20772_c0_seq2_m.32953 | PREDICTED: vestitone reductase-like [Vitis vinifera] | 36.68 | 11.953 | 6.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp20774_c0_seq1_m.26562 | PREDICTED: 60S acidic ribosomal protein P0 [Vitis vinifera] | 34.131 | 19.249 | 18.5 | 5 | 12 | 5 | 1.039 | 1.04 | 1.026 | 0.94 | 0.969 | 0.99 | 0.934 | 1.17E-02 |
| cds.Camellia_sinensis.comp20777_c0_seq1_m.37508 | PREDICTED: RNA-binding protein 7 [Vitis vinifera] | 22.001 | 1.4441 | 5.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp20780_c0_seq1_m.41262 | PREDICTED: pre-mRNA cleavage factor Im 25 kDa subunit 2 [Citrus sinensis] | 22.727 | 11.722 | 24.1 | 4 | 5 | 4 | 0.952 | 0.959 | 1.122 | 1.16 | 0.883 | 0.943 | 0.985 | 8.52E-01 |

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| cds.Camellia_sinensis.comp20783_c0_seq1_m.41641 | PREDICTED: peptidyl-prolyl cis-trans isomerase Pin1 isoform X2 [Juglans regia] | 12.926 | 20.673 | 30.5 | 4 | 7 | 4 | 0.99 | 1.041 | 0.923 | 1.033 | 0.978 | 1.037 | 1.032 | 4.63E-01 |
| cds.Camellia_sinensis.comp20786_c0_seq1_m.22268 | PREDICTED: magnesium-chelatase subunit ChlI, chloroplastic-like isoform X3 [Juglans | 46.468 | 165.09 | 42.9 | 17 | 35 | 17 | 1.005 | 1.003 | 1.01 | 0.991 | 0.983 | 0.99 | 0.982 | 5.32E-03 |
| cds.Camellia_sinensis.comp20791_c0_seq1_m.16520 | PREDICTED: probable zinc metalloprotease EGY2, chloroplastic isoform X2 [Nelumbo nucifera] | 56.973 | 9.562 | 7.9 | 4 | 6 | 4 | 0.958 | 1.041 | 1.032 | 0.932 | 0.991 | 1.01 | 0.968 | 4.12E-01 |

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| cds.Camellia_sinensis.comp20803_c0_seq1_m.21237 | PREDICTED: branched-chain-amino-acid aminotransferase 3, chloroplastic [Erythranthe guttata] | 45.781 | 56.399 | 29 | 13 | 19 | 13 | 1.012 | 1.005 | 1.02 | 0.959 | 0.98 | 0.986 | 0.963 | 1.64E-02 |
| cds.Camellia_sinensis.comp20807_c0_seq1_m.40489 | PREDICTED: elongation factor P-like [Gossypium hirsutum] | 24.476 | 58.747 | 44.5 | 9 | 17 | 9 | 1.041 | 1.06 | 1.052 | 0.946 | 0.944 | 0.941 | 0.898 | 3.96E-05 |
| cds.Camellia_sinensis.comp20815_c0_seq1_m.23773 | PREDICTED: cysteine synthase [Vitis vinifera] | 41.013 | 6.1021 | 12.8 | 5 | 7 | 4 | 0.961 | 0.994 | 1.006 | 1.058 | 1.026 | 0.998 | 1.041 | 1.40E-01 |
| cds.Camellia_sinensis.comp20820_c0_seq1_m.38571 | PREDICTED: glutathione S-transferase F9-like [Jatropha curcas] | 25.679 | 30.602 | 29 | 7 | 21 | 7 | 0.998 | 0.971 | 0.962 | 1.012 | 1.031 | 1.003 | 1.039 | 4.80E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20832_c0_seq1_m.31547 | PREDICTED: eukaryotic translation initiation factor 3 subunit G-B [Vitis vinifera] | 32.579 | 43.56 | 30.7 | 9 | 13 | 7 | 0.978 | 0.999 | 0.964 | 1.036 | 1.027 | 1.017 | 1.047 | 1.66E-02 |
| cds.Camellia_sinensis.comp20839_c0_seq2_m.26371 | PREDICTED: uncharacterized PKHD-type hydroxylase At1g22950-like [Nelumbo nucifera] | 29.493 | 3.2205 | 4.3 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp20841_c0_seq1_m.9399 | PREDICTED: subtilisin-like protease [Nicotiana sylvestris] | 82.946 | 2.3826 | 4.1 | 3 | 3 | 3 | 0.969 | 0.937 | 1.029 | 1.065 | 1.052 | 0.971 | 1.052 | 2.72E-01 |
| cds.Camellia_sinensis.comp20842_c0_seq1_m.13440 | PREDICTED: AT-hook motif nuclear-localized protein 9 [Ricinus communis] | 34.521 | 11.057 | 11.2 | 3 | 4 | 3 | 1.034 | 0.939 | 0.982 | 0.979 | 0.953 | 1.043 | 1.007 | 8.69E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20845_c1_seq1_m.52039 | PREDICTED: importin subunit alpha-1 [Cucumis melo] | 18.79 | 2.0114 | 18.3 | 4 | 4 | 1 | 0.957 | 0.995 | 0.976 | 1.015 | 1.029 | 1.045 | 1.055 | 1.88E-02 |
| cds.Camellia_sinensis.comp20846_c0_seq1_m.30367 | PREDICTED: prolyl-tRNA synthetase associated domain-containing protein 1 [Solanum tuberosum | 34.965 | 17.346 | 32 | 8 | 9 | 8 | 0.973 | 0.967 | 0.936 | 1.018 | 1.067 | 1.045 | 1.088 | 9.60E-03 |
| cds.Camellia_sinensis.comp20847_c0_seq1_m.23896 | condensation domain protein [Medicago truncatula] | 50.77 | 16.636 | 14.1 | 6 | 6 | 6 | 1.03 | 1.041 | 1.087 | 1.016 | 0.926 | 0.955 | 0.917 | 5.29E-02 |
| cds.Camellia_sinensis.comp20851_c0_seq1_m.29429 | PREDICTED: fructose-bisphosphate aldolase, cytoplasmic isozyme 1 [Theobroma cacao] | 36.427 | 140.53 | 41.1 | 9 | 27 | 9 | 1.034 | 1.054 | 1.02 | 0.96 | 0.93 | 0.981 | 0.924 | 1.20E-02 |
| cds.Camellia_sinensis.comp20857_c0_seq2_m.40730 | PREDICTED: histone H2A-like [Sesamum indicum] | 15.635 | 1.4511 | 15.6 | 3 | 8 | 1 | 1.11 | 1.094 | 1.112 | 0.866 | 0.903 | 0.888 | 0.801 | 7.69E-05 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20858_c0_seq1_m.19553 | PREDICTED: ethanolamine-phosphate cytidylyltransferase [Sesamum indicum] | 46.774 | 29.793 | 8.4 | 4 | 5 | 4 | 1.009 | 1.004 | 1.006 | 0.975 | 0.972 | 1.003 | 0.977 | 1.48E-01 |
| cds.Camellia_sinensis.comp20861_c0_seq1_m.45654 | transmembrane protein [Arabidopsis thaliana] | 12.461 | 33.199 | 18.9 | 2 | 7 | 2 | 0.92 | 0.983 | 1.03 | 1.061 | 0.931 | 1.075 | 1.046 | 4.82E-01 |
| cds.Camellia_sinensis.comp20862_c0_seq1_m.10575 | PREDICTED: dipeptidyl-peptidase 5 [Vitis vinifera] | 80.797 | 105.65 | 32.5 | 23 | 42 | 23 | 0.982 | 0.973 | 1.019 | 1.038 | 1.021 | 0.988 | 1.025 | 2.97E-01 |
| cds.Camellia_sinensis.comp20864_c0_seq1_m.32920 | Caffeoyl-CoA O-methyltransferase [Morus notabilis] | 27.553 | 18.841 | 33.1 | 7 | 10 | 7 | 1.168 | 1.096 | 1.118 | 0.852 | 0.881 | 0.893 | 0.776 | 4.19E-04 |
| cds.Camellia_sinensis.comp20865_c0_seq1_m.20015 | PREDICTED: switch-associated protein 70 [Vitis vinifera] | 52.855 | 70.111 | 38 | 15 | 24 | 15 | 0.971 | 0.966 | 0.992 | 1.025 | 1.018 | 1.021 | 1.046 | 5.72E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20867_c0_seq1_m.15016 | Protein kinase capable of phosphorylating tyrosine family protein [Populus trichocarpa] | 44.664 | 1.2566 | 4.5 | 2 | 2 | 2 | 1.005 | 0.975 | 1.074 | 1.03 | 0.894 | 1.028 | 0.967 | 5.55E-01 |
| cds.Camellia_sinensis.comp20873_c0_seq1_m.13915 | PREDICTED: synaptotagmin-2-like [Nelumbo nucifera] | 61.594 | 5.0706 | 12.3 | 8 | 13 | 3 | 0.952 | 0.99 | 0.94 | 1.038 | 1.057 | 1.047 | 1.09 | 6.24E-03 |
| cds.Camellia_sinensis.comp20874_c0_seq1_m.44718 | dihydroorotate dehydrogenase, putative [Medicago truncatula] | 15.902 | 4.0248 | 6.9 | 1 | 3 | 1 | 1.057 | 0.967 | 0.918 | 1.003 | 1.082 | 0.98 | 1.042 | 4.58E-01 |
| cds.Camellia_sinensis.comp20877_c0_seq1_m.38225 | PREDICTED: calcineurin subunit B-like [Daucus carota subsp. sativus] | 19.878 | 9.9636 | 26.3 | 4 | 4 | 3 | 1.045 | 1.032 | 1.124 | 1.012 | 0.92 | 0.863 | 0.873 | 6.21E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20881_c0_seq2_m.37337 | PREDICTED: abscisic acid receptor PYL8 [Vitis vinifera] | 19.935 | 1.6165 | 6.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp20882_c0_seq1_m.11112 | PREDICTED: protein TIC 62, chloroplastic [Sesamum indicum] | 31.947 | 55.397 | 52.8 | 10 | 37 | 6 | 1.119 | 1.059 | 1.04 | 0.916 | 0.909 | 0.924 | 0.854 | 2.22E-03 |
| cds.Camellia_sinensis.comp20882_c0_seq2_m.17004 | PREDICTED: protein TIC 62, chloroplastic [Populus euphratica] | 39.27 | 323.31 | 59.1 | 19 | 67 | 15 | 1.066 | 1.075 | 1.059 | 0.895 | 0.927 | 0.947 | 0.865 | 1.04E-03 |
| cds.Camellia_sinensis.comp20883_c0_seq1_m.38158 | PREDICTED: inosine triphosphate pyrophosphatase isoform X2 [Juglans regia] | 22.643 | 9.507 | 17 | 3 | 3 | 3 | 1.003 | 0.992 | 0.928 | 1.057 | 0.965 | 1.068 | 1.057 | 2.44E-01 |
| cds.Camellia_sinensis.comp20894_c0_seq2_m.33751 | Putative syntaxin-131 [Morus notabilis] | 15.86 | 3.1934 | 17.2 | 3 | 3 | 3 | 1.115 | 1.107 | 1.123 | 0.877 | 0.874 | 0.891 | 0.79 | 2.64E-06 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20894_c0_seq2_m.33752 | PREDICTED: syntaxin-132-like [Prunus mume] | 14.651 | 24.676 | 10.3 | 1 | 2 | 1 | 1.043 | 0.968 | 1.105 | 0.948 | 0.993 | 0.94 | 0.925 | 1.39E-01 |
| cds.Camellia_sinensis.comp20896_c0_seq1_m.33618 | PREDICTED: biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic-like [Nicotiana sylvestris] | 34.621 | 24.88 | 10.5 | 4 | 5 | 4 | 0.996 | 1.063 | 1.021 | 0.935 | 0.951 | 0.96 | 0.924 | 1.84E-02 |
| cds.Camellia_sinensis.comp20897_c0_seq2_m.55053 | oxidoreductase family protein [Populus trichocarpa] | 14.805 | 1.6042 | 5.8 | 1 | 1 | 1 | 0.927 | 1.014 | 0.908 | 1.086 | 1.068 | 1.028 | 1.117 | 4.13E-02 |
| cds.Camellia_sinensis.comp20901_c0_seq1_m.28740 | 40S ribosomal protein S2-4 [Medicago truncatula] | 30.281 | 128.94 | 48 | 16 | 33 | 10 | 1.096 | 1.067 | 1.087 | 0.927 | 0.913 | 0.865 | 0.832 | 1.20E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20902_c0_seq1_m.42673 | PREDICTED: ATP-dependent Clp protease adapter protein CLPS1, chloroplastic-like [Juglans regia] | 18.629 | 2.1974 | 11.1 | 3 | 3 | 3 | 0.969 | 1.039 | 1.042 | 0.956 | 1.034 | 0.969 | 0.97 | 4.22E-01 |
| cds.Camellia_sinensis.comp20904_c0_seq1_m.35646 | PREDICTED: psbP-like protein 1, chloroplastic [Sesamum indicum] | 28.08 | 75.084 | 29.6 | 9 | 20 | 9 | 1.013 | 0.993 | 0.989 | 0.968 | 1.023 | 1.007 | 1.001 | 9.67E-01 |
| cds.Camellia_sinensis.comp20914_c0_seq1_m.43257 | PREDICTED: dirigent protein 5 [Eucalyptus grandis] | 26.43 | 111.95 | 29.8 | 5 | 22 | 5 | 1.03 | 1.106 | 1.1 | 0.926 | 0.904 | 0.89 | 0.841 | 2.50E-03 |
| cds.Camellia_sinensis.comp20920_c0_seq1_m.53904 | PREDICTED: probable inactive receptor kinase RLK902 [Nicotiana attenuata] | 16.646 | 11.416 | 28.4 | 3 | 4 | 3 | 0.98 | 1.024 | 1.005 | 1.083 | 0.909 | 1.012 | 0.998 | 9.42E-01 |
| cds.Camellia_sinensis.comp20921_c0_seq1_m.19574 | PREDICTED: ruvB-like 2 [Sesamum indicum] | 51.623 | 74.693 | 36.8 | 16 | 24 | 16 | 0.941 | 0.95 | 0.995 | 1.042 | 1.035 | 1.058 | 1.086 | 1.08E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20923_c0_seq1_m.1885 | ketose-bisphosphate aldolase class-II family protein [Arabidopsis | 148.61 | 87.697 | 18.4 | 23 | 29 | 23 | 0.979 | 0.959 | 0.941 | 1.032 | 1.055 | 1.035 | 1.084 | 3.72E-03 |
| cds.Camellia_sinensis.comp20930_c0_seq1_m.34135 | transmembrane protein [Arabidopsis thaliana] | 19.655 | 16.86 | 12.8 | 1 | 2 | 1 | 1.055 | 0.944 | 0.952 | 0.939 | 1.03 | 1.081 | 1.034 | 5.83E-01 |
| cds.Camellia_sinensis.comp20933_c0_seq1_m.35813 | YbaK/prolyl-tRNA synthetase-related family protein [Populus trichocarpa] | 26.48 | 8.7232 | 9.7 | 2 | 3 | 2 | 0.897 | 0.951 | 1.049 | 1.101 | 1.034 | 1.002 | 1.083 | 2.04E-01 |
| cds.Camellia_sinensis.comp20935_c0_seq2_m.43476 | PREDICTED: KH domain-containing protein At4g18375-like [Sesamum indicum] | 24.413 | 23.783 | 14.1 | 3 | 3 | 3 | 0.985 | 1.067 | 1.078 | 1.027 | 0.963 | 0.888 | 0.919 | 1.70E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20936_c0_seq1_m.31963 | PREDICTED: tropinone reductase homolog isoform X1 [Sesamum indicum] | 33.917 | 3.5372 | 9 | 3 | 3 | 2 | 1.037 | 1.033 | 1.008 | 0.952 | 0.984 | 0.985 | 0.949 | 2.14E-02 |
| cds.Camellia_sinensis.comp20938_c0_seq1_m.40912 | PREDICTED: translationally-controlled tumor protein homolog [Prunus mume] | 25.486 | 28.697 | 29.1 | 8 | 20 | 5 | 1.045 | 0.957 | 0.989 | 0.965 | 1.04 | 1.016 | 1.01 | 7.79E-01 |
| cds.Camellia_sinensis.comp20939_c0_seq1_m.24698 | PREDICTED: protein LOW PSII ACCUMULATION 3, chloroplastic [Ziziphus jujuba] | 43.645 | 34.669 | 23.3 | 9 | 12 | 9 | 1.095 | 1.059 | 1.034 | 0.941 | 0.95 | 0.962 | 0.895 | 3.40E-03 |
| cds.Camellia_sinensis.comp20944_c0_seq1_m.33041 | PREDICTED: peroxidase 47 [Sesamum indicum] | 34.936 | 131.45 | 34.8 | 9 | 10 | 9 | 0.928 | 0.929 | 0.88 | 1.082 | 1.109 | 1.101 | 1.203 | 6.63E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20950_c0_seq1_m.28165 | nuclear protein [Arabidopsis thaliana] | 33.521 | 87.907 | 52.9 | 14 | 27 | 14 | 1.009 | 1.02 | 1.033 | 0.972 | 0.997 | 0.976 | 0.962 | 2.00E-02 |
| cds.Camellia_sinensis.comp20951_c0_seq1_m.28527 | PREDICTED: oligouridylate-binding protein 1-like [Prunus | 39.588 | 22.353 | 22.7 | 8 | 12 | 7 | 0.991 | 0.971 | 0.971 | 1.005 | 0.993 | 1.015 | 1.027 | 4.43E-02 |
| cds.Camellia_sinensis.comp20958_c0_seq1_m.33512 | PREDICTED: heterogeneous nuclear ribonucleoprotein H2 isoform X1 [Vitis vinifera] | 29.599 | 16.925 | 18.9 | 4 | 6 | 4 | | | | | | | | |
| cds.Camellia_sinensis.comp20960_c0_seq1_m.41449 | copper ion-binding protein [Medicago truncatula] | 12.664 | 3.4564 | 12.8 | 2 | 5 | 2 | 1.04 | 1.013 | 1.022 | 0.957 | 0.979 | 0.973 | 0.946 | 5.72E-03 |
| cds.Camellia_sinensis.comp20962_c0_seq1_m.8182 | PREDICTED: serine/threonine-protein kinase SAPK3 [Eucalyptus grandis] | 38.534 | 46.405 | 21.6 | 8 | 10 | 5 | 0.998 | 1.109 | 1.006 | 0.868 | 0.98 | 0.947 | 0.898 | 9.50E-02 |

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| cds.Camellia_sinensis.comp20972_c0_seq1_m.50792 | PREDICTED: nectarin-1 [Eucalyptus grandis] | 13.072 | 5.6161 | 14.5 | 2 | 4 | 2 | 0.967 | 0.929 | 0.884 | 1.063 | 1.102 | 1.084 | 1.169 | 5.00E-03 |
| cds.Camellia_sinensis.comp20973_c0_seq1_m.5748 | PREDICTED: protein TIC 100 [Solanum pennellii] | 98.759 | 3.4677 | 1.3 | 1 | 1 | 1 | 0.903 | 1.088 | 1.08 | 1.015 | 0.954 | 0.977 | 0.959 | 5.80E-01 |
| cds.Camellia_sinensis.comp20974_c0_seq1_m.17772 | PREDICTED: probable nucleoredoxin 1 [Ziziphus jujuba] | 64.438 | 116.53 | 37.8 | 19 | 36 | 19 | 0.898 | 0.887 | 0.894 | 1.104 | 1.126 | 1.113 | 1.248 | 2.60E-06 |
| cds.Camellia_sinensis.comp20976_c0_seq1_m.44117 | | 23.212 | 16.949 | 35.8 | 6 | 10 | 6 | 0.948 | 0.925 | 0.927 | 1.068 | 1.096 | 1.126 | 1.175 | 7.19E-04 |
| cds.Camellia_sinensis.comp20979_c0_seq1_m.1888 | PREDICTED: splicing factor 3B subunit 1 [Vitis vinifera] | 122.24 | 46.564 | 14.1 | 14 | 15 | 14 | 1.011 | 1.089 | 1.1 | 0.91 | 0.94 | 0.937 | 0.871 | 8.52E-03 |
| cds.Camellia_sinensis.comp20979_c0_seq1_m.1889 | PREDICTED: splicing factor 3B subunit 1 [Nelumbo nucifera] | 23.939 | 38.865 | 24 | 5 | 6 | 5 | 1.091 | 1.144 | 1.176 | 0.906 | 0.893 | 0.764 | 0.751 | 8.04E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp20982_c0_seq1_m.38132 | PREDICTED: U1 small nuclear ribonucleoprotein A-like isoform X1 [Sesamum indicum] | 28.725 | 6.9912 | 15.3 | 3 | 3 | 3 | 0.907 | 1.004 | 0.997 | 1.149 | 1.015 | 1.033 | 1.099 | 1.37E-01 |
| cds.Camellia_sinensis.comp20992_c0_seq1_m.20718 | PREDICTED: WD-40 repeat-containing protein MSI4-like [Juglans regia] | 51.128 | 15.053 | 12.2 | 4 | 7 | 3 | 1.044 | 1.008 | 0.972 | 1.018 | 0.972 | 0.99 | 0.985 | 5.90E-01 |
| cds.Camellia_sinensis.comp21000_c0_seq1_m.31884 | PREDICTED: sufE-like protein 1, chloroplastic/mitochondrial [Daucus carota subsp. sativus] | 39.422 | 26.638 | 19.6 | 5 | 6 | 5 | 0.941 | 1.003 | 1.067 | 1.033 | 1.042 | 0.94 | 1.001 | 9.76E-01 |
| cds.Camellia_sinensis.comp21005_c0_seq4_m.24618 | PREDICTED: protein phosphatase 2C 57 [Prunus mume] | 43.893 | 95.916 | 21.8 | 9 | 14 | 9 | 1.016 | 1.016 | 1.05 | 0.983 | 0.972 | 0.976 | 0.951 | 1.19E-02 |

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| cds.Camellia_sinensis.comp21006_c0_seq1_m.35903 | PREDICTED: tetrapyrrole-binding protein, chloroplastic [Juglans regia] | 30.146 | 2.4352 | 4.5 | 1 | 2 | 1 | 1.009 | 1.032 | 1.001 | 0.944 | 1.007 | 1.009 | 0.973 | 3.07E-01 |
| cds.Camellia_sinensis.comp21006_c1_seq1_m.26070 | tyrosine phosphatase, putative [Medicago truncatula] | 41.261 | 246.04 | 51 | 20 | 64 | 20 | 1.127 | 1.101 | 1.119 | 0.865 | 0.884 | 0.876 | 0.784 | 1.65E-05 |
| cds.Camellia_sinensis.comp21009_c0_seq1_m.28964 | PREDICTED: bifunctional L-3-cyanoalanine synthase/cysteine synthase 1, mitochondrial isoform X2 [Vitis | 41.896 | 86.35 | 24.1 | 9 | 24 | 8 | 1.013 | 1.023 | 1.016 | 1.015 | 0.943 | 0.978 | 0.962 | 2.09E-01 |
| cds.Camellia_sinensis.comp21010_c0_seq1_m.33119 | PREDICTED: S-formylglutathione hydrolase [Ipomoea nil] | 32.06 | 129.44 | 37.7 | 9 | 18 | 9 | 0.976 | 0.97 | 0.986 | 1.027 | 1.028 | 1.057 | 1.061 | 4.90E-03 |

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| cds.Camellia_sinensis.comp21016_c0_seq1_m.34450 | PREDICTED: translocon-associated protein subunit alpha-like [Juglans regia] | 24.909 | 10.233 | 5.7 | 1 | 2 | 1 | 1.07 | 1.097 | 1.027 | 0.957 | 0.891 | 0.944 | 0.874 | 9.88E-03 |
| cds.Camellia_sinensis.comp21017_c0_seq1_m.40078 | PREDICTED: ATP-dependent Clp protease ATP-binding subunit CLPT2, chloroplastic [Juglans regia] | 15.194 | 17.81 | 38.4 | 5 | 11 | 4 | 1.07 | 0.946 | 1.021 | 0.98 | 0.99 | 0.966 | 0.967 | 4.23E-01 |
| cds.Camellia_sinensis.comp21018_c0_seq1_m.6880 | PREDICTED: histidine--tRNA ligase, cytoplasmic isoform X1 [Nelumbo nucifera] | 98.124 | 66.042 | 21.7 | 18 | 26 | 18 | 1.005 | 0.988 | 1.002 | 1.002 | 0.998 | 0.973 | 0.993 | 5.22E-01 |
| cds.Camellia_sinensis.comp21019_c0_seq1_m.29951 | PREDICTED: bromodomain-containing protein 4-like [Ziziphus jujuba] | 32.216 | 119.45 | 48.4 | 13 | 28 | 13 | 0.995 | 0.992 | 1.008 | 1.007 | 1.007 | 0.988 | 1.002 | 7.87E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp21021_c0_seq2_m.32602 | PREDICTED: pre-mRNA-splicing factor ISY1 homolog [Beta vulgaris subsp. vulgaris] | 35.444 | 3.7839 | 7.9 | 3 | 3 | 3 | 1.017 | 1.092 | 1.047 | 0.983 | 0.948 | 0.912 | 0.901 | 2.51E-02 |
| cds.Camellia_sinensis.comp21022_c0_seq1_m.24264 | PREDICTED: GDSL esterase/lipase APG-like [Capsicum annuum] | 38.148 | 9.9561 | 12.9 | 4 | 5 | 4 | 1.01 | 1.11 | 1.039 | 0.825 | 1.02 | 0.983 | 0.895 | 1.84E-01 |
| cds.Camellia_sinensis.comp21024_c0_seq1_m.14426 | PREDICTED: eukaryotic peptide chain release factor GTP-binding subunit ERF3A-like isoform X2 [Ipomoea nil] | 52.283 | 32.7 | 24.4 | 11 | 19 | 11 | 0.986 | 0.966 | 0.946 | 1.028 | 1.003 | 1.055 | 1.065 | 2.92E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp21027_c0_seq1_m.39798 | PREDICTED: 14 kDa zinc-binding protein-like [Sesamum indicum] | 20.492 | 74.708 | 28.3 | 5 | 14 | 5 | 0.976 | 0.98 | 0.985 | 1.02 | 1.022 | 1.018 | 1.04 | 1.61E-04 |
| cds.Camellia_sinensis.comp21030_c0_seq1_m.29788 | PREDICTED: tropinone reductase homolog [Nicotiana attenuata] | 24.516 | 62.669 | 25.6 | 5 | 23 | 3 | 0.957 | 1.006 | 0.998 | 1.039 | 1.029 | 1.023 | 1.044 | 5.54E-02 |
| cds.Camellia_sinensis.comp21036_c0_seq1_m.27186 | PREDICTED: grpE protein homolog, mitochondrial [Sesamum indicum] | 41.759 | 90.694 | 24 | 9 | 21 | 9 | 1.134 | 1.11 | 1.119 | 0.869 | 0.876 | 0.898 | 0.786 | 3.63E-05 |
| cds.Camellia_sinensis.comp21039_c0_seq1_m.29908 | PREDICTED: 20 kDa chaperonin, chloroplastic-like [Nicotiana tabacum] | 21.783 | 76.983 | 40.9 | 9 | 26 | 9 | 1.053 | 0.985 | 1.001 | 0.979 | 0.994 | 0.993 | 0.976 | 3.12E-01 |

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| cds.Camellia_sinensis.comp21042_c0_seq1_m.43112 | PREDICTED: ferredoxin-thioredoxin reductase, variable chain [Theobroma cacao] | 22.79 | 105.78 | 34 | 7 | 18 | 7 | 1.031 | 0.988 | 0.977 | 0.995 | 1.002 | 0.998 | 1 | 9.97E-01 |
| cds.Camellia_sinensis.comp21045_c0_seq1_m.37610 | PREDICTED: probable plastid-lipid-associated protein 4, chloroplastic [Nicotiana attenuata] | 28.484 | 75.261 | 39.5 | 9 | 21 | 9 | 1.005 | 0.986 | 1.01 | 1.012 | 1.026 | 0.979 | 1.005 | 7.59E-01 |
| cds.Camellia_sinensis.comp21051_c0_seq1_m.38150 | PREDICTED: membrane steroid-binding protein 2-like [Arachis duranensis] | 23.941 | 95.77 | 35 | 6 | 15 | 6 | 0.958 | 0.961 | 0.961 | 1.016 | 1.014 | 1.064 | 1.074 | 4.54E-02 |
| cds.Camellia_sinensis.comp21052_c0_seq1_m.35948 | PREDICTED: 40S ribosomal protein S10-1-like [Gossypium hirsutum] | 20.106 | 35.307 | 39.6 | 7 | 20 | 6 | 0.963 | 1.008 | 0.98 | 0.976 | 1.01 | 1.013 | 1.016 | 4.17E-01 |

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| cds.Camellia_sinensis.comp21053_c0_seq1_m.8628 | PREDICTED: U3 small nucleolar RNA-associated protein 4 [Juglans regia] | 95.92 | 1.5142 | 0.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp210541_c0_seq1_m.51069 | PREDICTED: protein SRG1 [Vitis vinifera] | 17.632 | 1.1946 | 4.5 | 1 | 1 | 1 | 0.969 | 0.998 | 1.025 | 1.029 | 1.04 | 0.956 | 1.011 | 7.51E-01 |
| cds.Camellia_sinensis.comp21054_c0_seq1_m.28357 | PREDICTED: protein CHAPERONE-LIKE PROTEIN OF POR1, chloroplastic [Vitis vinifera] | 30.851 | 1.4176 | 2.9 | 1 | 1 | 1 | 0.985 | 0.989 | 1.074 | 0.957 | 0.961 | 1.041 | 0.971 | 4.93E-01 |
| cds.Camellia_sinensis.comp21055_c0_seq1_m.33724 | PREDICTED: serine/arginine-rich splicing factor SR30-like isoform X1 [Ipomoea nil] | 28.857 | 9.9276 | 12.7 | 3 | 3 | 3 | 0.993 | 1.065 | 1.053 | 0.99 | 0.965 | 0.938 | 0.93 | 5.34E-02 |

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| cds.Camellia_sinensis.comp21056_c0_seq2_m.25852 | PREDICTED: 2,3-dimethylmalate lyase isoform X1 [Theobroma cacao] | 37.181 | 181.62 | 53.7 | 15 | 35 | 15 | 0.977 | 0.993 | 0.978 | 1.015 | 1.033 | 1.021 | 1.041 | 5.46E-03 |
| cds.Camellia_sinensis.comp21057_c0_seq1_m.43189 | PREDICTED: photosystem I reaction center subunit VI, chloroplastic-like [Populus euphratica] | 15.264 | 11.344 | 13.2 | 3 | 10 | 3 | 0.996 | 0.977 | 1.02 | 0.976 | 1.006 | 1.004 | 0.998 | 8.92E-01 |
| cds.Camellia_sinensis.comp21061_c0_seq1_m.23387 | glycerol-3-phosphate acyltransferase 3 [Ricinus communis] | 42.707 | 1.1689 | 2.7 | 1 | 1 | 1 | 0.97 | 1.114 | 0.955 | 0.993 | 0.998 | 0.978 | 0.977 | 7.13E-01 |
| cds.Camellia_sinensis.comp21115_c0_seq1_m.30691 | PREDICTED: J domain-containing protein DDB_G0295729-like [Gossypium raimondii] | 39.797 | 2.0973 | 4.5 | 2 | 3 | 2 | 0.959 | 0.938 | 0.958 | 1.069 | 1.07 | 1.033 | 1.111 | 1.52E-03 |

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| cds.Camellia_sinensis.comp21134_c0_seq2_m.41738 | PREDICTED: single-stranded DNA-binding protein, mitochondrial-like [Nicotiana tabacum] | 25.165 | 5.5732 | 8.9 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp21139_c0_seq1_m.45245 | late embryogenesis abundant protein, putative [Medicago truncatula] | 18.743 | 9.1112 | 18.8 | 3 | 6 | 3 | 0.984 | 1.014 | 1.038 | 1.008 | 0.964 | 1.021 | 0.986 | 5.72E-01 |
| cds.Camellia_sinensis.comp21151_c0_seq2_m.38950 | PREDICTED: tropomyosin [Theobroma cacao] | 30.66 | 3.5383 | 5.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp21152_c0_seq1_m.42139 | PREDICTED: osmotin-like protein TPM-1 [Eucalyptus grandis] | 26.182 | 45.316 | 10.6 | 2 | 10 | 2 | 0.95 | 0.926 | 0.963 | 1.076 | 1.061 | 1.076 | 1.132 | 5.62E-04 |
| cds.Camellia_sinensis.comp21166_c0_seq1_m.51507 | PREDICTED: heparanase-like protein 3 [Juglans regia] | 15.463 | 1.3491 | 5.7 | 1 | 2 | 1 | 1.089 | 1.001 | 1.058 | 0.963 | 0.958 | 0.923 | 0.903 | 2.28E-02 |

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| cds.Camellia_sinensis.comp21169_c0_seq3_m.46243 | PREDICTED: probable protein phosphatase 2C 55 isoform X1 [Vitis vinifera] | 20.308 | 1.5837 | 5.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp21179_c0_seq1_m.19872 | PREDICTED: probable aspartyl aminopeptidase isoform X1 [Nelumbo nucifera] | 58.858 | 14.243 | 9.2 | 5 | 7 | 5 | 0.951 | 0.986 | 0.982 | 1.002 | 1.029 | 1.052 | 1.056 | 3.95E-02 |
| cds.Camellia_sinensis.comp21197_c0_seq3_m.57054 | plant/T7H20-70 protein [Medicago truncatula] | 12.866 | 24.987 | 26.3 | 2 | 2 | 2 | 0.751 | 0.648 | 0.629 | 1.42 | 1.348 | 1.319 | 2.015 | 2.82E-04 |
| cds.Camellia_sinensis.comp21209_c0_seq1_m.29021 | DUF1262 family protein [Medicago truncatula] | 44.286 | 28.627 | 14.4 | 5 | 8 | 5 | 0.862 | 0.92 | 0.882 | 1.129 | 1.16 | 1.109 | 1.276 | 4.60E-04 |
| cds.Camellia_sinensis.comp21227_c0_seq1_m.42571 | PREDICTED: D-tyrosyl-tRNA(Tyr) deacylase [Nelumbo nucifera] | 17.985 | 1.3983 | 4.9 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp21264_c0_seq1_m.20635 | PREDICTED: lysine histidine transporter 1-like [Lupinus angustifolius] | 50.233 | 1.9656 | 2.7 | 1 | 1 | 1 | 0.82 | 0.924 | 1.067 | 1.133 | 1.016 | 1.089 | 1.152 | 1.51E-01 |
| cds.Camellia_sinensis.comp21275_c0_seq1_m.12998 | PREDICTED: chaperonin 60 subunit alpha 2, chloroplastic-like [Populus euphratica] | 61.818 | 1.1618 | 6.2 | 3 | 5 | 2 | 1.088 | 0.963 | 0.975 | 0.98 | 0.892 | 1.095 | 0.981 | 7.75E-01 |
| cds.Camellia_sinensis.comp21315_c0_seq2_m.24203 | PREDICTED: fruit protein pKIWI502 [Vitis vinifera] | 32.794 | 36.921 | 29.5 | 7 | 10 | 6 | 1.02 | 0.979 | 0.991 | 1.002 | 1.013 | 0.993 | 1.006 | 6.73E-01 |
| cds.Camellia_sinensis.comp21350_c0_seq2_m.15219 | PREDICTED: carotenoid 9,10(9',10')-cleavage dioxygenase 1 [Juglans regia] | 61.464 | 148.92 | 41.7 | 19 | 42 | 19 | 0.969 | 0.99 | 0.977 | 1.023 | 1.024 | 1.018 | 1.044 | 2.70E-03 |

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| cds.Camellia_sinensis.comp21382_c0_seq1_m.50500 | PREDICTED: uncharacterized N-acetyltransferase p20-like [Daucus carota subsp. sativus] | 20.838 | 1.9119 | 9.2 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp21392_c0_seq2_m.8276 | PREDICTED: probable galactinol--sucrose galactosyltransferase 2 [Juglans regia] | 92.522 | 41.424 | 11.5 | 9 | 12 | 9 | 0.931 | 0.946 | 0.944 | 1.083 | 1.064 | 1.055 | 1.135 | 1.61E-04 |
| cds.Camellia_sinensis.comp21420_c0_seq1_m.45997 | PREDICTED: hevein-like preproprotein [Cicer arietinum] | 21.021 | 31.624 | 6.5 | 1 | 3 | 1 | 1.092 | 1.114 | 1.158 | 0.921 | 0.878 | 0.908 | 0.805 | 6.22E-04 |
| cds.Camellia_sinensis.comp21421_c0_seq2_m.33075 | PREDICTED: bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT [Juglans regia] | 24.71 | 5.2553 | 12.3 | 3 | 4 | 3 | 1.048 | 1.046 | 1.036 | 0.956 | 0.949 | 0.96 | 0.915 | 5.78E-05 |

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| cds.Camellia_sinensis.comp21484_c0_seq1_m.37700 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP20-2, chloroplastic [Jatropha curcas] | 33.366 | 32.118 | 21.6 | 6 | 8 | 6 | 0.955 | 0.962 | 1.048 | 1.036 | 0.985 | 0.996 | 1.018 | 6.19E-01 |
| cds.Camellia_sinensis.comp21558_c0_seq1_m.41743 | PREDICTED: aspartokinase 1, chloroplastic isoform X1 [Theobroma cacao] | 24.629 | 1.5891 | 9.9 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp21576_c0_seq1_m.22086 | PREDICTED: homogentisate 1,2-dioxygenase isoform X1 [Sesamum indicum] | 50.845 | 6.2946 | 5 | 2 | 2 | 2 | 0.858 | 0.991 | 0.93 | 1.056 | 1.088 | 1.115 | 1.173 | 2.26E-02 |
| cds.Camellia_sinensis.comp21606_c0_seq1_m.17315 | PREDICTED: 4-alpha-glucanotransferase, chloroplastic/amyloplastic [Vitis vinifera] | 65.701 | 7.3173 | 8.1 | 4 | 4 | 4 | 0.974 | 0.998 | 0.917 | 1.138 | 0.996 | 1.003 | 1.086 | 1.81E-01 |

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| cds.Camellia_sinensis.comp21721_c0_seq1_m.30161 | PREDICTED: 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase, chloroplastic [Vitis vinifera] | 35.778 | 49.58 | 38.6 | 13 | 24 | 13 | 1.015 | 1.009 | 0.986 | 1.004 | 0.99 | 0.982 | 0.989 | 3.60E-01 |
| cds.Camellia_sinensis.comp21779_c0_seq1_m.32092 | PREDICTED: heme-binding-like protein At3g10130, chloroplastic isoform X2 [Theobroma cacao] | 33.993 | 75.585 | 48.8 | 15 | 48 | 15 | 0.897 | 0.896 | 0.918 | 1.127 | 1.079 | 1.111 | 1.224 | 1.80E-04 |
| cds.Camellia_sinensis.comp21841_c0_seq1_m.43956 | PREDICTED: calcium-transporting ATPase 1, chloroplastic [Sesamum indicum] | 27.654 | 5.9469 | 7.7 | 2 | 2 | 1 | 0.932 | 0.932 | 1.067 | 0.977 | 1.06 | 1.052 | 1.054 | 3.59E-01 |

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| cds.Camellia_sinensis.comp21864_c0_seq1_m.30565 | PREDICTED: uncharacterized oxidoreductase C663.09c [Populus euphratica] | 32.941 | 7.4056 | 12 | 4 | 4 | 4 | 1.038 | 1.063 | 1 | 0.983 | 0.926 | 0.976 | 0.93 | 4.94E-02 |
| cds.Camellia_sinensis.comp21888_c0_seq1_m.48398 | PREDICTED: aldehyde dehydrogenase family 2 member B4, mitochondrial-like [Ziziphus jujuba] | 22.893 | 90.865 | 40.7 | 7 | 19 | 5 | 0.994 | 0.996 | 1.018 | 1.031 | 0.966 | 1.017 | 1.002 | 9.41E-01 |
| cds.Camellia_sinensis.comp21911_c0_seq1_m.38430 | PREDICTED: stromal 70 kDa heat shock-related protein, chloroplastic-like [Nelumbo nucifera] | 26.375 | 107.44 | 50.8 | 11 | 30 | 7 | 0.916 | 0.925 | 0.918 | 1.086 | 1.111 | 1.108 | 1.198 | 2.01E-05 |
| cds.Camellia_sinensis.comp21927_c0_seq1_m.31407 | PREDICTED: cytochrome P450 82C4-like [Prunus mume] | 48.089 | 17.329 | 12.3 | 5 | 7 | 5 | 0.864 | 0.929 | 0.909 | 1.12 | 1.126 | 1.107 | 1.241 | 6.04E-04 |

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| cds.Camellia_sinensis.comp21931_c0_seq1_m.22916 | Gut esterase (DUF1350) [Arabidopsis thaliana] | 49.425 | 60.939 | 23.6 | 8 | 11 | 8 | 0.973 | 0.931 | 0.973 | 1.037 | 1.031 | 1.001 | 1.067 | 2.42E-02 |
| cds.Camellia_sinensis.comp22064_c0_seq1_m.46500 | PREDICTED: chorismate synthase 1, chloroplastic [Beta vulgaris subsp. vulgaris] | 16.648 | 6.2342 | 11.3 | 1 | 2 | 1 | 1.064 | 1.095 | 1.036 | 1.021 | 0.872 | 0.902 | 0.875 | 5.48E-02 |
| cds.Camellia_sinensis.comp22069_c0_seq1_m.21640 | sodium/calcium exchanger family protein [Populus trichocarpa] | 61.145 | 39.276 | 11.6 | 5 | 9 | 5 | 0.963 | 0.985 | 0.962 | 0.996 | 0.998 | 1.019 | 1.035 | 3.06E-02 |
| cds.Camellia_sinensis.comp22081_c0_seq2_m.50310 | PREDICTED: soluble inorganic pyrophosphatase 1 [Vitis vinifera] | 14.788 | 13.996 | 22 | 3 | 9 | 1 | 1.044 | 1.038 | 1.109 | 0.916 | 1.004 | 0.882 | 0.878 | 4.05E-02 |
| cds.Camellia_sinensis.comp22085_c0_seq1_m.53888 | PREDICTED: IAA-amino acid hydrolase ILR1-like 4 [Cucumis sativus] | 16.799 | 1.9779 | 8.8 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp22097_c0_seq1_m.39846 | PREDICTED: small heat shock protein, chloroplastic [Theobroma cacao] | 24.684 | 4.7051 | 12.4 | 2 | 3 | 2 | 1.319 | 1.149 | 1.122 | 0.825 | 0.757 | 0.761 | 0.653 | 1.80E-03 |
| cds.Camellia_sinensis.comp22099_c0_seq1_m.36672 | PREDICTED: cationic peroxidase 1-like [Pyrus x bretschneideri] | 33.167 | 113.45 | 35.1 | 7 | 18 | 5 | 0.965 | 0.957 | 0.96 | 1.039 | 1.039 | 1.012 | 1.072 | 1.58E-03 |
| cds.Camellia_sinensis.comp22099_c0_seq5_m.53430 | PREDICTED: cationic peroxidase 1 [Vitis vinifera] | 15.99 | 19.699 | 32.7 | 4 | 7 | 2 | 1.064 | 0.959 | 1.133 | 0.934 | 0.965 | 0.994 | 0.917 | 1.76E-01 |
| cds.Camellia_sinensis.comp22154_c0_seq1_m.29275 | PREDICTED: putative methyltransferase At1g22800 [Jatropha curcas] | 26.418 | 2.2054 | 8.7 | 2 | 2 | 2 | 0.955 | 0.991 | 1.07 | 1.024 | 0.946 | 1.03 | 0.995 | 9.15E-01 |
| cds.Camellia_sinensis.comp22155_c0_seq1_m.29099 | PREDICTED: chromatin modification-related protein eaf-1 [Vitis vinifera] | 50.077 | 1.2709 | 2.2 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp22240_c0_seq1_m.28792 | PREDICTED: basic 7S globulin-like [Juglans regia] | 46.374 | 117.73 | 26.5 | 9 | 24 | 9 | 0.871 | 0.931 | 0.903 | 1.125 | 1.112 | 1.116 | 1.24 | 3.84E-04 |
| cds.Camellia_sinensis.comp22253_c0_seq1_m.45388 | PREDICTED: major allergen Pru ar 1-like [Nelumbo nucifera] | 17.754 | 87.068 | 73.1 | 11 | 35 | 11 | 0.848 | 0.819 | 0.827 | 1.191 | 1.207 | 1.175 | 1.433 | 5.00E-06 |
| cds.Camellia_sinensis.comp22261_c0_seq1_m.29034 | PREDICTED: pentatricopeptide repeat-containing protein At5g66520 [Vitis vinifera] | 40.697 | -2 | 2.2 | 1 | 1 | 1 | 0.99 | 1.025 | 1.084 | 1.047 | 0.949 | 0.914 | 0.939 | 2.57E-01 |
| cds.Camellia_sinensis.comp22286_c0_seq1_m.20934 | PREDICTED: zinc transporter 4, chloroplastic-like [Sesamum indicum] | 32.578 | 10.504 | 11.2 | 2 | 2 | 2 | 1.044 | 1.252 | 0.935 | 0.987 | 0.965 | 0.807 | 0.854 | 2.20E-01 |

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| cds.Camellia_sinensis.comp22317_c0_seq4_m.51213 | PREDICTED: GRIP and coiled-coil domain-containing protein 2 [Vitis vinifera] | 12.78 | -2 | 7.3 | 1 | 1 | 1 | 1.427 | 1.238 | 1.435 | 0.553 | 0.626 | 0.6 | 0.434 | 1.60E-04 |
| cds.Camellia_sinensis.comp22344_c0_seq1_m.13415 | PREDICTED: plant intracellular Ras-group-related LRR protein 4 [Ziziphus jujuba] | 63.672 | 2.5108 | 2.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp22415_c0_seq1_m.35402 | PREDICTED: DNA-directed RNA polymerases II and IV subunit 5A [Citrus sinensis] | 24.382 | 6.2704 | 9.2 | 2 | 2 | 2 | 0.967 | 1.002 | 1.01 | 0.999 | 0.928 | 1.105 | 1.018 | 7.85E-01 |
| cds.Camellia_sinensis.comp22451_c0_seq1_m.12748 | PREDICTED: heparanase-like protein 1 [Vitis vinifera] | 59.731 | 4.192 | 3.9 | 2 | 3 | 2 | 1.098 | 1.081 | 1.072 | 1.036 | 0.859 | 0.941 | 0.872 | 1.25E-01 |

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| cds.Camellia_sinensis.comp22492_c0_seq1_m.22766 | PREDICTED: beta-glucosidase BoGH3B-like [Ziziphus jujuba] | 54.998 | 11.594 | 8.2 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp22506_c0_seq1_m.10624 | PREDICTED: probably inactive leucine-rich repeat receptor-like protein kinase At5g48380 [Theobrom | 68.3 | 1.8432 | 3.1 | 2 | 2 | 2 | 0.931 | 0.917 | 0.917 | 1.139 | 1.16 | 0.98 | 1.186 | 8.89E-02 |
| cds.Camellia_sinensis.comp22532_c0_seq1_m.36840 | PREDICTED: probable carboxylesterase SOBER1-like [Vitis vinifera] | 29.776 | 1.2974 | 6.2 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp22552_c0_seq1_m.40751 | PREDICTED: plasma membrane-associated cation-binding protein 1 [Solanum tuberosum | 21.783 | 34.546 | 28.5 | 6 | 10 | 6 | 1.025 | 0.947 | 0.952 | 1.037 | 1.042 | 1.037 | 1.066 | 1.29E-01 |

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| cds.Camellia_sinensis.comp22553_c0_seq2_m.39461 | DUF3119 family protein [Medicago truncatula] | 21.637 | 18.46 | 14.3 | 2 | 5 | 2 | 1.011 | 0.978 | 1.03 | 1.005 | 0.986 | 0.973 | 0.982 | 3.64E-01 |
| cds.Camellia_sinensis.comp22574_c0_seq1_m.45157 | PREDICTED: lactoylglutathione lyase isoform X1 [Theobroma cacao] | 16.159 | 8.1878 | 16.1 | 2 | 2 | 2 | 0.991 | 0.963 | 0.932 | 1.045 | 1.003 | 1.083 | 1.085 | 4.57E-02 |
| cds.Camellia_sinensis.comp22579_c0_seq1_m.25302 | PREDICTED: scopoletin glucosyltransferase-like [Juglans regia] | 49.205 | 20.501 | 4.2 | 2 | 3 | 2 | 0.927 | 0.931 | 0.971 | 1.088 | 1.081 | 1.035 | 1.133 | 4.48E-03 |
| cds.Camellia_sinensis.comp22613_c0_seq1_m.28090 | PREDICTED: protein FMP32, mitochondrial [Ricinus communis] | 27.587 | 3.2806 | 8.6 | 2 | 2 | 2 | 0.956 | 1.02 | 1.033 | 0.984 | 0.986 | 1.033 | 0.998 | 9.56E-01 |
| cds.Camellia_sinensis.comp22625_c0_seq2_m.34958 | serotonin N-acetyltransferase 1, chloroplastic [Cajanus cajan] | 22.051 | 7.1629 | 11.7 | 2 | 3 | 2 | 0.939 | 1.012 | 1.023 | 1.035 | 0.963 | 1.032 | 1.019 | 6.27E-01 |

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| cds.Camellia_sinensis.comp22684_c0_seq1_m.56844 | PREDICTED: V-type proton ATPase subunit B 2 [Elaeis | 12.837 | 1.2244 | 26.7 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp22694_c0_seq1_m.17208 | PREDICTED: dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial-like [Nelumbo nucifera] | 51.101 | 107.25 | 28.5 | 14 | 31 | 8 | 1 | 0.995 | 0.988 | 0.992 | 1.001 | 1.018 | 1.009 | 3.28E-01 |
| cds.Camellia_sinensis.comp22699_c0_seq1_m.2313 | PREDICTED: intron-binding protein aquarius [Juglans regia] | 160.36 | 16.429 | 4.2 | 5 | 5 | 5 | 0.941 | 1.032 | 1.079 | 0.964 | 0.983 | 1.011 | 0.969 | 5.22E-01 |
| cds.Camellia_sinensis.comp22782_c0_seq1_m.41856 | cAMP-regulated phosphoprotein-like protein [Medicago truncatula] | 17.387 | 1.3302 | 6.5 | 1 | 1 | 1 | 0.936 | 1.099 | 1.022 | 1.05 | 0.937 | 0.97 | 0.967 | 6.04E-01 |

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| cds.Camellia_sinensis.comp22795_c1_seq1_m.34061 | PREDICTED: mitochondrial uncoupling protein 1 [Ziziphus jujuba] | 28.825 | 42.105 | 19.8 | 5 | 7 | 5 | 1.036 | 1.084 | 1.031 | 0.934 | 0.991 | 0.941 | 0.91 | 1.80E-02 |
| cds.Camellia_sinensis.comp22798_c0_seq1_m.33202 | PREDICTED: RPM1-interacting protein 4 [Vitis vinifera] | 28.326 | 17.158 | 11.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp22831_c0_seq1_m.33671 | PREDICTED: chloroplastic lipocalin [Vitis vinifera] | 42.169 | 118.47 | 26.1 | 9 | 22 | 9 | 1.006 | 0.923 | 0.959 | 1 | 1.059 | 1.005 | 1.061 | 1.27E-01 |
| cds.Camellia_sinensis.comp22839_c0_seq1_m.26890 | PREDICTED: peptide chain release factor APG3, chloroplastic [Vitis vinifera] | 47.322 | 60.411 | 18.7 | 8 | 11 | 8 | 1.012 | 1.03 | 1.025 | 0.948 | 0.965 | 0.981 | 0.944 | 6.54E-03 |
| cds.Camellia_sinensis.comp22895_c0_seq1_m.31295 | PREDICTED: aspartic proteinase PCS1 [Sesamum indicum] | 44.538 | 1.3414 | 2.5 | 1 | 1 | 1 | 0.941 | 1.138 | 1 | 0.996 | 0.964 | 0.969 | 0.951 | 4.57E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp22898_c0_seq1_m.56873 | Phosphoenolpyruvate carboxylase 2 [Morus notabilis] | 13.764 | 4.6863 | 25.8 | 3 | 6 | 1 | 0.886 | 0.945 | 0.955 | 1.136 | 1.088 | 1.031 | 1.168 | 1.32E-02 |
| cds.Camellia_sinensis.comp22944_c0_seq2_m.24036 | PREDICTED: protein IQ-DOMAIN 32 isoform X2 [Vitis vinifera] | 44.643 | 4.092 | 5.8 | 2 | 2 | 2 | 0.963 | 1.031 | 1.124 | 0.955 | 0.947 | 0.984 | 0.926 | 1.78E-01 |
| cds.Camellia_sinensis.comp22990_c0_seq1_m.25216 | PREDICTED: putative transferase At1g60990, chloroplastic [Juglans regia] | 45.821 | 1.5124 | 2.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp23016_c0_seq1_m.19417 | PREDICTED: transketolase, chloroplastic [Nelumbo nucifera] | 54.239 | 62.708 | 13.6 | 7 | 23 | 4 | 1.021 | 0.967 | 1.005 | 0.995 | 1.014 | 1.034 | 1.017 | 4.42E-01 |
| cds.Camellia_sinensis.comp23018_c0_seq1_m.18026 | PREDICTED: dnaJ homolog 1, mitochondrial-like [Sesamum | 55.904 | 65.371 | 28.8 | 16 | 27 | 9 | 1.149 | 1.133 | 1.113 | 0.831 | 0.85 | 0.894 | 0.758 | 2.98E-04 |

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| cds.Camellia_sinensis.comp23042_c0_seq1_m.25951 | PREDICTED: formamidase-like isoform X1 [Ziziphus jujuba] | 51.648 | 73.137 | 30 | 12 | 23 | 12 | 0.96 | 0.947 | 0.933 | 1.032 | 1.073 | 1.052 | 1.112 | 1.62E-03 |
| cds.Camellia_sinensis.comp23049_c0_seq1_m.34340 | PREDICTED: omega-amidase, chloroplastic [Theobroma cacao] | 29.561 | 1.4661 | 3.4 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp23119_c0_seq1_m.42782 | PREDICTED: disease resistance RPP13-like protein 4 [Capsicum annuum] | 31.325 | 20.403 | 9.1 | 2 | 2 | 2 | 0.853 | 1.096 | 0.878 | 1.067 | 1.126 | 1.018 | 1.136 | 1.90E-01 |
| cds.Camellia_sinensis.comp23125_c0_seq1_m.49092 | Ras-related protein Rab11D [Morus notabilis] | 14.03 | 18.378 | 26.8 | 3 | 4 | 3 | 0.913 | 0.915 | 1 | 1.059 | 1.008 | 1.136 | 1.133 | 5.36E-02 |
| cds.Camellia_sinensis.comp23136_c0_seq1_m.40278 | PREDICTED: probable glutathione S-transferase [Vitis vinifera] | 25.414 | 15.839 | 29.7 | 8 | 9 | 7 | 0.978 | 0.947 | 0.937 | 1.032 | 1.108 | 1.045 | 1.113 | 1.37E-02 |

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| cds.Camellia_sinensis.comp23155_c0_seq2_m.45028 | PREDICTED: peroxidase 17-like [Nicotiana tabacum] | 24.545 | 2.1519 | 6.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp23155_c0_seq3_m.55573 | PREDICTED: peroxidase 17-like [Prunus mume] | 14.426 | 1.4836 | 6.9 | 1 | 1 | 1 | 0.965 | 0.996 | 0.965 | 1.003 | 0.989 | 1.096 | 1.055 | 1.93E-01 |
| cds.Camellia_sinensis.comp23164_c0_seq1_m.40447 | PREDICTED: sorting nexin 2B [Daucus carota subsp. sativus] | 23.891 | 5.0371 | 12.4 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp23171_c0_seq1_m.26030 | PREDICTED: heat shock 70 kDa protein 8 [Ipomoea nil] | 49.514 | 4.7757 | 3.7 | 2 | 2 | 2 | 0.915 | 0.953 | 0.934 | 1.076 | 1.083 | 1.074 | 1.154 | 2.82E-04 |
| cds.Camellia_sinensis.comp23173_c0_seq1_m.24596 | PREDICTED: TOM1-like protein 2 isoform X2 [Populus euphratica] | 50.344 | 5.0933 | 5.8 | 3 | 4 | 3 | 0.972 | 0.987 | 0.974 | 1.075 | 1.081 | 1.032 | 1.087 | 5.68E-03 |

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| cds.Camellia_sinensis.comp23185_c0_seq1_m.52057 | PREDICTED: protein SIEVE ELEMENT OCCLUSION B [Vitis vinifera] | 19.138 | 17.087 | 23.2 | 4 | 6 | 4 | 0.937 | 0.917 | 0.911 | 1.061 | 1.101 | 1.106 | 1.182 | 4.39E-04 |
| cds.Camellia_sinensis.comp23200_c0_seq30_c0_seq3_m.35606 | PREDICTED: red chlorophyll catabolite reductase [Vitis vinifera] | 36.553 | 34.865 | 23.9 | 7 | 11 | 7 | 1.024 | 0.995 | 1.037 | 1.02 | 0.996 | 0.994 | 0.985 | 3.65E-01 |
| cds.Camellia_sinensis.comp23202_c0_seq1_m.39021 | glycoprotein family protein [Medicago truncatula] | 27.823 | 2.7613 | 4.1 | 1 | 1 | 1 | 0.966 | 1.203 | 0.843 | 0.991 | 1.01 | 0.993 | 0.994 | 9.67E-01 |
| cds.Camellia_sinensis.comp23207_c0_seq2_m.46038 | DNA-directed RNA polymerase subunit beta [Arabidopsis thaliana] | 26.32 | 5.4891 | 9.3 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp23208_c0_seq1_m.32620 | PREDICTED: cannabidiolic acid synthase-like [Sesamum indicum] | 40.208 | 1.5719 | 2.6 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp23208_c0_seq2_m.46046 | PREDICTED: berberine bridge enzyme-like 21 [Vitis vinifera] | 21.744 | 13.087 | 29.8 | 6 | 8 | 6 | 0.957 | 0.953 | 0.983 | 1.073 | 1.033 | 1.055 | 1.093 | 3.78E-03 |
| cds.Camellia_sinensis.comp23213_c0_seq1_m.25257 | PREDICTED: aspartate aminotransferase, mitochondrial isoform X1 [Sesamum | 48.715 | 23.843 | 23 | 10 | 13 | 10 | 1.056 | 1.035 | 1.002 | 0.967 | 0.975 | 1.004 | 0.952 | 6.34E-02 |
| cds.Camellia_sinensis.comp23229_c0_seq2_m.32276 | PREDICTED: ubiquinol oxidase 4, chloroplastic/chromoplastic [Vitis vinifera] | 40.851 | 61.033 | 26.4 | 9 | 21 | 9 | 1.031 | 1.004 | 1.044 | 0.952 | 0.969 | 0.978 | 0.942 | 1.26E-02 |
| cds.Camellia_sinensis.comp23234_c0_seq1_m.28763 | virus resistant/susceptible lipocalin [Solanum lycopersicum] | 34.159 | 5.3054 | 12.1 | 3 | 4 | 3 | 0.976 | 0.975 | 1.046 | 0.978 | 0.962 | 1.074 | 1.006 | 9.10E-01 |

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| cds.Camellia_sinensis.comp23253_c0_seq1_m.58877 | PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein Sgpp [Populus euphratica] | 11.591 | 1.3079 | 7.7 | 1 | 1 | 1 | 1.167 | 1.211 | 1.113 | 0.835 | 0.836 | 0.794 | 0.706 | 3.03E-04 |
| cds.Camellia_sinensis.comp23310_c0_seq2_m.42008 | PREDICTED: glycine-rich RNA-binding protein 4, mitochondrial [Vitis vinifera] | 15.692 | 27.621 | 41.4 | 5 | 5 | 5 | 1.012 | 0.963 | 1.012 | 1.074 | 0.952 | 1.043 | 1.027 | 5.49E-01 |
| cds.Camellia_sinensis.comp23332_c0_seq1_m.48713 | glutaredoxin 2 [Medicago truncatula] | 18.18 | 10.309 | 18.4 | 3 | 3 | 3 | 0.969 | 0.931 | 1.005 | 1.051 | 1.039 | 1.027 | 1.073 | 3.72E-02 |
| cds.Camellia_sinensis.comp23350_c0_seq1_m.44664 | PREDICTED: ABC transporter G family member 15-like isoform X1 [Nicotiana attenuata] | 18.589 | 2.1519 | 5.6 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp23354_c0_seq2_m.40883 | PREDICTED: probable ubiquitin-conjugating enzyme E2 18 [Jatropha curcas] | 18.272 | 2.774 | 9.3 | 2 | 4 | 2 | 0.976 | 1.011 | 0.974 | 0.996 | 1.061 | 0.955 | 1.017 | 6.47E-01 |
| cds.Camellia_sinensis.comp23356_c0_seq1_m.39580 | PREDICTED: NADP-dependent malic enzyme-like isoform X1 [Nicotiana tabacum] | 31.6 | 3.3679 | 14.6 | 3 | 7 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp23375_c0_seq1_m.15225 | bZIP transcription factor TRAB1-like [Nicotiana tabacum] | 47.506 | 2.0024 | 7.5 | 2 | 2 | 2 | 1.008 | 1.122 | 1.073 | 0.956 | 0.866 | 0.967 | 0.871 | 4.15E-02 |
| cds.Camellia_sinensis.comp23383_c0_seq1_m.31016 | PREDICTED: peroxidase 31 [Vitis vinifera] | 36.737 | 2.4008 | 3.6 | 1 | 1 | 1 | 0.976 | 1.283 | 1.093 | 0.91 | 0.905 | 0.82 | 0.786 | 5.24E-02 |

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| cds.Camellia_sinensis.comp23407_c0_seq1_m.35915 | PREDICTED: selT-like protein isoform X4 [Nicotiana tomentosiformis] | 25.471 | 1.1979 | 4.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp23411_c0_seq1_m.20884 | PREDICTED: UDP-arabinose 4-epimerase 1 [Prunus mume] | 45.894 | 1.4122 | 2.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp23442_c0_seq2_m.23113 | PREDICTED: protein TRIGALACTOSYLDIACYLGLYCEROL 1, chloroplastic isoform X1 [Juglans regia] | 38.318 | 2.6413 | 6.2 | 2 | 3 | 2 | 0.929 | 0.952 | 1.046 | 1.086 | 1.004 | 1.01 | 1.059 | 2.58E-01 |
| cds.Camellia_sinensis.comp23458_c0_seq1_m.12251 | PREDICTED: probable methyltransferase PMT14 [Theobroma cacao] | 69.76 | 13.154 | 8.9 | 5 | 5 | 5 | 1.031 | 1.151 | 1.183 | 0.903 | 0.731 | 0.976 | 0.776 | 5.39E-02 |

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| cds.Camellia_sinensis.comp23469_c0_seq2_m.34279 | 3-oxo-5-alpha-steroid 4-dehydrogenase [Medicago truncatula] | 25.884 | 1.4806 | 8.4 | 2 | 3 | 2 | 0.932 | 1.01 | 0.986 | 1.032 | 1.061 | 1.002 | 1.057 | 1.27E-01 |
| cds.Camellia_sinensis.comp23481_c0_seq1_m.49036 | PREDICTED: plant intracellular Ras-group-related LRR protein 1-like [Nicotiana attenuata] | 20.063 | 2.1263 | 8.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp23488_c0_seq1_m.40789 | PREDICTED: glutaredoxin-like [Juglans regia] | 12.711 | 16.597 | 31.7 | 3 | 5 | 3 | 0.934 | 0.973 | 0.949 | 1.001 | 1.089 | 1.083 | 1.111 | 2.44E-02 |
| cds.Camellia_sinensis.comp23492_c0_seq1_m.39466 | glutathione S-transferase DHAR2-like [Sesamum indicum] | 26.223 | 82.852 | 30.2 | 5 | 14 | 4 | 0.97 | 0.994 | 1.044 | 1.011 | 0.975 | 1.001 | 0.993 | 7.97E-01 |
| cds.Camellia_sinensis.comp23496_c0_seq1_m.44487 | | 20.864 | 10.646 | 6.3 | 1 | 2 | 1 | 0.947 | 0.979 | 1.028 | 0.937 | 1.025 | 1.096 | 1.035 | 5.54E-01 |

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| cds.Camellia_sinensis.comp23504_c0_seq1_m.19034 | PREDICTED: mitogen-activated protein kinase kinase 2 [Ziziphus jujuba] | 40.538 | 54.412 | 13.5 | 4 | 7 | 4 | 0.967 | 0.999 | 0.998 | 1.046 | 1.008 | 0.978 | 1.023 | 3.69E-01 |
| cds.Camellia_sinensis.comp23511_c0_seq1_m.35001 | universal stress family protein [Populus trichocarpa] | 20.237 | 5.7714 | 16.8 | 3 | 4 | 3 | 0.96 | 1.153 | 1.009 | 1.072 | 0.912 | 0.903 | 0.925 | 3.72E-01 |
| cds.Camellia_sinensis.comp23511_c0_seq2_m.39360 | PREDICTED: universal stress protein A-like protein [Nelumbo nucifera] | 21.602 | 12.205 | 25 | 5 | 8 | 5 | 0.993 | 1.016 | 1.032 | 0.982 | 0.947 | 1.055 | 0.981 | 5.88E-01 |
| cds.Camellia_sinensis.comp23527_c0_seq1_m.22234 | PREDICTED: alpha-L-fucosidase 1 [Juglans regia] | 60.611 | 3.8695 | 1.9 | 1 | 2 | 1 | 0.944 | 0.927 | 1.018 | 1.078 | 0.978 | 1.08 | 1.085 | 1.33E-01 |

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| cds.Camellia_sinensis.comp23540_c0_seq1_m.17687 | PREDICTED: protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic isoform X2 [Vitis vinifera] | 30.947 | 47.709 | 16.2 | 5 | 6 | 5 | 0.961 | 0.994 | 1.008 | 1.019 | 1.021 | 1.046 | 1.042 | 6.85E-02 |
| cds.Camellia_sinensis.comp23540_c0_seq1_m.17688 | PREDICTED: protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic [Eucalyptus grandis] | 11.466 | 32.127 | 42.2 | 3 | 8 | 3 | 0.971 | 0.993 | 0.947 | 1.071 | 0.956 | 1.099 | 1.074 | 1.96E-01 |
| cds.Camellia_sinensis.comp23543_c0_seq1_m.33026 | PREDICTED: cinnamoyl-CoA reductase 1 [Solanum tuberosum | 36.641 | 29.051 | 21.3 | 7 | 16 | 7 | 1.264 | 1.283 | 1.25 | 0.716 | 0.719 | 0.699 | 0.562 | 4.89E-07 |
| cds.Camellia_sinensis.comp23549_c0_seq1_m.33670 | PREDICTED: proactivator polypeptide-like 1 [Theobroma cacao] | 27.651 | 46.085 | 18.1 | 4 | 9 | 4 | 0.995 | 0.965 | 0.977 | 1.052 | 1.038 | 1.034 | 1.064 | 3.90E-03 |

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| cds.Camellia_sinensis.comp23551_c0_seq1_m.11022 | PREDICTED: transcription initiation factor TFIID subunit 15b [Sesamum indicum] | 41.732 | 30.181 | 13 | 5 | 8 | 5 | 1.125 | 1.148 | 1.05 | 0.864 | 0.864 | 0.914 | 0.795 | 2.24E-03 |
| cds.Camellia_sinensis.comp23552_c0_seq1_m.31138 | PREDICTED: ubiquitin-like domain-containing CTD phosphatase [Vitis vinifera] | 37.965 | 8.6382 | 6.6 | 2 | 2 | 2 | 1.068 | 1.062 | 1.041 | 0.916 | 0.962 | 0.938 | 0.888 | 1.82E-03 |
| cds.Camellia_sinensis.comp23582_c0_seq1_m.19162 | PREDICTED: acetolactate synthase small subunit 1, chloroplastic-like [Solanum tuberosum | 54.117 | 56.209 | 26.6 | 10 | 20 | 10 | 0.955 | 0.994 | 0.995 | 1.045 | 1.027 | 1.037 | 1.056 | 1.92E-02 |
| cds.Camellia_sinensis.comp23592_c0_seq1_m.24273 | endoribonuclease E-like protein [Medicago truncatula] | 48.129 | 1.3727 | 1.9 | 1 | 1 | 1 | 1.046 | 1.02 | 0.918 | 1.045 | 0.978 | 0.999 | 1.013 | 7.71E-01 |

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| cds.Camellia_sinensis.comp23594_c0_seq1_m.30848 | PREDICTED: translation initiation factor IF-2, chloroplastic isoform X1 [Sesamum indicum] | 28.92 | 6.8192 | 20.5 | 5 | 6 | 5 | 1.15 | 1.22 | 1.173 | 0.827 | 0.811 | 0.791 | 0.686 | 6.16E-05 |
| cds.Camellia_sinensis.comp23603_c1_seq1_m.31837 | PREDICTED: secretory carrier-associated membrane protein 2-like [Nicotiana tabacum] | 34.192 | 63.879 | 26.5 | 6 | 7 | 6 | 1.014 | 0.964 | 1.017 | 1.033 | 0.951 | 0.98 | 0.99 | 7.38E-01 |
| cds.Camellia_sinensis.comp23604_c0_seq1_m.10644 | muniscin carboxy-terminal mu-like domain protein protein [Medicago truncatula] | 32.731 | 4.8523 | 10 | 3 | 3 | 3 | 1.079 | 0.978 | 0.962 | 0.988 | 0.98 | 1.002 | 0.984 | 6.99E-01 |
| cds.Camellia_sinensis.comp23607_c0_seq1_m.42110 | NtPRp27-like protein precursor [Solanum tuberosum | 27.16 | 28.377 | 23.3 | 5 | 15 | 4 | 0.942 | 0.916 | 0.935 | 1.077 | 1.09 | 1.059 | 1.155 | 2.60E-04 |

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| cds.Camellia_sinensis.comp23618_c0_seq1_m.33504 | PREDICTED: thioredoxin-like protein AAED1, chloroplastic [Pyrus x bretschneideri] | 29.437 | 56.459 | 36.4 | 10 | 14 | 10 | 1.035 | 1.015 | 1.044 | 0.947 | 0.988 | 0.952 | 0.933 | 1.16E-02 |
| cds.Camellia_sinensis.comp23629_c1_seq1_m.46035 | PREDICTED: nuclear transcription factor Y subunit B-3 [Vitis vinifera] | 14.512 | 39.23 | 11.3 | 1 | 2 | 1 | 0.986 | 1.104 | 1.046 | 0.962 | 0.899 | 1.001 | 0.913 | 1.14E-01 |
| cds.Camellia_sinensis.comp23638_c0_seq2_m.33624 | PREDICTED: iron-sulfur cluster co-chaperone protein HscB, mitochondrial isoform X1 [Vitis | 31.34 | 3.3966 | 4.1 | 1 | 1 | 1 | 1.041 | 1.033 | 0.906 | 0.879 | 0.966 | 1.167 | 1.011 | 9.55E-01 |
| cds.Camellia_sinensis.comp23640_c0_seq1_m.22313 | PREDICTED: formate dehydrogenase, mitochondrial [Theobroma cacao] | 42.427 | 133.56 | 38.3 | 14 | 67 | 14 | 0.988 | 0.975 | 0.983 | 1.021 | 1.021 | 1.019 | 1.039 | 6.15E-04 |

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| cds.Camellia_sinensis.comp23644_c0_seq1_m.2851 | PREDICTED: DNA-directed RNA polymerase II subunit RPB2 [Ziziphus | 134.92 | 9.3801 | 3.1 | 3 | 4 | 3 | 1.122 | 1.136 | 1.161 | 0.891 | 0.862 | 0.848 | 0.761 | 1.01E-04 |
| cds.Camellia_sinensis.comp23661_c0_seq1_m.36437 | PREDICTED: vesicle-associated membrane protein 711 [Nicotiana tabacum] | 27.066 | 3.5117 | 16.2 | 4 | 6 | 4 | 1.019 | 1.016 | 1.016 | 0.998 | 0.99 | 0.976 | 0.971 | 4.81E-02 |
| cds.Camellia_sinensis.comp23677_c0_seq1_m.29418 | PREDICTED: protein STRICTOSIDINE SYNTHASE-LIKE 4-like [Juglans regia] | 41.47 | 23.551 | 18.5 | 7 | 11 | 7 | 1.009 | 0.995 | 0.97 | 0.951 | 1.029 | 1.018 | 1.008 | 7.95E-01 |
| cds.Camellia_sinensis.comp23686_c0_seq1_m.36715 | PREDICTED: probable thylakoid lumen protein sll1769 isoform X2 [Solanum tuberosum | 24.783 | 93.386 | 27.3 | 6 | 18 | 6 | 0.905 | 0.874 | 0.887 | 1.117 | 1.108 | 1.127 | 1.257 | 3.71E-05 |

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| cds.Camellia_sinensis.comp23687_c0_seq2_m.41874 | PREDICTED: universal stress protein PHOS32 [Eucalyptus grandis] | 20.396 | 10.02 | 19.7 | 3 | 5 | 3 | 0.855 | 1.029 | 0.945 | 1.152 | 1.06 | 1.046 | 1.152 | 8.04E-02 |
| cds.Camellia_sinensis.comp23689_c0_seq1_m.18354 | PREDICTED: xylose isomerase [Jatropha curcas] | 52.848 | 165.26 | 49.2 | 20 | 56 | 20 | 0.875 | 0.865 | 0.882 | 1.149 | 1.167 | 1.133 | 1.315 | 1.58E-05 |
| cds.Camellia_sinensis.comp23691_c0_seq1_m.18836 | PREDICTED: uridine kinase-like protein 1, chloroplastic [Nicotiana tabacum] | 54.733 | 13.916 | 9.4 | 4 | 4 | 4 | 1.007 | 1.118 | 1.016 | 0.929 | 0.984 | 0.985 | 0.923 | 1.08E-01 |
| cds.Camellia_sinensis.comp23696_c0_seq1_m.41908 | PREDICTED: 28 kDa ribonucleoprotein, chloroplastic-like [Nelumbo nucifera] | 18.588 | 84.4 | 62.4 | 10 | 31 | 8 | 1.017 | 1.007 | 1.037 | 0.976 | 0.973 | 0.971 | 0.954 | 5.76E-03 |
| cds.Camellia_sinensis.comp23709_c0_seq1_m.40618 | embryo-specific protein ATS3B-like [Cajanus cajan] | 21.885 | 79.669 | 19.4 | 3 | 12 | 3 | 0.955 | 0.917 | 0.828 | 1.107 | 1.112 | 1.106 | 1.231 | 3.86E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp23718_c0_seq2_m.39301 | PREDICTED: serine/arginine-rich splicing factor RSZ21-like isoform X1 [Arachis ipaensis] | 20.113 | 2.1786 | 7.3 | 1 | 1 | 1 | 1.057 | 1.037 | 0.991 | 0.944 | 0.997 | 0.97 | 0.944 | 7.96E-02 |
| cds.Camellia_sinensis.comp23719_c0_seq1_m.9918 | PREDICTED: THO complex subunit 4A [Arachis duranensis] | 24.963 | 31.904 | 30.7 | 7 | 11 | 5 | 1.093 | 1.122 | 1.048 | 0.887 | 0.914 | 0.948 | 0.842 | 3.44E-03 |
| cds.Camellia_sinensis.comp23725_c0_seq1_m.39683 | transferring glycosyl group transferase [Arabidopsis thaliana] | 25.464 | 7.86 | 8.6 | 2 | 4 | 2 | 0.959 | 0.974 | 0.965 | 1.005 | 1.111 | 1.008 | 1.078 | 1.56E-01 |
| cds.Camellia_sinensis.comp23726_c0_seq2_m.17993 | PREDICTED: polyadenylate-binding protein RBP47 [Vitis | 47.033 | 6.6267 | 6.3 | 3 | 3 | 3 | 0.918 | 1.006 | 1.03 | 1.026 | 1.054 | 0.99 | 1.039 | 3.75E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp23731_c0_seq1_m.24376 | PREDICTED: ATP phosphoribosyltransferase 2, chloroplastic-like [Nicotiana tabacum] | 44.373 | 48.254 | 21.1 | 8 | 11 | 8 | 0.975 | 1.036 | 0.99 | 1.019 | 1.001 | 0.988 | 1.002 | 9.05E-01 |
| cds.Camellia_sinensis.comp23736_c0_seq2_m.11787 | PREDICTED: translation factor GUF1 homolog, chloroplastic [Nelumbo nucifera] | 75.161 | 6.6564 | 5.9 | 4 | 4 | 4 | 1.066 | 1.089 | 1.062 | 0.899 | 0.939 | 0.948 | 0.866 | 1.36E-03 |
| cds.Camellia_sinensis.comp23737_c0_seq1_m.46339 |  | 18.499 | 49.485 | 17.3 | 2 | 4 | 2 | 1.037 | 0.987 | 0.985 | 1.014 | 0.954 | 1.027 | 0.995 | 8.71E-01 |
| cds.Camellia_sinensis.comp23742_c0_seq1_m.51948 | PREDICTED: probable glutathione S-transferase [Ricinus communis] | 12.013 | 1.1714 | 7.5 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp23767_c0_seq6_m.6889 | PREDICTED: pre-mRNA-processing factor 39 isoform X1 [Vitis vinifera] | 97.418 | 49.581 | 11.6 | 11 | 14 | 11 | 0.98 | 0.997 | 0.988 | 1.011 | 1.012 | 1.011 | 1.023 | 4.37E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp23775_c0_seq1_m.27773 | PREDICTED: probable 3-hydroxyisobutyrate dehydrogenase-like 2, mitochondrial [Fragaria vesca subsp. vesca] | 31.692 | 33.947 | 34.1 | 8 | 13 | 8 | 1.014 | 1.031 | 1.051 | 1.001 | 0.921 | 0.984 | 0.939 | 8.04E-02 |
| cds.Camellia_sinensis.comp23787_c0_seq1_m.25725 | PREDICTED: sporulation protein RMD1-like [Sesamum indicum] | 29.51 | 3.6775 | 7.1 | 2 | 2 | 2 | 0.892 | 0.999 | 0.988 | 1.014 | 1.062 | 1.073 | 1.094 | 8.63E-02 |
| cds.Camellia_sinensis.comp23789_c0_seq1_m.35175 | fiber protein Fb34 [Medicago truncatula] | 19.236 | 1.5592 | 5.1 | 1 | 1 | 1 | 0.9 | 0.889 | 0.891 | 1.198 | 1.074 | 1.097 | 1.257 | 2.12E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp23812_c0_seq3_m.16318 | PREDICTED: probable pre-mRNA-splicing factor ATP-dependent RNA helicase [Vigna radiata var. radiata] | 60.597 | 27.547 | 13.1 | 7 | 11 | 7 | 0.972 | 0.994 | 1.049 | 0.997 | 1.004 | 0.996 | 0.994 | 8.32E-01 |
| cds.Camellia_sinensis.comp23814_c0_seq1_m.30203 | PREDICTED: reticulon-like protein B8 [Vitis vinifera] | 27.492 | 28.028 | 23.7 | 6 | 10 | 6 | 1.047 | 0.999 | 1 | 0.983 | 0.978 | 0.992 | 0.969 | 1.27E-01 |
| cds.Camellia_sinensis.comp23815_c0_seq2_m.36254 | PREDICTED: ras-related protein RABC1 [Vitis vinifera] | 23.477 | 32.347 | 24.3 | 4 | 9 | 3 | 0.988 | 0.969 | 1.047 | 1.095 | 1.067 | 1.009 | 1.056 | 1.82E-01 |
| cds.Camellia_sinensis.comp23816_c0_seq1_m.50338 | PREDICTED: photosynthetic NDH subunit of subcomplex B 3, chloroplastic [Jatropha curcas] | 19.385 | 4.4973 | 5.6 | 1 | 2 | 1 | 1.155 | 1.115 | 1.098 | 0.94 | 0.836 | 0.826 | 0.773 | 4.08E-03 |

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| cds.Camellia_sinensis.comp23817_c0_seq1_m.16439 | PREDICTED: ATP-dependent RNA helicase DBP2-like [Nelumbo nucifera] | 60.974 | 3.7866 | 8 | 5 | 9 | 3 | 0.933 | 0.975 | 1.017 | 1.066 | 1.01 | 1.024 | 1.06 | 1.20E-01 |
| cds.Camellia_sinensis.comp23822_c0_seq1_m.12574 | PREDICTED: phenylalanine--tRNA ligase beta subunit, cytoplasmic-like [Nelumbo nucifera] | 66.507 | 25.283 | 21.1 | 11 | 15 | 11 | 0.944 | 1 | 0.948 | 1.076 | 1.071 | 1.042 | 1.103 | 9.66E-03 |
| cds.Camellia_sinensis.comp23829_c0_seq1_m.33036 | PREDICTED: annexin D4 [Vitis vinifera] | 37.33 | 25.58 | 25 | 9 | 14 | 9 | 1.078 | 1.078 | 1.043 | 0.901 | 0.926 | 0.929 | 0.862 | 5.25E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp23849_c0_seq15_m.12318 | PREDICTED: bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic-like isoform X1 [Daucus carota subsp. sativus] | 57.516 | 88.486 | 21.9 | 11 | 17 | 10 | 1.032 | 1.081 | 1.068 | 0.91 | 0.975 | 0.911 | 0.879 | 8.38E-03 |
| cds.Camellia_sinensis.comp23854_c0_seq1_m.38600 | ribosomal RNA small subunit methyltransferase G [Arabidopsis | 30.251 | 74.71 | 39.6 | 10 | 19 | 10 | 0.958 | 0.967 | 0.974 | 1.074 | 1.056 | 1.027 | 1.089 | 3.60E-03 |
| cds.Camellia_sinensis.comp23861_c0_seq1_m.37897 | probable calcium-binding protein CML21 [Cajanus cajan] | 26.354 | 16.126 | 19.2 | 4 | 4 | 4 | 1.121 | 1.01 | 1.03 | 1.01 | 0.945 | 0.921 | 0.91 | 8.92E-02 |

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| cds.Camellia_sinensis.comp23862_c0_seq2_m.17829 | PREDICTED: fe-S cluster assembly factor HCF101, chloroplastic [Vitis vinifera] | 42.728 | 68.602 | 19.4 | 6 | 9 | 6 | 1.04 | 1.004 | 1.055 | 0.97 | 0.937 | 0.941 | 0.919 | 9.98E-03 |
| cds.Camellia_sinensis.comp23866_c0_seq1_m.32836 | PREDICTED: probable prolyl 4-hydroxylase 4 [Ricinus communis] | 35.937 | 3.9901 | 6.8 | 2 | 2 | 2 | 1.071 | 1.074 | 0.945 | 0.945 | 0.976 | 0.98 | 0.939 | 2.32E-01 |
| cds.Camellia_sinensis.comp23873_c0_seq2_m.6052 | PREDICTED: DNA gyrase subunit A, chloroplastic/mitochondrial isoform X1 [Vitis vinifera] | 102.56 | 35.639 | 13.3 | 12 | 16 | 12 | 0.975 | 0.984 | 0.981 | 1.038 | 1.019 | 1.02 | 1.047 | 2.30E-03 |
| cds.Camellia_sinensis.comp23877_c0_seq1_m.18718 | PREDICTED: galactokinase-like [Ziziphus jujuba] | 54.462 | 184.09 | 45.3 | 18 | 36 | 15 | 0.981 | 0.967 | 0.964 | 1.026 | 0.996 | 1.01 | 1.041 | 1.63E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp23881_c0_seq1_m.36848 | PREDICTED: photosynthetic NDH subunit of subcomplex B 4, chloroplastic-like [Vitis vinifera] | 21.646 | 11.759 | 17.2 | 4 | 6 | 4 | 1.006 | 1.008 | 0.989 | 0.974 | 0.993 | 1.019 | 0.994 | 7.07E-01 |
| cds.Camellia_sinensis.comp23884_c0_seq1_m.19157 | PREDICTED: divinyl chlorophyllide a 8-vinyl-reductase, chloroplastic [Jatropha curcas] | 46.245 | 63.188 | 21 | 8 | 11 | 8 | 1.003 | 1.03 | 1.045 | 0.976 | 1.031 | 0.953 | 0.962 | 2.06E-01 |
| cds.Camellia_sinensis.comp23885_c0_seq1_m.9327 | PREDICTED: glycine-rich domain-containing protein 1-like [Juglans regia] | 87.586 | 3.4479 | 1.4 | 1 | 1 | 1 | 0.973 | 1.077 | 1.054 | 1.064 | 0.953 | 0.891 | 0.937 | 3.29E-01 |

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| cds.Camellia_sinensis.comp23891_c0_seq2_m.26046 | PREDICTED: aminoacyl tRNA synthase complex-interacting multifunctional protein 1 isoform X2 [Vitis vinifera] | 41.356 | 14.133 | 13.7 | 6 | 7 | 6 | 1.019 | 1.007 | 1.01 | 0.989 | 1.002 | 0.96 | 0.972 | 9.59E-02 |
| cds.Camellia_sinensis.comp23905_c0_seq1_m.37019 | PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein At3g48420 [Nicotiana | 27.422 | 72.802 | 40.3 | 10 | 23 | 10 | 1.027 | 1.02 | 1.029 | 0.969 | 1.002 | 0.973 | 0.957 | 1.56E-02 |
| cds.Camellia_sinensis.comp23914_c0_seq1_m.17817 | PREDICTED: aminopeptidase M1-like [Juglans regia] | 56.968 | 96.165 | 35.9 | 21 | 39 | 21 | 0.95 | 0.944 | 0.95 | 1.076 | 1.054 | 1.05 | 1.118 | 1.42E-04 |

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| cds.Camellia_sinensis.comp23927_c0_seq1_m.51036 | PREDICTED: thioredoxin M-type, chloroplastic-like [Fragaria vesca subsp. vesca] | 13.205 | 3.8723 | 15.3 | 2 | 8 | 1 | 1.042 | 1.05 | 0.985 | 1.032 | 0.961 | 0.954 | 0.958 | 2.49E-01 |
| cds.Camellia_sinensis.comp23928_c0_seq1_m.4633 | PREDICTED: coatomer subunit beta-1 [Theobroma cacao] | 105.71 | 98.623 | 23.8 | 19 | 29 | 19 | 1.027 | 1.017 | 0.99 | 0.97 | 1.026 | 1.006 | 0.989 | 6.15E-01 |
| cds.Camellia_sinensis.comp23930_c0_seq1_m.9730 | PREDICTED: long chain acyl-CoA synthetase 8 [Sesamum indicum] | 80.241 | 84.322 | 21.6 | 13 | 19 | 13 | 1.008 | 0.988 | 1.013 | 1.005 | 0.982 | 0.993 | 0.99 | 3.95E-01 |
| cds.Camellia_sinensis.comp23931_c0_seq1_m.30689 | PREDICTED: thylakoid membrane protein ssl2009-like [Nicotiana tabacum] | 24.727 | 82.523 | 13.3 | 3 | 5 | 3 | 1.079 | 1.085 | 1.047 | 0.937 | 0.969 | 0.902 | 0.874 | 4.60E-03 |

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| cds.Camellia_sinensis.comp23961_c0_seq1_m.41248 | nuclear transport factor 2 (NTF2) family protein [Medicago truncatula] | 23.204 | 19.266 | 45.8 | 10 | 20 | 10 | 1.048 | 1.024 | 1.011 | 0.943 | 0.986 | 0.999 | 0.95 | 6.40E-02 |
| cds.Camellia_sinensis.comp23966_c0_seq1_m.36614 | PREDICTED: 25.3 kDa vesicle transport protein [Ziziphus jujuba] | 25.392 | 49.328 | 28.9 | 7 | 11 | 7 | 0.899 | 0.908 | 0.991 | 1.056 | 1.062 | 1.054 | 1.134 | 5.53E-02 |
| cds.Camellia_sinensis.comp23975_c0_seq3_m.15198 | PREDICTED: YTH domain-containing family protein 1-like isoform X2 [Pyrus x bretschneideri] | 59.744 | 4.3401 | 4.1 | 2 | 2 | 2 | 0.966 | 1.01 | 0.929 | 1.007 | 1.085 | 1.021 | 1.072 | 1.06E-01 |
| cds.Camellia_sinensis.comp23980_c0_seq1_m.36708 | PREDICTED: 28 kDa ribonucleoprotein, chloroplastic [Vitis vinifera] | 21.557 | 15.883 | 18.5 | 4 | 5 | 4 | 1.014 | 1.063 | 1.028 | 0.938 | 1.029 | 0.983 | 0.95 | 1.62E-01 |

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| cds.Camellia_sinensis.comp23986_c0_seq2_m.42970 | PREDICTED: prefoldin subunit 1 isoform X1 [Vitis vinifera] | 14.505 | 16.108 | 36.5 | 5 | 6 | 5 | 0.886 | 0.897 | 0.946 | 1.065 | 1.067 | 1.142 | 1.2 | 3.98E-03 |
| cds.Camellia_sinensis.comp23989_c0_seq1_m.34980 | calcium-binding EF hand family protein [Populus trichocarpa] | 36.215 | 19.815 | 16.2 | 5 | 6 | 5 | 0.997 | 1.035 | 1.036 | 0.992 | 1.003 | 0.958 | 0.963 | 1.11E-01 |
| cds.Camellia_sinensis.comp23991_c0_seq1_m.8691 | PREDICTED: long chain acyl-CoA synthetase 9, chloroplastic [Vitis vinifera] | 76.838 | 53.751 | 17.2 | 9 | 17 | 9 | 1.036 | 0.991 | 1.018 | 0.981 | 0.985 | 0.977 | 0.967 | 6.11E-02 |
| cds.Camellia_sinensis.comp23998_c0_seq1_m.18906 | PREDICTED: DEAD-box ATP-dependent RNA helicase 20 [Ziziphus jujuba] | 55.594 | 71.087 | 36.3 | 17 | 23 | 15 | 0.989 | 1.015 | 0.985 | 0.981 | 1.029 | 0.999 | 1.007 | 7.16E-01 |

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| cds.Camellia_sinensis.comp24002_c0_seq1_m.29975 | PREDICTED: probable hydroxyacylglutathione hydrolase 2, chloroplastic [Capsicum annuum] | 39.225 | 29.218 | 20.1 | 6 | 9 | 6 | 1.05 | 1.081 | 1.073 | 0.948 | 0.915 | 0.903 | 0.863 | 9.64E-04 |
| cds.Camellia_sinensis.comp24003_c0_seq1_m.33142 | PREDICTED: phospholipid hydroperoxide glutathione peroxidase 1, chloroplastic-like [Sesamum indicum] | 31.524 | 76.61 | 34 | 8 | 26 | 8 | 1.051 | 0.992 | 1.015 | 0.955 | 0.981 | 0.978 | 0.953 | 6.32E-02 |
| cds.Camellia_sinensis.comp24028_c0_seq1_m.36099 | PREDICTED: UPF0235 protein At5g63440 [Ricinus communis] | 25.76 | 1.8266 | 6.9 | 2 | 2 | 2 | 1 | 1.346 | 0.933 | 0.894 | 0.879 | 0.928 | 0.824 | 2.52E-01 |
| cds.Camellia_sinensis.comp24036_c0_seq2_m.16475 | PREDICTED: probable beta-D-xylosidase 5 [Theobroma cacao] | 73.884 | 57.593 | 13.3 | 7 | 9 | 7 | 0.879 | 0.921 | 0.92 | 1.102 | 1.062 | 1.139 | 1.214 | 1.58E-03 |

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| cds.Camellia_sinensis.comp24048_c0_seq3_m.28524 | PREDICTED: histidine biosynthesis bifunctional protein hisIE, chloroplastic [Vitis vinifera] | 32.742 | 16.105 | 21.7 | 6 | 7 | 6 | 1.005 | 1.05 | 1.033 | 0.992 | 1.005 | 0.927 | 0.947 | 1.22E-01 |
| cds.Camellia_sinensis.comp24049_c0_seq1_m.38295 | peptide methionine sulfoxide reductase [Solanum lycopersicum] | 24.571 | 8.2113 | 16.5 | 4 | 5 | 4 | 1.037 | 1.019 | 0.992 | 1.004 | 0.931 | 1.014 | 0.968 | 3.24E-01 |
| cds.Camellia_sinensis.comp24050_c0_seq1_m.19288 | PREDICTED: protein RETICULATA-RELATED 1, chloroplastic-like [Solanum tuberosum | 60.605 | 5.2906 | 5 | 3 | 3 | 3 | 1.11 | 1.168 | 1.096 | 0.849 | 0.895 | 0.85 | 0.769 | 5.43E-04 |
| cds.Camellia_sinensis.comp24053_c0_seq1_m.10074 | PREDICTED: probable Xaa-Pro aminopeptidase P isoform X1 [Juglans regia] | 57.853 | 27.96 | 17.1 | 8 | 11 | 8 | 0.978 | 1.012 | 1.015 | 1.061 | 0.999 | 0.959 | 1.005 | 9.07E-01 |

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| cds.Camellia_sinensis.comp24053_c0_seq4_m.11134 | PREDICTED: probable Xaa-Pro aminopeptidase P [Vitis vinifera] | 23.791 | 8.4049 | 8.8 | 3 | 4 | 3 | 0.994 | 1.055 | 0.933 | 1.004 | 0.997 | 1.015 | 1.011 | 7.59E-01 |
| cds.Camellia_sinensis.comp24057_c0_seq1_m.30493 | PREDICTED: nuclear pore complex protein NUP35 [Ipomoea nil] | 35.989 | 7.8803 | 10.3 | 3 | 3 | 3 | 0.881 | 1.251 | 0.974 | 1.001 | 0.885 | 1.017 | 0.935 | 6.33E-01 |
| cds.Camellia_sinensis.comp24068_c0_seq1_m.34682 | calcium-binding EF hand family protein [Populus trichocarpa] | 18.464 | 8.907 | 23.6 | 4 | 10 | 4 | 0.962 | 1.028 | 0.961 | 1.016 | 1.028 | 1.033 | 1.043 | 1.38E-01 |
| cds.Camellia_sinensis.comp24075_c0_seq6_m.36125 | PREDICTED: rhodanese-like domain-containing protein 9, chloroplastic [Vitis vinifera] | 25.977 | 18.236 | 24.7 | 6 | 11 | 6 | 1.041 | 1.005 | 1.039 | 0.961 | 0.959 | 0.979 | 0.94 | 9.22E-03 |

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| cds.Camellia_sinensis.comp24077_c0_seq1_m.23151 | PREDICTED: 3-isopropylmalate dehydrogenase, chloroplastic [Vitis vinifera] | 43.362 | 45.791 | 26.2 | 11 | 21 | 11 | 1.015 | 1.045 | 1.008 | 1 | 0.976 | 0.972 | 0.961 | 4.81E-02 |
| cds.Camellia_sinensis.comp24078_c0_seq2_m.19441 | PREDICTED: SURP and G-patch domain-containing protein 1-like protein isoform X1 [Vitis vinifera] | 47.91 | 2.7308 | 5.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp24094_c0_seq1_m.8183 | PREDICTED: ATP-dependent DNA helicase RecQ-like [Prunus mume] | 99.53 | 1.4642 | 1.8 | 2 | 2 | 2 | 0.975 | 0.911 | 1.011 | 1.068 | 1.017 | 1.04 | 1.079 | 8.54E-02 |

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| cds.Camellia_sinensis.comp24100_c0_seq1_m.27039 | PREDICTED: LOW QUALITY PROTEIN: cell division protein FtsZ homolog 1, chloroplastic-like [Capsicum | 44.362 | 25.589 | 14.9 | 5 | 6 | 5 | 1.083 | 1.073 | 1.113 | 0.844 | 0.86 | 1.001 | 0.827 | 2.52E-02 |
| cds.Camellia_sinensis.comp24104_c0_seq1_m.25122 | PREDICTED: pentatricopeptide repeat-containing protein At1g61870, mitochondrial [Vitis vinifera] | 44.525 | 2.8009 | 3.8 | 2 | 2 | 2 | 1.108 | 1.105 | 1.078 | 0.922 | 0.918 | 0.847 | 0.816 | 2.16E-03 |
| cds.Camellia_sinensis.comp24112_c0_seq1_m.37222 | resistance to phytophthora protein, putative [Medicago | 26.883 | 1.3934 | 3.4 | 1 | 1 | 1 | 1.03 | 0.98 | 1.028 | 0.93 | 1.031 | 1.002 | 0.975 | 5.01E-01 |

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| cds.Camellia_sinensis.comp24113_c1_seq1_m.35659 | PREDICTED: alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic-like [Ipomoea nil] | 18.337 | 14.069 | 30 | 5 | 8 | 4 | 0.952 | 1.048 | 0.957 | 0.967 | 1.075 | 0.982 | 1.023 | 6.49E-01 |
| cds.Camellia_sinensis.comp24118_c0_seq1_m.41021 | PREDICTED: phenylalanine ammonia-lyase [Eucalyptus grandis] | 31.858 | 3.0121 | 22.6 | 5 | 9 | 2 | 1.095 | 1.193 | 1.162 | 0.847 | 0.873 | 0.795 | 0.729 | 1.08E-03 |
| cds.Camellia_sinensis.comp24120_c0_seq20_m.27368 | catalytic/coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] | 38.646 | 84.985 | 29.6 | 11 | 24 | 11 | 0.987 | 0.959 | 0.932 | 1.016 | 1.014 | 1.085 | 1.082 | 4.66E-02 |
| cds.Camellia_sinensis.comp24125_c0_seq1_m.34400 | PREDICTED: nuclear pore complex protein NUP54-like [Gossypium hirsutum] | 38.664 | 3.1382 | 3.4 | 1 | 1 | 1 | 0.918 | 1.473 | 0.889 | 1.043 | 0.883 | 0.793 | 0.829 | 4.12E-01 |

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| cds.Camellia_sinensis.comp24128_c0_seq1_m.15428 | PREDICTED: cytochrome P450 97B2, chloroplastic [Vitis vinifera] | 58.713 | 41.12 | 16 | 8 | 18 | 8 | 1.016 | 1.031 | 1.059 | 1.038 | 0.945 | 0.942 | 0.942 | 1.48E-01 |
| cds.Camellia_sinensis.comp24139_c0_seq1_m.34363 | PREDICTED: probable aminopyrimidine aminohydrolase, mitochondrial [Nicotiana tabacum] | 43.544 | 3.955 | 5.7 | 2 | 3 | 1 | 0.952 | 1.013 | 0.997 | 1.027 | 0.96 | 1.067 | 1.031 | 4.53E-01 |
| cds.Camellia_sinensis.comp24152_c0_seq1_m.44297 | PREDICTED: cysteine proteinase 15A-like [Ziziphus jujuba] | 28.609 | 7.9937 | 16.3 | 4 | 5 | 3 | 1.014 | 0.938 | 0.957 | 0.982 | 1.065 | 1.063 | 1.069 | 1.34E-01 |
| cds.Camellia_sinensis.comp24163_c0_seq1_m.42497 | PREDICTED: ribosome-binding factor PSRP1, chloroplastic [Citrus sinensis] | 25.735 | 3.7748 | 4.3 | 2 | 3 | 2 | 1.181 | 1.215 | 1.211 | 0.784 | 0.813 | 0.762 | 0.654 | 3.69E-05 |

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| cds.Camellia_sinensis.comp24164_c0_seq1_m.25907 | PREDICTED: protein ECERIFERUM 26 [Vitis vinifera] | 49.78 | 18.322 | 13.3 | 5 | 8 | 5 | 1.223 | 1.255 | 1.319 | 0.68 | 0.807 | 0.629 | 0.557 | 1.56E-03 |
| cds.Camellia_sinensis.comp24165_c0_seq1_m.18657 | PREDICTED: serine-threonine kinase receptor-associated protein-like [Ziziphus jujuba] | 37.337 | 75.928 | 29 | 9 | 15 | 9 | 0.962 | 0.987 | 0.958 | 1.028 | 1.038 | 1.024 | 1.063 | 3.84E-03 |
| cds.Camellia_sinensis.comp24168_c0_seq1_m.26608 | ribosomal RNA small subunit methyltransferase J [Arabidopsis | 41.529 | 44.173 | 17.8 | 5 | 9 | 5 | 1.074 | 1.107 | 1.229 | 0.87 | 0.803 | 0.843 | 0.738 | 2.98E-03 |
| cds.Camellia_sinensis.comp24176_c0_seq1_m.23265 | PREDICTED: mediator-associated protein 1 [Cucumis sativus] | 41.899 | 10.368 | 9.3 | 3 | 4 | 3 | 1.019 | 0.993 | 1.034 | 0.948 | 0.863 | 1.079 | 0.949 | 4.38E-01 |

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| cds.Camellia_sinensis.comp24182_c0_seq1_m.28653 | PREDICTED: L-galactose dehydrogenase [Fragaria vesca subsp. vesca] | 34.57 | 51.297 | 27.6 | 6 | 8 | 6 | 0.965 | 1.022 | 1.006 | 0.951 | 1.022 | 1.009 | 0.996 | 8.97E-01 |
| cds.Camellia_sinensis.comp24187_c0_seq2_m.39619 | PREDICTED: protein PEROXIN-4 [Ipomoea nil] | 17.701 | 2.7964 | 10.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24196_c0_seq1_m.46591 | PREDICTED: calcium-binding allergen Ole e 8 [Solanum tuberosum | 19.086 | 63.181 | 36.4 | 5 | 10 | 5 | 0.954 | 0.948 | 0.977 | 1.064 | 1.04 | 1.037 | 1.091 | 2.08E-03 |
| cds.Camellia_sinensis.comp24198_c0_seq1_m.52314 | PREDICTED: glutathione S-transferase L3 isoform X1 [Vitis vinifera] | 18.659 | 23.355 | 31.5 | 4 | 8 | 4 | 1.01 | 1.078 | 1.062 | 0.925 | 0.984 | 0.984 | 0.918 | 4.05E-02 |

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| cds.Camellia_sinensis.comp24205_c0_seq1_m.43355 | PREDICTED: ferredoxin-thioredoxin reductase catalytic chain, chloroplastic [Vitis | 16.333 | 32.415 | 36.1 | 6 | 12 | 6 | 0.987 | 1.03 | 0.971 | 1.012 | 1.022 | 0.997 | 1.014 | 4.87E-01 |
| cds.Camellia_sinensis.comp24206_c0_seq1_m.41922 | PREDICTED: CASP-like protein 1 [Sesamum indicum] | 20.47 | 14.223 | 26.4 | 5 | 9 | 5 | 0.785 | 0.771 | 0.76 | 1.206 | 1.294 | 1.253 | 1.62 | 2.38E-05 |
| cds.Camellia_sinensis.comp24207_c0_seq1_m.26848 | PREDICTED: ATP-citrate synthase alpha chain protein 2 [Vitis vinifera] | 46.486 | 26.406 | 12.8 | 6 | 12 | 3 | 1.043 | 0.971 | 1.002 | 1.007 | 1.021 | 1.04 | 1.017 | 4.85E-01 |
| cds.Camellia_sinensis.comp24208_c0_seq1_m.8550 | PREDICTED: DEAD-box ATP-dependent RNA helicase 37 [Vitis vinifera] | 66.283 | 26.201 | 23.9 | 12 | 14 | 11 | 0.936 | 0.993 | 0.962 | 1.027 | 1.042 | 1.037 | 1.074 | 1.50E-02 |

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| cds.Camellia_sinensis.comp24209_c0_seq1_m.15120 | PREDICTED: fatty acid amide hydrolase-like [Solanum tuberosum | 41.129 | 9.147 | 4.4 | 1 | 1 | 1 | 1.068 | 0.937 | 0.798 | 0.999 | 1.129 | 1.081 | 1.145 | 1.98E-01 |
| cds.Camellia_sinensis.comp24209_c0_seq1_m.15121 | PREDICTED: fatty acid amide hydrolase-like [Nicotiana attenuata] | 27.133 | 10.564 | 4.6 | 1 | 1 | 1 | 1.03 | 1.116 | 1.046 | 0.957 | 0.9 | 0.942 | 0.877 | 1.29E-02 |
| cds.Camellia_sinensis.comp24213_c0_seq1_m.7983 | PREDICTED: ABC transporter F family member 3 [Vitis vinifera] | 79.627 | 23.515 | 10.5 | 8 | 8 | 8 | 0.964 | 1.023 | 0.953 | 1.066 | 0.969 | 1.024 | 1.04 | 3.27E-01 |
| cds.Camellia_sinensis.comp24217_c0_seq2_m.21346 | PREDICTED: acyl-coenzyme A oxidase 4, peroxisomal isoform X2 [Vitis vinifera] | 47.726 | 56.518 | 26.1 | 11 | 16 | 2 | 0.997 | 0.905 | 0.914 | 0.987 | 1.098 | 1.118 | 1.137 | 6.09E-02 |
| cds.Camellia_sinensis.comp24234_c0_seq2_m.45260 | PREDICTED: EKC/KEOPS complex subunit Tprkb [Jatropha curcas] | 18.591 | 4.9074 | 17 | 2 | 3 | 2 | 1.012 | 0.944 | 0.9 | 1.024 | 1 | 1.134 | 1.106 | 1.23E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp24236_c0_seq1_m.38194 | PREDICTED: protein LSM12 homolog A [Sesamum | 22.235 | 1.1947 | 3.5 | 1 | 1 | 1 | 0.987 | 1.01 | 1.014 | 0.957 | 0.979 | 1.059 | 0.995 | 8.55E-01 |
| cds.Camellia_sinensis.comp24239_c0_seq1_m.27428 | S-adenosylmethionine synthase 2 [Nicotiana tabacum] | 40.335 | 3.5347 | 21.9 | 8 | 18 | 3 | 1.115 | 1.095 | 1.068 | 0.893 | 0.923 | 0.882 | 0.823 | 4.57E-04 |
| cds.Camellia_sinensis.comp24241_c0_seq1_m.41166 | PREDICTED: polyubiquitin 9 [Nelumbo nucifera] | 15.746 | 11.901 | 33.8 | 3 | 3 | 3 | 1.01 | 1.063 | 0.995 | 0.977 | 0.981 | 0.978 | 0.957 | 1.62E-01 |
| cds.Camellia_sinensis.comp24243_c0_seq8_m.7109 | PREDICTED: CCR4-NOT transcription complex subunit 3 isoform X2 [Vitis vinifera] | 94.569 | 4.8684 | 4.2 | 4 | 4 | 4 | 1.069 | 1.088 | 1.149 | 0.887 | 0.924 | 0.888 | 0.816 | 1.36E-03 |

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| cds.Camellia_sinensis.comp24249_c0_seq1_m.39115 | PREDICTED: aminoacyl tRNA synthase complex-interacting multifunctional protein 1 [Juglans regia] | 32.157 | 16.547 | 19 | 5 | 7 | 5 | 0.952 | 1.078 | 1.003 | 1.019 | 1.012 | 0.921 | 0.973 | 6.10E-01 |
| cds.Camellia_sinensis.comp24253_c0_seq1_m.39812 | PREDICTED: probable protein phosphatase 2C 39 [Nicotiana tabacum] | 22.663 | 11.711 | 19.3 | 4 | 8 | 2 | 0.969 | 1.027 | 0.988 | 1.014 | 1.039 | 0.979 | 1.016 | 5.47E-01 |
| cds.Camellia_sinensis.comp24256_c0_seq1_m.23885 | PREDICTED: GDT1-like protein 2, chloroplastic [Vitis vinifera] | 30.909 | 27.167 | 10 | 2 | 4 | 2 | 1.012 | 0.938 | 0.913 | 1.014 | 1.022 | 1.053 | 1.079 | 7.98E-02 |
| cds.Camellia_sinensis.comp24269_c0_seq1_m.20207 | PREDICTED: histone acetyltransferase type B catalytic subunit [Populus euphratica] | 55.461 | 5.7439 | 3.1 | 1 | 1 | 1 | 0.837 | 1.028 | 0.977 | 1.053 | 0.833 | 1.301 | 1.121 | 5.15E-01 |

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| cds.Camellia_sinensis.comp24271_c0_seq1_m.20938 | PREDICTED: glucan endo-1,3-beta-glucosidase 7 [Ricinus | 50.935 | -2 | 4.2 | 2 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24271_c0_seq2_m.36515 | PREDICTED: glucan endo-1,3-beta-glucosidase 7-like [Nicotiana tomentosif | 37.043 | 1.851 | 2.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24298_c0_seq1_m.23229 | PREDICTED: 3-ketoacyl-CoA synthase 6 [Sesamum indicum] | 56.181 | 4.7365 | 4.4 | 2 | 3 | 2 | 1.558 | 1.615 | 1.613 | 0.265 | 0.345 | 0.41 | 0.213 | 6.60E-03 |
| cds.Camellia_sinensis.comp24302_c0_seq1_m.35823 | PREDICTED: 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial-like [Jatropha | 32.437 | 6.4349 | 7.3 | 2 | 2 | 2 | 0.975 | 1 | 0.984 | 1.01 | 0.972 | 1.071 | 1.032 | 3.54E-01 |

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| cds.Camellia_sinensis.comp24308_c0_seq1_m.21367 | retinal-binding protein [Arabidopsis thaliana] | 50.785 | 15.149 | 11.8 | 5 | 5 | 5 | 0.971 | 1.029 | 0.989 | 1.022 | 0.989 | 1.014 | 1.012 | 5.72E-01 |
| cds.Camellia_sinensis.comp24317_c0_seq1_m.36665 | PREDICTED: peptide methionine sulfoxide reductase B5-like [Juglans regia] | 25.267 | 5.6683 | 12.1 | 3 | 3 | 2 | 0.979 | 1.059 | 1.049 | 0.972 | 0.987 | 0.96 | 0.946 | 1.00E-01 |
| cds.Camellia_sinensis.comp24327_c0_seq1_m.33972 | PREDICTED: probable plastid-lipid-associated protein 8, chloroplastic [Nicotiana attenuata] | 27.086 | 24.958 | 22.3 | 5 | 11 | 5 | 1.013 | 1.074 | 1.022 | 1.068 | 0.966 | 0.98 | 0.969 | 4.31E-01 |
| cds.Camellia_sinensis.comp24332_c0_seq1_m.38647 | PREDICTED: exosome complex component CSL4 [Juglans regia] | 21.225 | 1.578 | 5.1 | 1 | 1 | 1 | 0.952 | 1.094 | 0.884 | 1.072 | 1.036 | 0.981 | 1.054 | 4.53E-01 |

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| cds.Camellia_sinensis.comp24339_c0_seq1_m.48113 | PREDICTED: protein TOC75-3, chloroplastic [Nelumbo nucifera] | 22.376 | 1.9765 | 4.2 | 1 | 2 | 1 | 0.963 | 1.001 | 1.027 | 0.959 | 1.127 | 0.939 | 1.011 | 8.98E-01 |
| cds.Camellia_sinensis.comp24347_c0_seq2_m.31018 | PREDICTED: WD repeat-containing protein VIP3 [Nelumbo nucifera] | 34.135 | 5.0643 | 8.1 | 3 | 3 | 3 | 1.028 | 0.958 | 0.977 | 0.943 | 1.05 | 1.057 | 1.029 | 5.46E-01 |
| cds.Camellia_sinensis.comp24348_c0_seq1_m.32293 | PREDICTED: inositol polyphosphate multikinase beta [Vitis vinifera] | 35.803 | 8.9307 | 14.2 | 4 | 7 | 4 | 0.991 | 0.992 | 1.008 | 1.019 | 0.977 | 0.997 | 1.001 | 9.69E-01 |
| cds.Camellia_sinensis.comp24354_c0_seq1_m.32753 | PREDICTED: ankyrin repeat and SOCS box protein 13 [Citrus sinensis] | 23.706 | 3.5733 | 8.7 | 2 | 2 | 2 | 0.896 | 1.068 | 0.91 | 1.061 | 1.087 | 1.008 | 1.098 | 1.86E-01 |
| cds.Camellia_sinensis.comp24358_c0_seq1_m.18142 | neuronal PAS domain protein [Arabidopsis thaliana] | 61.288 | 2.8167 | 1.8 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp24369_c0_seq1_m.18459 | PREDICTED: vacuolar protein sorting-associated protein 4-like [Sesamum indicum] | 48.009 | 10.19 | 13.2 | 4 | 5 | 4 | | | | | | | | |
| cds.Camellia_sinensis.comp24377_c0_seq1_m.25327 | PREDICTED: ATG8-interacting protein 1 [Vitis vinifera] | 35 | 2.0884 | 3.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24380_c0_seq2_m.32547 | PREDICTED: cytochrome c oxidase subunit 5b-1, mitochondrial [Erythranthe guttata] | 18.348 | 48.906 | 41.2 | 7 | 14 | 7 | 0.961 | 0.97 | 0.95 | 1.048 | 1.068 | 1.008 | 1.084 | 1.11E-02 |
| cds.Camellia_sinensis.comp24387_c0_seq1_m.37312 | PREDICTED: temperature-induced lipocalin-1-like [Cucumis melo] | 21.394 | 4.5388 | 18.4 | 4 | 8 | 2 | 1.025 | 1.141 | 1.112 | 0.822 | 0.997 | 0.885 | 0.825 | 3.99E-02 |

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| cds.Camellia_sinensis.comp24387_c0_seq2_m.41361 | PREDICTED: apolipoprotein D [Populus euphratica] | 21.366 | 133.38 | 56.5 | 12 | 51 | 10 | 0.942 | 0.896 | 0.908 | 1.084 | 1.102 | 1.097 | 1.196 | 3.42E-04 |
| cds.Camellia_sinensis.comp24391_c0_seq1_m.25946 | PREDICTED: aminoacylase-1-like [Juglans regia] | 53.18 | 14.995 | 18.9 | 9 | 9 | 9 | 1.055 | 1.074 | 1.042 | 0.91 | 0.956 | 0.933 | 0.883 | 1.72E-03 |
| cds.Camellia_sinensis.comp24396_c0_seq1_m.28042 | PREDICTED: probable methyltransferase PMT2 [Fragaria vesca subsp. vesca] | 40.978 | 1.4661 | 5 | 2 | 2 | 2 | 1.294 | 1.166 | 1.112 | 0.787 | 0.737 | 0.835 | 0.66 | 1.96E-03 |
| cds.Camellia_sinensis.comp24397_c0_seq1_m.33080 | PREDICTED: LOW QUALITY PROTEIN: basic endochitinase [Vitis vinifera] | 36.672 | 21.069 | 4.1 | 1 | 1 | 1 | 0.826 | 0.854 | 0.872 | 1.105 | 1.272 | 1.132 | 1.375 | 2.38E-03 |
| cds.Camellia_sinensis.comp24400_c0_seq1_m.35973 | PREDICTED: ER membrane protein complex subunit 7 homolog [Theobroma cacao] | 23.115 | 4.7878 | 11.4 | 2 | 3 | 2 | 0.95 | 1.073 | 0.976 | 1.104 | 0.94 | 0.976 | 1.007 | 9.27E-01 |

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| cds.Camellia_sinensis.comp24411_c0_seq11_m.4822 | PREDICTED: ER membrane protein complex subunit 1 isoform X2 [Theobroma cacao] | 57.181 | 39.598 | 16 | 7 | 11 | 7 | 0.954 | 0.965 | 0.93 | 1.092 | 1.042 | 1.046 | 1.116 | 4.10E-03 |
| cds.Camellia_sinensis.comp24411_c0_seq1_m.4823 | PREDICTED: ER membrane protein complex subunit 1 [Jatropha curcas] | 54.821 | 30.399 | 18.2 | 7 | 12 | 7 | 0.942 | 0.953 | 1.009 | 1.041 | 1.052 | 1.017 | 1.071 | 4.26E-02 |
| cds.Camellia_sinensis.comp24412_c0_seq2_m.45149 | histone H2A variant 1 [Ananas comosus] | 18.569 | 10.066 | 20.5 | 4 | 8 | 3 | 1.096 | 1.131 | 1.175 | 0.896 | 0.838 | 0.84 | 0.757 | 7.21E-04 |
| cds.Camellia_sinensis.comp24413_c0_seq3_m.43397 | PREDICTED: putative phosphatidylglycerol/phosphatidylinositol transfer protein DDB_G0282179 [Vitis vinifera] | 21.198 | 28.096 | 25.3 | 5 | 14 | 5 | 1.01 | 0.987 | 1.018 | 1.001 | 0.985 | 1.007 | 0.993 | 5.57E-01 |

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| cds.Camellia_sinensis.comp24422_c1_seq1_m.11497 | PREDICTED: protein SUPPRESSOR OF GENE SILENCING 3 [Vitis vinifera] | 73.283 | 35.512 | 14.4 | 9 | 10 | 9 | 1.125 | 1.127 | 1.177 | 0.849 | 0.871 | 0.817 | 0.74 | 2.21E-04 |
| cds.Camellia_sinensis.comp24434_c0_seq1_m.27593 | Leucine-rich repeat (LRR) family protein [Arabidopsis thaliana] | 49.839 | 5.4427 | 10.3 | 4 | 5 | 4 | | | | | | | | |
| cds.Camellia_sinensis.comp24440_c0_seq1_m.28957 | PREDICTED: ATP synthase gamma chain, chloroplastic [Nelumbo nucifera] | 41.352 | 259.9 | 41.3 | 17 | 65 | 15 | 1.016 | 0.977 | 0.966 | 1.028 | 1.017 | 1.019 | 1.035 | 8.83E-02 |
| cds.Camellia_sinensis.comp24446_c0_seq1_m.37788 | PREDICTED: 30S ribosomal protein S9, chloroplastic-like [Nelumbo nucifera] | 22.414 | 6.9776 | 14.5 | 3 | 4 | 3 | 1.162 | 1.171 | 1.17 | 0.787 | 0.83 | 0.798 | 0.689 | 1.88E-03 |

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| cds.Camellia_sinensis.comp24452_c0_seq2_m.45813 | PREDICTED: histone-lysine N-methyltransferase setd3 [Nelumbo nucifera] | 26.399 | 1.3065 | 5.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24460_c0_seq1_m.6305 | PREDICTED: isoamylase 2, chloroplastic [Juglans regia] | 96.791 | 8.0471 | 5.9 | 5 | 5 | 5 | 1.01 | 1.016 | 1.025 | 0.949 | 0.989 | 0.969 | 0.953 | 1.87E-02 |
| cds.Camellia_sinensis.comp24465_c0_seq1_m.43939 | PREDICTED: histone deacetylase complex subunit SAP18 [Sesamum indicum] | 18.517 | 6.1553 | 15.2 | 3 | 7 | 3 | 1.005 | 1 | 0.966 | 1 | 1.042 | 1.01 | 1.027 | 2.00E-01 |
| cds.Camellia_sinensis.comp24471_c0_seq1_m.35807 | PREDICTED: REF/SRPP-like protein At1g67360 [Nicotiana | 28.646 | 37.627 | 28.5 | 6 | 10 | 6 | 0.915 | 0.878 | 0.892 | 1.106 | 1.092 | 1.106 | 1.231 | 8.17E-05 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp24482_c0_seq1_m.56983 | PREDICTED: guanylate-binding protein 7 isoform X2 [Ziziphus jujuba] | 13.418 | 1.8617 | 19.3 | 3 | 3 | 1 | 0.955 | 1.088 | 1.011 | 1.011 | 0.91 | 1.034 | 0.968 | 5.77E-01 |
| cds.Camellia_sinensis.comp24497_c0_seq1_m.37976 | PREDICTED: 50S ribosomal protein L9, chloroplastic [Daucus carota subsp. sativus] | 23.954 | 10.995 | 24.6 | 6 | 8 | 6 | 1.073 | 1.061 | 1.102 | 0.881 | 0.884 | 0.94 | 0.836 | 1.68E-03 |
| cds.Camellia_sinensis.comp24498_c0_seq3_m.31193 | PREDICTED: phosphoserine phosphatase, chloroplastic [Vitis vinifera] | 32.001 | 66.03 | 32.9 | 8 | 15 | 8 | 1.004 | 1.077 | 1.107 | 0.942 | 0.942 | 0.952 | 0.89 | 5.81E-02 |
| cds.Camellia_sinensis.comp24515_c0_seq2_m.18878 | PREDICTED: scarecrow-like protein 21 [Juglans regia] | 59.071 | 1.6917 | 1.7 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp24526_c0_seq2_m.10718 | DUF639 family protein [Medicago truncatula] | 61.831 | -2 | 1.3 | 1 | 1 | 1 | 1.092 | 0.849 | 1.006 | 0.931 | 1.088 | 1.035 | 1.036 | 6.78E-01 |

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| cds.Camellia_sinensis.comp24527_c0_seq1_m.54512 | palmitoyl-protein thioesterase 1-like [Cajanus cajan] | 15.457 | 17.119 | 33.8 | 3 | 5 | 3 | 1.068 | 1.056 | 1.053 | 0.917 | 0.995 | 0.947 | 0.9 | 1.18E-02 |
| cds.Camellia_sinensis.comp24528_c0_seq1_m.3142 | NADH-plastoquinone oxidoreductase subunit K (chloroplast) [Camellia pubicosta] | 32.237 | 48.051 | 12.4 | 3 | 5 | 3 | 0.919 | 0.963 | 0.97 | 1.026 | 0.988 | 1.059 | 1.077 | 4.69E-02 |
| cds.Camellia_sinensis.comp24528_c0_seq1_m.3143 | NADH-plastoquinone oxidoreductase subunit J (chloroplast) [Camellia crapnelliana] | 18.603 | 14.93 | 22.2 | 3 | 6 | 3 | 0.945 | 0.991 | 0.969 | 0.994 | 1.062 | 1.068 | 1.075 | 5.43E-02 |
| cds.Camellia_sinensis.comp24531_c1_seq1_m.29838 | PREDICTED: activator of 90 kDa heat shock protein ATPase homolog [Juglans regia] | 39.988 | 69.611 | 24.1 | 8 | 14 | 8 | 1.033 | 1.023 | 1.024 | 0.93 | 0.987 | 0.985 | 0.942 | 9.36E-02 |

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| cds.Camellia_sinensis.comp24543_c0_seq1_m.41193 | PREDICTED: putative phosphatidylglycerol/phosphatidylinositol transfer protein DDB_G0282179 [Jatropha curcas] | 21.35 | 14.003 | 13.8 | 2 | 4 | 2 | 1.161 | 1 | 0.962 | 0.887 | 0.983 | 0.985 | 0.914 | 2.61E-01 |
| cds.Camellia_sinensis.comp24545_c0_seq1_m.37377 | PREDICTED: multiple organellar RNA editing factor 8, chloroplastic/mitochondrial-like [Nicotiana tabacum] | 35.289 | 75.116 | 14 | 4 | 9 | 4 | 0.968 | 1.006 | 0.986 | 0.985 | 1.045 | 1.027 | 1.033 | 1.98E-01 |
| cds.Camellia_sinensis.comp24556_c0_seq1_m.40240 | PREDICTED: CDGSH iron-sulfur domain-containing protein NEET [Nelumbo nucifera] | 12.864 | 65.622 | 46.1 | 5 | 9 | 5 | 1.002 | 0.964 | 0.983 | 1.037 | 1.071 | 0.997 | 1.053 | 9.49E-02 |

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| cds.Camellia_sinensis.comp24560_c0_seq1_m.30511 | PREDICTED: high mobility group B protein 1-like [Nelumbo nucifera] | 19.386 | 3.8063 | 13.2 | 3 | 5 | 3 | 0.995 | 0.99 | 0.988 | 0.996 | 0.98 | 1.029 | 1.011 | 5.44E-01 |
| cds.Camellia_sinensis.comp24563_c0_seq1_m.34737 | PREDICTED: proteasome subunit alpha type-1-B [Sesamum indicum] | 30.23 | 110.66 | 48.7 | 13 | 29 | 13 | 0.983 | 0.972 | 0.967 | 1.024 | 1.031 | 1.04 | 1.059 | 9.58E-04 |
| cds.Camellia_sinensis.comp24569_c0_seq1_m.41022 | Ran-binding protein 1-b-like protein [Morus notabilis] | 25.916 | 22.214 | 20.2 | 5 | 9 | 3 | 1.098 | 1.084 | 1.033 | 0.898 | 0.921 | 0.905 | 0.847 | 1.18E-03 |
| cds.Camellia_sinensis.comp24569_c0_seq2_m.50549 | Ran-binding protein 1-b-like protein [Morus notabilis] | 20.64 | -2 | 28.3 | 4 | 6 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24570_c0_seq1_m.46922 | PREDICTED: S-adenosylmethionine synthase 5 [Prunus mume] | 15.734 | -2 | 31.2 | 4 | 11 | 1 | 1.165 | 1.143 | 1.073 | 0.821 | 0.9 | 0.858 | 0.763 | 1.74E-03 |

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| cds.Camellia_sinensis.comp24575_c0_seq1_m.42598 | PREDICTED: stress enhanced protein 2, chloroplastic [Vitis vinifera] | 20.571 | 5.1062 | 6.9 | 1 | 2 | 1 | 1.031 | 1.032 | 1.05 | 0.969 | 0.924 | 0.992 | 0.927 | 2.44E-02 |
| cds.Camellia_sinensis.comp24576_c0_seq1_m.41411 | PREDICTED: aquaporin TIP2-1 [Theobroma cacao] | 27.788 | 13.581 | 4.1 | 1 | 5 | 1 | 0.984 | 0.957 | 1.038 | 1.018 | 1.008 | 0.966 | 1.004 | 8.79E-01 |
| cds.Camellia_sinensis.comp24592_c0_seq1_m.28083 | PREDICTED: fructose-bisphosphate aldolase-lysine N-methyltransferase, chloroplastic [Gossypium raimondii] | 35.355 | 82.904 | 29.7 | 7 | 14 | 7 | 0.999 | 0.994 | 0.91 | 1.051 | 1.011 | 1.05 | 1.072 | 9.95E-02 |
| cds.Camellia_sinensis.comp24611_c0_seq1_m.24117 | PREDICTED: probable purple acid phosphatase 20 [Nicotiana tomentosiformis] | 47.727 | 6.0496 | 4.7 | 2 | 2 | 2 | 0.858 | 0.818 | 0.778 | 1.242 | 1.167 | 1.204 | 1.472 | 3.20E-04 |

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| cds.Camellia_sinensis.comp24615_c0_seq1_m.20658 | PREDICTED: pentatricopeptide repeat-containing protein At1g08070, chloroplastic [Ricinus communis] | 51.183 | -2 | 3.1 | 1 | 1 | 1 | 0.818 | 0.982 | 1.062 | 1.109 | 1.148 | 0.93 | 1.114 | 3.41E-01 |
| cds.Camellia_sinensis.comp24618_c0_seq1_m.22659 | PREDICTED: acyl-coenzyme A thioesterase 9, mitochondrial [Ricinus communis] | 58.206 | 5.288 | 3.9 | 3 | 3 | 3 | 1.101 | 1.114 | 1.069 | 0.928 | 0.867 | 0.899 | 0.82 | 1.02E-03 |
| cds.Camellia_sinensis.comp24620_c0_seq1_m.39124 | PREDICTED: ELAV-like protein 4 [Capsicum annuum] | 16.488 | 8.0107 | 17.4 | 3 | 4 | 3 | 0.93 | 0.946 | 0.981 | 1.036 | 1.058 | 1.056 | 1.103 | 4.64E-03 |
| cds.Camellia_sinensis.comp24637_c0_seq1_m.8160 | PREDICTED: subtilisin-like protease SBT1.7 [Theobroma cacao] | 81.53 | 12.217 | 1.9 | 1 | 4 | 1 | 0.975 | 1.027 | 1.047 | 0.964 | 1.026 | 0.967 | 0.97 | 3.57E-01 |

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| cds.Camellia_sinensis.comp24647_c0_seq1_m.25981 | PREDICTED: pentatricopeptide repeat-containing protein At3g13160, mitochondrial-like [Vitis vinifera] | 44.264 | 8.8348 | 15.5 | 7 | 8 | 7 | 0.971 | 0.975 | 0.985 | 0.982 | 1 | 1.016 | 1.023 | 1.03E-01 |
| cds.Camellia_sinensis.comp24652_c0_seq1_m.29323 | PREDICTED: COP9 signalosome complex subunit 5b [Vitis | 45.285 | 7.5576 | 4.7 | 2 | 2 | 2 | 0.986 | 0.955 | 0.974 | 1.097 | 1.001 | 1.008 | 1.066 | 1.12E-01 |
| cds.Camellia_sinensis.comp24653_c0_seq2_m.31027 | PREDICTED: 2-alkenal reductase (NADP(+)-dependent) [Vitis vinifera] | 37.835 | 71.031 | 33.7 | 11 | 31 | 11 | 0.927 | 0.907 | 0.89 | 1.103 | 1.096 | 1.111 | 1.215 | 9.79E-05 |
| cds.Camellia_sinensis.comp24656_c0_seq1_m.43752 | PREDICTED: acyl-coenzyme A thioesterase 9, mitochondrial-like [Nelumbo nucifera] | 22.055 | 3.1935 | 15.3 | 2 | 2 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp24675_c0_seq1_m.31705 | PREDICTED: malate dehydrogenase, glyoxysomal [Vitis vinifera] | 38.02 | 120.06 | 36.8 | 11 | 36 | 6 | 1.007 | 1.015 | 1.017 | 1.008 | 0.979 | 1.01 | 0.986 | 2.54E-01 |
| cds.Camellia_sinensis.comp24686_c0_seq1_m.24876 | PREDICTED: developmentally-regulated G-protein 3 [Arachis ipaensis] | 41.255 | 4.0422 | 6 | 2 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp24691_c0_seq1_m.35394 | PREDICTED: peptide deformylase 1A, chloroplastic [Nelumbo nucifera] | 31.64 | 20.343 | 21.1 | 6 | 10 | 6 | 0.999 | 1.034 | 1.01 | 0.99 | 0.997 | 1.004 | 0.983 | 1.92E-01 |
| cds.Camellia_sinensis.comp24697_c0_seq1_m.34694 | PREDICTED: ABC transporter I family member 17 [Citrus sinensis] | 31.094 | 15.69 | 25 | 6 | 7 | 6 | 1.011 | 1.059 | 1.068 | 0.907 | 0.946 | 0.954 | 0.895 | 8.54E-03 |

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| cds.Camellia_sinensis.comp24698_c0_seq1_m.27987 | PREDICTED: protein THYLAKOID FORMATION1, chloroplastic [Theobroma cacao] | 33.604 | 36.759 | 24.9 | 9 | 19 | 7 | 1.002 | 0.999 | 1.021 | 0.97 | 1.01 | 1.004 | 0.987 | 4.23E-01 |
| cds.Camellia_sinensis.comp24698_c0_seq2_m.30932 | PREDICTED: protein THYLAKOID FORMATION1, chloroplastic [Theobroma cacao] | 33.385 | 33.489 | 15.8 | 4 | 6 | 2 | 0.979 | 0.984 | 0.976 | 1.01 | 1.064 | 0.919 | 1.018 | 7.39E-01 |
| cds.Camellia_sinensis.comp24699_c0_seq1_m.33754 | | 44.555 | 3.2901 | 3.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24702_c0_seq1_m.41887 | PREDICTED: flavonoid 3'-monooxygenase-like [Sesamum indicum] | 32.159 | 10.81 | 11.5 | 4 | 5 | 3 | 1.072 | 1.069 | 1.069 | 0.934 | 0.856 | 0.983 | 0.864 | 6.71E-02 |

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| cds.Camellia_sinensis.comp24714_c0_seq1_m.50851 | PREDICTED: superoxide dismutase [Cu-Zn], chloroplastic [Ziziphus jujuba] | 16.015 | 46.255 | 24.2 | 3 | 7 | 2 | 0.914 | 0.901 | 0.887 | 1.087 | 1.112 | 1.129 | 1.232 | 1.20E-04 |
| cds.Camellia_sinensis.comp24729_c0_seq1_m.48307 | PREDICTED: 50S ribosomal protein L31, chloroplastic [Vitis vinifera] | 15.72 | 8.7437 | 8.6 | 1 | 2 | 1 | 1.267 | 1.176 | 1.112 | 0.759 | 0.825 | 0.797 | 0.67 | 8.78E-04 |
| cds.Camellia_sinensis.comp24732_c0_seq1_m.20638 | PREDICTED: ankyrin-1 [Theobroma cacao] | 49.125 | 25.226 | 8.3 | 3 | 4 | 3 | 0.97 | 1.004 | 0.992 | 1.072 | 0.989 | 0.991 | 1.029 | 3.80E-01 |
| cds.Camellia_sinensis.comp24762_c0_seq1_m.20309 | PREDICTED: pentatricopeptide repeat-containing protein At1g60770 isoform X1 [Vitis vinifera] | 56.417 | 1.8303 | 1.8 | 1 | 1 | 1 | 1.029 | 1.195 | 1.103 | 0.876 | 0.898 | 0.878 | 0.797 | 6.88E-03 |

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| cds.Camellia_sinensis.comp24764_c0_seq1_m.35070 | PREDICTED: 2-hydroxyisoflavanone dehydratase-like [Juglans regia] | 36.259 | 45.113 | 23.2 | 8 | 15 | 8 | 1.104 | 1.077 | 1.072 | 0.899 | 0.892 | 0.891 | 0.824 | 3.77E-05 |
| cds.Camellia_sinensis.comp24776_c0_seq1_m.41694 | PREDICTED: V-type proton ATPase subunit E-like [Nelumbo | 26.154 | -2 | 18.3 | 4 | 6 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24793_c0_seq2_m.35781 | PREDICTED: thiosulfate sulfurtransferase 18 isoform X2 [Solanum tuberosum | 18.216 | 1.5694 | 6.1 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24796_c0_seq1_m.33620 | PREDICTED: malignant T-cell-amplified sequence 1 homolog [Vitis vinifera] | 20.114 | 38.701 | 23.2 | 4 | 4 | 4 | 1.005 | 1.05 | 0.931 | 1.013 | 1.001 | 1.007 | 1.012 | 7.50E-01 |

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| cds.Camellia_sinensis.comp24798_c0_seq3_m.39242 | PREDICTED: protein OSB2, chloroplastic-like [Nicotiana tomentosiformis] | 29.829 | 11.605 | 8.8 | 2 | 2 | 2 | 0.956 | 0.995 | 1.02 | 1.01 | 0.947 | 1.085 | 1.024 | 6.34E-01 |
| cds.Camellia_sinensis.comp24800_c0_seq1_m.24723 | PREDICTED: cysteine desulfurase 1, chloroplastic [Juglans regia] | 38.377 | 12.252 | 7.2 | 2 | 3 | 2 | 0.99 | 1.026 | 1.057 | 1.076 | 0.985 | 0.88 | 0.957 | 4.86E-01 |
| cds.Camellia_sinensis.comp24800_c0_seq1_m.24724 | PREDICTED: cysteine desulfurase 1, chloroplastic [Juglans regia] | 13.55 | 30.472 | 28.5 | 4 | 5 | 4 | 1.005 | 1.04 | 1.021 | 0.961 | 0.979 | 0.991 | 0.956 | 2.79E-02 |
| cds.Camellia_sinensis.comp24811_c0_seq1_m.33849 | PREDICTED: polyadenylate-binding protein 2-like isoform X1 [Juglans | 25.195 | 2.9257 | 8.6 | 2 | 5 | 1 | 0.999 | 0.979 | 1.003 | 1.031 | 1.016 | 0.978 | 1.015 | 4.53E-01 |

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| cds.Camellia_sinensis.comp24815_c0_seq1_m.38451 | PREDICTED: sm-like protein LSM1B [Ziziphus jujuba] | 14.502 | 1.6751 | 12.5 | 1 | 1 | 1 | 0.876 | 1.278 | 1.054 | 1.151 | 0.925 | 0.738 | 0.877 | 4.66E-01 |
| cds.Camellia_sinensis.comp24818_c0_seq1_m.28200 | PREDICTED: phenylalanine ammonia-lyase 1 [Daucus carota subsp. sativus] | 45.753 | 19.992 | 40.3 | 16 | 32 | 7 | 1.376 | 1.315 | 1.268 | 0.616 | 0.661 | 0.625 | 0.48 | 2.07E-05 |
| cds.Camellia_sinensis.comp24820_c0_seq1_m.37845 | PREDICTED: expansin-like A2 [Ricinus communis] | 16.401 | 18.858 | 37.2 | 6 | 13 | 6 | 0.795 | 0.877 | 0.785 | 1.213 | 1.189 | 1.19 | 1.462 | 4.37E-04 |
| cds.Camellia_sinensis.comp24823_c0_seq2_m.39697 | PREDICTED: surfeit locus protein 1 isoform X1 [Theobroma cacao] | 27.913 | 5.6172 | 8.4 | 1 | 1 | 1 | 0.94 | 1.094 | 1.075 | 1.003 | 0.946 | 0.952 | 0.933 | 2.60E-01 |
| cds.Camellia_sinensis.comp24827_c1_seq1_m.11253 | PREDICTED: outer envelope protein 80, chloroplastic-like [Gossypium hirsutum] | 74.32 | 60.844 | 20.8 | 15 | 21 | 15 | 0.977 | 0.983 | 0.986 | 1.035 | 1.049 | 1.022 | 1.054 | 2.72E-03 |

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| cds.Camellia_sinensis.comp24834_c0_seq1_m.22223 | PREDICTED: 30S ribosomal protein S1, chloroplastic [Nelumbo nucifera] | 44.723 | 86.905 | 30.7 | 12 | 36 | 12 | 1.022 | 1.003 | 1.026 | 0.974 | 0.979 | 0.981 | 0.962 | 5.92E-03 |
| cds.Camellia_sinensis.comp24836_c0_seq1_m.42562 | PREDICTED: protein translation factor SUI1 homolog [Nelumbo nucifera] | 11.503 | 2.1725 | 8.8 | 1 | 1 | 1 | 1.004 | 0.985 | 0.998 | 0.965 | 1.068 | 0.989 | 1.012 | 7.47E-01 |
| cds.Camellia_sinensis.comp24839_c0_seq2_m.23278 | PREDICTED: thiol-disulfide oxidoreductase LTO1-like [Juglans regia] | 36.864 | 2.5888 | 3.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24851_c0_seq1_m.28271 | PREDICTED: 40S ribosomal protein S18 [Erythranthe guttata] | 17.698 | 121.85 | 50 | 7 | 15 | 7 | 1.128 | 1.127 | 1.147 | 0.82 | 0.861 | 0.833 | 0.739 | 4.01E-05 |
| cds.Camellia_sinensis.comp24864_c0_seq1_m.40533 | | 19.3 | 7.8641 | 11 | 2 | 4 | 2 | 1.148 | 1.107 | 1.083 | 0.881 | 0.869 | 0.88 | 0.788 | 1.76E-04 |

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| cds.Camellia_sinensis.comp24869_c0_seq1_m.29354 | PREDICTED: pyridoxal reductase, chloroplastic isoform X2 [Vitis vinifera] | 42.971 | 56.826 | 13.5 | 4 | 8 | 4 | 0.934 | 0.961 | 1.011 | 1.024 | 1.048 | 1.041 | 1.071 | 4.56E-02 |
| cds.Camellia_sinensis.comp24875_c0_seq1_m.21153 | PREDICTED: 60S ribosomal protein L4 [Ziziphus jujuba] | 44.76 | 78.066 | 38 | 13 | 22 | 8 | 1.125 | 1.15 | 1.145 | 0.848 | 0.853 | 0.857 | 0.748 | 1.25E-06 |
| cds.Camellia_sinensis.comp24877_c0_seq2_m.56801 | PREDICTED: probable carboxylesterase 2 [Vitis vinifera] | 12.678 | 4.7303 | 25.8 | 3 | 5 | 2 | 0.929 | 0.932 | 0.946 | 1.031 | 1.147 | 1.047 | 1.149 | 1.51E-02 |
| cds.Camellia_sinensis.comp24881_c0_seq1_m.50454 | PREDICTED: aquaporin PIP1-3 [Theobroma cacao] | 15.394 | 5.476 | 19.9 | 2 | 2 | 2 | 0.943 | 0.949 | 0.904 | 1.123 | 1.049 | 1.066 | 1.158 | 4.62E-03 |
| cds.Camellia_sinensis.comp24882_c0_seq1_m.23939 | PREDICTED: aspartic proteinase nepenthesin-1 [Sesamum indicum] | 46.761 | 37.286 | 11.7 | 4 | 8 | 4 | 0.984 | 0.92 | 0.979 | 1.092 | 1.065 | 1.054 | 1.114 | 1.08E-02 |

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| cds.Camellia_sinensis.comp24886_c1_seq1_m.31333 | PREDICTED: protein PAT1 homolog 1 [Vitis vinifera] | 47.621 | 2.0401 | 4.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24889_c0_seq2_m.48066 | PREDICTED: putative uridine kinase C227.14 isoform X2 [Theobroma cacao] | 18.111 | 1.2708 | 8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp24904_c0_seq1_m.37443 | PREDICTED: histone H1.1-like [Tarenaya hassleriana] | 25.451 | 2.4282 | 4.1 | 1 | 3 | 1 | 1.067 | 1.012 | 0.968 | 0.936 | 1.041 | 0.972 | 0.968 | 4.77E-01 |
| cds.Camellia_sinensis.comp24910_c0_seq1_m.13294 | PREDICTED: endo-1,3;1,4-beta-D-glucanase [Vitis vinifera] | 28.153 | 86.932 | 35.6 | 10 | 32 | 10 | 1.005 | 0.988 | 0.989 | 0.977 | 0.997 | 1.005 | 0.999 | 9.22E-01 |
| cds.Camellia_sinensis.comp24910_c0_seq1_m.13295 | PREDICTED: probable chalcone--flavonone isomerase 3 [Prunus mume] | 23.229 | 80.777 | 23.4 | 5 | 10 | 5 | 1.326 | 1.256 | 1.273 | 0.771 | 0.733 | 0.635 | 0.555 | 6.03E-04 |

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| cds.Camellia_sinensis.comp24911_c0_seq1_m.38588 | PREDICTED: 40S ribosomal protein S11-like [Daucus carota subsp. sativus] | 17.858 | 12.377 | 35.2 | 7 | 8 | 7 | 1.2 | 1.215 | 1.197 | 0.766 | 0.767 | 0.774 | 0.639 | 7.59E-08 |
| cds.Camellia_sinensis.comp24917_c0_seq1_m.41745 | PREDICTED: ATP synthase subunit b', chloroplastic [Theobroma cacao] | 24.011 | 64.13 | 36.2 | 8 | 42 | 8 | 1.003 | 0.995 | 0.976 | 1.006 | 1.005 | 1.046 | 1.028 | 1.51E-01 |
| cds.Camellia_sinensis.comp24926_c0_seq1_m.49132 | Translation machinery associated TMA7 [Arabidopsis thaliana] | 11.151 | 2.0296 | 11.8 | 1 | 2 | 1 | 0.988 | 1.052 | 1.043 | 0.986 | 1.04 | 0.899 | 0.949 | 3.13E-01 |
| cds.Camellia_sinensis.comp24932_c0_seq1_m.38826 | PREDICTED: 17.3 kDa class II heat shock protein-like [Nicotiana attenuata] | 18.083 | 62.033 | 48.8 | 5 | 15 | 5 | 1.028 | 1.046 | 0.97 | 0.96 | 1.016 | 0.983 | 0.972 | 3.75E-01 |

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| cds.Camellia_sinensis.comp24934_c0_seq1_m.49073 | photosystem II 5 kDa protein, chloroplastic-like [Cajanus cajan] | 11.748 | 15.377 | 11.5 | 1 | 9 | 1 | 0.985 | 1.05 | 0.961 | 0.989 | 1.035 | 0.987 | 1.005 | 8.67E-01 |
| cds.Camellia_sinensis.comp24944_c0_seq1_m.7395 | PREDICTED: heat shock 70 kDa protein 16 [Nicotiana tomentosiformis] | 85.424 | 3.8599 | 6 | 6 | 9 | 4 | 0.973 | 0.953 | 0.982 | 1.068 | 1.018 | 0.989 | 1.057 | 8.30E-02 |
| cds.Camellia_sinensis.comp24950_c0_seq1_m.34056 | PREDICTED: chlorophyll a-b binding protein 4, chloroplastic [Vitis vinifera] | 28.417 | 38.296 | 25 | 5 | 17 | 5 | 0.892 | 0.848 | 0.915 | 1.095 | 1.127 | 1.18 | 1.281 | 1.36E-03 |
| cds.Camellia_sinensis.comp24956_c0_seq1_m.23294 | PREDICTED: peroxidase 42 [Eucalyptus grandis] | 37.589 | 27.808 | 24 | 6 | 6 | 6 | 1.202 | 1.251 | 1.235 | 0.749 | 0.773 | 0.725 | 0.609 | 2.14E-05 |

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| cds.Camellia_sinensis.comp24958_c0_seq1_m.31985 | PREDICTED: ribulose bisphosphate carboxylase small chain, chloroplastic isoform X1 [Juglans regia] | 20.359 | 132.75 | 61.5 | 14 | 95 | 10 | 1.042 | 1.151 | 1.169 | 0.88 | 0.876 | 0.857 | 0.777 | 2.46E-03 |
| cds.Camellia_sinensis.comp24983_c0_seq1_m.16904 | BTB/POZ domain-containing protein [Morus notabilis] | 63.368 | 6.9201 | 5.5 | 3 | 3 | 2 | 0.772 | 0.994 | 1.05 | 1.161 | 1.159 | 0.923 | 1.152 | 3.01E-01 |
| cds.Camellia_sinensis.comp24992_c0_seq1_m.29544 | PREDICTED: probable aquaporin PIP-type 7a [Gossypium raimondii] | 31.672 | 3.8657 | 8.8 | 3 | 3 | 3 | 1.019 | 0.969 | 1.049 | 0.996 | 1.026 | 0.97 | 0.985 | 6.32E-01 |
| cds.Camellia_sinensis.comp25004_c0_seq2_m.48898 | PREDICTED: histone H4-like [Zea mays] | 11.409 | 80.118 | 58.3 | 7 | 40 | 7 | 1.105 | 1.078 | 1.089 | 0.875 | 0.898 | 0.858 | 0.804 | 1.35E-04 |
| cds.Camellia_sinensis.comp25017_c0_seq1_m.47244 | PREDICTED: 40S ribosomal protein S27-2-like [Nelumbo nucifera] | 14.794 | 5.6452 | 15.9 | 2 | 6 | 2 | 0.991 | 0.951 | 1.024 | 0.997 | 1.017 | 0.988 | 1.012 | 6.18E-01 |

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| cds.Camellia_sinensis.comp25019_c0_seq1_m.18730 | PREDICTED: beta-glucosidase 12 [Vitis vinifera] | 57.105 | 33.283 | 17.6 | 10 | 17 | 9 | 1.054 | 0.987 | 0.993 | 0.957 | 1.019 | 0.964 | 0.969 | 3.37E-01 |
| cds.Camellia_sinensis.comp25031_c0_seq2_m.30005 | selenocysteine methyltransferase family protein [Populus trichocarpa] | 37.444 | 4.5281 | 10.2 | 4 | 4 | 4 | 0.958 | 0.951 | 0.993 | 1.027 | 1.06 | 1.033 | 1.075 | 1.18E-02 |
| cds.Camellia_sinensis.comp25034_c0_seq2_m.32478 | PREDICTED: L-ascorbate peroxidase 1, cytosolic isoform X2 [Phoenix dactylifera] | 27.549 | 64.454 | 41.6 | 9 | 46 | 9 | 1.003 | 1.001 | 1.026 | 0.982 | 1.005 | 1.002 | 0.986 | 2.74E-01 |
| cds.Camellia_sinensis.comp25035_c0_seq1_m.34370 | PREDICTED: photosystem II 22 kDa protein, chloroplastic [Vitis vinifera] | 28.292 | 96.184 | 29.2 | 7 | 25 | 5 | 1.031 | 1.045 | 1.029 | 0.963 | 0.976 | 0.962 | 0.934 | 5.39E-04 |

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| cds.Camellia_sinensis.comp25036_c0_seq1_m.20734 | PREDICTED: S-adenosylmethionine synthase 2 [Eucalyptus grandis] | 43.081 | 157.68 | 42.7 | 15 | 44 | 7 | 1.149 | 1.106 | 1.14 | 0.849 | 0.875 | 0.863 | 0.762 | 4.41E-05 |
| cds.Camellia_sinensis.comp25037_c0_seq1_m.30194 | PREDICTED: flavonol synthase/flavanone 3-hydroxylase-like [Prunus mume] | 37.581 | 105.57 | 29.6 | 10 | 30 | 10 | 1.37 | 1.357 | 1.379 | 0.599 | 0.605 | 0.604 | 0.44 | 6.50E-09 |
| cds.Camellia_sinensis.comp25050_c0_seq1_m.47802 | PREDICTED: histone H2A.1-like [Prunus mume] | 19.906 | 2.7071 | 13.4 | 4 | 8 | 2 | 1.226 | 1.072 | 1.062 | 0.776 | 0.808 | 1.004 | 0.77 | 4.54E-02 |
| cds.Camellia_sinensis.comp25052_c0_seq1_m.4227 | PREDICTED: 1,4-alpha-glucan-branching enzyme 3, chloroplastic/amyloplastic isoform X2 [Ziziphus jujuba] | 88.202 | 2.5393 | 1.8 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp25080_c0_seq1_m.33148 | PREDICTED: signal peptidase complex catalytic subunit SEC11A-like [Glycine max] | 22.599 | 6.3722 | 5.4 | 1 | 1 | 1 | 0.948 | 0.986 | 1.004 | 1.077 | 0.993 | 1.014 | 1.05 | 1.80E-01 |
| cds.Camellia_sinensis.comp25087_c0_seq1_m.41266 | PREDICTED: 60S ribosomal protein L22-2-like [Ziziphus jujuba] | 13.995 | 24.424 | 25.8 | 3 | 4 | 3 | 1.024 | 1.122 | 1.104 | 0.916 | 0.871 | 0.879 | 0.82 | 3.56E-03 |
| cds.Camellia_sinensis.comp25092_c0_seq2_m.43164 | PREDICTED: 60S ribosomal protein L36-2 [Eucalyptus grandis] | 12.443 | 2.8655 | 9.1 | 1 | 2 | 1 | 1.009 | 1.037 | 1.068 | 0.909 | 0.962 | 1.011 | 0.925 | 8.84E-02 |
| cds.Camellia_sinensis.comp25104_c0_seq1_m.37456 | tubulin alpha-6 chain, putative [Medicago truncatula] | 24.424 | 4.2641 | 8.8 | 2 | 2 | 2 | 1.055 | 1.028 | 0.979 | 0.919 | 0.961 | 1.052 | 0.958 | 3.83E-01 |

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| cds.Camellia_sinensis.comp25121_c0_seq2_m.47958 | PREDICTED: cell division topological specificity factor homolog, chloroplastic-like [Sesamum indicum] | 18.014 | 13.464 | 16.9 | 2 | 3 | 2 | 0.982 | 1.013 | 1.031 | 0.955 | 0.992 | 1.034 | 0.985 | 6.01E-01 |
| cds.Camellia_sinensis.comp25125_c0_seq15_c0_seq1_m.14406 | PREDICTED: lycopene beta cyclase, chloroplastic [Vitis vinifera] | 56.64 | 4.5273 | 4.2 | 2 | 3 | 2 | 1.164 | 1.126 | 1.032 | 0.902 | 0.859 | 0.884 | 0.796 | 4.18E-03 |
| cds.Camellia_sinensis.comp25139_c0_seq1_m.10006 | PREDICTED: protein transport protein SEC23 [Citrus sinensis] | 36.04 | 5.3776 | 10.8 | 2 | 3 | 1 | 0.9 | 1.183 | 0.954 | 0.93 | 1.018 | 1.026 | 0.979 | 8.75E-01 |
| cds.Camellia_sinensis.comp25156_c0_seq1_m.24729 | transmembrane protein, putative [Medicago truncatula] | 32.997 | 3.4805 | 7.1 | 2 | 2 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp25164_c0_seq1_m.15760 | PREDICTED: beta-hexosaminidase 1 isoform X2 [Ziziphus jujuba] | 25.448 | 14.385 | 24.4 | 5 | 7 | 4 | 1.035 | 1.045 | 1.006 | 0.996 | 0.979 | 0.946 | 0.947 | 4.40E-02 |
| cds.Camellia_sinensis.comp25164_c0_seq2_m.15762 | PREDICTED: beta-hexosaminidase 1 [Vitis vinifera] | 36.014 | 28.244 | 17.4 | 5 | 10 | 5 | 1.039 | 1.006 | 1.053 | 0.932 | 0.954 | 0.965 | 0.92 | 8.12E-03 |
| cds.Camellia_sinensis.comp25169_c0_seq1_m.2215 | PREDICTED: 5-oxoprolinase [Vitis vinifera] | 138.23 | 69.564 | 12.9 | 14 | 19 | 14 | 0.92 | 0.985 | 0.978 | 1.042 | 1.017 | 1.056 | 1.08 | 3.29E-02 |
| cds.Camellia_sinensis.comp25190_c0_seq1_m.35088 | PREDICTED: 40S ribosomal protein S6-like [Cucumis sativus] | 28.255 | 52.56 | 31.7 | 7 | 12 | 4 | 1.158 | 1.139 | 1.154 | 0.799 | 0.829 | 0.86 | 0.721 | 1.17E-04 |
| cds.Camellia_sinensis.comp25196_c0_seq1_m.48078 | PREDICTED: 14 kDa proline-rich protein DC2.15-like [Erythranthe guttata] | 17.32 | 1.5248 | 5.5 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp25199_c0_seq1_m.17068 | PREDICTED: ATP-dependent 6-phosphofructokinase 4, chloroplastic [Eucalyptus grandis] | 62.915 | 12.251 | 14.4 | 8 | 12 | 5 | 1.016 | 1.028 | 1.051 | 0.943 | 1.026 | 0.952 | 0.944 | 1.09E-01 |
| cds.Camellia_sinensis.comp25200_c0_seq2_m.44828 | PREDICTED: 60S ribosomal protein L44-like [Gossypium hirsutum] | 12.015 | 2.2006 | 14.3 | 2 | 2 | 2 | 1.061 | 1.143 | 1.055 | 0.891 | 0.862 | 0.967 | 0.835 | 1.33E-02 |
| cds.Camellia_sinensis.comp25206_c0_seq1_m.25459 | PREDICTED: cellulose synthase-like protein E6 [Vitis vinifera] | 16.051 | 1.3796 | 6.3 | 1 | 1 | 1 | 1.023 | 0.991 | 0.968 | 0.998 | 1.026 | 1.001 | 1.014 | 4.72E-01 |
| cds.Camellia_sinensis.comp25217_c0_seq2_m.33462 | PREDICTED: F-box only protein 21 isoform X2 [Nicotiana tomentosiformis] | 24.903 | 54.619 | 22.2 | 4 | 8 | 4 | 1.052 | 1.01 | 1.025 | 0.974 | 0.953 | 0.989 | 0.945 | 2.38E-02 |

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| cds.Camellia_sinensis.comp25221_c0_seq1_m.44708 | PREDICTED: protein mago nashi homolog [Theobrom | 20.474 | 23.169 | 36.8 | 5 | 9 | 5 | 0.966 | 1.009 | 0.975 | 1.059 | 0.984 | 0.979 | 1.024 | 4.55E-01 |
| cds.Camellia_sinensis.comp25223_c0_seq1_m.19626 | PREDICTED: patatin-like protein 2 [Vitis vinifera] | 57.26 | 41.313 | 21.2 | 10 | 15 | 10 | 0.974 | 0.987 | 1.01 | 1.003 | 0.993 | 1.023 | 1.016 | 3.07E-01 |
| cds.Camellia_sinensis.comp25228_c1_seq6_m.28157 | transmembrane protein [Arabidopsis thaliana] | 40.642 | 43.251 | 21.7 | 8 | 11 | 8 | 1.043 | 1.066 | 1.022 | 0.932 | 0.925 | 0.973 | 0.904 | 7.08E-03 |
| cds.Camellia_sinensis.comp25234_c0_seq1_m.45771 | PREDICTED: EG45-like domain containing protein [Prunus mume] | 13.442 | 132.07 | 50 | 5 | 17 | 5 | 1.009 | 1.02 | 0.97 | 0.989 | 0.999 | 0.996 | 0.995 | 7.74E-01 |
| cds.Camellia_sinensis.comp25240_c0_seq1_m.1075 | NADH-plastoquinone oxidoreductase subunit 5 (chloroplast) [Camellia leptophylla] | 85.037 | 26.413 | 1.5 | 1 | 2 | 1 | 0.996 | 0.917 | 1.015 | 1.034 | 1.034 | 1.022 | 1.055 | 2.23E-01 |

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| cds.Camellia_sinensis.comp25250_c0_seq1_m.27012 | PREDICTED: stress-induced-phosphoprotein 1 [Gossypium hirsutum] | 13.865 | 1.5886 | 7.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp25270_c0_seq1_m.513 | PREDICTED: dnaJ homolog subfamily C GRV2 isoform X2 [Prunus | 244.54 | 25.411 | 4.1 | 7 | 7 | 7 | 0.93 | 1 | 1.019 | 1.013 | 0.963 | 1.022 | 1.017 | 6.40E-01 |
| cds.Camellia_sinensis.comp25271_c1_seq1_m.35482 | PREDICTED: heterodimeric geranylgeranyl pyrophosphate synthase small subunit, chloroplastic-like [Populus euphratica] | 37.437 | 35.722 | 22.8 | 8 | 11 | 8 | 1.037 | 1.058 | 1.076 | 0.93 | 0.947 | 0.952 | 0.892 | 8.79E-04 |
| cds.Camellia_sinensis.comp25276_c0_seq1_m.33734 | PREDICTED: dihydroflavonol 4-reductase-like [Vitis vinifera] | 38.478 | 14.842 | 9.9 | 3 | 4 | 3 | 0.931 | 1.011 | 0.957 | 1.063 | 1.056 | 0.982 | 1.07 | 1.28E-01 |

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| cds.Camellia_sinensis.comp25284_c0_seq1_m.47591 | Dihydrolipoyl dehydrogenase [Morus notabilis] | 12.205 | 6.3063 | 36 | 3 | 5 | 2 | 1.032 | 0.959 | 0.993 | 1.055 | 0.902 | 1.067 | 1.013 | 8.61E-01 |
| cds.Camellia_sinensis.comp25296_c0_seq1_m.51429 | PREDICTED: probable non-specific lipid-transfer protein AKCS9 [Fragaria vesca subsp. vesca] | 13.126 | 3.9386 | 19.2 | 2 | 2 | 2 | 0.925 | 0.955 | 0.92 | 1.14 | 1.022 | 1.073 | 1.155 | 1.30E-02 |
| cds.Camellia_sinensis.comp25299_c0_seq1_m.39018 | 50S ribosomal protein L34 [Arabidopsis thaliana] | 22.839 | 15.99 | 19.6 | 4 | 5 | 4 | 1.016 | 0.969 | 1.018 | 1.007 | 1.001 | 0.98 | 0.995 | 8.03E-01 |
| cds.Camellia_sinensis.comp25300_c0_seq1_m.38412 | PREDICTED: 50S ribosomal protein L29, chloroplastic [Gossypium raimondii] | 24.866 | 26.5 | 19 | 4 | 5 | 4 | 1.097 | 1.071 | 1.093 | 0.97 | 0.889 | 0.892 | 0.844 | 4.40E-03 |

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| cds.Camellia_sinensis.comp25311_c0_seq1_m.7542 | PREDICTED: calnexin homolog 1-like [Nicotiana tabacum] | 62.823 | 92.933 | 33.2 | 15 | 21 | 15 | 1.029 | 0.988 | 1.01 | 1.008 | 0.995 | 0.971 | 0.982 | 3.34E-01 |
| cds.Camellia_sinensis.comp25312_c0_seq3_m.20634 | PREDICTED: 5'-adenylylsulfate reductase 3, chloroplastic-like [Nicotiana tabacum] | 52.173 | 23.034 | 12 | 5 | 6 | 5 | 0.914 | 0.944 | 0.974 | 1.036 | 1.119 | 1.103 | 1.15 | 9.50E-03 |
| cds.Camellia_sinensis.comp25316_c0_seq1_m.8737 | PREDICTED: translation initiation factor IF-2, chloroplastic-like [Nelumbo nucifera] | 81.562 | 49.172 | 14.6 | 10 | 12 | 10 | 1.103 | 1.11 | 1.107 | 0.897 | 0.895 | 0.862 | 0.799 | 3.38E-03 |
| cds.Camellia_sinensis.comp25317_c0_seq1_m.7453 | PREDICTED: magnesium-chelatase subunit ChlD, chloroplastic isoform X1 [Nelumbo | 77.766 | 15.358 | 12 | 8 | 9 | 8 | 1.088 | 1.042 | 1.085 | 0.986 | 0.836 | 0.861 | 0.835 | 2.54E-02 |

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| cds.Camellia_sinensis.comp25344_c0_seq1_m.53989 | | 9.9658 | 12.967 | 18.3 | 1 | 1 | 1 | 0.886 | 0.734 | 0.986 | 1.152 | 1.15 | 1.149 | 1.324 | 7.91E-02 |
| cds.Camellia_sinensis.comp25349_c0_seq1_m.49225 | PREDICTED: thioredoxin-like protein CXXS1 [Theobroma cacao] | 16.177 | 4.8822 | 7 | 1 | 2 | 1 | 0.989 | 0.865 | 0.886 | 1.091 | 1.135 | 1.067 | 1.202 | 1.47E-02 |
| cds.Camellia_sinensis.comp25361_c0_seq1_m.33769 | Heavy metal transport/detoxification superfamily protein [Arabidopsis thaliana] | 22.167 | 50.225 | 18 | 2 | 4 | 2 | 1.052 | 1.063 | 0.973 | 0.918 | 0.952 | 0.989 | 0.926 | 9.50E-02 |
| cds.Camellia_sinensis.comp25366_c0_seq1_m.40729 | ATP-dependent Clp protease ATP-binding subunit [Arabidopsis thaliana] | 27.259 | 15.557 | 6.4 | 1 | 1 | 1 | 1.007 | 1.004 | 1.074 | 0.928 | 1.068 | 0.923 | 0.946 | 3.38E-01 |
| cds.Camellia_sinensis.comp25367_c0_seq1_m.46441 | calcium-dependent kinase [Medicago truncatula] | 11.617 | 5.8756 | 25.5 | 2 | 2 | 2 | 1.02 | 0.959 | 0.941 | 1.147 | 0.918 | 1.033 | 1.061 | 4.64E-01 |

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| cds.Camellia_sinensis.comp25370_c0_seq1_m.26624 | PREDICTED: translocon-associated protein subunit beta [Vitis vinifera] | 21.146 | 46.895 | 20.5 | 2 | 5 | 2 | 0.937 | 1.004 | 1.016 | 1.038 | 1.043 | 1.038 | 1.055 | 1.66E-01 |
| cds.Camellia_sinensis.comp25383_c0_seq1_m.46956 | polyketide cyclase/dehydrase and lipid transporter [Medicago truncatula] | 16.041 | 2.5326 | 11.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp25396_c0_seq1_m.35631 | PREDICTED: premnaspirodiene oxygenase-like [Vitis vinifera] | 38.624 | 3.331 | 3.5 | 1 | 1 | 1 | 1.074 | 0.895 | 1.051 | 1.027 | 0.928 | 1.027 | 0.987 | 8.82E-01 |
| cds.Camellia_sinensis.comp25398_c0_seq1_m.42073 | PREDICTED: eukaryotic translation initiation factor 3 subunit G [Vitis vinifera] | 26.215 | 101.71 | 41.2 | 9 | 12 | 7 | 1.036 | 0.996 | 1.066 | 0.988 | 0.982 | 0.98 | 0.952 | 1.34E-01 |
| cds.Camellia_sinensis.comp25412_c0_seq1_m.11339 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 [Ziziphus jujuba] | 44.12 | 58.21 | 21.4 | 7 | 15 | 7 | 0.958 | 0.954 | 0.954 | 1.039 | 1.032 | 1.044 | 1.087 | 2.07E-05 |

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| cds.Camellia_sinensis.comp25412_c0_seq1_m.11340 | PREDICTED: succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial-like [Nelumbo nucifera] | 31.441 | 81.003 | 29.4 | 7 | 16 | 4 | 1.047 | 0.99 | 0.956 | 0.998 | 0.983 | 1.027 | 1.005 | 8.60E-01 |
| cds.Camellia_sinensis.comp25412_c0_seq2_m.34327 | PREDICTED: succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial-like [Nelumbo nucifera] | 34.504 | 11.8 | 20.3 | 6 | 10 | 3 | 0.97 | 1.073 | 1.028 | 0.988 | 0.945 | 0.926 | 0.931 | 1.12E-01 |
| cds.Camellia_sinensis.comp25416_c0_seq1_m.20324 | PREDICTED: eukaryotic translation initiation factor 3 subunit J-like [Juglans regia] | 25.642 | 4.8247 | 6.6 | 1 | 1 | 1 | 0.997 | 1.114 | 1.076 | 0.821 | 0.888 | 1.087 | 0.877 | 2.02E-01 |

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| cds.Camellia_sinensis.comp25419_c0_seq1_m.11908 | PREDICTED: 3-oxoacyl-[acyl-carrier-protein] synthase II, chloroplastic [Vitis | 61.051 | 31.903 | 10.6 | 5 | 6 | 5 | 0.963 | 1 | 0.997 | 1.072 | 0.988 | 0.996 | 1.032 | 3.35E-01 |
| cds.Camellia_sinensis.comp25420_c0_seq1_m.34045 | PREDICTED: protein BOBBER 1 [Sesamum indicum] | 33.459 | 43.941 | 37.2 | 13 | 21 | 13 | 1.078 | 1.075 | 1.083 | 0.912 | 0.91 | 0.936 | 0.852 | 6.36E-05 |
| cds.Camellia_sinensis.comp25432_c0_seq1_m.14970 | PREDICTED: beta-glucosidase BoGH3B-like [Malus domestica] | 71.667 | 77.376 | 23 | 11 | 27 | 10 | 0.925 | 0.915 | 0.921 | 1.104 | 1.087 | 1.075 | 1.183 | 3.80E-05 |
| cds.Camellia_sinensis.comp25440_c0_seq1_m.32595 | PREDICTED: 2-hydroxyisoflavanone dehydratase-like [Vitis vinifera] | 37.254 | 15.621 | 2.9 | 1 | 1 | 1 | 0.942 | 0.961 | 0.979 | 1.038 | 1.045 | 1.058 | 1.09 | 2.28E-03 |
| cds.Camellia_sinensis.comp25442_c0_seq1_m.40798 | PREDICTED: 40S ribosomal protein S15 [Ricinus communis] | 17.202 | 10.646 | 19.2 | 2 | 5 | 1 | 1.215 | 1.125 | 1.264 | 0.756 | 0.871 | 0.713 | 0.649 | 3.18E-03 |

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| cds.Camellia_sinensis.comp25442_c0_seq2_m.41805 | PREDICTED: 40S ribosomal protein S15 [Ricinus communis] | 17.174 | -2 | 19.2 | 2 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp25445_c0_seq1_m.13251 | PREDICTED: plastidic glucose transporter 4-like [Juglans regia] | 57.807 | 2.5803 | 2.9 | 2 | 2 | 2 | 0.967 | 1.009 | 0.97 | 1.012 | 1.055 | 1.002 | 1.042 | 1.22E-01 |
| cds.Camellia_sinensis.comp25446_c0_seq1_m.13292 | SLH domain protein [Arabidopsis thaliana] | 27.662 | 8.3149 | 8.4 | 2 | 2 | 2 | 1.037 | 1.05 | 0.951 | 0.995 | 0.93 | 1.036 | 0.975 | 5.93E-01 |
| cds.Camellia_sinensis.comp25446_c0_seq1_m.13293 | SLH domain protein [Arabidopsis thaliana] | 25.983 | 13.56 | 11.1 | 2 | 2 | 2 | 1.003 | 1.049 | 1.092 | 1.029 | 0.961 | 0.872 | 0.91 | 1.51E-01 |
| cds.Camellia_sinensis.comp25448_c0_seq1_m.6626 | plant/MEB5-like protein [Medicago truncatula] | 94.205 | 4.9459 | 3.1 | 2 | 2 | 2 | 1.07 | 0.971 | 1.094 | 1.025 | 0.793 | 1.04 | 0.912 | 3.59E-01 |

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| cds.Camellia_sinensis.comp25454_c0_seq1_m.28314 | PREDICTED: naringenin,2-oxoglutarate 3-dioxygenase [Ziziphus | 44.491 | 178.49 | 49.4 | 18 | 49 | 18 | 1.386 | 1.375 | 1.399 | 0.556 | 0.589 | 0.561 | 0.41 | 5.66E-07 |
| cds.Camellia_sinensis.comp25455_c0_seq1_m.29329 | FAD-dependent oxidoreductase family protein [Populus trichocarpa] | 40.614 | 5.0158 | 5.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp25470_c0_seq1_m.21842 | PREDICTED: outer envelope pore protein 37, chloroplastic [Solanum pennellii] | 41.219 | 26.377 | 20.6 | 6 | 9 | 6 | 0.99 | 0.998 | 0.968 | 1.012 | 1.013 | 1 | 1.023 | 8.23E-02 |
| cds.Camellia_sinensis.comp25474_c0_seq1_m.11244 | PREDICTED: probable tRNA (guanine(26)-N(2))-dimethyltransferase 2 isoform X1 [Vitis vinifera] | 66.23 | 1.6165 | 1.5 | 1 | 1 | 1 | 1.025 | 0.983 | 1.169 | 0.928 | 0.929 | 0.96 | 0.887 | 9.23E-02 |

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| cds.Camellia_sinensis.comp25476_c0_seq1_m.42537 | alba DNA/RNA-binding protein [Medicago truncatula] | 14.425 | 26.296 | 30.2 | 5 | 8 | 1 | 0.923 | 0.943 | 0.939 | 1.074 | 1.173 | 0.985 | 1.152 | 1.12E-01 |
| cds.Camellia_sinensis.comp25488_c0_seq1_m.16338 | PREDICTED: protein disulfide isomerase-like 1-4 [Populus euphratica] | 64.24 | 102.49 | 28.5 | 15 | 20 | 15 | 1.115 | 1.113 | 1.082 | 0.912 | 0.881 | 0.883 | 0.808 | 1.38E-04 |
| cds.Camellia_sinensis.comp25494_c0_seq1_m.22116 | PREDICTED: casein kinase II subunit alpha-like isoform X1 [Nicotiana tabacum] | 51.354 | 12.596 | 12.9 | 5 | 6 | 5 | 0.974 | 1.02 | 0.989 | 1.077 | 0.98 | 0.99 | 1.021 | 5.66E-01 |
| cds.Camellia_sinensis.comp25497_c0_seq1_m.43426 | PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 [Eucalyptus grandis] | 13.387 | 38.348 | 45.2 | 6 | 13 | 6 | 1.017 | 1.025 | 1.098 | 0.966 | 0.967 | 0.941 | 0.915 | 2.74E-02 |
| cds.Camellia_sinensis.comp25498_c0_seq1_m.39612 | transmembrane protein, putative [Medicago truncatula] | 26.761 | 3.9404 | 12.4 | 3 | 3 | 3 | 0.985 | 0.987 | 0.984 | 0.992 | 1.01 | 1.008 | 1.018 | 8.84E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25502_c0_seq1_m.37641 | abscisic stress-ripening protein 2-like [Citrus sinensis] | 23.762 | 59.028 | 34.3 | 5 | 17 | 5 | 1.231 | 1.097 | 1.134 | 0.802 | 0.836 | 0.855 | 0.72 | 1.10E-03 |
| cds.Camellia_sinensis.comp25510_c0_seq3_m.18506 | PREDICTED: ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplastic[Citrus sinensis] | 35.027 | 1.3106 | 3.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp25510_c0_seq3_m.18507 | PREDICTED: ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplastic-like isoform X4 [Theobroma cacao] | 26.164 | 2.7583 | 5.3 | 1 | 1 | 1 | 0.968 | 1.121 | 1.047 | 0.948 | 1.016 | 0.903 | 0.914 | 1.77E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25522_c0_seq1_m.12388 | PREDICTED: dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex,mitochondrial isoform X1 [Sesamum indicum] | 37.435 | 184.02 | 41.9 | 12 | 24 | 12 | 1.021 | 0.986 | 0.983 | 1.015 | 1.002 | 1.005 | 1.011 | 4.46E-01 |
| cds.Camellia_sinensis.comp25522_c0_seq1_m.12389 | PREDICTED: dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex,mitochondrial-like [Juglans regia] | 30.446 | 49.675 | 26.2 | 7 | 13 | 7 | 1.014 | 0.978 | 0.976 | 0.997 | 1 | 1.035 | 1.022 | 2.84E-01 |
| cds.Camellia_sinensis.comp25540_c0_seq1_m.38260 | | 23.186 | 19.294 | 20.2 | 4 | 6 | 4 | 1.049 | 1.043 | 1.026 | 0.948 | 0.94 | 0.959 | 0.913 | 5.00E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25544_c0_seq1_m.33642 | PREDICTED: UPF0301 protein Cpha266_0885 [Citrus sinensis] | 31.92 | 1.1885 | 9.2 | 2 | 2 | 2 | 1.12 | 1.31 | 1.04 | 0.819 | 0.752 | 0.912 | 0.716 | 1.93E-02 |
| cds.Camellia_sinensis.comp25549_c0_seq1_m.3438 | PREDICTED: hexokinase-1 isoform X1 [Vitis vinifera] | 59.434 | 103.99 | 33.8 | 14 | 27 | 14 | 0.933 | 0.955 | 1.021 | 1.049 | 1.029 | 1.034 | 1.07 | 6.91E-02 |
| cds.Camellia_sinensis.comp25551_c0_seq2_m.25546 | transglutaminase family protein [Medicago truncatula] | 25.884 | 2.0705 | 4.1 | 1 | 1 | 1 | 0.878 | 0.961 | 1.008 | 0.98 | 1.162 | 1.043 | 1.119 | 1.58E-01 |
| cds.Camellia_sinensis.comp25552_c0_seq1_m.33134 | PREDICTED: probable carboxylesterase 12 [Juglans regia] | 37.866 | 16.149 | 13.9 | 4 | 5 | 4 | 0.985 | 1.084 | 1.088 | 0.901 | 0.959 | 0.954 | 0.891 | 4.02E-02 |
| cds.Camellia_sinensis.comp25559_c0_seq1_m.36815 | PREDICTED: outer envelope pore protein 16-3, chloroplastic/mitochondrial [Ricinus communis] | 24.653 | 4.1982 | 12.4 | 3 | 5 | 3 | 0.988 | 1.024 | 0.97 | 1.02 | 1.028 | 0.935 | 1 | 9.93E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25562_c0_seq2_m.49216 | PREDICTED: 1-aminocyclopropane-1-carboxylate oxidase [Gossypium hirsutum] | 11.278 | 1.4641 | 8.9 | 1 | 1 | 1 | 1.056 | 1.22 | 1.184 | 0.926 | 0.742 | 0.843 | 0.726 | 1.43E-02 |
| cds.Camellia_sinensis.comp25568_c0_seq1_m.32625 | transmembrane protein [Arabidopsis thaliana] | 33.457 | 27.254 | 15.3 | 4 | 8 | 4 | 1.039 | 1.034 | 1.033 | 0.936 | 0.976 | 0.967 | 0.927 | 2.72E-02 |
| cds.Camellia_sinensis.comp25586_c0_seq1_m.20566 | PREDICTED: aminoacylase-1 isoform X2 [Vitis vinifera] | 49.15 | 88.904 | 33.2 | 12 | 19 | 12 | 0.948 | 0.984 | 0.955 | 1.053 | 1.052 | 1.048 | 1.092 | 1.65E-02 |
| cds.Camellia_sinensis.comp25603_c0_seq1_m.23574 | uncharacterized LOC107793530 [Nicotiana tabacum] | 44.036 | 20.097 | 14.8 | 5 | 5 | 5 | 1.017 | 1.003 | 1.033 | 0.93 | 0.991 | 1.025 | 0.965 | 2.88E-01 |
| cds.Camellia_sinensis.comp25606_c0_seq1_m.24811 | PREDICTED: signal recognition particle 43 kDa protein, chloroplastic [Solanum tuberosum | 47.758 | 49.651 | 28.7 | 14 | 17 | 14 | 0.992 | 0.973 | 1.004 | 1.015 | 1.019 | 0.988 | 1.018 | 2.55E-01 |

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| cds.Camellia_sinensis.comp25607_c0_seq1_m.14266 | PREDICTED: adenosylhomocysteinase [Ziziphus jujuba] | 53.495 | 190.33 | 59 | 25 | 75 | 20 | 1.048 | 1.055 | 1.05 | 0.937 | 0.957 | 0.943 | 0.9 | 8.35E-05 |
| cds.Camellia_sinensis.comp25618_c0_seq1_m.43246 | PREDICTED: polyadenylate-binding protein RBP45B-like isoform X3 [Solanum lycopersic | 23.911 | 6.1499 | 5.3 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp25621_c0_seq1_m.42677 | PREDICTED: protein transport protein Sec61 subunit beta [Cucumis sativus] | 11.735 | 1.5189 | 9.9 | 1 | 1 | 1 | 1.016 | 1.01 | 0.995 | 1.034 | 0.927 | 1.023 | 0.988 | 7.22E-01 |
| cds.Camellia_sinensis.comp25622_c0_seq1_m.8997 | PREDICTED: DNA repair helicase UVH6 isoform X2 [Sesamum indicum] | 31.119 | 1.927 | 3.3 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp25623_c0_seq1_m.20018 | PREDICTED: rhomboid-like protein 20 [Vitis vinifera] | 32.669 | 2.6345 | 6.5 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp25629_c0_seq1_m.41703 | PREDICTED: probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial [Sesamum indicum] | 21.912 | 60.521 | 61.1 | 10 | 16 | 10 | 1.034 | 1.041 | 0.991 | 0.955 | 0.956 | 0.976 | 0.942 | 2.41E-02 |
| cds.Camellia_sinensis.comp25645_c0_seq1_m.23361 | PREDICTED: delta-aminolevulinic acid dehydratase, chloroplastic [Populus euphratica] | 46.982 | 69.501 | 27.9 | 10 | 20 | 10 | 1.028 | 1.081 | 1.065 | 0.913 | 0.929 | 0.964 | 0.884 | 4.90E-03 |

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| cds.Camellia_sinensis.comp25651_c0_seq1_m.34569 | PREDICTED: 50S ribosomal protein L13, chloroplastic-like [Capsicum annuum] | 22.568 | 11.41 | 17.6 | 3 | 4 | 3 | 1.036 | 1.024 | 1.038 | 0.982 | 0.99 | 0.955 | 0.945 | 8.26E-03 |
| cds.Camellia_sinensis.comp25652_c0_seq1_m.11281 | PREDICTED: paramyosin [Erythranthe guttata] | 17.273 | 1.9099 | 7.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp25652_c0_seq2_m.20881 | PREDICTED: paramyosin isoform X2 [Vitis vinifera] | 43.386 | 2.4085 | 6.5 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp25658_c0_seq1_m.38497 | Cu/Zn superoxide dismutase family protein [Populus trichocarpa] | 15.167 | 67.447 | 40.1 | 5 | 20 | 4 | 0.932 | 0.931 | 0.941 | 1.055 | 1.095 | 1.091 | 1.156 | 3.00E-04 |
| cds.Camellia_sinensis.comp25663_c0_seq1_m.7758 | PREDICTED: protein SMAX1-LIKE 4 [Vitis vinifera] | 106.65 | 1.6125 | 1.3 | 1 | 1 | 1 | 1.085 | 1.001 | 1.118 | 1.062 | 0.893 | 0.837 | 0.871 | 1.45E-01 |

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| cds.Camellia_sinensis.comp25664_c0_seq2_m.46175 | PREDICTED: protein disulfide isomerase-like 5-1 [Vitis vinifera] | 16.911 | 2.3361 | 12.8 | 2 | 3 | 1 | 1.003 | 1.062 | 0.978 | 0.979 | 1.006 | 0.976 | 0.973 | 3.64E-01 |
| cds.Camellia_sinensis.comp25664_c0_seq3_m.47339 | PREDICTED: protein disulfide isomerase-like 5-1 [Vitis vinifera] | 16.908 | 8.5579 | 15.4 | 3 | 5 | 2 | 1.038 | 1.079 | 1.023 | 0.977 | 0.832 | 1.043 | 0.908 | 2.19E-01 |
| cds.Camellia_sinensis.comp25680_c0_seq1_m.17593 | PSI reaction center subunit II [Citrus sinensis] | 25.308 | 137.71 | 48.7 | 11 | 83 | 11 | 1.017 | 1.033 | 1.01 | 0.986 | 0.997 | 0.976 | 0.967 | 2.08E-02 |
| cds.Camellia_sinensis.comp25691_c0_seq2_m.8971 | PREDICTED: 5'-nucleotidase domain-containing protein 4-like isoform X2 [Juglans regia] | 67.005 | 98.762 | 20 | 10 | 18 | 10 | 0.938 | 0.99 | 0.964 | 1.03 | 1.032 | 1.029 | 1.069 | 5.05E-02 |
| cds.Camellia_sinensis.comp25692_c0_seq2_m.33412 | PREDICTED: urease accessory protein G [Ziziphus jujuba] | 32.046 | 71.654 | 30.6 | 7 | 14 | 7 | 1.038 | 1.046 | 1.066 | 0.919 | 0.966 | 0.947 | 0.899 | 2.96E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25696_c0_seq1_m.13773 | PREDICTED: threonine dehydratase biosynthetic, chloroplastic [Nelumbo nucifera] | 66.833 | 10.193 | 8 | 5 | 6 | 5 | 1.021 | 1.025 | 1.01 | 1.019 | 0.989 | 0.973 | 0.975 | 1.54E-01 |
| cds.Camellia_sinensis.comp25697_c0_seq1_m.5308 | PREDICTED: lon protease homolog, mitochondrial-like [Nelumbo nucifera] | 109.28 | 41.408 | 16.5 | 12 | 15 | 12 | 1 | 0.961 | 0.951 | 0.994 | 1.027 | 1.003 | 1.038 | 1.05E-01 |
| cds.Camellia_sinensis.comp25700_c0_seq1_m.51328 | PREDICTED: 40S ribosomal protein S6 [Musa acuminata subsp. malaccensis] | 20.093 | 5.7845 | 13.1 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp25711_c0_seq1_m.4368 | PREDICTED: lethal(2) giant larvae protein homolog SRO77-like isoform X1 [Prunus | 121.56 | 8.1733 | 3.5 | 4 | 5 | 4 | 1.031 | 0.901 | 1.035 | 0.984 | 1.046 | 1.012 | 1.025 | 6.14E-01 |

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| cds.Camellia_sinensis.comp25717_c0_seq2_m.450 | PREDICTED: 30S ribosomal protein S20, chloroplastic-like [Nicotiana attenuata] | 20.293 | 4.4965 | 4.9 | 1 | 1 | 1 | 1.08 | 1.091 | 1.205 | 0.873 | 0.901 | 0.825 | 0.77 | 3.86E-03 |
| cds.Camellia_sinensis.comp25720_c0_seq20_m.26153 | actin cross-linking protein [Medicago truncatula] | 33.561 | 1.3064 | 3 | 1 | 1 | 1 | 1.034 | 1.197 | 1.049 | 0.894 | 0.838 | 0.968 | 0.823 | 3.60E-02 |
| cds.Camellia_sinensis.comp25723_c0_seq13_m.34156 | PREDICTED: fatty-acid-binding protein 1 [Jatropha curcas] | 33.225 | 59.404 | 25.7 | 8 | 11 | 8 | 0.995 | 0.991 | 0.993 | 1.038 | 1.011 | 1.001 | 1.024 | 1.64E-01 |
| cds.Camellia_sinensis.comp25724_c0_seq14_m.19500 | nucleoporin protein Ndc1-Nup [Medicago truncatula] | 62.648 | 1.4679 | 3.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp25726_c0_seq16_m.23728 | PREDICTED: prostaglandin E synthase 2 [Jatropha curcas] | 27.428 | 5.8107 | 10.5 | 4 | 5 | 3 | 0.998 | 0.974 | 1.023 | 0.984 | 1.049 | 0.944 | 0.994 | 8.51E-01 |

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| cds.Camellia_sinensis.comp25728_c0_seq2_m.49862 | PREDICTED: thioredoxin-1 isoform X1 [Juglans regia] | 15.412 | 13.626 | 7.7 | 1 | 7 | 1 | 1.009 | 0.975 | 0.993 | 1.025 | 0.985 | 1.008 | 1.014 | 4.20E-01 |
| cds.Camellia_sinensis.comp25744_c0_seq1_m.47627 | PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 [Nicotiana tabacum] | 12.779 | 4.9561 | 8.6 | 1 | 1 | 1 | 1.056 | 0.884 | 0.906 | 1.048 | 1.02 | 1.101 | 1.113 | 1.40E-01 |
| cds.Camellia_sinensis.comp25745_c0_seq1_m.29044 | PREDICTED: mitogen-activated protein kinase kinase 5-like [Capsicum annuum] | 39.991 | 9.3595 | 7.2 | 2 | 4 | 2 | 0.914 | 0.979 | 0.914 | 1.217 | 1.032 | 1.043 | 1.173 | 5.37E-02 |
| cds.Camellia_sinensis.comp25747_c1_seq1_m.2467 | PREDICTED: splicing factor 3B subunit 3 [Vitis vinifera] | 135 | 53.97 | 15.3 | 18 | 22 | 18 | 0.975 | 0.975 | 0.985 | 1.054 | 1.026 | 1.022 | 1.057 | 5.76E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25759_c0_seq1_m.36958 | PAP fibrillin domain protein,expressed protein [Medicago truncatula] | 29.924 | 62.065 | 23.3 | 6 | 8 | 6 | 1.017 | 0.996 | 1.006 | 1.023 | 1.032 | 0.987 | 1.008 | 6.44E-01 |
| cds.Camellia_sinensis.comp25763_c0_seq1_m.4976 | PREDICTED: DExH-box ATP-dependent RNA helicase DExH10 [Nelumbo nucifera] | 114.92 | 1.6781 | 2.5 | 3 | 3 | 3 | 0.969 | 0.968 | 1.026 | 0.941 | 1.11 | 1 | 1.03 | 6.27E-01 |
| cds.Camellia_sinensis.comp25769_c0_seq1_m.24383 | PREDICTED: peroxisomal adenine nucleotide carrier 1 [Citrus sinensis] | 36.089 | 2.25 | 4 | 1 | 1 | 1 | 0.843 | 0.986 | 1.124 | 0.885 | 0.608 | 1.557 | 1.033 | 9.05E-01 |
| cds.Camellia_sinensis.comp25800_c0_seq1_m.33226 | PREDICTED: peroxidase 12 [Fragaria vesca subsp. vesca] | 39.358 | 117.25 | 30.7 | 12 | 28 | 12 | 0.978 | 1.031 | 1.027 | 1.019 | 0.99 | 1.009 | 0.994 | 7.78E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25801_c0_seq3_m.46501 | PREDICTED: probable plastid-lipid-associated protein 11 isoform X3 [Juglans regia] | 22.254 | 19.049 | 34.7 | 7 | 8 | 7 | 0.946 | 0.991 | 1.021 | 1.113 | 0.971 | 0.982 | 1.037 | 5.22E-01 |
| cds.Camellia_sinensis.comp25806_c0_seq1_m.33587 | PREDICTED: NAD(P)H-quinone oxidoreductase subunit M, chloroplastic-like [Gossypium hirsutum] | 25.57 | 45.372 | 39.7 | 10 | 12 | 10 | 1.013 | 1.009 | 0.959 | 1.002 | 1.029 | 1.005 | 1.018 | 3.97E-01 |
| cds.Camellia_sinensis.comp25808_c0_seq1_m.685 | PREDICTED: protein TSS [Vitis vinifera] | 181.39 | 34.367 | 6.1 | 10 | 10 | 8 | 1.096 | 1.067 | 1.138 | 0.942 | 0.839 | 0.864 | 0.801 | 4.88E-03 |
| cds.Camellia_sinensis.comp25808_c0_seq1_m.686 | PREDICTED: protein TSS [Ricinus communis] | 35.378 | 4.5563 | 6.4 | 2 | 2 | 2 | 0.968 | 0.883 | 0.937 | 1.111 | 1.034 | 1.097 | 1.163 | 1.23E-02 |

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| cds.Camellia_sinensis.comp25819_c1_seq1_m.34973 | PREDICTED: protein TIC 21, chloroplastic [Sesamum indicum] | 23.708 | 6.6089 | 6.2 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp25823_c0_seq1_m.34065 | PREDICTED: B-cell receptor-associated protein 31-like [Nicotiana tabacum] | 25.52 | 13.796 | 19 | 4 | 6 | 4 | 1.053 | 1.007 | 1.052 | 0.957 | 1.014 | 0.915 | 0.927 | 8.37E-02 |
| cds.Camellia_sinensis.comp25824_c0_seq1_m.44079 | plastid transcriptionally active protein [Medicago truncatula] | 16.976 | 3.6322 | 5.6 | 1 | 2 | 1 | 0.982 | 1.012 | 0.956 | 1.038 | 0.985 | 1.042 | 1.039 | 1.94E-01 |
| cds.Camellia_sinensis.comp25834_c0_seq1_m.24919 | PREDICTED: probable fructose-bisphosphate aldolase 3, chloroplastic [Sesamum indicum] | 44.523 | 93.59 | 42.6 | 14 | 24 | 13 | 1.013 | 1.011 | 1.02 | 0.983 | 0.969 | 1.014 | 0.974 | 1.28E-01 |
| cds.Camellia_sinensis.comp25838_c0_seq1_m.32758 | HN1-like protein [Medicago truncatula] | 37.07 | 10.787 | 18.6 | 4 | 5 | 3 | 0.942 | 1.056 | 1.027 | 0.996 | 1 | 0.974 | 0.982 | 6.51E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25843_c0_seq1_m.35993 | PREDICTED: NADP-dependent malic enzyme isoform X4 [Nelumbo nucifera] | 33.802 | 2.0501 | 7.4 | 3 | 3 | 2 | 1.018 | 0.912 | 0.973 | 1.064 | 1.035 | 1.017 | 1.073 | 1.07E-01 |
| cds.Camellia_sinensis.comp25849_c0_seq1_m.26650 | PREDICTED: NEDD8-activating enzyme E1 catalytic subunit isoform X1 [Eucalyptus grandis] | 49.6 | 42.073 | 21.2 | 7 | 8 | 7 | 0.913 | 0.902 | 0.981 | 1.088 | 1.073 | 1.027 | 1.14 | 1.39E-02 |
| cds.Camellia_sinensis.comp25857_c0_seq1_m.29195 | PREDICTED: aldose 1-epimerase [Vitis vinifera] | 40.357 | 18.702 | 11.2 | 4 | 6 | 4 | 1.037 | 0.987 | 0.908 | 1.017 | 0.972 | 1.058 | 1.039 | 4.39E-01 |
| cds.Camellia_sinensis.comp25860_c0_seq1_m.29489 | PREDICTED: pirin-like protein [Vitis vinifera] | 38.139 | 5.561 | 4.4 | 1 | 1 | 1 | 0.987 | 1.205 | 1.038 | 0.96 | 0.902 | 0.901 | 0.855 | 7.36E-02 |
| cds.Camellia_sinensis.comp25862_c0_seq1_m.10282 | PREDICTED: ABC transporter G family member 7 [Vitis vinifera] | 82.033 | 19.904 | 10.2 | 7 | 8 | 7 | 1.008 | 1.026 | 1.016 | 0.964 | 0.96 | 1.005 | 0.96 | 5.85E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25863_c0_seq1_m.22745 | acetyl-CoA carboxylase beta subunit (chloroplast) [Camellia sinensis] | 57.987 | 20.483 | 18 | 7 | 8 | 7 | 1.034 | 0.985 | 0.989 | 1.035 | 0.967 | 0.959 | 0.984 | 6.05E-01 |
| cds.Camellia_sinensis.comp25866_c0_seq1_m.12227 | PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial isoform X1 [Capsicum | 81.741 | 130.03 | 27.4 | 17 | 31 | 17 | 0.992 | 1.022 | 0.993 | 1.012 | 1.003 | 0.994 | 1.001 | 9.50E-01 |
| cds.Camellia_sinensis.comp25868_c0_seq1_m.24454 | PREDICTED: heterogeneous nuclear ribonucleoprotein 1-like [Malus domestica] | 36.016 | 52.275 | 22.9 | 6 | 16 | 5 | 1.008 | 0.996 | 0.989 | 1.014 | 0.993 | 0.979 | 0.998 | 8.45E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25879_c0_seq1_m.41545 | PREDICTED: serine/threonine-protein phosphatase 6 regulatory subunit 2 isoform X1 [Vitis vinifera] | 23.261 | 70.13 | 24.4 | 3 | 3 | 3 | 1.062 | 0.991 | 1.002 | 0.999 | 0.907 | 1.009 | 0.954 | 3.02E-01 |
| cds.Camellia_sinensis.comp25884_c0_seq1_m.21957 | PREDICTED: DNA ligase 1 [Camelina sativa] | 42.672 | 5.2113 | 6.6 | 2 | 3 | 2 | 1.187 | 1.256 | 1.178 | 0.711 | 0.73 | 0.871 | 0.638 | 2.48E-03 |
| cds.Camellia_sinensis.comp25886_c0_seq2_m.41532 | PREDICTED: AP-2 complex subunit sigma [Sesamum indicum] | 17.123 | 4.5003 | 12.7 | 2 | 2 | 2 | 0.915 | 0.911 | 0.964 | 1.078 | 1.085 | 1.082 | 1.163 | 1.42E-02 |
| cds.Camellia_sinensis.comp25907_c0_seq2_m.21991 | PREDICTED: ADP,ATP carrier protein 3, mitochondrial [Eucalyptus grandis] | 41.431 | 62.364 | 23 | 10 | 40 | 5 | 0.955 | 0.957 | 1.003 | 1.041 | 1.047 | 1.023 | 1.067 | 2.01E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25913_c0_seq1_m.35215 | PREDICTED: multiple organellar RNA editing factor 2, chloroplastic [Nelumbo nucifera] | 26.916 | 8.1784 | 15.9 | 4 | 8 | 4 | 1.045 | 1.044 | 1.072 | 0.922 | 0.894 | 0.96 | 0.878 | 4.34E-03 |
| cds.Camellia_sinensis.comp25919_c0_seq1_m.29927 | PREDICTED: RNA-binding protein sym-2 isoform X1 [Daucus carota subsp. sativus] | 43.031 | 16.416 | 19.8 | 6 | 8 | 6 | 0.981 | 0.999 | 0.967 | 1 | 1.04 | 1.066 | 1.054 | 6.63E-02 |
| cds.Camellia_sinensis.comp25924_c0_seq1_m.26348 | glycoside hydrolase family 28 family protein [Populus trichocarpa] | 49.412 | 37.121 | 11.6 | 5 | 5 | 5 | 0.929 | 0.965 | 1.012 | 0.994 | 1.024 | 1.062 | 1.06 | 1.35E-01 |
| cds.Camellia_sinensis.comp25931_c0_seq1_m.22736 | PREDICTED: sugar transport protein 14-like [Ipomoea nil] | 56.199 | 24.9 | 8.9 | 3 | 5 | 3 | 0.913 | 0.983 | 0.925 | 1.103 | 1.098 | 0.908 | 1.102 | 2.40E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp25952_c0_seq2_m.14551 | PREDICTED: cyclin-dependent kinase C-2 [Vitis vinifera] | 57.561 | 2.5708 | 4.6 | 3 | 4 | 2 | 1.031 | 0.972 | 0.996 | 1.09 | 0.956 | 0.967 | 1.005 | 9.48E-01 |
| cds.Camellia_sinensis.comp25955_c0_seq1_m.37552 | PREDICTED: 60S ribosomal protein L6-1-like [Pyrus x bretschneideri] | 26.046 | 12.725 | 28.8 | 7 | 11 | 4 | 1.132 | 1.114 | 1.149 | 0.884 | 0.875 | 0.848 | 0.768 | 6.36E-05 |
| cds.Camellia_sinensis.comp25955_c0_seq2_m.40421 | PREDICTED: 60S ribosomal protein L6-1-like [Pyrus x bretschneideri] | 27.725 | 26.374 | 31.4 | 8 | 13 | 5 | 1.092 | 1.153 | 1.116 | 0.868 | 0.907 | 0.855 | 0.783 | 4.97E-04 |
| cds.Camellia_sinensis.comp25987_c0_seq1_m.41894 | PREDICTED: malate dehydrogenase, glyoxysomal [Fragaria vesca subsp. vesca] | 16.653 | 9.0496 | 35.4 | 5 | 8 | 3 | 0.927 | 1.032 | 0.988 | 1.071 | 1.03 | 1.021 | 1.059 | 1.65E-01 |
| cds.Camellia_sinensis.comp25989_c0_seq1_m.19437 | PREDICTED: cysteine proteinase COT44 [Citrus sinensis] | 40.341 | 127.46 | 32.5 | 9 | 20 | 8 | 1.097 | 1.086 | 1.059 | 0.909 | 0.895 | 0.93 | 0.843 | 3.65E-04 |

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| cds.Camellia_sinensis.comp25990_c0_seq1_m.47421 | PREDICTED: probable glutathione S-transferase [Nicotiana attenuata] | 16.041 | 6.961 | 27.7 | 7 | 20 | 5 | 1.027 | 0.975 | 0.947 | 0.974 | 0.974 | 1.056 | 1.019 | 6.37E-01 |
| cds.Camellia_sinensis.comp25995_c0_seq1_m.33788 | PREDICTED: multiple organellar RNA editing factor 1, mitochondrial [Vitis vinifera] | 42.7 | 7.3164 | 9.4 | 3 | 4 | 3 | 1.055 | 0.98 | 1.015 | 0.966 | 0.955 | 1.027 | 0.967 | 3.34E-01 |
| cds.Camellia_sinensis.comp25996_c0_seq2_m.49305 |  | 15.109 | 50.048 | 24.4 | 2 | 3 | 2 | 1.032 | 0.969 | 0.878 | 0.983 | 1.078 | 1.071 | 1.088 | 1.99E-01 |
| cds.Camellia_sinensis.comp25998_c0_seq1_m.11174 | PREDICTED: protein FRIGIDA [Sesamum indicum] | 78.87 | 9.8811 | 5.8 | 4 | 4 | 4 | 1.023 | 1.059 | 0.999 | 0.959 | 0.948 | 1.028 | 0.953 | 1.83E-01 |
| cds.Camellia_sinensis.comp26010_c0_seq1_m.30863 | PREDICTED: putative 12-oxophytodienoate reductase 11 [Theobroma cacao] | 40.996 | 102.17 | 30.2 | 9 | 17 | 8 | 0.942 | 0.998 | 0.973 | 1.002 | 1.012 | 1.023 | 1.043 | 7.75E-02 |

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| cds.Camellia_sinensis.comp26013_c0_seq1_m.23914 | PREDICTED: triose phosphate/phosphate translocator, chloroplastic [Vitis vinifera] | 48.08 | 45.616 | 12.5 | 6 | 12 | 6 | 0.921 | 0.913 | 0.958 | 1.073 | 1.083 | 1.082 | 1.16 | 6.00E-04 |
| cds.Camellia_sinensis.comp26015_c0_seq1_m.29474 | thiamine monophosphate synthase [Medicago truncatula] | 32.552 | 43.382 | 30.5 | 8 | 11 | 8 | 1.008 | 0.977 | 0.974 | 1.001 | 1.067 | 0.986 | 1.032 | 3.06E-01 |
| cds.Camellia_sinensis.comp26016_c0_seq1_m.33501 | PREDICTED: V-type proton ATPase subunit E [Sesamum | 26.333 | 69.18 | 45.9 | 10 | 23 | 7 | 1 | 0.982 | 0.962 | 1.01 | 1.026 | 1.04 | 1.045 | 3.52E-02 |
| cds.Camellia_sinensis.comp26018_c0_seq1_m.23404 | PREDICTED: serine--tRNA ligase [Vitis vinifera] | 46.11 | 37.742 | 23.9 | 9 | 10 | 9 | 1.019 | 1.043 | 1.027 | 0.984 | 0.977 | 0.976 | 0.951 | 2.32E-03 |
| cds.Camellia_sinensis.comp26023_c0_seq1_m.31133 | uncharacterized LOC107830728 [Nicotiana tabacum] | 31.217 | 67.113 | 19.8 | 5 | 9 | 5 | 1.054 | 1.056 | 0.95 | 0.983 | 1.028 | 0.94 | 0.964 | 4.57E-01 |

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| cds.Camellia_sinensis.comp26027_c0_seq1_m.7122 | PREDICTED: probable galactinol--sucrose galactosyltransferase 6 isoform X1 [Populus euphratica] | 93.927 | 323.31 | 34.1 | 25 | 62 | 25 | 1.11 | 1.106 | 1.111 | 0.88 | 0.89 | 0.872 | 0.794 | 1.43E-06 |
| cds.Camellia_sinensis.comp26033_c0_seq1_m.41032 | PREDICTED: coiled-coil domain-containing protein 25 isoform X1 [Vitis vinifera] | 25.144 | 1.1908 | 7 | 2 | 2 | 2 | 1.059 | 1.163 | 1.098 | 0.854 | 0.818 | 0.979 | 0.798 | 2.00E-02 |
| cds.Camellia_sinensis.comp26040_c0_seq1_m.20949 | uncharacterized LOC107810057 [Nicotiana tabacum] | 47.193 | 1.5038 | 1.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp26042_c0_seq1_m.30245 | PREDICTED: putative lactoylglutathione lyase isoform X2 [Vitis vinifera] | 32.799 | 25.911 | 45 | 12 | 48 | 1 | 0.942 | 0.955 | 0.989 | 1.045 | 1.08 | 1.023 | 1.091 | 1.54E-02 |

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| cds.Camellia_sinensis.comp26042_c0_seq2_m.31341 | PREDICTED: putative lactoylglutathione lyase isoform X2 [Vitis vinifera] | 32.712 | 144.92 | 49 | 13 | 56 | 2 | 0.942 | 0.966 | 0.953 | 1.057 | 1.051 | 1.043 | 1.101 | 3.01E-04 |
| cds.Camellia_sinensis.comp26046_c0_seq1_m.33895 | PREDICTED: DNA-damage-repair/toleration protein DRT102 [Nelumbo nucifera] | 35.947 | 96.526 | 33.2 | 9 | 18 | 9 | 0.953 | 0.963 | 0.958 | 1.04 | 1.03 | 1.036 | 1.081 | 4.33E-05 |
| cds.Camellia_sinensis.comp260594_c0_seq1_m.50831 | PREDICTED: non-specific phospholipase C4 isoform X2 [Vitis vinifera] | 20.397 | 9.6276 | 17.1 | 3 | 4 | 3 | 0.933 | 1.044 | 1.122 | 0.85 | 0.966 | 1.085 | 0.936 | 4.85E-01 |
| cds.Camellia_sinensis.comp26059_c0_seq1_m.33749 | PREDICTED: NADH--cytochrome b5 reductase 1 [Jatropha curcas] | 33.016 | 29.643 | 20 | 7 | 10 | 6 | 0.991 | 0.971 | 1.002 | 0.973 | 1.012 | 0.977 | 0.999 | 9.64E-01 |

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| cds.Camellia_sinensis.comp26061_c0_seq1_m.36997 | PREDICTED: aminopeptidase M1 isoform X2 [Vitis vinifera] | 39.536 | 29.099 | 17.5 | 6 | 12 | 5 | 0.956 | 0.98 | 0.922 | 1.052 | 1.073 | 1.055 | 1.113 | 4.66E-03 |
| cds.Camellia_sinensis.comp26068_c0_seq1_m.26871 | PREDICTED: biotin carboxyl carrier protein of acetyl-CoA carboxylase [Prunus mume] | 30.685 | 13.609 | 18.4 | 5 | 7 | 5 | 1.013 | 1.07 | 1.021 | 0.98 | 0.991 | 0.978 | 0.95 | 4.42E-02 |
| cds.Camellia_sinensis.comp26073_c0_seq1_m.30288 | PREDICTED: 33 kDa ribonucleoprotein, chloroplastic [Juglans regia] | 35.214 | 49.763 | 19.3 | 6 | 10 | 6 | 1.016 | 1.004 | 1.07 | 0.981 | 0.969 | 0.976 | 0.947 | 5.27E-02 |
| cds.Camellia_sinensis.comp26081_c0_seq1_m.45814 | PREDICTED: L10-interacting MYB domain-containing protein-like [Cucumis melo] | 19.175 | 3.2047 | 6.1 | 1 | 1 | 1 | 0.907 | 0.959 | 0.958 | 0.993 | 1.252 | 0.966 | 1.137 | 2.22E-01 |

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| cds.Camellia_sinensis.comp26091_c0_seq1_m.17776 | PREDICTED: protein TIC 56, chloroplastic-like [Gossypium hirsutum] | 59.411 | 12.805 | 9.8 | 5 | 6 | 5 | 0.933 | 1.032 | 1.008 | 1.044 | 1.029 | 1.003 | 1.035 | 3.46E-01 |
| cds.Camellia_sinensis.comp26098_c0_seq4_m.50935 | PREDICTED: macrophage migration inhibitory factor homolog [Eucalyptu | 13.099 | 46.866 | 15.6 | 2 | 5 | 2 | 1.024 | 0.992 | 1.011 | 1.005 | 0.991 | 1.017 | 0.995 | 7.18E-01 |
| cds.Camellia_sinensis.comp26102_c0_seq1_m.29197 | PREDICTED: phosphopantothenate--cysteine ligase 2-like [Juglans regia] | 36.207 | 22.255 | 12.9 | 4 | 4 | 4 | 1.062 | 1.021 | 0.974 | 0.998 | 1.009 | 0.922 | 0.958 | 3.20E-01 |
| cds.Camellia_sinensis.comp26103_c1_seq1_m.10502 | PREDICTED: violaxanthin de-epoxidase, chloroplastic [Vitis vinifera] | 53.757 | 137.54 | 38.3 | 14 | 25 | 14 | 0.96 | 0.988 | 0.965 | 1.052 | 1.026 | 1.06 | 1.077 | 4.94E-03 |

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| cds.Camellia_sinensis.comp26108_c0_seq1_m.26404 | PREDICTED: GDSL esterase/lipase At1g09390-like isoform X1 [Juglans regia] | 42.298 | 2.0821 | 2.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp26112_c0_seq1_m.42689 | PREDICTED: dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 1, mitochondrial-like isoform X3 [Populus euphratica] | 21.758 | -2 | 33.3 | 7 | 11 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp26118_c0_seq1_m.40510 | PREDICTED: auxin-binding protein ABP19a [Eucalyptus grandis] | 22.317 | 22.198 | 15.6 | 3 | 14 | 3 | 0.992 | 0.94 | 0.987 | 1.009 | 1.029 | 1.008 | 1.044 | 8.08E-02 |

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| cds.Camellia_sinensis.comp26123_c0_seq1_m.25847 | PREDICTED: heavy metal-associated isoprenylated plant protein 3-like isoform X2 [Juglans regia] | 39.119 | 2.0889 | 3.3 | 1 | 1 | 1 | 0.896 | 0.973 | 1.006 | 1.137 | 0.991 | 1.033 | 1.099 | 1.51E-01 |
| cds.Camellia_sinensis.comp26126_c0_seq1_m.48294 | PREDICTED: ras-related protein RABD2a-like [Nicotiana tabacum] | 17.122 | 1.5292 | 28 | 5 | 11 | 1 | 1.01 | 1.027 | 0.996 | 1.008 | 0.978 | 0.989 | 0.981 | 1.97E-01 |
| cds.Camellia_sinensis.comp26133_c0_seq1_m.13320 | PREDICTED: regulation of nuclear pre-mRNA domain-containing protein 1B-like [Prunus mume] | 60.867 | 3.8386 | 4.3 | 3 | 3 | 3 | 0.993 | 1.007 | 0.98 | 1.027 | 1.001 | 1.005 | 1.018 | 1.90E-01 |

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| cds.Camellia_sinensis.comp26136_c0_seq1_m.26384 | PREDICTED: probable tocopherol O-methyltransferase, chloroplastic isoform X4 [Juglans regia] | 39.994 | 31.387 | 23.6 | 7 | 10 | 7 | 1.004 | 1.005 | 1.049 | 0.982 | 0.986 | 0.975 | 0.962 | 6.18E-02 |
| cds.Camellia_sinensis.comp26137_c0_seq1_m.14029 | PREDICTED: flavonoid 3',5'-hydroxylase 2-like [Jatropha curcas] | 57.074 | 16.113 | 17.6 | 8 | 10 | 8 | 1.242 | 1.363 | 1.379 | 0.639 | 0.682 | 0.588 | 0.479 | 1.65E-04 |
| cds.Camellia_sinensis.comp26138_c0_seq1_m.38810 | PREDICTED: non-symbiotic hemoglobin 1 [Ricinus communis] | 26.452 | 34.161 | 31.9 | 8 | 16 | 8 | 0.979 | 0.979 | 0.974 | 1.03 | 1.065 | 1.003 | 1.057 | 8.81E-02 |
| cds.Camellia_sinensis.comp26139_c1_seq1_m.19052 | PREDICTED: UDP-glucose 4-epimerase GEPI48 [Sesamum indicum] | 37.964 | 139.53 | 51.1 | 15 | 39 | 14 | 0.974 | 0.94 | 0.941 | 1.059 | 1.092 | 1.045 | 1.119 | 2.98E-03 |

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| cds.Camellia_sinensis.comp26157_c0_seq1_m.39234 | PREDICTED: proteasome subunit beta type-1-like [Nicotiana tabacum] | 24.645 | 6.4214 | 32.3 | 6 | 9 | 2 | 0.938 | 0.973 | 0.983 | 1.082 | 1.023 | 1.006 | 1.075 | 5.15E-02 |
| cds.Camellia_sinensis.comp26157_c0_seq2_m.39673 | PREDICTED: proteasome subunit beta type-1 [Ziziphus jujuba] | 25.058 | 111.77 | 54.4 | 10 | 15 | 6 | 0.994 | 0.959 | 0.94 | 1.022 | 1.059 | 1.031 | 1.076 | 2.00E-02 |
| cds.Camellia_sinensis.comp26160_c0_seq10_c0_seq1_m.26066 | PREDICTED: probable alpha-amylase 2 [Jatropha curcas] | 46.952 | 4.5604 | 6.3 | 3 | 3 | 3 | 1.097 | 0.953 | 0.976 | 0.972 | 0.982 | 1.015 | 0.981 | 7.23E-01 |
| cds.Camellia_sinensis.comp26168_c0_seq1_m.29601 | PREDICTED: peroxidase 73 [Vitis vinifera] | 35.455 | 29.482 | 34.9 | 9 | 17 | 7 | 1.011 | 1.044 | 1.031 | 0.986 | 0.945 | 0.946 | 0.932 | 1.40E-02 |
| cds.Camellia_sinensis.comp26171_c0_seq2_m.40947 | PREDICTED: NADPH--cytochrome P450 reductase 2 [Prunus mume] | 20.603 | 4.2638 | 7.5 | 1 | 1 | 1 | 1.296 | 1.3 | 1.218 | 0.754 | 0.658 | 0.691 | 0.551 | 1.85E-04 |

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| cds.Camellia_sinensis.comp26177_c0_seq1_m.41667 | PREDICTED: 60S ribosomal protein L31 [Juglans regia] | 14.069 | 19.705 | 33.1 | 3 | 3 | 3 | 1.113 | 1.042 | 1.099 | 0.951 | 0.87 | 0.913 | 0.84 | 5.96E-03 |
| cds.Camellia_sinensis.comp26178_c0_seq1_m.25671 | E3 ubiquitin-protein ligase [Arabidopsis thaliana] | 52.465 | 13.562 | 8.9 | 4 | 5 | 4 | 1.016 | 0.858 | 0.981 | 0.951 | 0.985 | 1.166 | 1.087 | 3.73E-01 |
| cds.Camellia_sinensis.comp26181_c0_seq1_m.29403 | PREDICTED: protein LOW PSII ACCUMULATION 3, chloroplastic [Vitis vinifera] | 37.155 | 8.0744 | 8.6 | 3 | 6 | 3 | 1.007 | 0.993 | 1.016 | 0.987 | 1.024 | 0.992 | 0.996 | 7.57E-01 |
| cds.Camellia_sinensis.comp26184_c0_seq1_m.32281 | PREDICTED: guanine nucleotide-binding protein subunit beta-like protein [Erythranthe guttata] | 35.931 | 136.94 | 36.7 | 10 | 29 | 10 | 0.959 | 0.959 | 0.954 | 1.043 | 1.052 | 1.017 | 1.084 | 1.48E-03 |

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| cds.Camellia_sinensis.comp26187_c0_seq1_m.24832 | PREDICTED: 40S ribosomal protein S3a [Sesamum indicum] | 29.806 | 68.408 | 48.7 | 10 | 22 | 10 | 1.097 | 1.12 | 1.091 | 0.845 | 0.876 | 0.866 | 0.782 | 5.51E-05 |
| cds.Camellia_sinensis.comp26191_c0_seq11_c0_seq1_m.25177 | PREDICTED: embryogenesis-associated protein EMB8 isoform X1 [Nelumbo nucifera] | 44.928 | 3.538 | 5.8 | 1 | 1 | 1 | 0.707 | 1.247 | 1.171 | 1.188 | 1.033 | 0.704 | 0.936 | 8.15E-01 |
| cds.Camellia_sinensis.comp26199_c0_seq1_m.17298 | PREDICTED: pto-interacting protein 1 isoform X2 [Sesamum indicum] | 38.825 | 74.727 | 34.4 | 11 | 19 | 10 | 0.986 | 0.957 | 0.995 | 1.016 | 1.012 | 1.022 | 1.038 | 3.62E-02 |
| cds.Camellia_sinensis.comp26206_c0_seq2_m.39660 | PREDICTED: binding partner of ACD11 1 [Theobroma cacao] | 27.643 | 22.639 | 31.5 | 8 | 13 | 6 | 1.103 | 1.02 | 1.045 | 0.97 | 0.957 | 0.945 | 0.907 | 1.60E-02 |
| cds.Camellia_sinensis.comp26206_c0_seq3_m.40252 | PREDICTED: binding partner of ACD11 1 [Theobroma cacao] | 27.591 | 12.816 | 25.6 | 7 | 10 | 6 | 0.985 | 0.966 | 0.997 | 0.972 | 1.055 | 1.045 | 1.042 | 2.13E-01 |

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| cds.Camellia_sinensis.comp26210_c0_seq1_m.33336 | PREDICTED: protein SGT1 homolog A-like [Jatropha curcas] | 36.949 | 14.116 | 26.7 | 9 | 10 | 8 | 0.973 | 0.959 | 0.971 | 1.036 | 1.001 | 1.041 | 1.06 | 1.13E-02 |
| cds.Camellia_sinensis.comp26219_c0_seq1_m.29148 | PREDICTED: protein SLOW GREEN 1, chloroplastic-like isoform X2 [Gossypium hirsutum] | 45.082 | 4.3655 | 7.6 | 3 | 3 | 3 | 0.957 | 0.898 | 0.947 | 1.096 | 1.082 | 1.052 | 1.153 | 3.52E-03 |
| cds.Camellia_sinensis.comp26222_c0_seq1_m.35005 | PREDICTED: GDT1-like protein 4 [Cucumis melo] | 24.773 | 1.5575 | 3.9 | 1 | 1 | 1 | 0.981 | 0.977 | 0.983 | 1.061 | 0.978 | 1.037 | 1.046 | 2.10E-01 |
| cds.Camellia_sinensis.comp26231_c0_seq1_m.27340 | PREDICTED: isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial isoform X1 [Ricinus | 40.735 | 51.525 | 25 | 9 | 16 | 9 | 0.976 | 0.998 | 0.986 | 1.036 | 1.015 | 1.034 | 1.042 | 1.07E-02 |

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| cds.Camellia_sinensis.comp26232_c0_seq32_m.36763 | DNA-binding protein [Medicago truncatula] | 24.035 | 2.8459 | 5.1 | 1 | 1 | 1 | 0.98 | 1.047 | 1.134 | 0.96 | 0.947 | 0.933 | 0.898 | 7.04E-02 |
| cds.Camellia_sinensis.comp26236_c1_seq1_m.48309 | | 18.403 | 4.3686 | 10.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp26246_c0_seq1_m.30448 | bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase-like [Gossypium | 35.01 | 7.5402 | 13.8 | 4 | 5 | 3 | 1.053 | 1.05 | 1.026 | 0.914 | 1.018 | 0.932 | 0.915 | 5.87E-02 |
| cds.Camellia_sinensis.comp26248_c0_seq1_m.28827 | PREDICTED: 3-deoxy-manno-octulosonate cytidylyltransferase, mitochondrial-like isoform X1 [Nicotiana attenuata] | 34.261 | 105.94 | 32.6 | 6 | 11 | 6 | 0.998 | 0.978 | 0.982 | 1.015 | 1.014 | 0.992 | 1.021 | 9.58E-02 |

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| cds.Camellia_sinensis.comp26250_c0_seq1_m.2532 | PREDICTED: starch synthase 3, chloroplastic/amyloplastic isoform X1 [Ziziphus jujuba] | 83.105 | 47.688 | 21.2 | 12 | 13 | 12 | 1.055 | 1.097 | 1.072 | 0.909 | 0.914 | 0.91 | 0.848 | 4.78E-03 |
| cds.Camellia_sinensis.comp26250_c0_seq1_m.2533 | PREDICTED: starch synthase 3, chloroplastic/amyloplastic [Vitis vinifera] | 62.555 | 13.859 | 11.7 | 6 | 7 | 6 | 1.182 | 1.131 | 1.058 | 0.849 | 0.829 | 0.917 | 0.77 | 4.12E-03 |
| cds.Camellia_sinensis.comp26251_c0_seq1_m.32703 | Glutelin type-B 5 [Morus notabilis] | 39.432 | 54.639 | 30.6 | 11 | 18 | 11 | 0.909 | 0.925 | 0.921 | 1.077 | 1.076 | 1.09 | 1.177 | 1.84E-05 |
| cds.Camellia_sinensis.comp26252_c0_seq1_m.25284 | PREDICTED: beta-glucosidase 12-like [Nicotiana sylvestris] | 56.574 | 24.816 | 12 | 6 | 9 | 5 | 1.011 | 0.973 | 0.967 | 1.039 | 1.005 | 1.026 | 1.04 | 7.97E-02 |
| cds.Camellia_sinensis.comp26255_c0_seq2_m.14870 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP20-1 isoform X1 [Nelumbo nucifera] | 20.505 | 4.3603 | 6.4 | 1 | 1 | 1 | 1.112 | 1.17 | 1.064 | 0.903 | 0.839 | 0.884 | 0.785 | 2.32E-03 |

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| cds.Camellia_sinensis.comp26268_c0_seq1_m.37228 | PREDICTED: probable protein phosphatase 2C 58 [Sesamum indicum] | 31.569 | 10.595 | 10.8 | 3 | 5 | 1 | 0.965 | 0.874 | 1.065 | 1.041 | 1.013 | 1.063 | 1.073 | 2.77E-01 |
| cds.Camellia_sinensis.comp26270_c0_seq1_m.8002 | PREDICTED: casein kinase 1-like protein HD16 isoform X2 [Ipomoea nil] | 78.982 | 1.5441 | 2.1 | 1 | 1 | 1 | 0.997 | 0.859 | 1.104 | 0.986 | 1.017 | 1.05 | 1.031 | 6.58E-01 |
| cds.Camellia_sinensis.comp26273_c0_seq1_m.33649 | PREDICTED: adenylate kinase, chloroplastic-like [Populus euphratica] | 33.475 | 28.9 | 21.3 | 6 | 14 | 5 | 0.99 | 1.034 | 0.937 | 1.013 | 0.992 | 1.002 | 1.016 | 6.08E-01 |
| cds.Camellia_sinensis.comp26283_c0_seq1_m.30031 | PREDICTED: signal recognition particle receptor subunit beta-like [Sesamum indicum] | 29.25 | 16.622 | 23.4 | 5 | 9 | 5 | 0.982 | 0.951 | 0.947 | 1.103 | 0.987 | 1.047 | 1.089 | 6.81E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26285_c0_seq1_m.46008 | PREDICTED: glutathione S-transferase T1 [Ricinus communis] | 19.873 | 10.854 | 14.1 | 2 | 2 | 2 | 0.99 | 0.986 | 1.066 | 0.957 | 1.016 | 0.992 | 0.975 | 4.57E-01 |
| cds.Camellia_sinensis.comp26288_c0_seq1_m.43846 | PREDICTED: subtilisin-like protease SBT3.11 [Pyrus x bretschneideri] | 14.398 | 36.904 | 34.1 | 4 | 7 | 4 | 0.945 | 0.92 | 0.901 | 1.095 | 1.104 | 1.134 | 1.205 | 4.24E-04 |
| cds.Camellia_sinensis.comp26290_c0_seq1_m.21347 | PREDICTED: eukaryotic initiation factor 4A-3 [Vitis vinifera] | 46.559 | 78.079 | 33.5 | 16 | 28 | 14 | 0.971 | 0.961 | 0.977 | 1.031 | 1.021 | 1.037 | 1.062 | 8.19E-04 |
| cds.Camellia_sinensis.comp26296_c0_seq1_m.39538 | PREDICTED: phosphopantetheine adenylyltransferase [Theobroma cacao] | 26.013 | 19.037 | 30.8 | 7 | 9 | 7 | 0.988 | 1.026 | 0.97 | 1.025 | 0.996 | 1.012 | 1.016 | 4.23E-01 |
| cds.Camellia_sinensis.comp26305_c0_seq1_m.2721 | PREDICTED: protein TPLATE [Ipomoea nil] | 101.42 | 7.7555 | 3.2 | 2 | 2 | 2 | 1.148 | 1.054 | 0.924 | 0.896 | 0.98 | 0.978 | 0.913 | 2.76E-01 |

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| cds.Camellia_sinensis.comp26309_c0_seq1_m.35452 | PREDICTED: mitochondrial import receptor subunit TOM20 [Vitis vinifera] | 27.97 | 57.458 | 37.2 | 10 | 15 | 10 | 0.915 | 0.958 | 0.969 | 1.044 | 1.093 | 1.092 | 1.136 | 5.28E-03 |
| cds.Camellia_sinensis.comp26322_c0_seq32_m.1497 | PREDICTED: ARF guanine-nucleotide exchange factor GNOM [Jatropha curcas] | 139.95 | 1.9317 | 2.2 | 3 | 3 | 3 | 1.193 | 0.963 | 1.029 | 0.957 | 0.879 | 0.955 | 0.876 | 1.36E-01 |
| cds.Camellia_sinensis.comp26336_c0_seq1_m.25208 | PREDICTED: glutamate dehydrogenase 2 [Theobroma cacao] | 47.284 | 9.4171 | 13.9 | 5 | 7 | 2 | 0.96 | 1.212 | 0.925 | 0.97 | 0.977 | 0.958 | 0.938 | 5.72E-01 |
| cds.Camellia_sinensis.comp26365_c0_seq1_m.37925 | PREDICTED: aldose 1-epimerase-like [Nicotiana tabacum] | 34.723 | 12.984 | 17.5 | 6 | 9 | 6 | 0.972 | 0.936 | 0.924 | 1.028 | 1.04 | 1.086 | 1.114 | 8.86E-03 |

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| cds.Camellia_sinensis.comp26377_c0_seq1_m.30105 | PREDICTED: protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha [Vitis vinifera] | 28.17 | 24.113 | 18.3 | 4 | 4 | 4 | 0.943 | 0.992 | 0.986 | 1.044 | 1.029 | 1.023 | 1.06 | 2.68E-02 |
| cds.Camellia_sinensis.comp26384_c0_seq1_m.38788 | PREDICTED: 40S ribosomal protein S12 [Nelumbo nucifera] | 15.184 | 18.403 | 56.2 | 6 | 11 | 3 | 1.021 | 0.983 | 1.141 | 0.968 | 0.838 | 1.043 | 0.906 | 2.67E-01 |
| cds.Camellia_sinensis.comp26384_c0_seq2_m.39037 | PREDICTED: 40S ribosomal protein S12 [Nelumbo nucifera] | 15.152 | 27.678 | 62.5 | 7 | 12 | 4 | 0.959 | 0.986 | 0.959 | 1.025 | 1.08 | 1.013 | 1.074 | 3.12E-02 |
| cds.Camellia_sinensis.comp26388_c0_seq1_m.18287 | PREDICTED: probable transaldolase [Sesamum indicum] | 48.969 | 95.198 | 35.3 | 13 | 20 | 13 | 0.954 | 1.013 | 0.974 | 1.042 | 1.037 | 1.015 | 1.052 | 5.80E-02 |

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| cds.Camellia_sinensis.comp26389_c0_seq1_m.39277 | PREDICTED: ESCRT-related protein CHMP1B-like [Nelumbo nucifera] | 22.603 | 28.494 | 32.5 | 7 | 8 | 7 | 1.042 | 1.06 | 1.064 | 0.979 | 0.914 | 0.951 | 0.898 | 6.78E-03 |
| cds.Camellia_sinensis.comp26398_c0_seq2_m.42894 | PREDICTED: miraculin [Theobroma cacao] | 24.856 | 4.7454 | 9.9 | 2 | 3 | 2 | 0.733 | 0.826 | 0.764 | 1.235 | 1.352 | 1.182 | 1.622 | 7.95E-04 |
| cds.Camellia_sinensis.comp26401_c0_seq4_m.10602 | PREDICTED: uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic [Nicotiana sylvestris] | 80.481 | 8.1099 | 6.8 | 5 | 5 | 4 | | | | | | | | |
| cds.Camellia_sinensis.comp26404_c0_seq1_m.35741 | PREDICTED: superoxide dismutase [Fe], chloroplastic [Vitis vinifera] | 34.096 | 33.438 | 22.7 | 6 | 11 | 6 | 1.011 | 0.999 | 0.963 | 0.966 | 1.044 | 1.013 | 1.017 | 5.76E-01 |

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| cds.Camellia_sinensis.comp26405_c0_seq1_m.42130 | PREDICTED: eukaryotic translation initiation factor [Vitis vinifera] | 22.537 | 21.756 | 23.2 | 5 | 7 | 5 | 0.954 | 0.984 | 0.977 | 1.025 | 1.006 | 1.009 | 1.043 | 1.88E-02 |
| cds.Camellia_sinensis.comp26408_c0_seq1_m.45653 | PREDICTED: brain acid soluble protein 1 homolog [Pyrus x bretschneideri] | 17.82 | 8.249 | 7.3 | 1 | 1 | 1 | 0.911 | 0.924 | 0.917 | 1.162 | 1.025 | 1.1 | 1.194 | 4.04E-02 |
| cds.Camellia_sinensis.comp26411_c0_seq1_m.4265 | PREDICTED: vacuolar protein-sorting-associated protein 11 homolog isoform X3 [Vitis vinifera] | 108.63 | 10.183 | 8 | 8 | 9 | 8 | 1.04 | 0.988 | 1.039 | 0.987 | 0.972 | 0.978 | 0.958 | 6.99E-02 |
| cds.Camellia_sinensis.comp26419_c0_seq1_m.19908 | PREDICTED: probable xyloglucan endotransglucosylase/hydrolase protein 6 [Juglans regia] | 32.893 | 26.298 | 26.8 | 8 | 11 | 6 | 1.24 | 1.256 | 1.279 | 0.758 | 0.72 | 0.685 | 0.573 | 5.66E-05 |

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| cds.Camellia_sinensis.comp26421_c0_seq2_m.36917 | PREDICTED: peptidyl-prolyl cis-trans isomerase CYP23 [Populus euphratica] | 26.056 | 1.1538 | 4.3 | 1 | 1 | 1 | 1.042 | 0.983 | 1.005 | 0.98 | 0.949 | 1.042 | 0.981 | 5.66E-01 |
| cds.Camellia_sinensis.comp26429_c0_seq1_m.30304 | PREDICTED: protein SLOW GREEN 1, chloroplastic-like [Nelumbo nucifera] | 37.781 | 6.4794 | 9.3 | 3 | 4 | 3 | 0.912 | 1.008 | 0.974 | 1.049 | 1.033 | 1.051 | 1.083 | 5.50E-02 |
| cds.Camellia_sinensis.comp26433_c0_seq1_m.39369 | PREDICTED: signal peptidase complex subunit 3B [Arachis ipaensis] | 19.062 | 8.4826 | 6.6 | 1 | 1 | 1 | 0.986 | 0.918 | 0.95 | 1.044 | 1.079 | 1.046 | 1.11 | 1.07E-02 |
| cds.Camellia_sinensis.comp26441_c0_seq1_m.17335 | PREDICTED: protein DETOXIFICATION 40-like [Daucus carota subsp. sativus] | 59.44 | 2.5212 | 3.8 | 2 | 2 | 2 | 1.05 | 1.075 | 1.09 | 0.828 | 0.826 | 1.107 | 0.859 | 2.40E-01 |

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| cds.Camellia_sinensis.comp26443_c0_seq1_m.27088 | PREDICTED: guanylate kinase 2, chloroplastic/mitochondrial [Ipomoea nil] | 33.997 | 3.1263 | 5.9 | 2 | 2 | 2 | 0.943 | 0.941 | 0.91 | 1.069 | 1.115 | 1.054 | 1.159 | 1.98E-03 |
| cds.Camellia_sinensis.comp26447_c0_seq1_m.21594 | import inner membrane translocase subunit [Arabidopsis thaliana] | 41.221 | 20.511 | 19.9 | 6 | 7 | 6 | 1.035 | 1.034 | 0.947 | 0.959 | 1.17 | 1.015 | 1.042 | 5.88E-01 |
| cds.Camellia_sinensis.comp26451_c0_seq1_m.29519 | PREDICTED: nitrilase-like protein 2 isoform X1 [Solanum pennellii] | 35.051 | 224.18 | 67.1 | 18 | 44 | 16 | 1.019 | 1.024 | 1.007 | 0.981 | 0.986 | 0.973 | 0.964 | 4.30E-03 |
| cds.Camellia_sinensis.comp26453_c0_seq1_m.38607 | PREDICTED: chaperone protein DnaJ-like [Gossypium hirsutum] | 13.938 | 4.1846 | 18.3 | 3 | 3 | 3 | 0.943 | 0.935 | 0.957 | 1.033 | 1.083 | 1.077 | 1.126 | 1.92E-03 |

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| cds.Camellia_sinensis.comp26455_c0_seq1_m.33143 | PREDICTED: proline--tRNA ligase, cytoplasmic [Arachis ipaensis] | 45.73 | 11.776 | 30 | 10 | 13 | 4 | 1.066 | 1.06 | 1.088 | 0.901 | 0.938 | 0.954 | 0.869 | 1.68E-03 |
| cds.Camellia_sinensis.comp26455_c1_seq1_m.45521 | PREDICTED: proline--tRNA ligase, cytoplasmic-like [Nelumbo nucifera] | 17.849 | 18.132 | 34 | 5 | 5 | 3 | 1.167 | 1.049 | 1.073 | 0.802 | 0.936 | 0.879 | 0.796 | 1.43E-02 |
| cds.Camellia_sinensis.comp26458_c0_seq2_m.35806 | dimethylallyl, adenosine tRNA methylthiotransferase [Arabidopsis thaliana] | 27.97 | 75.965 | 28.4 | 7 | 17 | 7 | 0.993 | 0.964 | 0.982 | 0.993 | 1.034 | 1.009 | 1.033 | 9.06E-02 |
| cds.Camellia_sinensis.comp26460_c0_seq1_m.7641 | PREDICTED: ferric reduction oxidase 7, chloroplastic isoform X1 [Vitis vinifera] | 83.622 | 31.494 | 8.9 | 6 | 7 | 6 | 1.031 | 1.042 | 1.059 | 0.938 | 0.953 | 0.944 | 0.905 | 3.84E-04 |

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| cds.Camellia_sinensis.comp26464_c0_seq1_m.23457 | PREDICTED: aspartate aminotransferase, cytoplasmic [Theobroma cacao] | 52.11 | 52.291 | 30.5 | 12 | 18 | 11 | 0.936 | 0.965 | 0.989 | 1.032 | 1.032 | 1.023 | 1.068 | 1.50E-02 |
| cds.Camellia_sinensis.comp26465_c0_seq1_m.51897 | PREDICTED: 3-hydroxybenzoate 6-hydroxylase 1 [Ricinus communis] | 16.335 | 1.425 | 6.2 | 1 | 1 | 1 | 0.975 | 1.013 | 0.939 | 1.022 | 1.002 | 1.063 | 1.055 | 1.29E-01 |
| cds.Camellia_sinensis.comp26474_c0_seq1_m.6815 | PREDICTED: WD repeat-containing protein 75 [Juglans regia] | 91.437 | 4.875 | 2.7 | 2 | 2 | 2 | 0.961 | 1.096 | 0.989 | 1.068 | 0.866 | 1.03 | 0.973 | 7.15E-01 |
| cds.Camellia_sinensis.comp26478_c0_seq1_m.44479 | PREDICTED: adrenodoxin-like protein 2, mitochondrial [Sesamum indicum] | 19.988 | 1.6865 | 7.2 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp26484_c0_seq1_m.27782 | PREDICTED: protein PELOTA 1 [Nicotiana | 42.383 | 2.0467 | 2.1 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp26490_c0_seq1_m.14796 | PREDICTED: carboxyl-terminal-processing peptidase 3, chloroplastic [Sesamum indicum] | 59.942 | 11.041 | 7.8 | 4 | 5 | 4 | 0.973 | 1.025 | 1.004 | 1.024 | 0.995 | 0.99 | 1.002 | 9.01E-01 |
| cds.Camellia_sinensis.comp26493_c0_seq1_m.11502 | PREDICTED: mitochondrial Rho GTPase 1 [Vitis vinifera] | 71.486 | 26.78 | 16.7 | 11 | 14 | 9 | 0.991 | 0.987 | 1.026 | 0.987 | 1.019 | 0.985 | 0.996 | 8.07E-01 |
| cds.Camellia_sinensis.comp26495_c1_seq2_m.22967 | PREDICTED: nudix hydrolase 19, chloroplastic [Solanum tuberosum | 21.613 | 34.288 | 25.5 | 5 | 6 | 5 | 1.121 | 0.961 | 0.989 | 1.064 | 0.794 | 1.063 | 0.951 | 6.27E-01 |
| cds.Camellia_sinensis.comp26495_c1_seq2_m.22968 | PREDICTED: nudix hydrolase 19, chloroplastic-like [Malus domestica] | 21.464 | 15.087 | 15.6 | 3 | 3 | 3 | 1.02 | 0.982 | 0.997 | 1.014 | 0.998 | 1 | 1.004 | 7.34E-01 |

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| cds.Camellia_sinensis.comp26498_c0_seq1_m.17905 | PREDICTED: probable 26S proteasome non-ATPase regulatory subunit 3 [Vitis vinifera] | 55.354 | 107.85 | 41.1 | 18 | 30 | 18 | 0.996 | 1 | 1.018 | 1.002 | 1.024 | 0.961 | 0.991 | 6.63E-01 |
| cds.Camellia_sinensis.comp26504_c0_seq2_m.48391 | PREDICTED: replication factor C subunit 2 [Lupinus angustifolius] | 16.02 | 18.242 | 28.4 | 3 | 3 | 3 | 0.986 | 0.945 | 0.934 | 1.106 | 1.036 | 1.018 | 1.103 | 3.16E-02 |
| cds.Camellia_sinensis.comp26506_c0_seq1_m.23107 | PREDICTED: altered inheritance of mitochondria protein 32 [Vitis vinifera] | 44.506 | 53.279 | 21.8 | 8 | 22 | 7 | 1.077 | 1.077 | 1.052 | 0.913 | 0.923 | 0.904 | 0.855 | 9.56E-05 |
| cds.Camellia_sinensis.comp26512_c0_seq1_m.11629 | PREDICTED: chaperone protein DnaJ [Citrus sinensis] | 34.913 | 49.411 | 31.8 | 8 | 11 | 8 | 1.042 | 1.05 | 1.092 | 0.926 | 0.947 | 0.936 | 0.882 | 1.40E-03 |

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| cds.Camellia_sinensis.comp26513_c0_seq2_m.30635 | PREDICTED: THO complex subunit 3 [Sesamum indicum] | 35.12 | 4.2404 | 6.4 | 2 | 2 | 2 | 1.014 | 1.001 | 1.083 | 0.991 | 1.001 | 0.915 | 0.938 | 1.63E-01 |
| cds.Camellia_sinensis.comp26525_c0_seq1_m.24481 | PREDICTED: 26S protease regulatory subunit S10B homolog B [Vigna radiata var. radiata] | 44.597 | 124.64 | 49.5 | 18 | 32 | 17 | 0.991 | 0.987 | 0.964 | 1.043 | 1.006 | 1.029 | 1.046 | 2.94E-02 |
| cds.Camellia_sinensis.comp26526_c0_seq2_m.10699 | PREDICTED: actin-related protein 5-like isoform X2 [Juglans regia] | 35.546 | 1.2195 | 3.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp26531_c0_seq1_m.8009 | PREDICTED: phospholipase D alpha 1 [Sesamum indicum] | 101.33 | 104.61 | 33 | 27 | 40 | 23 | 0.968 | 0.968 | 0.959 | 1.046 | 1.005 | 1.065 | 1.076 | 1.36E-02 |

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| cds.Camellia_sinensis.comp26543_c0_seq1_m.53696 | PREDICTED: probable mediator of RNA polymerase II transcription subunit 37c, partial [Raphanus sativus] | 16.527 | 3.4618 | 19.9 | 3 | 7 | 1 | 0.944 | 0.972 | 1.242 | 0.901 | 0.914 | 1.028 | 0.9 | 3.63E-01 |
| cds.Camellia_sinensis.comp26551_c0_seq1_m.14734 | PREDICTED: GPI transamidase component PIG-T [Vitis vinifera] | 74.92 | 1.9067 | 1.3 | 1 | 3 | 1 | 1.025 | 0.983 | 1.035 | 0.94 | 1.046 | 0.986 | 0.977 | 5.22E-01 |
| cds.Camellia_sinensis.comp26555_c0_seq1_m.49470 | PREDICTED: 60S ribosomal protein L28-2-like [Nelumbo nucifera] | 19.166 | 18.148 | 32.2 | 6 | 10 | 6 | 1.141 | 1.081 | 1.164 | 0.847 | 0.835 | 0.855 | 0.749 | 2.40E-04 |
| cds.Camellia_sinensis.comp26557_c0_seq1_m.48630 | PREDICTED: phenylalanine ammonia-lyase [Nelumbo nucifera] | 14.501 | 3.5862 | 33.8 | 4 | 4 | 2 | 1.442 | 1.345 | 1.454 | 0.473 | 0.552 | 0.597 | 0.382 | 1.83E-04 |

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| cds.Camellia_sinensis.comp26559_c0_seq1_m.17417 | PREDICTED: aspartate--tRNA ligase 2, cytoplasmic-like [Nelumbo nucifera] | 60.841 | 128.93 | 33.9 | 17 | 31 | 17 | 1.02 | 0.999 | 1.004 | 0.992 | 0.992 | 0.984 | 0.982 | 5.49E-02 |
| cds.Camellia_sinensis.comp26584_c0_seq2_m.37309 | PREDICTED: universal stress protein PHOS32 [Ipomoea nil] | 25.465 | 51.074 | 24.8 | 5 | 9 | 5 | 0.998 | 1.012 | 1.033 | 0.984 | 0.989 | 0.952 | 0.961 | 6.40E-02 |
| cds.Camellia_sinensis.comp26587_c0_seq1_m.16802 | | 50.306 | 1.4097 | 2.3 | 1 | 1 | 1 | 0.942 | 0.961 | 0.955 | 1.102 | 0.91 | 1.154 | 1.108 | 3.14E-01 |
| cds.Camellia_sinensis.comp26589_c0_seq1_m.29291 | 26S proteasome regulatory subunit RPN13 [Cajanus cajan] | 40.619 | 24.896 | 12 | 3 | 3 | 3 | 0.979 | 0.979 | 1.033 | 1.022 | 1.003 | 1.021 | 1.018 | 3.83E-01 |
| cds.Camellia_sinensis.comp26590_c0_seq1_m.37732 | putative linoleate 9S-lipoxygenase 5 [Morus notabilis] | 37.758 | 8.548 | 17 | 5 | 7 | 3 | 1.073 | 1.068 | 1.028 | 0.88 | 1.014 | 0.923 | 0.889 | 5.28E-02 |

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| cds.Camellia_sinensis.comp26592_c1_seq1_m.15592 | PREDICTED: betaine aldehyde dehydrogenase 1, chloroplastic [Ziziphus jujuba] | 57.088 | 109.51 | 26.4 | 11 | 20 | 11 | 1.009 | 0.987 | 0.973 | 0.996 | 1.008 | 1.015 | 1.017 | 2.32E-01 |
| cds.Camellia_sinensis.comp26604_c0_seq4_m.22113 | PREDICTED: phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and protein-tyrosine-phosphatase PTEN2A[Ricinus communis] | 47.181 | 8.6407 | 13.6 | 5 | 5 | 5 | 0.976 | 1.123 | 1.047 | 1.001 | 0.918 | 0.937 | 0.908 | 1.18E-01 |
| cds.Camellia_sinensis.comp26610_c0_seq1_m.1613 | PREDICTED: ABC transporter B family member 19 [Ricinus | 136.05 | 1.8935 | 3.3 | 4 | 4 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp26614_c0_seq1_m.15318 | PREDICTED: beta-fructofuranosidase, insoluble isoenzyme CWINV1 [Eucalyptus grandis] | 65.106 | 62.079 | 23.1 | 13 | 20 | 13 | 0.937 | 0.99 | 0.984 | 1.036 | 1.046 | 1.039 | 1.072 | 1.66E-02 |
| cds.Camellia_sinensis.comp26617_c0_seq1_m.24495 | DUF4336 domain protein [Medicago truncatula] | 50.59 | 55.652 | 15.4 | 8 | 11 | 8 | 0.997 | 0.982 | 0.954 | 1.026 | 0.995 | 1.03 | 1.04 | 8.01E-02 |
| cds.Camellia_sinensis.comp26626_c0_seq1_m.37458 | rubredoxin family protein [Populus trichocarpa] | 17.331 | 7.4221 | 15.7 | 3 | 6 | 3 | 0.993 | 0.977 | 0.99 | 0.989 | 0.99 | 1.051 | 1.024 | 3.29E-01 |
| cds.Camellia_sinensis.comp26628_c0_seq1_m.25079 | Protein XAP5 CIRCADIAN TIMEKEEPER [Morus notabilis] | 33.574 | 5.7626 | 7.2 | 1 | 1 | 1 | 0.818 | 1.194 | 1.05 | 1.022 | 0.935 | 1.003 | 0.967 | 8.53E-01 |
| cds.Camellia_sinensis.comp26630_c0_seq1_m.40606 | PREDICTED: 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic-like [Jatropha curcas] | 16.555 | 1.8012 | 14.6 | 2 | 3 | 2 | 1.033 | 0.912 | 1.076 | 0.842 | 1.074 | 1.06 | 0.985 | 8.52E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26631_c0_seq1_m.33058 | PREDICTED: non-functional NADPH-dependent codeinone reductase 2-like [Daucus carota subsp. sativus] | 36.923 | 145.33 | 55.2 | 18 | 56 | 16 | 0.924 | 0.934 | 0.942 | 1.063 | 1.084 | 1.064 | 1.147 | 8.28E-05 |
| cds.Camellia_sinensis.comp26640_c0_seq1_m.35494 | PREDICTED: endonuclease 1 [Nicotiana attenuata] | 35.181 | 3.5282 | 2.3 | 1 | 1 | 1 | 1.014 | 1.011 | 1.067 | 0.96 | 0.972 | 0.978 | 0.941 | 3.01E-02 |
| cds.Camellia_sinensis.comp26646_c0_seq1_m.24007 | saccharopine dehydrogenase [Medicago truncatula] | 33.778 | 39.351 | 15.9 | 5 | 7 | 5 | 0.957 | 0.956 | 0.992 | 1.056 | 1.004 | 1.071 | 1.078 | 3.18E-02 |
| cds.Camellia_sinensis.comp26646_c0_seq1_m.24008 | Saccharopine dehydrogenase [Arabidopsis thaliana] | 17.77 | 7.0217 | 10.6 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp26652_c1_seq1_m.22429 | PREDICTED: protein BTR1 isoform X2 [Vitis vinifera] | 34.778 | 42.686 | 26.6 | 8 | 11 | 6 | 0.984 | 1.032 | 1.047 | 0.962 | 0.954 | 0.965 | 0.941 | 3.30E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26652_c1_seq3_m.38958 | PREDICTED: protein BTR1 isoform X2 [Vitis vinifera] | 26.963 | 9.3883 | 26 | 6 | 7 | 4 | 1.093 | 0.839 | 0.735 | 1.072 | 1.143 | 1.138 | 1.257 | 1.10E-01 |
| cds.Camellia_sinensis.comp26653_c0_seq1_m.18036 | PREDICTED: transducin beta-like protein 2 [Nicotiana sylvestris] | 46.342 | 23.642 | 14 | 5 | 8 | 5 | 1.004 | 1.042 | 1.033 | 1.076 | 0.923 | 0.964 | 0.962 | 4.39E-01 |
| cds.Camellia_sinensis.comp26664_c0_seq1_m.10560 | PREDICTED: N6-adenosine-methyltransferase MT-A70-like [Vitis vinifera] | 80.741 | 5.5668 | 4.1 | 3 | 3 | 3 | 1.053 | 1.095 | 1.001 | 1.048 | 0.99 | 0.814 | 0.906 | 2.67E-01 |
| cds.Camellia_sinensis.comp26664_c1_seq1_m.34799 | PREDICTED: ATP-dependent Clp protease proteolytic subunit 4, chloroplastic [Theobroma cacao] | 26.034 | 52.37 | 30.3 | 9 | 19 | 9 | 1.027 | 1.02 | 0.987 | 0.982 | 1.01 | 0.991 | 0.983 | 3.18E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26669_c0_seq1_m.26830 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 12 isoform X2 [Jatropha curcas] | 50.13 | 21.586 | 24.6 | 11 | 12 | 9 | 1.005 | 1.078 | 1.027 | 0.997 | 0.985 | 0.911 | 0.93 | 1.07E-01 |
| cds.Camellia_sinensis.comp26669_c0_seq2_m.41168 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 12 isoform X2 [Vitis vinifera] | 34.753 | 3.3538 | 13.6 | 4 | 5 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp26669_c0_seq3_m.54299 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 12 [Beta vulgaris subsp. vulgaris] | 13.355 | 1.9094 | 23.2 | 3 | 4 | 1 | 0.946 | 1.048 | 0.947 | 1.114 | 0.981 | 0.986 | 1.048 | 4.40E-01 |
| cds.Camellia_sinensis.comp26675_c0_seq1_m.28276 | PREDICTED: translation initiation factor eIF-2B subunit alpha-like [Nicotiana tabacum] | 44.337 | 18.744 | 18.5 | 6 | 7 | 6 | 0.897 | 0.935 | 0.969 | 1.139 | 1.036 | 1.064 | 1.156 | 1.57E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26676_c0_seq2_m.53628 | PREDICTED: ER membrane protein complex subunit 10 [Gossypium raimondii] | 16.642 | 2.4278 | 6.6 | 2 | 2 | 2 | 0.974 | 1.044 | 0.978 | 0.992 | 1.039 | 0.985 | 1.007 | 8.18E-01 |
| cds.Camellia_sinensis.comp26677_c1_seq1_m.34526 | PREDICTED: cysteine proteinase inhibitor 6 [Theobroma cacao] | 27.371 | 40.686 | 31.6 | 6 | 9 | 6 | 1.001 | 0.995 | 0.963 | 1 | 1.036 | 1.03 | 1.036 | 9.41E-02 |
| cds.Camellia_sinensis.comp26685_c0_seq3_m.18193 | PREDICTED: asparagine--tRNA ligase, chloroplastic/mitochondrial isoform X1 [Vitis vinifera] | 46.624 | 1.9691 | 2.1 | 1 | 2 | 1 | 0.953 | 0.941 | 1.027 | 1.036 | 1.042 | 1.024 | 1.062 | 9.35E-02 |
| cds.Camellia_sinensis.comp26685_c0_seq3_m.18196 | PREDICTED: asparagine--tRNA ligase, chloroplastic/mitochondrial-like [Ipomoea nil] | 11.378 | 13.148 | 40.4 | 4 | 9 | 3 | 0.953 | 0.957 | 0.985 | 1.022 | 1.022 | 1.028 | 1.061 | 4.90E-03 |

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| cds.Camellia_sinensis.comp26692_c0_seq1_m.29062 | PREDICTED: ACT domain-containing protein ACR11-like [Daucus carota subsp. sativus] | 31.506 | 97.028 | 31.3 | 9 | 32 | 9 | 1.009 | 0.994 | 0.985 | 1.01 | 1.016 | 0.982 | 1.007 | 6.28E-01 |
| cds.Camellia_sinensis.comp26701_c0_seq2_m.39566 | PREDICTED: universal stress protein PHOS34 [Eucalyptus grandis] | 18.265 | 28.105 | 14.1 | 2 | 4 | 2 | 1.005 | 1.048 | 1.083 | 0.943 | 0.975 | 1.021 | 0.937 | 1.09E-01 |
| cds.Camellia_sinensis.comp26706_c0_seq1_m.26738 | esterase/lipase/thioesterase family protein [Populus trichocarpa] | 44.093 | 4.2696 | 5.3 | 2 | 2 | 2 | 1.039 | 0.978 | 1.006 | 1.027 | 0.985 | 0.971 | 0.987 | 6.13E-01 |
| cds.Camellia_sinensis.comp26707_c0_seq1_m.474 | PREDICTED: pre-mRNA-processing-splicing factor 8A [Theobroma cacao] | 268.39 | 25.359 | 3.9 | 9 | 10 | 9 | 1.162 | 1.193 | 1.139 | 0.882 | 0.833 | 0.843 | 0.732 | 1.42E-04 |

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| cds.Camellia_sinensis.comp26709_c0_seq1_m.43631 | PREDICTED: non-specific lipid-transfer protein 1-like [Pyrus x bretschneideri] | 12.235 | 1.3564 | 7.6 | 1 | 1 | 1 | 0.946 | 1.007 | 1.001 | 1.043 | 0.999 | 1.023 | 1.038 | 1.89E-01 |
| cds.Camellia_sinensis.comp26709_c0_seq2_m.48095 | PREDICTED: non-specific lipid-transfer protein 1-like [Pyrus x bretschneideri] | 12.209 | 6.9332 | 28.8 | 3 | 6 | 3 | 0.824 | 0.811 | 0.787 | 1.247 | 1.173 | 1.205 | 1.497 | 5.73E-05 |
| cds.Camellia_sinensis.comp26712_c0_seq1_m.45153 | PREDICTED: NHP2-like protein 1 [Prunus mume] | 16.063 | 30.39 | 26.5 | 3 | 6 | 3 | 0.973 | 0.994 | 0.982 | 0.996 | 1.028 | 1.053 | 1.043 | 7.05E-02 |
| cds.Camellia_sinensis.comp26713_c0_seq1_m.41573 | PREDICTED: probable NAD(P)H dehydrogenase (quinone) FQR1-like 1 [Vigna radiata var. radiata] | 21.664 | 47.978 | 46.3 | 8 | 17 | 3 | 1.053 | 1.024 | 1.047 | 0.912 | 0.988 | 1.067 | 0.95 | 3.10E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26714_c0_seq2_m.30909 | PREDICTED: peptidyl-tRNA hydrolase 2, mitochondrial isoform X2 [Ipomoea | 19.996 | 1.4244 | 9.4 | 2 | 2 | 2 | 1.034 | 1.046 | 1.006 | 1.071 | 0.901 | 0.946 | 0.946 | 3.29E-01 |
| cds.Camellia_sinensis.comp26720_c0_seq1_m.28521 | PREDICTED: probable fructokinase-7 [Prunus mume] | 41.129 | 7.6147 | 13.2 | 5 | 8 | 4 | 0.874 | 1.088 | 1.05 | | 0.856 | 1.05 | 0.949 | 6.80E-01 |
| cds.Camellia_sinensis.comp26723_c0_seq1_m.17388 | PREDICTED: 11-oxo-beta-amyrin 30-oxidase isoform X2 [Vitis vinifera] | 60.915 | 5.9051 | 3.5 | 2 | 2 | 2 | 0.931 | 0.957 | 0.922 | 1.053 | 1.067 | 1.1 | 1.146 | 1.34E-03 |
| cds.Camellia_sinensis.comp26729_c0_seq1_m.8066 | PREDICTED: beta-amyrin synthase [Sesamum indicum] | 87.518 | 16.013 | 5.9 | 4 | 4 | 4 | 0.92 | 0.931 | 1.032 | 1.046 | 1.061 | 1.089 | 1.109 | 5.30E-02 |

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| cds.Camellia_sinensis.comp26732_c0_seq1_m.22473 | PREDICTED: tetratricopeptide repeat protein 38-like isoform X3 [Gossypium raimondii] | 53.338 | 1.649 | 4.9 | 2 | 2 | 2 | 0.981 | 1.013 | 0.853 | 1.051 | 1.071 | 1.051 | 1.115 | 1.72E-01 |
| cds.Camellia_sinensis.comp26744_c0_seq1_m.29380 | PREDICTED: thioredoxin reductase 1-like [Nelumbo | 36.433 | 108.08 | 26.5 | 7 | 14 | 7 | 0.99 | 0.935 | 0.981 | 1.028 | 1.026 | 1.033 | 1.062 | 7.65E-02 |
| cds.Camellia_sinensis.comp26747_c0_seq1_m.38478 | PREDICTED: arogenate dehydrogenase 1, chloroplastic isoform X1 [Vitis vinifera] | 31.278 | 41.475 | 16.7 | 5 | 6 | 5 | 0.818 | 0.848 | 0.827 | 1.224 | 1.13 | 1.184 | 1.419 | 1.62E-04 |
| cds.Camellia_sinensis.comp26749_c0_seq1_m.45343 | PREDICTED: myosin-5-like [Glycine max] | 15.088 | 12.69 | 27.3 | 4 | 19 | 4 | 1.081 | 1.059 | 1.057 | 0.889 | 0.919 | 0.95 | 0.863 | 1.94E-03 |

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| cds.Camellia_sinensis.comp26757_c0_seq1_m.10442 | PREDICTED: probable inactive serine/threonine-protein kinase scy1 [Ziziphus jujuba] | 89.205 | 12.923 | 2.7 | 1 | 1 | 1 | 0.868 | 1.012 | 1.018 | 1.257 | 1.014 | 0.879 | 1.087 | 5.53E-01 |
| cds.Camellia_sinensis.comp26760_c0_seq1_m.52107 | PREDICTED: pectinesterase-like [Eucalyptus grandis] | 12.065 | 3.3867 | 22.9 | 2 | 2 | 2 | 0.977 | 1.007 | 0.986 | 1.037 | 1.065 | 0.945 | 1.026 | 5.49E-01 |
| cds.Camellia_sinensis.comp26767_c0_seq1_m.54690 | PREDICTED: adenosylhomocysteinase-like [Phoenix dactylifera] | 15.401 | 10.569 | 25 | 3 | 9 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp26768_c0_seq1_m.36038 | PREDICTED: carbonic anhydrase 2 isoform X1 [Ricinus communis] | 31.143 | 100.27 | 57.1 | 13 | 36 | 11 | 0.95 | 0.947 | 0.976 | 1.006 | 1.017 | 1.037 | 1.065 | 8.46E-03 |
| cds.Camellia_sinensis.comp26774_c0_seq1_m.44152 | PREDICTED: sm-like protein LSM2 [Vitis vinifera] | 14.696 | 7.3939 | 10.2 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26781_c0_seq1_m.31960 | PREDICTED: methionine aminopeptidase 1B, chloroplastic [Juglans regia] | 40.922 | 24.306 | 15.2 | 7 | 10 | 7 | 1.058 | 1.119 | 1.097 | 0.932 | 0.892 | 0.914 | 0.836 | 9.99E-04 |
| cds.Camellia_sinensis.comp26783_c0_seq1_m.33779 | PREDICTED: translin-associated protein X [Nelumbo nucifera] | 32.049 | 1.8397 | 3.2 | 1 | 1 | 1 | 0.991 | 0.865 | 1.019 | 1.046 | 1.043 | 1.058 | 1.095 | 2.09E-01 |
| cds.Camellia_sinensis.comp26785_c0_seq1_m.34625 | NAD-dependent epimerase/dehydratase family protein [Medicago truncatula] | 31.725 | 104.5 | 24.3 | 6 | 15 | 6 | 0.957 | 0.895 | 0.906 | 1.076 | 1.089 | 1.099 | 1.183 | 1.42E-03 |
| cds.Camellia_sinensis.comp26789_c0_seq2_m.42230 | PREDICTED: universal stress protein A-like protein [Vitis vinifera] | 17.846 | 9.5695 | 19.9 | 3 | 5 | 3 | 0.978 | 0.97 | 0.926 | 1.079 | 1.031 | 1.107 | 1.119 | 1.38E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26795_c0_seq1_m.42493 | PREDICTED: protein CURVATURE THYLAKOID 1C, chloroplastic [Eucalyptus grandis] | 16.607 | 61.411 | 18.4 | 3 | 8 | 3 | 0.948 | 0.971 | 0.907 | 1.093 | 1.026 | 1.012 | 1.108 | 2.99E-02 |
| cds.Camellia_sinensis.comp26800_c0_seq1_m.39501 | PREDICTED: thioredoxin [Vitis vinifera] | 22.95 | 75.526 | 25.2 | 5 | 21 | 4 | 1.013 | 1.057 | 1.006 | 0.974 | 0.951 | 0.969 | 0.941 | 2.36E-02 |
| cds.Camellia_sinensis.comp26812_c0_seq1_m.34139 | PREDICTED: transmembrane ascorbate ferrireductase 1 [Sesamum indicum] | 25.265 | 34.592 | 4.8 | 1 | 4 | 1 | 0.834 | 0.748 | 0.738 | 1.216 | 1.26 | 1.272 | 1.616 | 3.02E-04 |
| cds.Camellia_sinensis.comp26815_c0_seq1_m.28445 | PREDICTED: peroxidase 3-like [Nelumbo nucifera] | 35.276 | 83.046 | 36.5 | 11 | 19 | 11 | 1 | 1.012 | 1.014 | 0.979 | 0.997 | 0.995 | 0.982 | 6.38E-02 |
| cds.Camellia_sinensis.comp26817_c0_seq1_m.39868 | PREDICTED: outer envelope pore protein 21, chloroplastic-like [Juglans regia] | 19.349 | 30.634 | 25.1 | 3 | 4 | 3 | 1.007 | 1.019 | 0.982 | 1.006 | 0.974 | 0.884 | 0.952 | 2.79E-01 |

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| cds.Camellia_sinensis.comp26819_c0_seq1_m.6333 | PREDICTED: alpha-amylase 3, chloroplastic [Vitis vinifera] | 102.14 | 72.676 | 19.9 | 17 | 25 | 17 | 1.068 | 1.049 | 1.072 | 0.898 | 0.939 | 0.951 | 0.874 | 1.94E-03 |
| cds.Camellia_sinensis.comp26828_c0_seq1_m.56452 | PREDICTED: beta-galactosidase 1-like isoform X3 [Eucalyptus grandis] | 12.448 | 1.3163 | 7.3 | 1 | 2 | 1 | 0.73 | 0.768 | 0.694 | 1.271 | 1.311 | 1.322 | 1.781 | 5.63E-05 |
| cds.Camellia_sinensis.comp26832_c0_seq1_m.42570 | PREDICTED: cytochrome b5 [Nicotiana attenuata] | 15.231 | 2.5349 | 35.8 | 3 | 6 | 1 | 0.97 | 0.969 | 1.103 | 0.972 | 0.992 | 1.004 | 0.976 | 6.31E-01 |
| cds.Camellia_sinensis.comp26832_c0_seq2_m.43366 | PREDICTED: cytochrome b5 [Nicotiana attenuata] | 15.213 | 31.552 | 44 | 5 | 10 | 3 | 1.005 | 0.968 | 1.014 | 1.008 | 1.047 | 1.016 | 1.028 | 2.04E-01 |
| cds.Camellia_sinensis.comp26838_c0_seq2_m.16845 | FAD/NAD(P)-binding oxidoreductase family protein [Arabidopsis thaliana] | 54.792 | 1.2285 | 3 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26839_c0_seq3_m.11391 | FG-GAP repeat-containing family protein [Populus trichocarpa] | 74.282 | 6.56 | 4 | 3 | 3 | 3 | 1.015 | 1.001 | 1.019 | 0.923 | 1.051 | 0.993 | 0.978 | 5.91E-01 |
| cds.Camellia_sinensis.comp26850_c0_seq1_m.10545 | PREDICTED: SUMO-activating enzyme subunit 2 [Prunus mume] | 72.285 | 49.95 | 11 | 7 | 8 | 7 | 0.941 | 0.958 | 0.947 | 1.08 | 1.067 | 1.035 | 1.118 | 1.24E-03 |
| cds.Camellia_sinensis.comp26854_c0_seq2_m.50755 | PREDICTED: NAD-dependent malic enzyme 59 kDa isoform, mitochondrial [Sesamum indicum] | 11.659 | 5.1399 | 19.5 | 3 | 5 | 2 | 0.987 | 0.922 | 1.014 | 1.015 | 1.037 | 1.042 | 1.059 | 1.22E-01 |
| cds.Camellia_sinensis.comp26865_c0_seq1_m.29633 | PREDICTED: ycf54-like protein [Nicotiana tabacum] | 25.386 | 107.35 | 49.6 | 9 | 21 | 9 | 1.092 | 1.031 | 1.058 | 0.939 | 0.901 | 0.926 | 0.87 | 2.46E-03 |

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| cds.Camellia_sinensis.comp26866_c0_seq1_m.30905 | PREDICTED: soluble inorganic pyrophosphatase 6, chloroplastic-like [Nicotiana attenuata] | 33.053 | 157.73 | 38.2 | 11 | 33 | 11 | 1.031 | 1.03 | 1.034 | 0.963 | 0.966 | 0.977 | 0.939 | 1.58E-04 |
| cds.Camellia_sinensis.comp26867_c0_seq1_m.23170 | PREDICTED: fructose-1,6-bisphosphatase, chloroplastic [Glycine max] | 45.155 | 247.91 | 39.1 | 16 | 42 | 16 | 1.005 | 0.945 | 0.946 | 1.022 | 1.058 | 1.02 | 1.07 | 4.41E-02 |
| cds.Camellia_sinensis.comp26874_c0_seq2_m.34359 | PREDICTED: binding partner of ACD11 1-like [Nicotiana tabacum] | 27.172 | 48.964 | 31.6 | 8 | 15 | 5 | 0.93 | 1.005 | 0.988 | 1.021 | 1.023 | 1.073 | 1.066 | 8.69E-02 |
| cds.Camellia_sinensis.comp26874_c0_seq3_m.40819 | PREDICTED: binding partner of ACD11 1 [Vitis vinifera] | 23.873 | 44.805 | 30.2 | 6 | 8 | 5 | 0.983 | 1.028 | 1.002 | 1.033 | 0.996 | 1.011 | 1.009 | 6.20E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26887_c0_seq1_m.34748 | PREDICTED: neurofilament heavy polypeptide [Vitis vinifera] | 29.224 | 40.323 | 27.8 | 6 | 9 | 6 | 1.203 | 1.22 | 1.195 | 0.795 | 0.754 | 0.794 | 0.648 | 1.97E-05 |
| cds.Camellia_sinensis.comp26888_c0_seq1_m.47435 | PREDICTED: endochitinase EP3 [Daucus carota subsp. sativus] | 16.327 | 13.09 | 19.5 | 5 | 8 | 5 | 0.952 | 0.951 | 0.944 | 1.063 | 1.07 | 1.028 | 1.11 | 1.18E-03 |
| cds.Camellia_sinensis.comp26892_c0_seq1_m.37174 | PREDICTED: ras-related protein RABB1b [Ricinus communis] | 23.346 | 21.749 | 30.8 | 5 | 9 | 3 | 1.003 | 0.939 | 1.067 | 0.981 | 1.033 | 1.036 | 1.014 | 7.40E-01 |
| cds.Camellia_sinensis.comp26895_c0_seq1_m.15701 | PREDICTED: polyadenylate-binding protein 2-like [Jatropha | 63.383 | 53.805 | 19.5 | 8 | 10 | 7 | 0.939 | 1.038 | 0.932 | 1.004 | 0.986 | 1.091 | 1.059 | 2.84E-01 |

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| cds.Camellia_sinensis.comp26900_c0_seq1_m.38174 | PREDICTED: histidine-containing phosphotransfer protein 1-like isoform X1 [Erythranthe guttata] | 19.911 | 6.3023 | 13.2 | 2 | 3 | 2 | 0.8 | 1.147 | 0.835 | 1.126 | 1.017 | 1.118 | 1.172 | 2.22E-01 |
| cds.Camellia_sinensis.comp26907_c0_seq5_m.36751 | plasma membrane fusion protein [Arabidopsis thaliana] | 25.319 | 47.2 | 30.7 | 5 | 12 | 5 | 0.946 | 1.031 | 1.072 | 1.028 | 1.016 | 0.972 | 0.989 | 8.21E-01 |
| cds.Camellia_sinensis.comp26914_c0_seq1_m.26134 | PREDICTED: peroxisomal and mitochondrial division factor 2 [Daucus carota subsp. sativus] | 47.848 | 34.428 | 25.5 | 13 | 15 | 13 | 0.977 | 0.978 | 0.979 | 1.032 | 0.954 | 1.05 | 1.035 | 3.76E-01 |
| cds.Camellia_sinensis.comp26921_c1_seq1_m.42103 | PREDICTED: cytochrome b-c1 complex subunit 7-2 isoform X1 [Vitis vinifera] | 14.728 | 26.058 | 42.3 | 4 | 12 | 4 | 0.96 | 0.989 | 0.956 | 1.008 | 1.024 | 1.013 | 1.048 | 1.55E-02 |

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| cds.Camellia_sinensis.comp26923_c0_seq1_m.22885 | PREDICTED: vacuolar protein sorting-associated protein 9A isoform X1 [Vitis vinifera] | 53.125 | 5.3548 | 3.8 | 1 | 1 | 1 | 0.929 | 1.107 | 0.833 | 1.094 | 1.067 | 0.997 | 1.101 | 3.07E-01 |
| cds.Camellia_sinensis.comp26927_c0_seq1_m.27964 | PREDICTED: 4-sulfomuconolactone hydrolase [Prunus mume] | 36.974 | 5.0534 | 10.8 | 4 | 4 | 4 | 0.996 | 1.026 | 1.006 | 0.957 | 0.998 | 1.022 | 0.983 | 4.59E-01 |
| cds.Camellia_sinensis.comp26935_c0_seq3_m.37978 | PREDICTED: monothiol glutaredoxin-S7, chloroplastic [Populus euphratica] | 19.607 | 16.85 | 25 | 3 | 6 | 3 | 0.975 | 0.978 | 1.036 | 1.032 | 0.969 | 1.006 | 1.006 | 8.33E-01 |
| cds.Camellia_sinensis.comp26950_c0_seq5_m.39635 | acetyltransferase (GNAT) domain protein [Medicago truncatula] | 20.016 | 1.3934 | 4.6 | 1 | 1 | 1 | 1.08 | 1.105 | 1.056 | 0.985 | 0.887 | 0.874 | 0.847 | 1.38E-02 |
| cds.Camellia_sinensis.comp26957_c0_seq1_m.38574 | transmembrane protein [Arabidopsis thaliana] | 23.198 | 4.0528 | 8.1 | 2 | 4 | 2 | 1.002 | 0.997 | 0.956 | 1.014 | 0.987 | 1.055 | 1.034 | 2.43E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26961_c0_seq2_m.46775 | PREDICTED: superoxide dismutase [Cu-Zn] 2 [Eucalyptus grandis] | 16.883 | 30.185 | 47.9 | 7 | 12 | 7 | 0.994 | 0.952 | 0.957 | 1.042 | 1.022 | 1.064 | 1.078 | 1.40E-02 |
| cds.Camellia_sinensis.comp26963_c0_seq1_m.25102 | PREDICTED: protein RETICULATA-RELATED 3, chloroplastic-like [Pyrus x bretschneideri] | 24.801 | 6.4192 | 14.2 | 3 | 3 | 3 | 0.989 | 1.052 | 1.044 | 0.942 | 0.963 | 1.011 | 0.945 | 1.19E-01 |
| cds.Camellia_sinensis.comp26967_c0_seq1_m.16638 | PREDICTED: citrate synthase, mitochondrial [Ipomoea nil] | 52.713 | 77.626 | 26.1 | 12 | 23 | 12 | 1.028 | 1.034 | 1.005 | 0.98 | 0.986 | 0.983 | 0.962 | 1.15E-02 |
| cds.Camellia_sinensis.comp26973_c0_seq1_m.39125 | PREDICTED: CBL-interacting serine/threonine-protein kinase 23 isoform X2 [Ziziphus jujuba] | 14.419 | 1.5675 | 6.2 | 1 | 1 | 1 | 1.037 | 1.055 | 1.076 | 0.959 | 0.967 | 0.9 | 0.892 | 1.02E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26976_c0_seq1_m.27661 | PREDICTED: translation initiation factor IF-3 [Ricinus communis] | 31.233 | 28.789 | 13.9 | 3 | 6 | 3 | 1.234 | 1.202 | 1.17 | 0.792 | 0.79 | 0.772 | 0.653 | 1.82E-05 |
| cds.Camellia_sinensis.comp26980_c0_seq1_m.12038 | PREDICTED: transmembrane 9 superfamily member 8-like [Solanum tuberosum | 74.085 | 14.942 | 5.6 | 4 | 4 | 4 | 1.035 | 1.029 | 1.049 | 0.946 | 0.971 | 0.891 | 0.902 | 1.64E-02 |
| cds.Camellia_sinensis.comp26983_c0_seq12_m.33669 | PREDICTED: THO complex subunit 4A-like [Juglans regia] | 28.209 | 15.891 | 24.8 | 8 | 13 | 1 | 1.134 | 1.08 | 1.206 | 0.834 | 0.851 | 0.859 | 0.744 | 8.78E-04 |
| cds.Camellia_sinensis.comp26983_c0_seq13_m.33647 | PREDICTED: THO complex subunit 4A-like isoform X1 [Nelumbo nucifera] | 28.224 | 4.6827 | 25 | 8 | 12 | 2 | 1.054 | 1.095 | 1.07 | 0.847 | 0.94 | 0.976 | 0.858 | 2.44E-02 |
| cds.Camellia_sinensis.comp26983_c0_seq15_m.36240 | PREDICTED: THO complex subunit 4B-like [Juglans regia] | 28.281 | 2.4998 | 8 | 2 | 2 | 1 | 1.007 | 0.996 | 0.902 | 0.95 | 1.039 | 1.114 | 1.068 | 3.24E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp26983_c0_seq93_m.28144 | PREDICTED: THO complex subunit 4D [Solanum pennellii] | 22.581 | 6.3836 | 14.7 | 3 | 4 | 3 | 1.156 | 1.179 | 1.26 | 0.781 | 0.879 | 0.697 | 0.656 | 4.06E-03 |
| cds.Camellia_sinensis.comp26989_c0_seq19_c0_seq1_m.41111 | PREDICTED: putative L-ascorbate peroxidase 6 isoform X1 [Vitis vinifera] | 17.682 | 17.501 | 39.5 | 6 | 10 | 6 | 0.979 | 0.968 | 1.014 | 1.036 | 1.031 | 1.005 | 1.037 | 9.38E-02 |
| cds.Camellia_sinensis.comp26991_c0_seq1_m.16685 | PREDICTED: signal recognition particle 54 kDa protein 2 [Theobroma cacao] | 55.31 | 21.603 | 15.2 | 6 | 7 | 6 | 0.978 | 1.007 | 1.047 | 0.99 | 1.02 | 1 | 0.993 | 7.63E-01 |
| cds.Camellia_sinensis.comp26996_c0_seq1_m.34338 | PREDICTED: THO complex subunit 7A [Sesamum indicum] | 27.826 | 3.4659 | 9.2 | 2 | 2 | 2 | 0.97 | 1.059 | 1.032 | 1.008 | 0.895 | 1.042 | 0.962 | 4.92E-01 |
| cds.Camellia_sinensis.comp27000_c0_seq1_m.42120 | PREDICTED: mitochondrial acidic protein MAM33 isoform X2 [Solanum tuberosum | 25.95 | 2.3507 | 5.2 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp27010_c0_seq1_m.9726 | PREDICTED: putative beta-D-xylosidase [Jatropha curcas] | 83.377 | 148.26 | 26.1 | 16 | 42 | 16 | 0.922 | 0.934 | 0.918 | 1.074 | 1.051 | 1.093 | 1.16 | 2.83E-04 |
| cds.Camellia_sinensis.comp27016_c0_seq1_m.34053 |  | 26.014 | 26.705 | 14 | 3 | 6 | 3 | 1.129 | 1.104 | 1.004 | 0.881 | 0.879 | 0.91 | 0.825 | 7.08E-03 |
| cds.Camellia_sinensis.comp27021_c0_seq1_m.30589 | uncharacterized LOC100274051 [Zea mays] | 21.662 | 11.98 | 19.6 | 3 | 6 | 3 | 0.925 | 0.999 | 0.96 | 0.956 | 1.115 | 1.066 | 1.088 | 1.80E-01 |
| cds.Camellia_sinensis.comp27022_c0_seq1_m.35616 | PREDICTED: B-cell receptor-associated protein 31-like [Nicotiana tabacum] | 24.807 | 35.457 | 14.4 | 3 | 9 | 3 | 1.005 | 1.004 | 0.99 | 1.004 | 0.969 | 1.023 | 0.999 | 9.45E-01 |
| cds.Camellia_sinensis.comp27034_c0_seq1_m.33320 | PREDICTED: dihydrofolate reductase [Vitis vinifera] | 32.39 | 61.654 | 9.1 | 2 | 3 | 2 | 1.401 | 1.392 | 1.43 | 0.561 | 0.682 | 0.507 | 0.414 | 9.54E-03 |

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| cds.Camellia_sinensis.comp27037_c0_seq1_m.58749 | PREDICTED: putative quinone-oxidoreductase homolog, chloroplastic [Prunus mume] | 11.67 | 1.4625 | 16.3 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp27042_c0_seq1_m.32393 | heme oxygenase 1, chloroplastic-like [Nicotiana tabacum] | 33.028 | 29.896 | 25.1 | 7 | 8 | 4 | 1.039 | 0.976 | 1.023 | 0.984 | 0.991 | 0.975 | 0.971 | 2.08E-01 |
| cds.Camellia_sinensis.comp27042_c0_seq2_m.32684 | heme oxygenase 1, chloroplastic-like [Nicotiana tabacum] | 31.142 | 1.9489 | 16.2 | 5 | 5 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp27045_c0_seq1_m.3580 | PREDICTED: nuclear pore complex protein NUP96 [Vitis vinifera] | 118.16 | 1.225 | 2.8 | 3 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp27046_c0_seq1_m.56718 | PREDICTED: nitrilase-like protein 2 [Ricinus communis] | 13.564 | 1.2095 | 30.6 | 3 | 4 | 1 | 0.953 | 1.033 | 1.073 | 0.961 | 0.997 | 0.992 | 0.964 | 3.93E-01 |

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| cds.Camellia_sinensis.comp27049_c0_seq1_m.21867 | PREDICTED: protein disulfide-isomerase 5-2 [Ricinus communis] | 48.982 | 32.986 | 24.1 | 11 | 14 | 11 | 0.946 | 0.949 | 0.976 | 1.035 | 1.074 | 1.056 | 1.102 | 2.60E-03 |
| cds.Camellia_sinensis.comp27051_c0_seq1_m.17273 | PREDICTED: anthranilate synthase alpha subunit 2, chloroplastic-like isoform X2 [Nicotiana tabacum] | 65.075 | 190.48 | 45.6 | 23 | 48 | 23 | 1.013 | 1.013 | 1 | 0.982 | 0.984 | 0.988 | 0.976 | 6.70E-03 |
| cds.Camellia_sinensis.comp27055_c0_seq15_m.10230 | PREDICTED: coronatine-insensitive protein 1 [Theobroma cacao] | 66.812 | 12.836 | 11.3 | 6 | 7 | 6 | 0.87 | 0.958 | 1.015 | 1.02 | 1.042 | 1.084 | 1.107 | 1.00E-01 |
| cds.Camellia_sinensis.comp27058_c0_seq28_m.48495 | PREDICTED: LOW QUALITY PROTEIN: auxilin-related protein 1-like [Malus domestica] | 12.134 | 1.7325 | 9.5 | 1 | 3 | 1 | 1.021 | 0.923 | 0.953 | 1.014 | 1.1 | 1.044 | 1.09 | 8.56E-02 |

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| cds.Camellia_sinensis.comp27064_c0_seq1_m.17481 | PREDICTED: putative clathrin assembly protein At2g01600 [Nelumbo | 62.405 | 5.1308 | 8.9 | 5 | 5 | 4 | 1.05 | 0.979 | 0.96 | 1.092 | 0.942 | 0.985 | 1.01 | 8.73E-01 |
| cds.Camellia_sinensis.comp27065_c0_seq2_m.4908 | PREDICTED: DUF724 domain-containing protein 6-like isoform X1 [Ipomoea nil] | 107.66 | 3.7258 | 2.4 | 2 | 2 | 2 | 1.266 | 1.394 | 1.269 | 0.768 | 0.586 | 0.631 | 0.505 | 1.36E-03 |
| cds.Camellia_sinensis.comp27076_c0_seq1_m.35798 | PREDICTED: electron transfer flavoprotein subunit beta, mitochondrial [Ziziphus jujuba] | 27.725 | 9.3105 | 18.3 | 5 | 6 | 5 | 0.965 | 0.978 | 1.006 | 0.993 | 1.04 | 1.023 | 1.036 | 1.23E-01 |
| cds.Camellia_sinensis.comp27084_c0_seq1_m.9619 | PREDICTED: KH domain-containing protein At4g18375-like [Glycine max] | 30.529 | 8.7639 | 6.2 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp27087_c0_seq1_m.46535 | PREDICTED: UPF0664 stress-induced protein C29B12.11c [Nelumbo nucifera] | 23.128 | 1.9467 | 12.3 | 2 | 2 | 2 | 0.87 | 0.884 | 0.917 | 1.307 | 1.02 | 1.061 | 1.268 | 4.17E-02 |
| cds.Camellia_sinensis.comp27088_c0_seq1_m.12753 | PREDICTED: probable Xaa-Pro aminopeptidase P isoform X1 [Jatropha curcas] | 72.33 | 43.018 | 18.3 | 10 | 15 | 10 | 0.97 | 1.005 | 0.992 | 1.009 | 1.012 | 1.008 | 1.021 | 1.84E-01 |
| cds.Camellia_sinensis.comp27093_c0_seq2_m.50004 | PREDICTED: non-specific lipid transfer protein GPI-anchored 2 [Vitis vinifera] | 12.438 | 2.2611 | 15 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp27102_c0_seq1_m.14624 | PREDICTED: T-complex protein 1 subunit epsilon [Nicotiana tabacum] | 59.216 | 55.034 | 27.1 | 15 | 23 | 15 | 0.933 | 0.937 | 0.926 | 1.065 | 1.072 | 1.054 | 1.141 | 2.27E-05 |

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| cds.Camellia_sinensis.comp27106_c0_seq1_m.24540 | Urease accessory protein UreH [Morus notabilis] | 39.907 | 10.675 | 3.2 | 1 | 2 | 1 | 0.968 | 1.035 | 1.088 | 0.997 | 0.89 | 1.029 | 0.943 | 3.48E-01 |
| cds.Camellia_sinensis.comp27110_c0_seq1_m.8651 | PREDICTED: conserved oligomeric Golgi complex subunit 7 [Theobroma cacao] | 92.826 | 6.2268 | 3.6 | 3 | 3 | 3 | 1.046 | 0.962 | 1.029 | 1.042 | 0.958 | 0.968 | 0.977 | 5.66E-01 |
| cds.Camellia_sinensis.comp27112_c0_seq1_m.40457 | PREDICTED: inactive protein RESTRICTED TEV MOVEMENT 2-like [Daucus carota subsp. sativus] | 20.996 | 11.634 | 11.1 | 2 | 2 | 2 | 0.995 | 1.005 | 0.993 | 0.951 | 1.055 | 1.008 | 1.007 | 8.59E-01 |
| cds.Camellia_sinensis.comp27114_c0_seq1_m.26893 | PREDICTED: GDSL esterase/lipase At3g26430-like [Juglans regia] | 46.596 | 2.4876 | 4 | 2 | 2 | 2 | 0.925 | 0.988 | 0.984 | 1.049 | 1.017 | 1.063 | 1.08 | 3.66E-02 |

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| cds.Camellia_sinensis.comp27117_c0_seq1_m.17061 | PREDICTED: monodehydroascorbate reductase isoform X1 [Vitis vinifera] | 47.223 | 214.76 | 54.6 | 22 | 77 | 21 | 0.937 | 0.907 | 0.932 | 1.071 | 1.113 | 1.082 | 1.177 | 4.42E-04 |
| cds.Camellia_sinensis.comp27120_c0_seq1_m.24219 | PREDICTED: yrdC domain-containing protein, mitochondrial isoform X1 [Ricinus | 31.143 | 3.5953 | 8.7 | 2 | 2 | 2 | 0.953 | 0.977 | 1.138 | 1.004 | 1.036 | 0.908 | 0.961 | 6.04E-01 |
| cds.Camellia_sinensis.comp27125_c0_seq4_m.4548 | PREDICTED: phytochrome E isoform X4 [Jatropha curcas] | 62.441 | 4.3643 | 4.3 | 3 | 3 | 3 | 0.975 | 0.901 | 1.349 | 0.893 | 0.868 | 1.01 | 0.859 | 3.54E-01 |
| cds.Camellia_sinensis.comp27125_c0_seq4_m.4549 | PREDICTED: phytochrome E-like [Juglans regia] | 26.036 | 2.4561 | 6.1 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp27127_c0_seq1_m.44386 | PREDICTED: 3-ketoacyl-CoA synthase 11 isoform X2 [Gossypium raimondii] | 24.21 | 1.1574 | 3.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp27140_c0_seq1_m.23629 | PREDICTED: anthocyanidin 3-O-glucosyltransferase 7 [Vitis vinifera] | 50.677 | 82.478 | 25 | 10 | 18 | 10 | 1.134 | 1.114 | 1.12 | 0.837 | 0.859 | 0.885 | 0.766 | 9.79E-05 |
| cds.Camellia_sinensis.comp27153_c0_seq1_m.21972 | PREDICTED: structural maintenance of chromosomes protein 2-1-like [Ziziphus jujuba] | 42.454 | 40.153 | 22 | 7 | 10 | 2 | 1.04 | 1.067 | 1.099 | 0.912 | 0.946 | 0.926 | 0.868 | 1.82E-03 |
| cds.Camellia_sinensis.comp27154_c0_seq1_m.24675 | PREDICTED: probable xyloglucan endotransglucosylase/hydrolase protein B [Populus euphratica] | 35.618 | 2.2642 | 10.4 | 3 | 3 | 2 | 0.917 | 1.087 | 0.855 | 1.051 | 1.023 | 1.091 | 1.107 | 2.22E-01 |

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| cds.Camellia_sinensis.comp27157_c0_seq1_m.20519 | PREDICTED: putative GEM-like protein 3 [Erythranthe guttata] | 46.435 | 1.5661 | 2.1 | 1 | 1 | 1 | 1.059 | 1.019 | 1.02 | 0.933 | 1.003 | 0.96 | 0.935 | 5.10E-02 |
| cds.Camellia_sinensis.comp27164_c0_seq1_m.29784 | PREDICTED: hypersensitive-induced response protein 2 [Solanum tuberosum | 31.467 | 86.661 | 43.7 | 12 | 33 | 9 | 0.927 | 0.915 | 0.898 | 1.104 | 1.091 | 1.084 | 1.197 | 7.64E-05 |
| cds.Camellia_sinensis.comp27166_c0_seq1_m.22873 | PREDICTED: U5 small nuclear ribonucleoprotein 40 kDa protein [Ziziphus jujuba] | 39.294 | 13.206 | 12.1 | 4 | 4 | 4 | 1.016 | 1.005 | 1.01 | 0.994 | 1.01 | 1.02 | 0.998 | 7.87E-01 |
| cds.Camellia_sinensis.comp27168_c0_seq1_m.28325 | PREDICTED: SUMO-activating enzyme subunit 1B-1 isoform X1 [Vitis vinifera] | 36.092 | 19.113 | 24.8 | 7 | 11 | 7 | 0.972 | 0.944 | 0.962 | 1.016 | 1.058 | 1.073 | 1.093 | 8.46E-03 |

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| cds.Camellia_sinensis.comp27172_c0_seq1_m.28250 | PREDICTED: protein phosphatase methylesterase 1 [Sesamum indicum] | 42.216 | 8.1527 | 7.4 | 3 | 3 | 3 | 0.926 | 1.074 | 1.021 | 1.032 | 1.044 | 0.923 | 0.993 | 9.11E-01 |
| cds.Camellia_sinensis.comp27178_c0_seq1_m.9522 | PREDICTED: peroxisomal fatty acid beta-oxidation multifunctional protein AIM1 [Theobroma cacao] | 78.867 | 84.702 | 22.7 | 17 | 23 | 17 | 0.933 | 0.941 | 0.944 | 1.07 | 1.06 | 1.081 | 1.139 | 4.00E-05 |
| cds.Camellia_sinensis.comp27182_c0_seq1_m.41959 | PREDICTED: peptidyl-prolyl cis-trans isomerase CYP19-3 [Ziziphus jujuba] | 22.574 | 4.7934 | 17.9 | 5 | 10 | 3 | 1.01 | 0.99 | 0.985 | 1.019 | 1.063 | 0.94 | 1.012 | 7.79E-01 |
| cds.Camellia_sinensis.comp27190_c0_seq1_m.27944 | PREDICTED: 60S ribosomal protein L13a-4 [Sesamum indicum] | 23.641 | 14.441 | 27.7 | 6 | 9 | 2 | 1.094 | 1.124 | 1.142 | 0.87 | 0.869 | 0.873 | 0.777 | 2.50E-03 |

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| cds.Camellia_sinensis.comp27190_c0_seq2_m.27972 | PREDICTED: 60S ribosomal protein L13a-4 [Sesamum indicum] | 29.869 | 1.7124 | 18.8 | 5 | 8 | 1 | 1.209 | 1.188 | 1.133 | 0.771 | 0.818 | 0.824 | 0.684 | 1.83E-04 |
| cds.Camellia_sinensis.comp27196_c0_seq1_m.30399 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 2 [Vitis vinifera] | 28.068 | 38.259 | 14.4 | 3 | 4 | 3 | 0.99 | 0.944 | 0.963 | 1.075 | 1.013 | 1.039 | 1.079 | 2.58E-02 |
| cds.Camellia_sinensis.comp27198_c0_seq1_m.23934 | PREDICTED: obg-like ATPase 1 [Vigna radiata var. radiata] | 29.577 | 54.091 | 50 | 12 | 19 | 12 | 1.004 | 0.999 | 1.03 | 1.016 | 0.979 | 0.996 | 0.986 | 3.84E-01 |
| cds.Camellia_sinensis.comp27198_c0_seq1_m.23935 | PREDICTED: obg-like ATPase 1 [Prunus mume] | 18.39 | 44.921 | 42.9 | 7 | 10 | 7 | 1.046 | 1.04 | 1.053 | 0.975 | 0.971 | 0.941 | 0.92 | 2.06E-03 |
| cds.Camellia_sinensis.comp27203_c0_seq1_m.29469 | PREDICTED: disease resistance RPP13-like protein 4 [Capsicum annuum] | 48.541 | 2.4185 | 6.6 | 3 | 3 | 3 | | | | | | | | |

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| cds.Camellia_sinensis.comp27207_c0_seq1_m.37062 | PREDICTED: vesicle transport v-SNARE 13 [Vitis vinifera] | 24.858 | 23.796 | 32.1 | 6 | 7 | 6 | 1.012 | 1.051 | 1.007 | 0.989 | 0.967 | 0.978 | 0.956 | 3.94E-02 |
| cds.Camellia_sinensis.comp27211_c0_seq2_m.37491 | 50S ribosomal protein L10, chloroplastic [Nicotiana tabacum] | 11.866 | 24.576 | 51.4 | 6 | 15 | 6 | 1.022 | 1.02 | 0.976 | 0.968 | 1.011 | 0.994 | 0.985 | 4.89E-01 |
| cds.Camellia_sinensis.comp27212_c0_seq1_m.12901 | PREDICTED: delta-1-pyrroline-5-carboxylate dehydrogenase 12A1, mitochondrial isoform | 67.784 | 114.71 | 33.6 | 18 | 29 | 18 | 0.941 | 0.957 | 0.924 | 1.047 | 1.04 | 1.059 | 1.115 | 6.80E-04 |
| cds.Camellia_sinensis.comp27213_c0_seq1_m.21055 | PREDICTED: mitochondrial carnitine/acylcarnitine carrier-like protein [Juglans regia] | 30.569 | 54.968 | 45.8 | 13 | 18 | 13 | 1.028 | 1.051 | 1.03 | 0.985 | 0.952 | 0.941 | 0.926 | 7.42E-03 |

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| cds.Camellia_sinensis.comp27214_c0_seq5_m.34668 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP16-1, chloroplastic isoform X2 [Vitis vinifera] | 15.426 | 6.9752 | 17.3 | 1 | 1 | 1 | 1.002 | 0.899 | 1.018 | 1.085 | 1.08 | 0.939 | 1.063 | 3.79E-01 |
| cds.Camellia_sinensis.comp27215_c0_seq1_m.14883 | PREDICTED: heterogeneous nuclear ribonucleoprotein Q [Sesamum indicum] | 53.327 | 3.4461 | 2.3 | 1 | 1 | 1 | 1.103 | 1.038 | 1.079 | 1.033 | 0.791 | 0.943 | 0.859 | 1.22E-01 |
| cds.Camellia_sinensis.comp27216_c0_seq1_m.30162 | PREDICTED: early nodulin-like protein 2 [Ipomoea nil] | 35.952 | 4.6579 | 9.5 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp27224_c0_seq2_m.34734 | PREDICTED: macro domain-containing protein VPA0103-like isoform X3 [Nicotiana tabacum] | 30.955 | 84.034 | 29.5 | 6 | 9 | 6 | 1.028 | 1.019 | 1.018 | 0.956 | 1.085 | 0.926 | 0.968 | 5.47E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp27225_c0_seq1_m.28449 | anthocyanidin reductase [Vitis vinifera] | 36.273 | 62.198 | 30.3 | 11 | 25 | 6 | 1.404 | 1.342 | 1.365 | 0.559 | 0.608 | 0.576 | 0.424 | 3.32E-06 |
| cds.Camellia_sinensis.comp27225_c0_seq2_m.28877 | anthocyanidin reductase [Vitis vinifera] | 37.459 | 8.2769 | 20.5 | 7 | 18 | 2 | 1.311 | 1.253 | 1.313 | 0.684 | 0.687 | 0.663 | 0.525 | 2.24E-06 |
| cds.Camellia_sinensis.comp27225_c1_seq1_m.31047 | PREDICTED: PLASMODESMATA CALLOSE-BINDING PROTEIN 3 [Vitis vinifera] | 20.119 | 4.4973 | 5 | 1 | 1 | 1 | 0.991 | 0.99 | 0.976 | 0.99 | 1.061 | 1.005 | 1.033 | 2.07E-01 |
| cds.Camellia_sinensis.comp27228_c0_seq2_m.28667 | PREDICTED: pentatricopeptide repeat-containing protein At4g36680, mitochondrial [Vitis vinifera] | 43.584 | 3.058 | 3.1 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp27229_c0_seq1_m.34263 | PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B-like [Sesamum indicum] | 12.075 | 1.42 | 15 | 2 | 3 | 1 | 0.988 | 0.898 | 1.032 | 1.085 | 1.033 | 0.987 | 1.064 | 2.70E-01 |
| cds.Camellia_sinensis.comp27229_c0_seq5_m.51936 | PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B-like [Ipomoea nil] | 11.971 | 3.7679 | 28.3 | 4 | 5 | 3 | 1.111 | 1.049 | 1.091 | 0.918 | 0.853 | 0.955 | 0.839 | 8.92E-03 |
| cds.Camellia_sinensis.comp27241_c0_seq1_m.23938 | PREDICTED: IAA-amino acid hydrolase ILR1-like 3 [Vitis vinifera] | 48.017 | 8.8507 | 6.7 | 3 | 3 | 2 | 0.99 | 0.914 | 1.051 | 1.037 | 0.962 | 1.061 | 1.036 | 5.16E-01 |
| cds.Camellia_sinensis.comp27255_c0_seq1_m.26215 | PREDICTED: GEM-like protein 1 [Theobroma cacao] | 37.906 | 21.443 | 8 | 3 | 4 | 3 | 0.974 | 1.024 | 0.969 | 1.017 | 0.996 | 1.005 | 1.017 | 4.05E-01 |

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| cds.Camellia_sinensis.comp27256_c0_seq1_m.18069 | PREDICTED: triose phosphate/phosphate translocator, non-green plastid, chloroplastic-like [Nicotiana attenuata] | 53.315 | 6.5504 | 5.6 | 2 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp27260_c0_seq2_m.11556 | PREDICTED: protein MODIFIER OF SNC1 11 isoform X1 [Vitis vinifera] | 22.318 | 45.149 | 41.2 | 6 | 10 | 6 | 1.021 | 1.05 | 0.99 | 1 | 0.975 | 1 | 0.972 | 2.10E-01 |
| cds.Camellia_sinensis.comp27260_c0_seq3_m.14275 | PREDICTED: dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex,chloroplastic [Vitis vinifera] | 49.889 | 51.545 | 28.3 | 11 | 15 | 10 | 0.998 | 1.017 | 0.979 | 1.014 | 1.011 | 0.979 | 1.003 | 8.43E-01 |

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| cds.Camellia_sinensis.comp27269_c0_seq1_m.35694 | PREDICTED: thylakoid lumenal 16.5 kDa protein, chloroplastic [Ziziphus jujuba] | 25.127 | 42.701 | 32.3 | 6 | 16 | 6 | 1.061 | 1.02 | 0.969 | 0.994 | 0.953 | 0.988 | 0.962 | 2.66E-01 |
| cds.Camellia_sinensis.comp27274_c0_seq1_m.37043 | PREDICTED: RPM1-interacting protein 4-like [Sesamum indicum] | 26.671 | 1.4361 | 5.3 | 1 | 1 | 1 | 1.154 | 0.967 | 1.008 | 0.97 | 0.952 | 0.934 | 0.913 | 1.79E-01 |
| cds.Camellia_sinensis.comp27275_c0_seq2_m.35346 | PREDICTED: 60S ribosomal protein L15 [Nicotiana tabacum] | 24.139 | 2.7825 | 6.9 | 2 | 3 | 2 | 1.041 | 1.087 | 1.091 | 0.959 | 0.923 | 0.9 | 0.864 | 3.60E-03 |
| cds.Camellia_sinensis.comp27280_c0_seq1_m.38417 | PREDICTED: mitochondrial fission 1 protein A-like [Nicotiana tabacum] | 18.391 | 1.9523 | 9.4 | 2 | 2 | 2 | 1.044 | 1.018 | 1.06 | 0.955 | 0.966 | 0.954 | 0.921 | 2.72E-03 |
| cds.Camellia_sinensis.comp27284_c0_seq1_m.31468 | PREDICTED: 60S ribosomal protein L17-2 [Ziziphus jujuba] | 24.958 | 43.431 | 25.7 | 5 | 9 | 3 | 1.08 | 1.096 | 1.122 | 0.918 | 0.932 | 0.854 | 0.82 | 2.40E-03 |

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| cds.Camellia_sinensis.comp27284_c0_seq2_m.32028 | PREDICTED: 60S ribosomal protein L17-2 [Juglans regia] | 20.667 | 5.7439 | 21.3 | 4 | 7 | 2 | 1.074 | 1.111 | 1.136 | 0.891 | 0.901 | 0.866 | 0.8 | 3.80E-04 |
| cds.Camellia_sinensis.comp27285_c0_seq1_m.35727 | putative mannitol dehydrogenase [Morus notabilis] | 31.595 | 16.138 | 10.5 | 3 | 5 | 3 | 0.947 | 0.976 | 0.941 | 1.087 | 1.042 | 1.041 | 1.107 | 5.04E-03 |
| cds.Camellia_sinensis.comp27285_c0_seq3_m.45741 | PREDICTED: probable mannitol dehydrogenase [Ricinus communis] | 23.235 | 2.5407 | 7 | 2 | 3 | 2 | 0.934 | 0.942 | 0.976 | 1.064 | 1.073 | 1.039 | 1.114 | 2.88E-03 |
| cds.Camellia_sinensis.comp27288_c0_seq1_m.48383 | 60S ribosomal protein L37a-2 [Medicago truncatula] | 12.721 | 6.8785 | 21.2 | 2 | 3 | 2 | 0.932 | 1.233 | 1.076 | 0.895 | 0.915 | 0.943 | 0.849 | 1.29E-01 |
| cds.Camellia_sinensis.comp27289_c0_seq2_m.43364 | | 10.996 | 2.0836 | 11.9 | 1 | 2 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp27290_c0_seq4_m.33441 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic isoform X3 [Vitis vinifera] | 24.796 | 43.753 | 32.5 | 7 | 21 | 7 | 1.019 | 0.977 | 0.962 | 0.995 | 0.979 | 1.011 | 1.009 | 6.59E-01 |
| cds.Camellia_sinensis.comp27292_c0_seq1_m.33110 | PREDICTED: 14-3-3 protein 7 [Ricinus communis] | 28.896 | 141.62 | 60.5 | 17 | 48 | 14 | 0.977 | 0.949 | 0.905 | 1.04 | 1.063 | 1.086 | 1.126 | 9.52E-03 |
| cds.Camellia_sinensis.comp27300_c1_seq1_m.38184 | PREDICTED: chlorophyll a-b binding protein CP29.1, chloroplastic [Ricinus communis] | 24.283 | 115.72 | 46.2 | 10 | 50 | 7 | 1.036 | 0.955 | 0.969 | 0.982 | 1.034 | 1.008 | 1.022 | 4.96E-01 |
| cds.Camellia_sinensis.comp27300_c1_seq2_m.42952 | PREDICTED: chlorophyll a-b binding protein CP29.1, chloroplastic [Ricinus communis] | 30.03 | 74.473 | 34.8 | 8 | 26 | 5 | 1.063 | 1.05 | 1.013 | 0.965 | 0.936 | 0.985 | 0.923 | 1.82E-02 |

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| cds.Camellia_sinensis.comp27314_c0_seq1_m.30117 | PREDICTED: eukaryotic translation initiation factor 2 subunit alpha-like [Sesamum indicum] | 41.484 | 31.367 | 14.7 | 5 | 6 | 5 | 1.008 | 0.995 | 1.011 | 0.86 | 1.082 | 1.044 | 0.991 | 8.60E-01 |
| cds.Camellia_sinensis.comp27316_c0_seq1_m.17284 | PREDICTED: extensin-like [Nicotiana tabacum] | 63.117 | 16.687 | 11 | 6 | 7 | 6 | 1.016 | 1.018 | 0.957 | 0.97 | 0.939 | 1.028 | 0.982 | 6.08E-01 |
| cds.Camellia_sinensis.comp27319_c0_seq1_m.22934 | PREDICTED: acetylornithine aminotransferase, mitochondrial-like [Jatropha curcas] | 49.89 | 110.15 | 31.2 | 11 | 18 | 10 | 1.007 | 1.021 | 1.013 | 0.957 | 0.999 | 0.97 | 0.962 | 4.37E-02 |
| cds.Camellia_sinensis.comp27322_c0_seq1_m.25140 | PREDICTED: patatin-like protein 2 isoform X2 [Arachis duranensis] | 49.106 | 1.5436 | 1.6 | 1 | 2 | 1 | 0.93 | 0.977 | 0.966 | 1.026 | 1.039 | 1.086 | 1.097 | 1.55E-02 |

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| cds.Camellia_sinensis.comp27322_c0_seq2_m.31542 | Patatin group A-3 [Morus notabilis] | 44.871 | 21.276 | 17.2 | 6 | 7 | 6 | 1.073 | 0.942 | 0.948 | 1.035 | 1.065 | 0.946 | 1.028 | 6.38E-01 |
| cds.Camellia_sinensis.comp27327_c0_seq1_m.25811 | PREDICTED: poly(U)-specific endoribonuclease-B [Vitis vinifera] | 51.393 | 4.3687 | 5.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp27330_c0_seq10_c0_seq1_m.15051 | PREDICTED: protein ASPARTIC PROTEASE IN GUARD CELL 1 [Ricinus communis] | 47.863 | 11.358 | 10 | 4 | 6 | 4 | 1.101 | 1.086 | 1.071 | 0.925 | 0.942 | 0.94 | 0.862 | 1.15E-04 |
| cds.Camellia_sinensis.comp27335_c0_seq1_m.32917 | PREDICTED: beta-glucosidase 13 [Vitis vinifera] | 42.59 | 22.017 | 12.4 | 5 | 10 | 5 | 1.093 | 1.083 | 1.122 | 0.943 | 0.886 | 0.886 | 0.823 | 1.12E-03 |
| cds.Camellia_sinensis.comp27336_c0_seq2_m.51245 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 12-like [Nicotiana attenuata] | 20.875 | 25.691 | 33.3 | 8 | 8 | 3 | 0.989 | 1.039 | 0.942 | 0.992 | 0.994 | 1.056 | 1.024 | 5.25E-01 |

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| cds.Camellia_sinensis.comp27339_c0_seq2_m.35031 | PREDICTED: chlorophyll a-b binding protein 13, chloroplastic-like [Nelumbo nucifera] | 28.901 | 23.494 | 26.1 | 5 | 48 | 3 | 0.947 | 0.941 | 0.969 | 1.045 | 1.047 | 1.02 | 1.089 | 2.22E-03 |
| cds.Camellia_sinensis.comp27339_c0_seq4_m.43220 | PREDICTED: chlorophyll a-b binding protein 5, chloroplastic [Sesamum indicum] | 20.154 | 58.365 | 44.4 | 6 | 59 | 2 | 1.021 | 0.927 | 1.019 | 0.964 | 1.051 | 0.98 | 1.009 | 8.27E-01 |
| cds.Camellia_sinensis.comp27339_c0_seq6_m.50345 | PREDICTED: chlorophyll a-b binding protein of LHCII type 1 [Musa acuminata subsp. malaccensi | 11.014 | 1.5478 | 75 | 3 | 7 | 1 | 0.922 | 1.005 | 1.007 | 1.095 | 0.999 | 1 | 1.055 | 2.76E-01 |
| cds.Camellia_sinensis.comp27341_c0_seq3_m.47505 | PREDICTED: autophagy-related protein 8C [Sesamum indicum] | 13.707 | 2.3951 | 19.3 | 3 | 3 | 3 | 0.965 | 0.962 | 0.942 | 1.055 | 1.022 | 1.076 | 1.099 | 4.96E-03 |

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| cds.Camellia_sinensis.comp27350_c0_seq10_c0_seq1_m.24260 | PREDICTED: chalcone synthase 1 [Juglans regia] | 48.966 | 67.923 | 32.2 | 11 | 35 | 2 | 1.518 | 1.391 | 1.424 | 0.472 | 0.54 | 0.506 | 0.35 | 2.17E-05 |
| cds.Camellia_sinensis.comp27350_c0_seq2_m.26012 | PREDICTED: chalcone synthase 1 [Juglans regia] | 49.033 | -2 | 30.6 | 10 | 33 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp27354_c0_seq3_m.28181 | PREDICTED: geranylgeranyl pyrophosphate synthase, chloroplastic-like [Sesamum indicum] | 40.703 | 5.1704 | 8.8 | 3 | 3 | 3 | 1.031 | 1.057 | 1.072 | 0.979 | 0.946 | 0.911 | 0.897 | 1.02E-02 |
| cds.Camellia_sinensis.comp27359_c0_seq1_m.43821 | PREDICTED: delta(1)-pyrroline-2-carboxylate reductase [Prunus mume] | 21.424 | 49.743 | 28.1 | 5 | 10 | 5 | 0.939 | 0.953 | 0.983 | 1.059 | 1.069 | 1.042 | 1.103 | 3.16E-03 |

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| cds.Camellia_sinensis.comp27362_c0_seq1_m.50066 | PREDICTED: pyrophosphate-energized vacuolar membrane proton pump 1-like isoform X1 [Nicotiana sylvestris] | 17.116 | 54.456 | 44.8 | 7 | 15 | 2 | 0.969 | 0.918 | 1.023 | 0.97 | 1.016 | 1.051 | 1.044 | 3.30E-01 |
| cds.Camellia_sinensis.comp27363_c0_seq2_m.28875 | PREDICTED: protein FLX-like 4 [Jatropha curcas] | 34.278 | 12.847 | 22.5 | 7 | 10 | 7 | 0.958 | 0.987 | 0.986 | 1.015 | 1.034 | 1.013 | 1.045 | 2.04E-02 |
| cds.Camellia_sinensis.comp27367_c0_seq1_m.14464 | PREDICTED: probable inorganic phosphate transporter 1-3 [Sesamum indicum] | 59.078 | 28.096 | 11.1 | 6 | 9 | 5 | 1.007 | 0.983 | 0.99 | 0.962 | 1.015 | 1.005 | 1.001 | 9.81E-01 |

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| cds.Camellia_sinensis.comp27369_c0_seq2_m.41742 | PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial-like [Sesamum indicum] | 19.867 | 8.1251 | 18.9 | 4 | 10 | 4 | 1.067 | 1.048 | 1.031 | 0.972 | 0.949 | 0.936 | 0.908 | 2.88E-03 |
| cds.Camellia_sinensis.comp27370_c0_seq1_m.26641 | PREDICTED: DNA damage-inducible protein 1 [Pyrus x bretschneideri] | 44.15 | 132.92 | 44.1 | 13 | 17 | 13 | 0.958 | 0.998 | 0.933 | 1.049 | 1.043 | 1.062 | 1.092 | 1.22E-02 |
| cds.Camellia_sinensis.comp27372_c0_seq1_m.36694 | PREDICTED: probable carbohydrate esterase At4g34215 [Lupinus angustifolius] | 27.091 | 2.8298 | 8.5 | 2 | 3 | 2 | 0.945 | 0.927 | 0.973 | 0.919 | 1.164 | 1.093 | 1.116 | 2.18E-01 |

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| cds.Camellia_sinensis.comp27373_c0_seq1_m.22325 | PREDICTED: diphosphomevalonate decarboxylase MVD2-like [Nicotiana attenuata] | 46.451 | 19.857 | 19.7 | 9 | 14 | 9 | 0.997 | 0.964 | 0.968 | 1.02 | 1.03 | 1.019 | 1.048 | 1.37E-02 |
| cds.Camellia_sinensis.comp27376_c0_seq1_m.23506 | PREDICTED: adenylyltransferase and sulfurtransferase MOCS3 [Ricinus communis] | 55.286 | 12.52 | 11 | 5 | 6 | 5 | 0.966 | 0.944 | 0.945 | 1.056 | 1.062 | 1.077 | 1.119 | 2.97E-04 |
| cds.Camellia_sinensis.comp27377_c0_seq1_m.43994 | PREDICTED: protease Do-like 5, chloroplastic isoform X1 [Nelumbo nucifera] | 26.525 | 35.48 | 13.5 | 3 | 6 | 3 | 1.008 | 0.985 | 0.955 | 1.018 | 1.047 | 1.029 | 1.05 | 5.15E-02 |
| cds.Camellia_sinensis.comp27380_c1_seq10_c1_seq1_m.39390 | COPI associated protein [Medicago truncatula] | 22.395 | 6.7332 | 9.1 | 2 | 2 | 2 | 0.932 | 0.991 | 1.012 | 1.045 | 1.045 | 0.999 | 1.052 | 1.49E-01 |

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| cds.Camellia_sinensis.comp27381_c0_seq1_m.37044 | DNA-binding family protein [Populus trichocarpa] | 15.279 | 38.968 | 34.3 | 4 | 8 | 4 | 0.959 | 0.961 | 0.993 | 1.026 | 1.021 | 1.046 | 1.062 | 1.12E-02 |
| cds.Camellia_sinensis.comp27384_c0_seq1_m.32444 | PREDICTED: xyloglucan endotransglucosylase/hydrolase protein 9 [Gossypium arboreum] | 33.85 | 4.9624 | 12.5 | 4 | 5 | 4 | 1.145 | 1.211 | 1.132 | 0.887 | 0.77 | 0.834 | 0.714 | 1.82E-03 |
| cds.Camellia_sinensis.comp27385_c1_seq2_m.39231 | PREDICTED: ADP-ribosylation factor 1 isoform X1 [Fragaria vesca subsp. vesca] | 20.666 | 80.293 | 32 | 6 | 24 | 6 | 1.012 | 0.994 | 0.98 | 1.006 | 1.008 | 0.991 | 1.006 | 5.83E-01 |
| cds.Camellia_sinensis.comp27386_c1_seq1_m.47223 | PREDICTED: 60S acidic ribosomal protein P3-like [Nelumbo nucifera] | 12.775 | 42.232 | 21.6 | 2 | 5 | 2 | 1.006 | 1.061 | 1.1 | 0.937 | 0.981 | 0.924 | 0.897 | 2.69E-02 |

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| cds.Camellia_sinensis.comp27397_c0_seq1_m.13150 | PREDICTED: clathrin interactor EPSIN 1 [Vitis vinifera] | 41.831 | 6.3554 | 8.5 | 2 | 2 | 2 | 1.166 | 1.098 | 1.042 | 0.852 | 0.853 | 0.952 | 0.804 | 1.12E-02 |
| cds.Camellia_sinensis.comp27397_c0_seq1_m.13151 | PREDICTED: clathrin interactor EPSIN 1 isoform X2 [Theobroma cacao] | 15.393 | 2.8204 | 21.5 | 3 | 4 | 3 | 1.086 | 1.064 | 1.06 | 0.943 | 0.904 | 0.929 | 0.865 | 5.57E-04 |
| cds.Camellia_sinensis.comp27402_c0_seq1_m.37995 | PREDICTED: membrane steroid-binding protein 2-like [Sesamum indicum] | 21.237 | 5.9064 | 12.4 | 2 | 2 | 2 | 1.07 | 1.159 | 1.04 | 0.89 | 0.898 | 0.921 | 0.829 | 5.34E-03 |
| cds.Camellia_sinensis.comp27422_c0_seq1_m.41621 | PREDICTED: purple acid phosphatase 3-like [Ziziphus jujuba] | 32.283 | 80.407 | 16.6 | 4 | 7 | 4 | 0.992 | 1.02 | 0.957 | 1.055 | 0.956 | 1.007 | 1.017 | 6.64E-01 |
| cds.Camellia_sinensis.comp27425_c0_seq2_m.35521 | PREDICTED: PHD finger protein Alfin1 [Vitis vinifera] | 27.815 | 1.9488 | 4 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp27426_c0_seq1_m.30120 | PREDICTED: ras-related protein RABA1f [Tarenaya hassleriana] | 24.061 | 37.428 | 42.1 | 8 | 17 | 3 | 0.977 | 0.978 | 1.01 | 1.039 | 1.037 | 1.01 | 1.041 | 4.81E-02 |
| cds.Camellia_sinensis.comp27440_c0_seq2_m.52441 | | 14.454 | 3.4121 | 8.5 | 1 | 1 | 1 | 0.995 | 0.971 | 0.919 | 1.028 | 1.021 | 1.082 | 1.085 | 5.12E-02 |
| cds.Camellia_sinensis.comp27449_c0_seq1_m.35876 | PREDICTED: alpha carbonic anhydrase 1, chloroplastic [Prunus mume] | 30.787 | 10.077 | 9.7 | 3 | 5 | 3 | 0.927 | 0.937 | 0.961 | 1.024 | 1.109 | 1.017 | 1.115 | 2.21E-02 |
| cds.Camellia_sinensis.comp27451_c0_seq1_m.19603 | C2 domain-containing family protein [Populus trichocarpa] | 45.301 | 6.4934 | 4.6 | 2 | 3 | 2 | 0.989 | 0.93 | 0.916 | 1.024 | 1.097 | 1.065 | 1.124 | 1.91E-02 |
| cds.Camellia_sinensis.comp27452_c0_seq1_m.38379 | PREDICTED: acyl carrier protein 1, chloroplastic-like [Citrus sinensis] | 19.958 | 11.939 | 8.1 | 1 | 2 | 1 | 1.035 | 1.178 | 1.142 | 0.8 | 0.903 | 0.915 | 0.78 | 1.27E-02 |

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| cds.Camellia_sinensis.comp27462_c0_seq1_m.16642 | PREDICTED: protein DEK [Solanum lycopersicum] | 31.461 | 2.6542 | 4.4 | 1 | 1 | 1 | 0.956 | 0.895 | 1.039 | 1.081 | 1.05 | 1.008 | 1.086 | 1.53E-01 |
| cds.Camellia_sinensis.comp27462_c0_seq1_m.16643 | PREDICTED: DNA ligase 1 [Theobroma cacao] | 25.547 | -2 | 3.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp27465_c0_seq4_m.42355 | PREDICTED: 2-phytyl-1,4-beta-naphthoquinone methyltransferase, chloroplastic isoform X2 [Citrus sinensis] | 14.761 | 2.5349 | 12.7 | 2 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp27469_c0_seq1_m.34207 | cupin family protein [Medicago truncatula] | 22.025 | 28.122 | 19.7 | 3 | 7 | 3 | 1.034 | 1.013 | 0.959 | 0.98 | 1.003 | 1.005 | 0.994 | 8.27E-01 |
| cds.Camellia_sinensis.comp27470_c0_seq2_m.29756 | plasma protein [Arabidopsis thaliana] | 21.261 | 1.8331 | 10.9 | 2 | 2 | 2 | 0.903 | 0.888 | 1.055 | 1.091 | 1.007 | 1.092 | 1.121 | 1.29E-01 |

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| cds.Camellia_sinensis.comp27471_c0_seq1_m.27836 | PREDICTED: probable plastid-lipid-associated protein 3, chloroplastic [Nelumbo nucifera] | 42.804 | 41.71 | 26.3 | 8 | 16 | 7 | 1.092 | 1.141 | 1.127 | 0.883 | 0.815 | 0.867 | 0.763 | 6.02E-04 |
| cds.Camellia_sinensis.comp27471_c0_seq2_m.31372 | PREDICTED: plastoglobulin-1, chloroplastic-like [Ziziphus jujuba] | 39.315 | 207.37 | 41.1 | 12 | 34 | 11 | 0.954 | 0.962 | 0.947 | 1.052 | 1.062 | 1.043 | 1.103 | 1.43E-04 |
| cds.Camellia_sinensis.comp27478_c0_seq1_m.19271 | PREDICTED: histone deacetylase 6 [Vitis vinifera] | 53.96 | 8.1069 | 7.6 | 3 | 3 | 3 | 0.845 | 0.985 | 1 | 1.115 | 0.984 | 1.036 | 1.108 | 1.85E-01 |
| cds.Camellia_sinensis.comp27480_c0_seq2_m.34221 | PREDICTED: ATP-dependent Clp protease proteolytic subunit-related protein 2, chloroplastic [Nelumbo nucifera] | 33.025 | 62.439 | 18.1 | 6 | 15 | 6 | 0.97 | 1.026 | 1.05 | 0.994 | 0.955 | 0.965 | 0.957 | 1.72E-01 |

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| cds.Camellia_sinensis.comp27483_c0_seq1_m.24196 | PREDICTED: UDP-glycosyltransferase 84B1 [Vitis vinifera] | 53.436 | 106.81 | 10.9 | 4 | 5 | 4 | 1.012 | 1.001 | 0.96 | 1.025 | 1.014 | 1.029 | 1.032 | 1.30E-01 |
| cds.Camellia_sinensis.comp27490_c0_seq1_m.38291 | PREDICTED: acyl-acyl carrier protein thioesterase ATL3, chloroplastic-like [Ziziphus jujuba] | 25.853 | 3.4594 | 8.3 | 2 | 2 | 2 | 1.046 | 1.066 | 0.967 | 0.959 | 0.882 | 1.072 | 0.946 | 4.17E-01 |
| cds.Camellia_sinensis.comp27497_c0_seq1_m.32426 | PREDICTED: translin [Theobroma cacao] | 33.965 | 13.927 | 13.4 | 4 | 4 | 4 | 1.057 | 0.99 | 0.987 | 0.961 | 0.983 | 1.02 | 0.977 | 4.60E-01 |
| cds.Camellia_sinensis.comp27498_c0_seq1_m.4383 | PREDICTED: protein QUIRKY [Capsicum annuum] | 89.603 | 12.862 | 5.6 | 3 | 3 | 3 | 0.967 | 0.826 | 1.02 | 1.065 | 0.964 | 1.078 | 1.105 | 2.32E-01 |

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| cds.Camellia_sinensis.comp27502_c0_seq1_m.16363 | PREDICTED: ribonuclease III domain-containing protein RNC1, chloroplastic-like isoform X1 [Daucus carota subsp. sativus] | 62.479 | 3.4285 | 6.6 | 4 | 4 | 4 | 0.998 | 0.922 | 0.954 | 1.035 | 1.069 | 1.042 | 1.095 | 2.20E-02 |
| cds.Camellia_sinensis.comp27505_c0_seq1_m.31043 | PREDICTED: magnesium protoporphyrin IX methyltransferase, chloroplastic-like [Ipomoea | 36.571 | 105.07 | 37.5 | 11 | 18 | 11 | 1.091 | 1.059 | 1.061 | 0.932 | 0.874 | 0.956 | 0.86 | 5.96E-03 |
| cds.Camellia_sinensis.comp27506_c0_seq1_m.52015 | PREDICTED: glutamate synthase [NADH], amyloplastic-like [Nicotiana tomentosiformis] | 18.876 | 2.0804 | 4.7 | 1 | 1 | 1 | 0.95 | 0.999 | 0.964 | 1.037 | 0.992 | 1.077 | 1.066 | 8.54E-02 |

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| cds.Camellia_sinensis.comp27508_c0_seq1_m.20620 | PREDICTED: inter-alpha-trypsin inhibitor heavy chain H3-like [Zea mays] | 55.889 | 11.287 | 6.6 | 3 | 4 | 3 | 1.033 | 1.094 | 0.984 | 0.906 | 0.963 | 0.977 | 0.915 | 8.21E-02 |
| cds.Camellia_sinensis.comp27511_c0_seq1_m.39327 | PREDICTED: lipid phosphate phosphatase gamma, chloroplastic-like [Sesamum indicum] | 25.546 | 8.7639 | 6.7 | 2 | 2 | 2 | 0.944 | 1.027 | 1.023 | 1.012 | 0.978 | 1.031 | 1.009 | 7.78E-01 |
| cds.Camellia_sinensis.comp27513_c0_seq1_m.27540 | PREDICTED: thiol protease aleurain-like [Ziziphus jujuba] | 42.854 | 42.194 | 19.2 | 7 | 16 | 7 | 1.049 | 1.012 | 1.032 | 0.974 | 0.956 | 0.973 | 0.939 | 6.22E-03 |
| cds.Camellia_sinensis.comp27514_c0_seq1_m.30024 | PREDICTED: reticulon-like protein B9 [Nicotiana tabacum] | 25.305 | 1.3201 | 4.1 | 1 | 1 | 1 | 1.007 | 1.01 | 1.018 | 1.02 | 0.904 | 1.047 | 0.979 | 6.58E-01 |

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| cds.Camellia_sinensis.comp27520_c0_seq1_m.29804 | PREDICTED: probable serine/threonine-protein kinase roco9 [Arachis ipaensis] | 21.767 | 49.026 | 41.5 | 7 | 10 | 7 | 1.029 | 0.976 | 0.952 | 1.01 | 0.98 | 1.023 | 1.019 | 5.06E-01 |
| cds.Camellia_sinensis.comp27520_c0_seq1_m.29805 | PREDICTED: probable serine/threonine-protein kinase roco9 [Vigna radiata var. radiata] | 14.541 | 8.1939 | 24 | 3 | 7 | 3 | 0.99 | 0.98 | 1.027 | 1.025 | 1.011 | 0.956 | 0.998 | 9.44E-01 |
| cds.Camellia_sinensis.comp27533_c1_seq1_m.26941 | PREDICTED: protein PHR1-LIKE 1-like [Malus domestica] | 26.186 | 2.2212 | 3.7 | 1 | 1 | 1 | 1.077 | 1.104 | 1.031 | 0.994 | 0.938 | 0.845 | 0.865 | 4.60E-02 |
| cds.Camellia_sinensis.comp27536_c0_seq1_m.28571 | PREDICTED: spermidine sinapoyl-CoA acyltransferase [Juglans regia] | 47.381 | 17.178 | 5.4 | 2 | 2 | 2 | 1.008 | 1.061 | 1.102 | 0.96 | 0.987 | 0.881 | 0.892 | 5.51E-02 |

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| cds.Camellia_sinensis.comp27550_c0_seq1_m.19114 | PREDICTED: cinnamate beta-D-glucosyltransferase-like [Juglans regia] | 54.496 | 68.16 | 26.1 | 11 | 20 | 11 | 1.055 | 1.122 | 1.066 | 0.936 | 0.944 | 0.921 | 0.864 | 2.00E-03 |
| cds.Camellia_sinensis.comp27555_c0_seq1_m.29295 | PREDICTED: threonine synthase, chloroplastic [Sesamum indicum] | 50.394 | 4.5286 | 12.9 | 5 | 6 | 2 | 1.023 | 0.956 | 1.038 | 1.057 | 1.033 | 0.906 | 0.993 | 8.82E-01 |
| cds.Camellia_sinensis.comp27557_c0_seq2_m.24018 | PREDICTED: alpha-1,4 glucan phosphorylase L isozyme, chloroplastic/amyloplastic [Vitis vinifera] | 50.548 | 2.3968 | 5.7 | 3 | 3 | 1 | 0.998 | 1.124 | 1.067 | 0.9 | 0.958 | 0.946 | 0.879 | 3.14E-02 |
| cds.Camellia_sinensis.comp27561_c0_seq1_m.6073 | PREDICTED: probable plastidic glucose transporter 1 isoform X1 [Vitis vinifera] | 61.63 | 18.549 | 5.5 | 3 | 4 | 3 | 1.021 | 0.953 | 1.017 | 0.998 | 1.02 | 1.038 | 1.022 | 4.32E-01 |

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| cds.Camellia_sinensis.comp27561_c0_seq1_m.6074 | PREDICTED: fruit protein pKIWI501-like [Juglans regia] | 17.479 | 80.553 | 61 | 11 | 28 | 11 | 1.073 | 1.06 | 1.069 | 0.864 | 0.951 | 0.954 | 0.865 | 4.65E-02 |
| cds.Camellia_sinensis.comp27564_c0_seq1_m.19725 | PREDICTED: low-temperature-induced cysteine proteinase [Theobroma cacao] | 57.02 | 5.8985 | 3.1 | 1 | 1 | 1 | 0.876 | 0.79 | 0.712 | 1.169 | 1.275 | 1.245 | 1.551 | 2.48E-03 |
| cds.Camellia_sinensis.comp27568_c0_seq1_m.34771 | PREDICTED: multiple organellar RNA editing factor 3, mitochondrial [Vitis vinifera] | 30.604 | 1.4425 | 4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp27568_c0_seq3_m.38351 | PREDICTED: DAG protein, chloroplastic [Daucus carota subsp. sativus] | 25.737 | 56.057 | 13.7 | 2 | 6 | 2 | 1.151 | 1.15 | 1.042 | 0.877 | 0.879 | 0.869 | 0.785 | 1.85E-02 |
| cds.Camellia_sinensis.comp27570_c0_seq1_m.24938 | ATPase subunit 1 (mitochondrion) [Nelumbo nucifera] | 50.087 | 197.27 | 47.5 | 21 | 64 | 19 | 1.021 | 1.017 | 1.021 | 0.982 | 0.977 | 0.977 | 0.96 | 4.20E-05 |

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| cds.Camellia_sinensis.comp27573_c0_seq1_m.18451 | PREDICTED: long chain base biosynthesis protein 2a [Vitis vinifera] | 57.173 | 20.358 | 9.6 | 6 | 6 | 6 | 0.977 | 0.983 | 1.031 | 1.025 | 1.025 | 1.018 | 1.026 | 2.73E-01 |
| cds.Camellia_sinensis.comp27578_c0_seq1_m.30937 | transmembrane protein, putative [Medicago truncatula] | 28.655 | 2.1442 | 8.5 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp27580_c0_seq1_m.32417 | PREDICTED: 3-ketoacyl-CoA thiolase 2, peroxisomal [Prunus mume] | 41.837 | 7.6884 | 11.8 | 4 | 9 | 2 | 1.097 | 0.946 | 1.029 | 0.985 | 0.998 | 0.941 | 0.952 | 3.61E-01 |
| cds.Camellia_sinensis.comp27582_c0_seq1_m.20285 | PREDICTED: cytochrome P450 71A1-like isoform X2 [Populus euphratica] | 58.265 | 37.586 | 6.4 | 3 | 4 | 3 | 0.934 | 1.02 | 0.947 | 1.07 | 1.034 | 1.065 | 1.092 | 3.88E-02 |
| cds.Camellia_sinensis.comp27590_c0_seq1_m.35340 | PREDICTED: psbP domain-containing protein 5, chloroplastic [Vitis vinifera] | 28.41 | 24.618 | 22.4 | 5 | 7 | 5 | 1.01 | 1.039 | 1.087 | 0.952 | 0.957 | 0.93 | 0.905 | 1.28E-02 |

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| cds.Camellia_sinensis.comp27591_c1_seq1_m.40290 | PREDICTED: probable calcium-binding protein CML13 [Sesamum indicum] | 20.266 | 57.214 | 74 | 12 | 20 | 12 | 1.021 | 0.971 | 1.02 | 0.993 | 0.992 | 1.004 | 0.992 | 6.86E-01 |
| cds.Camellia_sinensis.comp27592_c0_seq1_m.4230 | PREDICTED: serine/threonine-protein phosphatase PP1 [Citrus sinensis] | 36.258 | 7.066 | 12.2 | 4 | 4 | 3 | 0.996 | 0.934 | 1.002 | 1.005 | 1.05 | 1.027 | 1.051 | 1.23E-01 |
| cds.Camellia_sinensis.comp27596_c0_seq1_m.19392 | PREDICTED: methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial [Ipomoea nil] | 60.211 | 84.661 | 20 | 9 | 14 | 9 | 0.986 | 1.018 | 1.008 | 1.016 | 1.019 | 0.981 | 1.001 | 9.38E-01 |

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| cds.Camellia_sinensis.comp27604_c0_seq1_m.28659 | PREDICTED: zinc finger CCCH domain-containing protein 14 [Vitis vinifera] | 31.76 | 44.513 | 23.4 | 6 | 10 | 5 | 1.001 | 0.984 | 1.038 | 1.003 | 0.991 | 0.949 | 0.974 | 3.08E-01 |
| cds.Camellia_sinensis.comp27615_c0_seq1_m.25272 | uncharacterized LOC8278573 precursor [Ricinus communis] | 43.521 | 24.778 | 14.6 | 4 | 5 | 4 | 0.927 | 0.827 | 0.888 | 1.108 | 1.174 | 1.15 | 1.299 | 2.16E-03 |
| cds.Camellia_sinensis.comp27622_c0_seq1_m.29090 | PREDICTED: protein CHAPERONE-LIKE PROTEIN OF POR1, chloroplastic [Erythranthe guttata] | 28.077 | 22.179 | 6.4 | 1 | 2 | 1 | 0.958 | 0.984 | 1.071 | 0.966 | 1.09 | 0.947 | 0.997 | 9.44E-01 |
| cds.Camellia_sinensis.comp27628_c0_seq1_m.33687 | PREDICTED: formimidoyltransferase-cyclodeaminase-like [Juglans regia] | 32.116 | 12.239 | 13.8 | 4 | 6 | 4 | 0.969 | 0.983 | 1.052 | 0.994 | 0.984 | 0.964 | 0.979 | 4.93E-01 |

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| cds.Camellia_sinensis.comp27630_c0_seq1_m.38510 | PREDICTED: 40S ribosomal protein S8 isoform X2 [Zea mays] | 28.739 | 2.8368 | 19.8 | 4 | 5 | 1 | 0.994 | 1.088 | 1.265 | 0.882 | 0.889 | 0.869 | 0.789 | 8.13E-02 |
| cds.Camellia_sinensis.comp27630_c0_seq2_m.38611 | PREDICTED: 40S ribosomal protein S8-like [Oryza brachyantha] | 25.06 | 34.033 | 29.3 | 5 | 9 | 2 | 1.172 | 0.984 | 1.124 | 0.826 | 0.895 | 0.992 | 0.827 | 6.40E-02 |
| cds.Camellia_sinensis.comp27634_c0_seq1_m.32545 | rubredoxin family protein [Arabidopsis lyrata subsp. lyrata] | 28.596 | 35.847 | 22.9 | 6 | 10 | 6 | 1.097 | 1.038 | 1.011 | 0.941 | 0.955 | 0.976 | 0.913 | 2.61E-02 |
| cds.Camellia_sinensis.comp27636_c0_seq1_m.40910 | PREDICTED: basic transcription factor 3 [Eucalyptus grandis] | 21.115 | 4.7737 | 9.7 | 3 | 5 | 3 | 1.141 | 1.131 | 1.128 | 0.85 | 0.849 | 0.829 | 0.744 | 2.38E-06 |
| cds.Camellia_sinensis.comp27639_c0_seq1_m.6860 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 14 [Vitis vinifera] | 63.227 | 59.972 | 15.2 | 7 | 11 | 7 | 0.95 | 0.938 | 0.984 | 1.051 | 1.058 | 1.06 | 1.103 | 2.48E-03 |

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| cds.Camellia_sinensis.comp27639_c0_seq1_m.6861 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 14 isoform X2 [Ricinus communis] | 35.039 | 8.6086 | 13.1 | 4 | 7 | 4 | 0.953 | 1.015 | 0.988 | 1.051 | 1.034 | 0.984 | 1.038 | 2.37E-01 |
| cds.Camellia_sinensis.comp27643_c0_seq3_m.32360 | PREDICTED: phosphatidate cytidylyltransferase 4, chloroplastic [Theobroma cacao] | 39.497 | 2.1629 | 4.6 | 2 | 2 | 2 | 0.78 | 1.023 | 1 | 1.041 | 1.127 | 1.076 | 1.157 | 1.64E-01 |
| cds.Camellia_sinensis.comp27644_c0_seq2_m.7911 | PREDICTED: neutral ceramidase [Gossypium raimondii] | 86.825 | 15.218 | 8.1 | 6 | 7 | 6 | 0.988 | 1.046 | 0.998 | 1.02 | 0.936 | 1.028 | 0.984 | 6.59E-01 |
| cds.Camellia_sinensis.comp27648_c0_seq1_m.18793 | PREDICTED: serine carboxypeptidase-like 17 [Juglans regia] | 53.498 | 4.0866 | 4.5 | 2 | 2 | 2 | 1.12 | 1.125 | 0.993 | 0.909 | 0.899 | 0.929 | 0.845 | 1.66E-02 |

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| cds.Camellia_sinensis.comp27652_c0_seq1_m.42586 | PREDICTED: iron-sulfur assembly protein IscA-like 1, mitochondrial [Ricinus communis] | 15.238 | 1.8241 | 8.5 | 1 | 1 | 1 | 0.992 | 1.034 | 0.931 | 1.066 | 0.967 | 1.023 | 1.033 | 4.71E-01 |
| cds.Camellia_sinensis.comp27657_c0_seq1_m.25906 | sucrase-related family protein [Populus trichocarpa] | 47.584 | 2.3719 | 5.1 | 2 | 2 | 2 | 1.055 | 1.015 | 0.978 | 1.056 | 0.965 | 0.935 | 0.97 | 5.00E-01 |
| cds.Camellia_sinensis.comp27658_c0_seq1_m.25591 | plant/F14D7-9 protein [Medicago truncatula] | 32.41 | 40.931 | 17.4 | 4 | 4 | 3 | 0.983 | 0.985 | 0.991 | 1.066 | 0.955 | 1.035 | 1.033 | 4.44E-01 |
| cds.Camellia_sinensis.comp27664_c0_seq1_m.40058 | PREDICTED: SKP1-like protein 1A isoform X1 [Nicotiana tomentosiformis] | 17.537 | 35.622 | 35.5 | 9 | 17 | 6 | 1.004 | 0.975 | 0.984 | 1.013 | 1.044 | 1.017 | 1.037 | 4.56E-02 |
| cds.Camellia_sinensis.comp27671_c0_seq1_m.35572 | PREDICTED: eukaryotic initiation factor 4A-8 [Pyrus x bretschneideri] | 28.743 | 112.64 | 53 | 14 | 44 | 5 | 0.933 | 0.965 | 0.931 | 1.047 | 1.053 | 1.124 | 1.14 | 6.98E-03 |

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| cds.Camellia_sinensis.comp27684_c0_seq1_m.34303 | protein ACI14 [Solanum lycopersicum] | 35.892 | 9.3945 | 9.4 | 3 | 3 | 3 | 0.962 | 1.128 | 0.956 | 1.016 | 0.936 | 1.01 | 0.972 | 6.92E-01 |
| cds.Camellia_sinensis.comp27692_c0_seq1_m.36580 | | 21.543 | 48.246 | 37.8 | 6 | 7 | 6 | 0.927 | 0.974 | 1.022 | 1.063 | 0.97 | 1.038 | 1.051 | 2.77E-01 |
| cds.Camellia_sinensis.comp27695_c0_seq1_m.29118 | Translation initiation factor eIF-2B subunit delta [Morus notabilis] | 42.783 | 3.6592 | 5.5 | 2 | 3 | 2 | 1.136 | 1.078 | 1.101 | 0.868 | 0.867 | 0.919 | 0.801 | 8.19E-04 |
| cds.Camellia_sinensis.comp27701_c0_seq1_m.17363 | PREDICTED: plant intracellular Ras-group-related LRR protein 1-like [Ziziphus jujuba] | 57.25 | 2.0581 | 1.9 | 1 | 2 | 1 | 0.96 | 0.937 | 1.032 | 1.077 | 0.959 | 1.056 | 1.056 | 3.09E-01 |
| cds.Camellia_sinensis.comp27704_c0_seq1_m.12820 | PREDICTED: hsp70-Hsp90 organizing protein 3-like [Ipomoea nil] | 65.897 | 183.96 | 54.5 | 32 | 54 | 24 | 1.031 | 1.057 | 1.082 | 0.946 | 0.941 | 0.94 | 0.892 | 1.48E-02 |

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| cds.Camellia_sinensis.comp27704_c0_seq2_m.25696 | PREDICTED: hsp70-Hsp90 organizing protein 3-like [Ipomoea nil] | 53.506 | 93.35 | 39.8 | 20 | 28 | 12 | 1.026 | 1.006 | 1.059 | 0.987 | 0.999 | 0.973 | 0.957 | 6.07E-02 |
| cds.Camellia_sinensis.comp27710_c0_seq1_m.9599 | PREDICTED: KH domain-containing protein HEN4 isoform X1 [Vitis vinifera] | 74.492 | 20.156 | 10 | 7 | 8 | 7 | 1.01 | 1.011 | 1.007 | 1.017 | 0.993 | 0.981 | 0.988 | 3.64E-01 |
| cds.Camellia_sinensis.comp27714_c0_seq1_m.38025 | PREDICTED: 50S ribosomal protein L19-1, chloroplastic-like isoform X1 [Juglans regia] | 25.873 | 3.04 | 10.9 | 3 | 4 | 3 | 0.976 | 0.979 | 0.901 | 1.164 | 1.011 | 1.011 | 1.116 | 1.18E-01 |
| cds.Camellia_sinensis.comp27728_c0_seq1_m.13497 | PREDICTED: histone-lysine N-methyltransferase setd3 isoform X1 [Vitis vinifera] | 39.396 | 4.1534 | 4.9 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp27728_c0_seq2_m.30113 | PREDICTED: histone-lysine N-methyltransferase setd3-like [Nicotiana tabacum] | 16.996 | 1.3464 | 5.9 | 1 | 1 | 1 | 1.035 | 0.953 | 1.114 | 0.993 | 0.936 | 0.97 | 0.935 | 2.43E-01 |
| cds.Camellia_sinensis.comp27742_c0_seq1_m.29999 | PREDICTED: methyltransferase-like protein 7A [Vitis vinifera] | 35.948 | 9.6453 | 6.6 | 2 | 4 | 2 | 0.953 | 0.977 | 1.015 | 1.04 | 1.004 | 1.084 | 1.062 | 1.05E-01 |
| cds.Camellia_sinensis.comp27744_c0_seq1_m.47324 | PREDICTED: probable glutathione S-transferase parC [Nelumbo nucifera] | 13.161 | 8.4596 | 35.7 | 6 | 14 | 6 | 1.006 | 0.983 | 0.958 | 0.985 | 1.04 | 1.028 | 1.036 | 1.80E-01 |
| cds.Camellia_sinensis.comp27745_c0_seq1_m.30721 | PREDICTED: protein FLX-like 3 [Nicotiana tabacum] | 30.174 | 36.913 | 32.1 | 10 | 15 | 9 | 0.967 | 0.948 | 0.984 | 1.029 | 1.025 | 1.049 | 1.07 | 6.24E-03 |

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| cds.Camellia_sinensis.comp27752_c0_seq1_m.38156 | PREDICTED: protein LOW PSII ACCUMULATION 2, chloroplastic [Jatropha curcas] | 11.417 | 14.846 | 26.4 | 3 | 4 | 3 | 1.028 | 1.084 | 1.292 | 0.749 | 0.988 | 0.834 | 0.755 | 5.64E-02 |
| cds.Camellia_sinensis.comp27753_c0_seq1_m.42051 | PREDICTED: peroxidase 12 [Eucalyptus grandis] | 22.094 | 34.611 | 25.5 | 4 | 7 | 4 | 0.96 | 1.005 | 0.998 | 1.044 | 0.996 | 1.015 | 1.031 | 1.96E-01 |
| cds.Camellia_sinensis.comp27764_c0_seq3_m.29841 | starch-binding domain-containing protein [Solanum lycopersicum] | 47.353 | 8.2614 | 9.3 | 3 | 3 | 3 | 0.997 | 1.073 | 1.043 | 0.989 | 0.876 | 1.021 | 0.927 | 2.06E-01 |
| cds.Camellia_sinensis.comp27766_c0_seq2_m.40392 | PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform-like [Ziziphus jujuba] | 23.479 | 21.093 | 26.8 | 6 | 10 | 5 | 0.956 | 0.942 | 0.98 | 1.077 | 1.034 | 1.029 | 1.091 | 9.26E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp27767_c0_seq1_m.16273 | PREDICTED: abscisate beta-glucosyltransferase [Eucalyptus grandis] | 53.201 | 65.096 | 17.5 | 9 | 15 | 9 | 0.952 | 0.982 | 0.981 | 1.07 | 0.993 | 1.015 | 1.056 | 9.11E-02 |
| cds.Camellia_sinensis.comp27776_c0_seq1_m.46698 | transmembrane protein, putative [Medicago truncatula] | 18.786 | 3.3119 | 12.2 | 2 | 2 | 2 | 0.995 | 1.033 | 1.001 | 0.92 | 1.087 | 0.97 | 0.983 | 7.18E-01 |
| cds.Camellia_sinensis.comp27782_c0_seq1_m.29375 | PREDICTED: ATP synthase subunit O, mitochondrial [Erythranthe guttata] | 32.228 | 78.023 | 39.3 | 12 | 34 | 12 | 1.036 | 0.998 | 1.03 | 0.986 | 0.978 | 0.968 | 0.957 | 2.63E-02 |
| cds.Camellia_sinensis.comp27787_c0_seq2_m.44511 | PREDICTED: ras-related protein RABB1c isoform X1 [Amborella trichopoda] | 21.341 | 95.928 | 43.1 | 6 | 12 | 4 | 0.998 | 0.993 | 0.974 | 0.998 | 1.041 | 1.076 | 1.051 | 1.01E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp27788_c0_seq1_m.26729 | PREDICTED: Golgi to ER traffic protein 4 homolog [Sesamum indicum] | 37.336 | 4.5838 | 7 | 2 | 2 | 2 | 0.995 | 1.059 | 0.91 | 1.009 | 0.947 | 1.087 | 1.027 | 6.77E-01 |
| cds.Camellia_sinensis.comp27792_c0_seq1_m.11601 | PREDICTED: mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS1-like [Nicotiana attenuata] | 23.408 | 14.129 | 25.7 | 5 | 7 | 5 | 1.05 | 1.069 | 1.157 | 0.897 | 0.884 | 0.926 | 0.826 | 4.42E-03 |
| cds.Camellia_sinensis.comp27796_c0_seq4_m.39734 | PREDICTED: 5-formyltetrahydrofolate cyclo-ligase-like protein COG0212 isoform X2 [Nicotiana tomentosiformis] | 28.227 | 8.1476 | 15 | 4 | 4 | 4 | 0.969 | 0.954 | 1.027 | 0.992 | 1.034 | 1.002 | 1.026 | 3.61E-01 |

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| cds.Camellia_sinensis.comp27798_c0_seq1_m.6496 | PREDICTED: protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1-like [Solanum tuberosum | 100.35 | 7.4288 | 6.9 | 7 | 8 | 7 | 1.06 | 1.048 | 0.999 | 0.98 | 0.93 | 0.943 | 0.918 | 2.37E-02 |
| cds.Camellia_sinensis.comp27802_c0_seq1_m.27276 | PREDICTED: V-type proton ATPase subunit C [Nicotiana | 42.381 | 76.035 | 25.9 | 11 | 16 | 11 | 0.993 | 1.005 | 0.988 | 1.02 | 1.005 | 1.013 | 1.017 | 5.97E-02 |
| cds.Camellia_sinensis.comp27806_c0_seq1_m.43057 | PREDICTED: 60S ribosomal protein L24-like [Jatropha curcas] | 18.518 | 11.774 | 12.3 | 3 | 4 | 3 | 1.077 | 1.122 | 1.101 | 0.895 | 0.914 | 0.895 | 0.819 | 1.36E-04 |
| cds.Camellia_sinensis.comp27811_c0_seq1_m.22502 | PREDICTED: protein ABCI7, chloroplastic [Vitis vinifera] | 55.575 | 29.628 | 9.7 | 5 | 7 | 4 | 0.992 | 1.027 | 1.03 | 0.964 | 0.983 | 0.986 | 0.962 | 5.06E-02 |

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| cds.Camellia_sinensis.comp27812_c0_seq1_m.19185 | PREDICTED: inorganic phosphate transporter 1-4-like [Sesamum indicum] | 58.905 | 11.545 | 7.3 | 5 | 5 | 4 | 0.867 | 0.915 | 0.95 | 1.184 | 1.017 | 1.102 | 1.209 | 2.13E-02 |
| cds.Camellia_sinensis.comp27818_c0_seq1_m.24693 | PREDICTED: alpha-1,4-glucan-protein synthase [UDP-forming] 2 [Malus domestica] | 49.056 | 79.383 | 35.3 | 15 | 32 | 7 | 1.038 | 1.036 | 1.018 | 0.995 | 0.982 | 0.973 | 0.954 | 6.32E-03 |
| cds.Camellia_sinensis.comp27818_c0_seq2_m.27266 | PREDICTED: alpha-1,4-glucan-protein synthase [UDP-forming] [Pyrus x bretschneideri] | 48.174 | 8.9578 | 23.5 | 11 | 25 | 3 | 1.083 | 1.004 | 1.054 | 0.968 | 0.971 | 0.923 | 0.911 | 2.81E-02 |
| cds.Camellia_sinensis.comp27819_c0_seq2_m.28471 | PREDICTED: high mobility group B protein 10 isoform X2 [Vitis vinifera] | 36.777 | 1.3388 | 2.1 | 1 | 1 | 1 | 0.988 | 1.107 | 1.038 | 0.93 | 1.04 | 0.898 | 0.915 | 1.81E-01 |

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| cds.Camellia_sinensis.comp27828_c0_seq1_m.36752 | PREDICTED: 3-oxoacyl-[acyl-carrier-protein] reductase FabG-like [Nicotiana tabacum] | 29.725 | 18.371 | 19.4 | 5 | 7 | 5 | 0.961 | 0.949 | 0.942 | 1.081 | 1.039 | 1.039 | 1.108 | 2.12E-03 |
| cds.Camellia_sinensis.comp27829_c0_seq1_m.21294 | PREDICTED: calcium-dependent protein kinase SK5-like [Solanum tuberosum | 48.345 | 14.644 | 12.1 | 4 | 7 | 4 | 0.958 | 0.956 | 1.055 | 1.079 | 0.943 | 1.03 | 1.028 | 6.24E-01 |
| cds.Camellia_sinensis.comp27847_c0_seq1_m.40758 | PREDICTED: ADP-ribosylation factor-like protein 8A isoform X1 [Capsicum annuum] | 25.298 | 24.817 | 27.7 | 5 | 9 | 4 | 0.995 | 0.99 | 0.999 | 1.049 | 1.065 | 0.95 | 1.027 | 5.56E-01 |
| cds.Camellia_sinensis.comp27855_c0_seq2_m.26247 | PREDICTED: very-long-chain enoyl-CoA reductase isoform X1 [Vitis vinifera] | 36.396 | 6.2256 | 9 | 3 | 4 | 3 | 1.099 | 1.257 | 1.193 | 0.876 | 0.743 | 0.791 | 0.679 | 3.32E-03 |

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| cds.Camellia_sinensis.comp27863_c0_seq1_m.16442 | PREDICTED: internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial-like [Sesamum | 56.426 | 7.8437 | 6.8 | 4 | 5 | 4 | 0.919 | 0.957 | 1.018 | 0.999 | 1.016 | 1.029 | 1.052 | 1.73E-01 |
| cds.Camellia_sinensis.comp27864_c0_seq1_m.32651 | PREDICTED: 40S ribosomal protein S6-like [Musa acuminata subsp. malaccensis] | 28.348 | 5.7212 | 17.7 | 4 | 7 | 1 | 1.013 | 1.393 | 0.983 | 0.898 | 0.851 | 0.836 | 0.763 | 8.52E-02 |
| cds.Camellia_sinensis.comp27865_c0_seq1_m.35278 | PREDICTED: protein CURVATURE THYLAKOID 1D, chloroplastic isoform X2 [Vitis vinifera] | 23.502 | 19.589 | 16.2 | 3 | 4 | 3 | 0.959 | 1.017 | 1.037 | 1.011 | 1.016 | 0.971 | 0.995 | 8.74E-01 |
| cds.Camellia_sinensis.comp27866_c0_seq2_m.50182 | PREDICTED: 21 kDa protein [Prunus mume] | 14.686 | 11.886 | 16.2 | 2 | 2 | 2 | 1.001 | 0.972 | 0.987 | 0.992 | 1.056 | 1.005 | 1.031 | 2.16E-01 |

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| cds.Camellia_sinensis.comp27870_c0_seq1_m.37067 | PREDICTED: clathrin light chain 2-like [Cucumis sativus] | 29.03 | 11.628 | 20.5 | 5 | 8 | 4 | 1.029 | 1.071 | 1.043 | 0.995 | 0.93 | 0.949 | 0.914 | 1.81E-02 |
| cds.Camellia_sinensis.comp27877_c0_seq1_m.49510 | PREDICTED: prolyl endopeptidase [Jatropha curcas] | 22.529 | 29.787 | 30.6 | 6 | 21 | 4 | 0.994 | 0.991 | 0.975 | 0.986 | 1 | 0.985 | 1.004 | 6.55E-01 |
| cds.Camellia_sinensis.comp27879_c0_seq1_m.18135 | aspartate aminotransferase 2 family protein [Populus trichocarpa] | 24.805 | 55.619 | 56.4 | 12 | 23 | 12 | 1.016 | 1.005 | 1.003 | 0.979 | 1 | 0.972 | 0.976 | 6.00E-02 |
| cds.Camellia_sinensis.comp27879_c0_seq2_m.30639 | PREDICTED: aspartate aminotransferase, chloroplastic [Vitis vinifera] | 26.489 | 196.54 | 56 | 12 | 38 | 11 | 0.982 | 1.007 | 0.985 | 1.028 | 0.999 | 0.998 | 1.017 | 2.47E-01 |
| cds.Camellia_sinensis.comp27880_c1_seq2_m.22949 | PREDICTED: pectinesterase [Ricinus communis] | 53.21 | 6.199 | 2 | 1 | 2 | 1 | 0.958 | 1.07 | 1.033 | 1.027 | 0.917 | 1.004 | 0.963 | 4.72E-01 |

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| cds.Camellia_sinensis.comp27898_c0_seq1_m.15788 | PREDICTED: protein EDS1L-like [Nicotiana tabacum] | 70.017 | 2.1 | 3.4 | 2 | 2 | 2 | 1.125 | 1.007 | 1.024 | 0.89 | 0.887 | 1.046 | 0.894 | 1.53E-01 |
| cds.Camellia_sinensis.comp27901_c0_seq1_m.30576 | PREDICTED: phosphomannomutase [Vitis vinifera] | 35.57 | 31.106 | 24 | 7 | 11 | 7 | 1.062 | 1.025 | 1.04 | 0.97 | 0.96 | 0.965 | 0.926 | 1.98E-03 |
| cds.Camellia_sinensis.comp27903_c0_seq1_m.9824 | PREDICTED: E3 ubiquitin-protein ligase KEG isoform X2 [Vitis vinifera] | 56.061 | 59.81 | 20.2 | 9 | 12 | 9 | 0.955 | 1.038 | 0.952 | 1.059 | 1.021 | 1.042 | 1.06 | 1.22E-01 |
| cds.Camellia_sinensis.comp27907_c0_seq1_m.42167 | PREDICTED: protein SRG1 [Theobroma cacao] | 32.276 | 4.8274 | 15.2 | 4 | 5 | 4 | 0.923 | 1 | 1.013 | 1.041 | 1.036 | 0.964 | 1.036 | 4.08E-01 |
| cds.Camellia_sinensis.comp27911_c0_seq1_m.14961 | PREDICTED: CBS domain-containing protein CBSCBSPB5 isoform X2 [Eucalyptu | 24.753 | 5.6274 | 6.6 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp27922_c0_seq2_m.27931 | PREDICTED: SAL1 phosphatase-like isoform X2 [Glycine max] | 15.268 | 18.903 | 26.6 | 4 | 7 | 4 | 1.012 | 0.992 | 0.982 | 1.021 | 0.985 | 1.019 | 1.013 | 4.27E-01 |
| cds.Camellia_sinensis.comp27928_c0_seq2_m.41003 | PREDICTED: FAD synthetase 2, chloroplastic [Daucus carota subsp. sativus] | 23.008 | 1.8726 | 4.4 | 1 | 1 | 1 | 0.977 | 1.073 | 0.93 | 1.056 | 0.912 | 1.062 | 1.017 | 8.18E-01 |
| cds.Camellia_sinensis.comp27929_c0_seq1_m.29995 | PREDICTED: probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial [Theobroma cacao] | 36.431 | 37.046 | 13.6 | 3 | 4 | 3 | 0.942 | 0.923 | 0.93 | 1.032 | 1.117 | 1.085 | 1.157 | 3.68E-03 |
| cds.Camellia_sinensis.comp27931_c0_seq1_m.36596 | structural constituent of ribosome protein [Medicago truncatula] | 30.169 | 5.015 | 11.5 | 3 | 5 | 3 | 0.882 | 1.038 | 0.976 | 1.023 | 1.089 | 1.043 | 1.089 | 1.61E-01 |

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| cds.Camellia_sinensis.comp27939_c0_seq1_m.20010 | PREDICTED: bifunctional purple acid phosphatase 26-like [Juglans regia] | 56.306 | 6.5291 | 3.9 | 1 | 1 | 1 | 1.106 | 0.797 | 1.048 | 1.106 | 1.126 | 0.834 | 1.039 | 7.95E-01 |
| cds.Camellia_sinensis.comp27947_c0_seq1_m.40362 | PREDICTED: eukaryotic translation initiation factor 4B3-like [Nicotiana tabacum] | 33.886 | 3.253 | 3.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp27949_c0_seq1_m.37702 | PREDICTED: ras-related protein RHN1 isoform X2 [Vitis vinifera] | 20.595 | 56.108 | 41.8 | 7 | 15 | 5 | 0.952 | 0.935 | 0.946 | 1.01 | 1.066 | 1.095 | 1.119 | 9.96E-03 |
| cds.Camellia_sinensis.comp27949_c0_seq2_m.38344 | PREDICTED: ras-related protein RHN1 isoform X1 [Vitis vinifera] | 22.398 | 4.9477 | 25.5 | 4 | 10 | 2 | 0.936 | 0.937 | 0.902 | 1.055 | 1.142 | 1.085 | 1.183 | 3.14E-03 |

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| cds.Camellia_sinensis.comp27950_c0_seq1_m.26267 | PREDICTED: diaminopimelate epimerase, chloroplastic [Vitis vinifera] | 33.412 | 47.806 | 20.2 | 5 | 8 | 5 | 1.044 | 0.98 | 0.981 | 0.976 | 0.993 | 1.003 | 0.989 | 6.59E-01 |
| cds.Camellia_sinensis.comp27953_c0_seq1_m.41972 | PREDICTED: neutral/alkaline invertase 3, chloroplastic [Vitis vinifera] | 23.421 | 8.1818 | 5.1 | 1 | 1 | 1 | 0.953 | 1.002 | 1.06 | 0.957 | 1.015 | 1.024 | 0.994 | 8.84E-01 |
| cds.Camellia_sinensis.comp27960_c0_seq1_m.32009 | PREDICTED: calnexin homolog [Nelumbo nucifera] | 35.4 | 18.662 | 9.3 | 2 | 3 | 2 | 1.27 | 0.94 | 1.088 | 0.845 | 0.817 | 0.993 | 0.805 | 1.14E-01 |
| cds.Camellia_sinensis.comp27965_c0_seq1_m.30992 | PREDICTED: persulfide dioxygenase ETHE1 homolog, mitochondrial-like [Nicotiana attenuata] | 24.57 | 4.618 | 10.7 | 2 | 2 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp27972_c0_seq1_m.37314 | tagatose-6-phosphate ketose/aldose isomerase, putative (Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein) [Arabidopsis thaliana] | 24.541 | 4.8023 | 20.1 | 4 | 5 | 4 | 1.006 | 0.969 | 0.994 | 0.995 | 1.007 | 1.039 | 1.024 | 2.32E-01 |
| cds.Camellia_sinensis.comp27975_c0_seq1_m.40790 | PREDICTED: calmodulin-binding protein 60 C isoform X2 [Vitis vinifera] | 28.407 | 1.5849 | 9.4 | 3 | 3 | 1 | 0.943 | 1.024 | 1.05 | 0.941 | 1.013 | 1.039 | 0.992 | 8.68E-01 |
| cds.Camellia_sinensis.comp27976_c0_seq2_m.13381 | PREDICTED: glutamyl-tRNA(Gln) amidotransferase subunit A, chloroplastic/mitochondrial [Ipomoea | 57.917 | 158.92 | 35.4 | 14 | 23 | 14 | 1.016 | 0.992 | 1.02 | 0.999 | 0.963 | 0.982 | 0.972 | 1.09E-01 |

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| cds.Camellia_sinensis.comp27982_c0_seq1_m.46320 | PREDICTED: thioredoxin-like protein Clot [Prunus mume] | 15.003 | 4.7147 | 14.4 | 2 | 3 | 2 | 1.008 | 0.973 | 0.997 | 0.938 | 1.067 | 1.024 | 1.017 | 7.11E-01 |
| cds.Camellia_sinensis.comp27989_c0_seq2_m.7925 | PREDICTED: ABC transporter F family member 4-like [Cucumis melo] | 76.984 | 11.67 | 8.2 | 4 | 4 | 4 | 1.004 | 1.096 | 1.027 | 1.006 | 0.878 | 1.042 | 0.936 | 3.07E-01 |
| cds.Camellia_sinensis.comp27991_c0_seq2_m.43729 | PREDICTED: probable calcium-binding protein CML20 [Pyrus x bretschneideri] | 19.305 | 15.527 | 26.6 | 4 | 6 | 4 | 1.092 | 1.115 | 1.023 | 0.914 | 0.896 | 0.939 | 0.851 | 5.36E-03 |
| cds.Camellia_sinensis.comp27994_c0_seq1_m.4637 | PREDICTED: protein ENHANCED DISEASE RESISTANCE 2 isoform X2 [Prunus | 52.503 | 1.2203 | 2.8 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp27995_c0_seq2_m.34073 | PREDICTED: NADPH-dependent pterin aldehyde reductase [Vitis vinifera] | 26.09 | 13.616 | 30.8 | 8 | 11 | 8 | 0.932 | 0.995 | 1.028 | 0.964 | 0.936 | 1.018 | 0.987 | 7.60E-01 |
| cds.Camellia_sinensis.comp27998_c0_seq1_m.15252 | PREDICTED: glucose-1-phosphate adenylyltransferase large subunit 3, chloroplastic/amyloplastic [Vitis vinifera] | 57.648 | 216.71 | 40 | 17 | 31 | 16 | 1.034 | 0.982 | 1.011 | 0.996 | 1.023 | 0.977 | 0.99 | 6.36E-01 |
| cds.Camellia_sinensis.comp28002_c0_seq1_m.43612 | PREDICTED: S-adenosylmethionine synthase 5 [Vitis vinifera] | 16.905 | 8.329 | 33.8 | 5 | 13 | 1 | 1.185 | 1.116 | 1.175 | 0.749 | 0.859 | 0.866 | 0.712 | 2.52E-03 |
| cds.Camellia_sinensis.comp28011_c0_seq1_m.30896 | PREDICTED: 1-aminocyclopropane-1-carboxylate oxidase homolog 1-like [Nelumbo nucifera] | 43.315 | 43.911 | 18.7 | 7 | 12 | 7 | 0.984 | 1.005 | 1.044 | 1 | 1.003 | 0.967 | 0.979 | 3.76E-01 |

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| cds.Camellia_sinensis.comp28015_c0_seq1_m.40723 | PREDICTED: 2-alkenal reductase (NADP(+)-dependent) isoform X2 [Sesamum indicum] | 15.401 | 3.0054 | 19 | 2 | 3 | 1 | 0.917 | 1.047 | 0.97 | 1.119 | 0.962 | 1.011 | 1.054 | 4.27E-01 |
| cds.Camellia_sinensis.comp28022_c0_seq1_m.46866 | PREDICTED: remorin [Cucumis melo] | 18.086 | 53.093 | 39.9 | 10 | 18 | 9 | 0.93 | 0.915 | 0.938 | 1.075 | 1.098 | 1.099 | 1.176 | 9.69E-05 |
| cds.Camellia_sinensis.comp28024_c0_seq1_m.49734 | PREDICTED: 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase-like [Malus domestica] | 13.603 | 1.6773 | 13.9 | 2 | 6 | 1 | 1.014 | 0.982 | 0.958 | 0.978 | 1.035 | 1.018 | 1.026 | 3.36E-01 |

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| cds.Camellia_sinensis.comp28027_c0_seq2_m.24842 | PREDICTED: probable L-ascorbate peroxidase 6, chloroplastic isoform X1 [Ipomoea nil] | 46.949 | 227.17 | 54.2 | 22 | 70 | 22 | 1.031 | 1.005 | 1.005 | 0.954 | 0.995 | 0.983 | 0.964 | 7.29E-02 |
| cds.Camellia_sinensis.comp28030_c0_seq10_c0_seq1_m.24237 | enoyl-CoA hydratase/isomerase family protein [Populus trichocarpa] | 50.105 | 27.293 | 12.9 | 6 | 8 | 6 | 1.425 | 1.421 | 1.381 | 0.502 | 0.508 | 0.547 | 0.368 | 2.02E-06 |
| cds.Camellia_sinensis.comp28032_c0_seq12_c0_seq1_m.26675 | PREDICTED: NADP-dependent D-sorbitol-6-phosphate dehydrogenase [Ricinus communis] | 38.055 | 20.426 | 22.1 | 8 | 11 | 8 | 0.991 | 0.996 | 0.971 | 1.021 | 1.012 | 1.04 | 1.039 | 2.70E-02 |

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| cds.Camellia_sinensis.comp28043_c0_seq1_m.15070 | PREDICTED: AT-rich interactive domain-containing protein 5 isoform X1 [Ipomoea nil] | 50.837 | 4.2775 | 5.3 | 3 | 3 | 2 | 1.006 | 0.98 | 1.047 | 0.927 | 1.038 | 1.006 | 0.98 | 6.11E-01 |
| cds.Camellia_sinensis.comp28047_c0_seq1_m.35838 | PREDICTED: GTP-binding protein YPTM2 [Populus euphratica] | 22.733 | 104.91 | 56.2 | 9 | 17 | 3 | 0.943 | 0.99 | 0.975 | 1.066 | 0.993 | 1.075 | 1.078 | 6.21E-02 |
| cds.Camellia_sinensis.comp28047_c0_seq2_m.37543 | PREDICTED: GTP-binding protein YPTM2 [Populus euphratica] | 22.663 | 7.9338 | 48.3 | 8 | 15 | 2 | 0.955 | 0.985 | 0.974 | 0.971 | 1.047 | 1.083 | 1.064 | 1.42E-01 |
| cds.Camellia_sinensis.comp28047_c0_seq3_m.38110 | PREDICTED: GTP-binding protein YPTM2 [Theobroma cacao] | 22.397 | 11.844 | 43.8 | 7 | 14 | 3 | 0.938 | 0.968 | 0.9 | 1.076 | 1.059 | 1.049 | 1.135 | 4.78E-03 |
| cds.Camellia_sinensis.comp28052_c0_seq1_m.12818 | PREDICTED: quinolinate synthase, chloroplastic [Juglans regia] | 77.597 | 4.4983 | 3.7 | 3 | 3 | 3 | 0.913 | 0.927 | 0.991 | 1.034 | 1.107 | 1.103 | 1.146 | 1.53E-02 |

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| cds.Camellia_sinensis.comp28061_c0_seq1_m.27880 | PREDICTED: cell division cycle protein 27 homolog isoform X1 [Prunus | 36.516 | 40.68 | 18.7 | 5 | 8 | 5 | 1.042 | 0.972 | 1.01 | 0.989 | 0.962 | 1.022 | 0.983 | 5.60E-01 |
| cds.Camellia_sinensis.comp28068_c0_seq1_m.20528 | PREDICTED: cysteine desulfurase, mitochondrial [Nelumbo nucifera] | 52.03 | 30.089 | 18.7 | 8 | 10 | 8 | 1.01 | 1.002 | 0.982 | 1.004 | 0.985 | 0.957 | 0.984 | 3.73E-01 |
| cds.Camellia_sinensis.comp28071_c0_seq1_m.22627 | chloroplast sedoheptulose-1,7-bisphosphatase [Solanum lycopersicum] | 42.433 | 175.21 | 52.7 | 20 | 78 | 20 | 1.05 | 1.031 | 0.999 | 0.954 | 0.989 | 0.969 | 0.945 | 3.52E-02 |
| cds.Camellia_sinensis.comp28079_c0_seq1_m.3191 | PREDICTED: NF-X1-type zinc finger protein NFXL1 [Vitis vinifera] | 121.82 | 1.9529 | 0.9 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp28080_c0_seq2_m.39935 | PREDICTED: 60S ribosomal protein L11 [Ricinus communis] | 21.368 | 16.851 | 21.3 | 4 | 10 | 1 | 1.144 | 1.1 | 1.132 | 0.835 | 0.894 | 0.859 | 0.767 | 3.20E-04 |
| cds.Camellia_sinensis.comp28080_c0_seq3_m.40155 | PREDICTED: 60S ribosomal protein L11 [Amborella trichopoda] | 24.404 | 20.326 | 22.3 | 5 | 11 | 2 | 1.092 | 1.04 | 1.128 | 0.873 | 0.929 | 0.894 | 0.827 | 3.10E-03 |
| cds.Camellia_sinensis.comp28105_c0_seq1_m.34296 | PREDICTED: probable thiol methyltransferase 2 isoform X3 [Citrus sinensis] | 27.905 | 8.3268 | 12.1 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp28106_c0_seq1_m.46951 | PREDICTED: 60S ribosomal protein L21-1 [Daucus carota subsp. sativus] | 18.716 | 16.424 | 30.5 | 6 | 12 | 6 | 1.198 | 1.207 | 1.205 | 0.774 | 0.798 | 0.807 | 0.659 | 2.54E-06 |
| cds.Camellia_sinensis.comp28111_c0_seq1_m.41736 | PREDICTED: thioredoxin H-type [Prunus mume] | 13.804 | 19.626 | 52.8 | 7 | 20 | 6 | 1.015 | 1.01 | 0.92 | 1.077 | 0.999 | 1.022 | 1.052 | 2.59E-01 |

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| cds.Camellia_sinensis.comp28122_c0_seq1_m.8123 | PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 isoform X2 [Populus euphratica] | 91.731 | 4.2612 | 2.8 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp28123_c0_seq1_m.42227 | PREDICTED: glycine-rich RNA-binding protein GRP1A-like [Nelumbo nucifera] | 16.786 | 140.3 | 50 | 7 | 26 | 5 | 1.047 | 1.04 | 1.041 | 0.955 | 0.958 | 0.965 | 0.92 | 2.19E-05 |
| cds.Camellia_sinensis.comp28131_c0_seq1_m.18968 | PREDICTED: riboflavin biosynthesis protein PYRR, chloroplastic isoform X2 [Vitis vinifera] | 64.245 | 5.2259 | 3.2 | 3 | 3 | 3 | 0.963 | 1.013 | 0.995 | 1.006 | 1.026 | 1.012 | 1.025 | 1.99E-01 |

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| cds.Camellia_sinensis.comp28134_c0_seq1_m.30420 | PREDICTED: ABC transporter I family member 19 [Daucus carota subsp. | 33.344 | 3.7229 | 7.1 | 2 | 2 | 2 | 0.951 | 1.029 | 0.929 | 1.097 | 1.068 | 0.953 | 1.072 | 2.66E-01 |
| cds.Camellia_sinensis.comp28139_c0_seq1_m.39401 | PREDICTED: protein EMBRYO SAC DEVELOPMENT ARREST 3, chloroplastic [Citrus sinensis] | 23.422 | 1.2262 | 7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28142_c0_seq1_m.18076 | PREDICTED: trans-cinnamate 4-monooxygenase [Jatropha curcas] | 60.624 | 61.458 | 26.1 | 13 | 20 | 13 | 1.245 | 1.257 | 1.245 | 0.711 | 0.741 | 0.714 | 0.578 | 1.10E-06 |
| cds.Camellia_sinensis.comp28153_c0_seq1_m.44111 | PREDICTED: pentatricopeptide repeat-containing protein At1g12620-like [Nicotiana sylvestris] | 23.375 | -2 | 4.8 | 1 | 2 | 1 | 0.954 | 0.927 | 0.958 | 1.061 | 1.099 | 1.03 | 1.124 | 5.56E-03 |

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| cds.Camellia_sinensis.comp28154_c0_seq1_m.48869 | L-ascorbate peroxidase 5 [Solanum lycopersicum] | 18.71 | 1.2985 | 4.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28155_c0_seq1_m.11399 | PREDICTED: probable alpha-galactosidase B [Citrus sinensis] | 40.988 | 114.72 | 34.8 | 10 | 21 | 10 | 1.001 | 1 | 1.012 | 1.005 | 1.03 | 0.99 | 1.004 | 7.67E-01 |
| cds.Camellia_sinensis.comp28155_c0_seq1_m.11400 | PREDICTED: probable alpha-galactosidase B [Citrus sinensis] | 33.929 | 2.7771 | 5.7 | 2 | 3 | 2 | 0.951 | 0.969 | 0.946 | 1.061 | 1.046 | 1.052 | 1.102 | 3.17E-04 |
| cds.Camellia_sinensis.comp28156_c0_seq5_m.31264 | PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein At4g39970 [Ipomoea | 34.039 | 27.98 | 16.8 | 5 | 10 | 5 | 1.045 | 1.057 | 1.019 | 0.949 | 0.973 | 0.914 | 0.909 | 1.05E-02 |

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| cds.Camellia_sinensis.comp28158_c0_seq1_m.21407 | PREDICTED: isoaspartyl peptidase/L-asparaginase 1 [Vitis vinifera] | 34.597 | 58.738 | 20.8 | 6 | 9 | 6 | 1.004 | 0.963 | 0.982 | 1.035 | 0.984 | 1.035 | 1.036 | 1.68E-01 |
| cds.Camellia_sinensis.comp28166_c0_seq1_m.24152 | PREDICTED: calreticulin-3-like [Populus euphratica] | 46.459 | 17.718 | 21.8 | 8 | 12 | 6 | 1.056 | 1.083 | 1.075 | 0.921 | 0.906 | 0.896 | 0.847 | 1.16E-04 |
| cds.Camellia_sinensis.comp28167_c0_seq1_m.27410 | PREDICTED: patatin-like protein 2 [Vitis vinifera] | 45.447 | 55.067 | 23.2 | 10 | 10 | 10 | 0.961 | 0.99 | 0.97 | 1.076 | 1.017 | 1.005 | 1.061 | 6.25E-02 |
| cds.Camellia_sinensis.comp28168_c1_seq6_m.40232 | PREDICTED: ubiquitin-conjugating enzyme E2 10-like [Gossypium hirsutum] | 16.547 | 10.366 | 12.8 | 2 | 3 | 2 | 1.071 | 0.995 | 1.056 | 0.914 | 0.981 | 0.955 | 0.913 | 4.07E-02 |
| cds.Camellia_sinensis.comp28169_c0_seq1_m.38581 | PREDICTED: 60S ribosomal protein L13-1 [Nelumbo nucifera] | 23.908 | 22.169 | 23.7 | 5 | 8 | 5 | 1.136 | 1.116 | 1.11 | 0.855 | 0.887 | 0.865 | 0.775 | 3.95E-05 |

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| cds.Camellia_sinensis.comp28178_c0_seq1_m.24102 | PREDICTED: hepatocyte growth factor-regulated tyrosine kinase substrate isoform X3 [Juglans regia] | 32.126 | 7.1292 | 10.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp28181_c0_seq1_m.12362 | PREDICTED: DEAD-box ATP-dependent RNA helicase 53 [Vitis vinifera] | 41.29 | 6.3789 | 12.3 | 4 | 5 | 4 | 0.843 | 0.938 | 0.859 | 1.169 | 1.101 | 1.145 | 1.294 | 2.28E-03 |
| cds.Camellia_sinensis.comp28181_c0_seq1_m.12363 | PREDICTED: DEAD-box ATP-dependent RNA helicase 53-like [Citrus sinensis] | 28.392 | 8.1285 | 12.5 | 3 | 3 | 3 | 0.923 | 0.933 | 0.959 | 1.056 | 1.054 | 1.105 | 1.142 | 2.30E-03 |

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| cds.Camellia_sinensis.comp28208_c0_seq1_m.9743 | PREDICTED: delta-1-pyrroline-5-carboxylate synthase [Sesamum indicum] | 78.684 | 19.134 | 12.9 | 10 | 13 | 10 | 0.982 | 1.024 | 1.008 | 0.998 | 0.998 | 1.038 | 1.007 | 7.32E-01 |
| cds.Camellia_sinensis.comp28215_c0_seq8_m.14740 | PREDICTED: heterogeneous nuclear ribonucleoprotein 1-like [Juglans regia] | 47.577 | 138.5 | 13.7 | 5 | 16 | 4 | 1.001 | 0.983 | 0.975 | 1.012 | 0.997 | 1.019 | 1.023 | 8.44E-02 |
| cds.Camellia_sinensis.comp28217_c0_seq1_m.36291 | glycoprotein family protein [Medicago truncatula] | 28.787 | 8.2185 | 8.2 | 2 | 3 | 2 | 0.997 | 1.008 | 0.987 | 1.051 | 0.932 | 1.028 | 1.006 | 9.00E-01 |
| cds.Camellia_sinensis.comp28217_c0_seq2_m.36876 | glycoprotein family protein [Medicago truncatula] | 32.255 | 5.1714 | 5.9 | 2 | 2 | 2 | 1.096 | 1.088 | 1.054 | 0.901 | 0.957 | 0.885 | 0.847 | 3.30E-03 |
| cds.Camellia_sinensis.comp28222_c0_seq1_m.16700 | PREDICTED: glutathione reductase, cytosolic isoform X1 [Vitis vinifera] | 53.876 | 138.97 | 40.8 | 18 | 30 | 18 | 0.964 | 0.94 | 0.979 | 1.082 | 1.046 | 1.058 | 1.105 | 2.94E-03 |

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| cds.Camellia_sinensis.comp28223_c0_seq1_m.29677 | PREDICTED: peptidyl-prolyl cis-trans isomerase [Vitis vinifera] | 28.234 | 86.54 | 23.5 | 7 | 31 | 6 | 0.989 | 1.022 | 0.991 | 0.99 | 0.991 | 0.985 | 0.988 | 3.30E-01 |
| cds.Camellia_sinensis.comp28225_c0_seq1_m.30489 | PREDICTED: 50S ribosomal protein L35, chloroplastic-like [Erythranthe guttata] | 16.558 | 2.1519 | 9.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28227_c0_seq1_m.17295 | PREDICTED: sterol 14-demethylase-like [Ziziphus jujuba] | 55.457 | 4.7626 | 3.9 | 2 | 3 | 2 | 1.046 | 1.069 | 1.092 | 0.936 | 0.906 | 0.898 | 0.854 | 8.82E-04 |
| cds.Camellia_sinensis.comp28228_c0_seq1_m.35208 | PREDICTED: eukaryotic translation initiation factor 3 subunit A [Erythranthe guttata] | 35.716 | 8.756 | 27.5 | 4 | 6 | 1 | 1.045 | 0.98 | 1.008 | 1.022 | 1.003 | 0.947 | 0.98 | 5.26E-01 |

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| cds.Camellia_sinensis.comp28228_c0_seq2_m.35783 | PREDICTED: eukaryotic translation initiation factor 3 subunit A [Erythranthe guttata] | 35.827 | 1.2063 | 27.5 | 4 | 6 | 1 | 1.086 | 1.057 | 1.039 | 0.934 | 0.978 | 0.894 | 0.882 | 1.20E-02 |
| cds.Camellia_sinensis.comp28231_c0_seq1_m.12401 | PREDICTED: protein NUCLEAR FUSION DEFECTIVE 4-like [Jatropha curcas] | 64.249 | 10.79 | 5.8 | 4 | 4 | 4 | 1.031 | 1.046 | 1.001 | 0.903 | 0.972 | 1.05 | 0.95 | 3.10E-01 |
| cds.Camellia_sinensis.comp28234_c0_seq1_m.37114 | PREDICTED: thioredoxin-like protein slr0233 [Prunus mume] | 23.685 | 66.066 | 27.1 | 6 | 13 | 6 | 1.032 | 1.033 | 1.007 | 1.007 | 0.953 | 0.981 | 0.957 | 7.16E-02 |
| cds.Camellia_sinensis.comp28236_c1_seq1_m.20964 | PREDICTED: monodehydroascorbate reductase 4, peroxisomal [Vitis vinifera] | 53.216 | 31.229 | 17.8 | 8 | 13 | 8 | 0.968 | 0.95 | 0.966 | 1.029 | 1.056 | 1.065 | 1.092 | 1.78E-03 |

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| cds.Camellia_sinensis.comp28244_c0_seq1_m.32818 | PREDICTED: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial [Sesamum indicum] | 28.356 | 7.0782 | 16.5 | 4 | 7 | 4 | 1.006 | 0.944 | 1.041 | 0.97 | 0.988 | 1.005 | 0.991 | 7.89E-01 |
| cds.Camellia_sinensis.comp28247_c0_seq1_m.14164 | GTPase Era [Morus notabilis] | 54.209 | 3.5653 | 4.2 | 2 | 2 | 2 | 1.032 | 1.094 | 1.129 | 0.89 | 0.922 | 0.918 | 0.839 | 3.58E-03 |
| cds.Camellia_sinensis.comp28252_c0_seq1_m.26270 | PREDICTED: protein SLOW GREEN 1, chloroplastic-like [Nicotiana attenuata] | 40.33 | 17.016 | 6.8 | 3 | 6 | 3 | 1.009 | 0.953 | 0.969 | 1.007 | 1.058 | 1.036 | 1.058 | 6.37E-02 |
| cds.Camellia_sinensis.comp28255_c0_seq1_m.3638 | PREDICTED: mitochondrial arginine transporter BAC2-like isoform X1 [Nicotiana tabacum] | 41.072 | 1.1869 | 1.9 | 1 | 1 | 1 | 0.951 | 0.977 | 0.985 | 1.023 | 1.039 | 1.045 | 1.067 | 6.44E-03 |

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| cds.Camellia_sinensis.comp28256_c0_seq2_m.21404 | PREDICTED: probable endo-1,3(4)-beta-glucanase ARB_01444 [Daucus carota subsp. sativus] | 64.753 | 15.364 | 9.6 | 5 | 5 | 5 | 0.902 | 0.927 | 0.884 | 1.091 | 1.085 | 1.077 | 1.199 | 2.19E-04 |
| cds.Camellia_sinensis.comp28274_c0_seq1_m.4439 | PREDICTED: calmodulin-binding transcription activator 6 isoform X1 [Vitis vinifera] | 106.06 | 6.616 | 3.7 | 4 | 4 | 4 | 1.135 | 1.067 | 1.102 | 0.877 | 0.877 | 0.9 | 0.803 | 3.81E-04 |
| cds.Camellia_sinensis.comp28278_c0_seq1_m.37133 | PREDICTED: EKC/KEOPS complex subunit bud32 [Juglans regia] | 29.411 | 6.4551 | 8.8 | 2 | 2 | 2 | 1.085 | 0.992 | 1.13 | 0.94 | 0.888 | 0.951 | 0.867 | 3.17E-02 |

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| cds.Camellia_sinensis.comp28287_c0_seq1_m.16003 | PREDICTED: methionine--tRNA ligase, chloroplastic/mitochondrial [Vitis vinifera] | 69.586 | 55.997 | 15.6 | 8 | 9 | 8 | 1.038 | 0.993 | 0.975 | 0.998 | 0.996 | 0.986 | 0.991 | 6.82E-01 |
| cds.Camellia_sinensis.comp28290_c0_seq1_m.27632 | PREDICTED: ribokinase isoform X1 [Theobroma cacao] | 42.09 | 3.4232 | 7.5 | 4 | 4 | 4 | 0.993 | 1.001 | 0.984 | 0.99 | 1.015 | 1 | 1.009 | 3.63E-01 |
| cds.Camellia_sinensis.comp28292_c0_seq3_m.27179 | PREDICTED: thylakoid lumenal protein TL20.3, chloroplastic isoform X1 [Juglans regia] | 30.293 | 275.84 | 57.6 | 13 | 30 | 13 | 0.994 | 0.999 | 1.002 | 0.975 | 1.008 | 0.998 | 0.995 | 6.62E-01 |
| cds.Camellia_sinensis.comp28297_c0_seq1_m.31083 | NAD(P)-binding rossmann-fold protein [Medicago truncatula] | 39.069 | 74.143 | 46.1 | 15 | 37 | 6 | 0.979 | 0.998 | 0.967 | 1.033 | 1.025 | 1.017 | 1.044 | 1.30E-02 |

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| cds.Camellia_sinensis.comp28297_c0_seq2_m.34773 | NAD-dependent epimerase/dehydratase [Zea mays] | 27.944 | 158.94 | 61.2 | 15 | 31 | 6 | 1.066 | 1.011 | 1.038 | 0.926 | 0.966 | 0.958 | 0.915 | 1.14E-02 |
| cds.Camellia_sinensis.comp28300_c0_seq1_m.40644 | PREDICTED: 50S ribosomal protein L4, chloroplastic-like [Nelumbo nucifera] | 33.539 | 11.727 | 9.6 | 3 | 4 | 3 | 0.933 | 0.915 | 0.94 | 1.059 | 1.119 | 1.098 | 1.175 | 8.76E-04 |
| cds.Camellia_sinensis.comp28302_c1_seq1_m.15926 | PREDICTED: TOM1-like protein 2 [Vitis vinifera] | 67.699 | 11.354 | 2.3 | 1 | 1 | 1 | 0.989 | 0.851 | 0.992 | 1.127 | 1.115 | 0.959 | 1.13 | 1.67E-01 |
| cds.Camellia_sinensis.comp28303_c2_seq1_m.19063 | PREDICTED: cytochrome P450 704C1 [Theobroma cacao] | 57.329 | 168.42 | 47.5 | 22 | 40 | 22 | 1.066 | 1.008 | 1.02 | 0.966 | 0.967 | 0.963 | 0.936 | 6.11E-02 |
| cds.Camellia_sinensis.comp28305_c0_seq1_m.37395 | PREDICTED: ras-related protein RABH1b-like [Nicotiana tabacum] | 22.998 | 38.405 | 32.4 | 7 | 12 | 4 | 1.08 | 1.013 | 1.027 | 1.025 | 0.878 | 0.971 | 0.921 | 1.65E-01 |

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| cds.Camellia_sinensis.comp28312_c0_seq2_m.16725 | PREDICTED: 40S ribosomal protein S15a [Erythranthe guttata] | 14.787 | 10.525 | 25.4 | 4 | 8 | 4 | 0.97 | 0.953 | 0.976 | 1.031 | 1.086 | 1.031 | 1.086 | 1.18E-02 |
| cds.Camellia_sinensis.comp28313_c0_seq2_m.21555 | PREDICTED: DNA polymerase I isoform X1 [Theobroma cacao] | 47.596 | 8.8056 | 4 | 1 | 1 | 1 | 1.041 | 0.921 | 1.024 | 1.087 | 0.969 | 0.97 | 1.013 | 8.18E-01 |
| cds.Camellia_sinensis.comp28314_c0_seq2_m.31619 | BAG family molecular chaperone regulator 4 [Asparagus officinalis] | 41.296 | 5.1013 | 5.4 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp28329_c0_seq1_m.34253 | PREDICTED: 40S ribosomal protein S3-3-like [Nelumbo nucifera] | 26.352 | 72.336 | 56.6 | 13 | 25 | 6 | 0.944 | 0.937 | 0.953 | 1.033 | 1.005 | 1.048 | 1.089 | 3.00E-03 |
| cds.Camellia_sinensis.comp28333_c0_seq1_m.25292 | PREDICTED: alcohol dehydrogenase-like 1 [Sesamum indicum] | 50.616 | 64.179 | 20.3 | 7 | 9 | 7 | 0.958 | 1.007 | 1.002 | 1.107 | 1.009 | 0.977 | 1.042 | 3.76E-01 |

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| cds.Camellia_sinensis.comp28338_c0_seq1_m.35010 | PREDICTED: protein PALE CRESS, chloroplastic-like isoform X1 [Nicotiana tabacum] | 36.376 | 5.8212 | 8.4 | 3 | 4 | 3 | 1.045 | 0.947 | 1.006 | 0.99 | 0.958 | 1.002 | 0.984 | 6.50E-01 |
| cds.Camellia_sinensis.comp28341_c0_seq2_m.49807 | PREDICTED: 40S ribosomal protein S9-2 [Solanum pennellii] | 19.591 | 17.582 | 25 | 5 | 9 | 5 | 0.941 | 0.939 | 0.973 | 1.08 | 1.111 | 1.057 | 1.138 | 2.16E-03 |
| cds.Camellia_sinensis.comp28353_c0_seq2_m.15608 | PREDICTED: protein HOTHEAD-like isoform X1 [Nicotiana tabacum] | 60.774 | 1.272 | 1.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28356_c0_seq1_m.13732 | PREDICTED: mitochondrial Rho GTPase 1-like isoform X1 [Ipomoea nil] | 70.98 | 1.153 | 5.5 | 4 | 5 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp28357_c1_seq1_m.51060 | PREDICTED: cinnamoyl-CoA reductase 1-like isoform X2 [Populus euphratica] | 19.709 | 3.2853 | 12.8 | 3 | 4 | 3 | 0.894 | 1.041 | 1.023 | 1.006 | 1.033 | 1.031 | 1.038 | 4.65E-01 |
| cds.Camellia_sinensis.comp28358_c0_seq1_m.9158 | PREDICTED: subtilisin-like protease SBT1.9 [Vitis vinifera] | 84.728 | 2.3926 | 4.1 | 3 | 3 | 3 | 1.102 | 1.052 | 1.049 | 0.92 | 0.928 | 0.931 | 0.868 | 9.79E-04 |
| cds.Camellia_sinensis.comp28359_c0_seq1_m.6188 | PREDICTED: protein PLASTID MOVEMENT IMPAIRED 1 [Theobroma cacao] | 95.151 | 88.673 | 19.6 | 16 | 21 | 16 | 1.13 | 1.122 | 1.143 | 0.854 | 0.868 | 0.852 | 0.758 | 2.04E-06 |
| cds.Camellia_sinensis.comp28362_c0_seq1_m.34005 | DUF2358 family protein [Medicago truncatula] | 34.304 | 33.242 | 7.3 | 3 | 4 | 3 | 0.937 | 1 | 0.933 | 1.067 | 1.016 | 1.038 | 1.087 | 3.38E-02 |
| cds.Camellia_sinensis.comp28364_c1_seq2_m.35218 | PREDICTED: 40S ribosomal protein S5 [Vitis vinifera] | 23.957 | 57.408 | 33.5 | 8 | 18 | 8 | 0.972 | 0.98 | 0.977 | 1.059 | 1.039 | 1.037 | 1.07 | 6.76E-04 |

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| cds.Camellia_sinensis.comp28367_c0_seq1_m.37830 | PREDICTED: ras-related protein RABF1 [Vitis vinifera] | 21.816 | 4.6955 | 17.5 | 3 | 4 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp28371_c0_seq1_m.32315 | PREDICTED: (R,S)-reticuline 7-O-methyltransferase [Theobroma cacao] | 39.728 | 2.5522 | 3.6 | 1 | 1 | 1 | 0.977 | 0.838 | 0.99 | 1.274 | 0.941 | 1.021 | 1.154 | 2.61E-01 |
| cds.Camellia_sinensis.comp28373_c0_seq1_m.22341 | PREDICTED: aldehyde dehydrogenase family 3 member H1 isoform X1 [Prunus | 53.03 | 86.596 | 18.6 | 9 | 11 | 9 | 0.956 | 0.969 | 1.01 | 1.065 | 1.02 | 0.987 | 1.047 | 1.74E-01 |
| cds.Camellia_sinensis.comp28374_c1_seq1_m.35279 | PSII-associated proline-rich protein [Solanum lycopersicum] | 23.73 | 48.953 | 37.4 | 5 | 15 | 5 | 1.041 | 1.019 | 1.01 | 0.959 | 0.985 | 0.959 | 0.946 | 1.15E-02 |

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| cds.Camellia_sinensis.comp28406_c0_seq1_m.27823 | PREDICTED: ubiquitin fusion degradation protein 1 homolog isoform X2 [Populus euphratica] | 35.788 | 61.348 | 26.4 | 8 | 10 | 7 | 1.012 | 1.062 | 1.095 | 0.926 | 0.928 | 0.941 | 0.882 | 5.98E-03 |
| cds.Camellia_sinensis.comp28414_c0_seq1_m.22936 | PREDICTED: PTI1-like tyrosine-protein kinase 1 [Juglans regia] | 27.048 | 14.318 | 19.3 | 4 | 6 | 3 | 0.941 | 0.988 | 1.007 | 1.085 | 1.02 | 1.005 | 1.059 | 1.37E-01 |
| cds.Camellia_sinensis.comp28414_c0_seq4_m.53285 | protein kinase Pti1 [Glycine max] | 11.218 | 2.3462 | 8.1 | 1 | 1 | 1 | 1.02 | 0.987 | 0.954 | 0.902 | 1.062 | 1.079 | 1.028 | 7.06E-01 |
| cds.Camellia_sinensis.comp28415_c0_seq1_m.12957 | PREDICTED: transmembrane 9 superfamily member 9-like [Ziziphus jujuba] | 73.938 | 11.401 | 5.8 | 3 | 3 | 3 | 1.03 | 1.051 | 1.075 | 0.891 | 0.973 | 0.972 | 0.899 | 2.74E-02 |

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| cds.Camellia_sinensis.comp28417_c0_seq1_m.22464 | PREDICTED: glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Eucalyptus grandis] | 20.841 | 56.776 | 60 | 9 | 42 | 3 | 1.036 | 1.006 | 0.954 | 0.982 | 1.021 | 1.02 | 1.009 | 7.48E-01 |
| cds.Camellia_sinensis.comp28417_c0_seq1_m.22467 | glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Pyrus x bretschneideri] | 11.603 | 156.3 | 89.5 | 9 | 58 | 8 | 0.984 | 0.938 | 0.951 | 1.033 | 1.06 | 1.043 | 1.092 | 5.50E-03 |
| cds.Camellia_sinensis.comp28419_c0_seq1_m.38820 | PREDICTED: 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 2 [Nicotiana tabacum] | 23.712 | 14.581 | 29.4 | 6 | 7 | 5 | 0.919 | 0.955 | 1.043 | 1.058 | 1.026 | 1.026 | 1.066 | 1.68E-01 |
| cds.Camellia_sinensis.comp28425_c0_seq1_m.10099 | PREDICTED: heat shock cognate protein 80 [Ziziphus jujuba] | 62.23 | 267.5 | 45.3 | 27 | 68 | 14 | 1.112 | 1.084 | 1.104 | 0.873 | 0.881 | 0.899 | 0.804 | 4.29E-05 |

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| cds.Camellia_sinensis.comp28425_c0_seq1_m.10101 | PREDICTED: heat shock cognate protein 80 [Ziziphus jujuba] | 19.329 | 55.962 | 33.5 | 6 | 15 | 6 | 1.058 | 1.149 | 1.06 | 0.898 | 0.9 | 0.897 | 0.825 | 1.96E-02 |
| cds.Camellia_sinensis.comp28430_c0_seq1_m.26340 | PREDICTED: 12-oxophytodienoate reductase 3-like [Jatropha curcas] | 43.773 | 41.732 | 22.6 | 9 | 12 | 9 | 0.908 | 0.997 | 0.99 | 1.012 | 1.041 | 1.068 | 1.078 | 8.86E-02 |
| cds.Camellia_sinensis.comp28431_c0_seq1_m.36056 | PREDICTED: 60S ribosomal protein L10 [Vitis vinifera] | 27.358 | 17.045 | 21.2 | 5 | 6 | 5 | 1.151 | 1.104 | 1.095 | 0.84 | 0.859 | 0.853 | 0.762 | 8.26E-05 |
| cds.Camellia_sinensis.comp28435_c0_seq2_m.34929 | PREDICTED: NAP1-related protein 2 [Vitis vinifera] | 29.633 | 23.108 | 15.1 | 4 | 5 | 4 | 0.943 | 0.949 | 1.011 | 1.057 | 1.014 | 1.03 | 1.068 | 5.88E-02 |
| cds.Camellia_sinensis.comp28437_c0_seq1_m.30989 | PREDICTED: putative deoxyribonuclease TATDN1 [Juglans regia] | 36.31 | 1.4454 | 3.4 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp28438_c0_seq1_m.38905 | 60S acidic ribosomal protein family [Arabidopsis thaliana] | 11.5 | 31.842 | 36.3 | 2 | 6 | 2 | 1.037 | 0.913 | 0.878 | 1.024 | 1.096 | 1.069 | 1.128 | 8.63E-02 |
| cds.Camellia_sinensis.comp28445_c0_seq1_m.18163 | PREDICTED: bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic [Vitis vinifera] | 56.806 | 13.472 | 8.6 | 5 | 7 | 4 | 1.421 | 1.362 | 1.341 | 0.547 | 0.603 | 0.591 | 0.422 | 1.75E-05 |
| cds.Camellia_sinensis.comp28451_c0_seq4_m.34490 | PREDICTED: U1 small nuclear ribonucleoprotein A isoform X1 [Vitis vinifera] | 23.206 | 5.1279 | 10.6 | 2 | 3 | 2 | 1.063 | 1.017 | 1.115 | 1.014 | 0.919 | 0.868 | 0.877 | 6.48E-02 |

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| cds.Camellia_sinensis.comp28458_c0_seq2_m.12232 | PREDICTED: CBS domain-containing protein CBSCBSPB3-like isoform X1 [Nicotiana tabacum] | 58.901 | 64.476 | 29.4 | 11 | 12 | 11 | 0.988 | 1.043 | 0.99 | 0.989 | 0.963 | 0.995 | 0.976 | 2.94E-01 |
| cds.Camellia_sinensis.comp28473_c0_seq1_m.35295 | PREDICTED: probable 2-carboxy-D-arabinitol-1-phosphatase [Juglans regia] | 21.804 | 24.328 | 25.5 | 4 | 8 | 4 | 1.056 | 1.053 | 1.086 | 0.963 | 0.928 | 0.899 | 0.873 | 3.60E-03 |
| cds.Camellia_sinensis.comp28473_c0_seq1_m.35296 | PREDICTED: probable 2-carboxy-D-arabinitol-1-phosphatase isoform X2 [Ricinus communis] | 13.993 | 18.762 | 29.2 | 3 | 3 | 3 | 1.08 | 1.032 | 1.052 | 0.918 | 0.97 | 0.944 | 0.895 | 5.80E-03 |

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| cds.Camellia_sinensis.comp28481_c0_seq2_m.48310 | PREDICTED: cell division cycle protein 48 homolog [Arachis ipaensis] | 23.78 | 1.1683 | 23 | 5 | 11 | 1 | 1.08 | 1.03 | 1.084 | 0.9 | 0.936 | 0.955 | 0.874 | 4.90E-03 |
| cds.Camellia_sinensis.comp28483_c0_seq1_m.24621 | PREDICTED: protein TRANSPARENT TESTA GLABRA 1-like [Ziziphus jujuba] | 38.348 | 5.152 | 6.7 | 2 | 2 | 2 | 0.993 | 1.081 | 1.065 | 1.08 | 0.875 | 0.913 | 0.914 | 2.48E-01 |
| cds.Camellia_sinensis.comp28498_c0_seq1_m.36521 | PREDICTED: VAMP-like protein YKT61 [Ricinus communis] | 22.666 | 9.3791 | 29.1 | 6 | 6 | 6 | 0.949 | 0.98 | 1.017 | 1.037 | 1.069 | 0.985 | 1.049 | 1.99E-01 |
| cds.Camellia_sinensis.comp28499_c2_seq1_m.45054 | PREDICTED: thioredoxin-like 3-1, chloroplastic [Theobroma cacao] | 22.141 | 6.5676 | 21.7 | 5 | 9 | 4 | 0.989 | 1.013 | 0.957 | 1.005 | 1.016 | 1.052 | 1.039 | 1.53E-01 |

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| cds.Camellia_sinensis.comp28509_c0_seq1_m.24190 | PREDICTED: methionyl-tRNA formyltransferase [Citrus sinensis] | 32.367 | 3.3052 | 7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp28510_c0_seq1_m.34868 | PREDICTED: (DL)-glycerol-3-phosphatase 2 [Sesamum indicum] | 30.507 | 21.586 | 15.9 | 4 | 4 | 4 | 0.998 | 1.001 | 0.966 | 1.005 | 0.999 | 1.03 | 1.023 | 1.93E-01 |
| cds.Camellia_sinensis.comp28514_c0_seq1_m.2113 | PREDICTED: topless-related protein 1-like isoform X1 [Nicotiana sylvestris] | 122.45 | 20.443 | 10.6 | 11 | 13 | 7 | 0.993 | 0.987 | 1.054 | 1.025 | 0.963 | 0.985 | 0.98 | 5.07E-01 |
| cds.Camellia_sinensis.comp28516_c0_seq1_m.3672 | PREDICTED: importin-11 isoform X1 [Vitis vinifera] | 113.24 | 2.8156 | 1.5 | 1 | 1 | 1 | 1.022 | 0.93 | 0.976 | 1.152 | 0.926 | 1.014 | 1.056 | 4.99E-01 |

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| cds.Camellia_sinensis.comp28520_c0_seq1_m.30390 | PREDICTED: probable voltage-gated potassium channel subunit beta [Ricinus communis] | 38.515 | 28.049 | 25.9 | 12 | 22 | 12 | 1.014 | 1.027 | 1.021 | 1.001 | 0.962 | 0.971 | 0.958 | 2.70E-02 |
| cds.Camellia_sinensis.comp28522_c0_seq1_m.15851 | PREDICTED: protein DETOXIFICATION 41-like [Juglans regia] | 55.266 | 4.2103 | 2.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28524_c0_seq1_m.40659 | PREDICTED: thylakoid lumenal 15 kDa protein 1, chloroplastic-like isoform X2 [Populus euphratica] | 24.028 | 204.83 | 46.2 | 8 | 25 | 8 | 0.934 | 0.966 | 0.928 | 1.091 | 1.072 | 1.044 | 1.134 | 2.14E-03 |
| cds.Camellia_sinensis.comp28534_c0_seq1_m.8188 | PREDICTED: sucrose synthase 7-like [Nicotiana attenuata] | 98.673 | 71.657 | 24.1 | 21 | 28 | 19 | 0.933 | 0.922 | 0.99 | 1.059 | 1.052 | 1.063 | 1.116 | 3.85E-02 |

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| cds.Camellia_sinensis.comp28537_c0_seq1_m.11963 | PREDICTED: protein arginine N-methyltransferase 1.5 isoform X1 [Vitis vinifera] | 72.557 | 10.893 | 1.7 | 1 | 1 | 1 | 0.923 | 0.998 | 0.95 | 1.004 | 1.025 | 1.123 | 1.098 | 8.81E-02 |
| cds.Camellia_sinensis.comp28540_c0_seq1_m.17423 | PREDICTED: ATP-dependent 6-phosphofructokinase 5, chloroplastic-like isoform X1 [Juglans regia] | 60.305 | 8.6349 | 7.1 | 4 | 5 | 3 | 0.978 | 0.953 | 1.029 | 0.983 | 1.028 | 1.013 | 1.022 | 4.52E-01 |
| cds.Camellia_sinensis.comp28540_c0_seq1_m.17425 | | 12.923 | -2 | 11.4 | 1 | 1 | 1 | 1.036 | 1.02 | 0.998 | 0.965 | 1.04 | 0.942 | 0.965 | 3.14E-01 |
| cds.Camellia_sinensis.comp28542_c0_seq1_m.42075 | PREDICTED: ras-related protein Rab7 [Capsicum annuum] | 23.056 | 15.717 | 36.1 | 7 | 11 | 5 | 0.914 | 1.015 | 0.952 | 1 | 1.043 | 1.01 | 1.06 | 1.50E-01 |

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| cds.Camellia_sinensis.comp28543_c0_seq2_m.4228 | PREDICTED: putative acyl-activating enzyme 19 isoform X4 [Pyrus x bretschneideri] | 105.76 | -2 | 1.3 | 1 | 1 | 1 | 0.974 | 1.117 | 0.933 | 0.862 | 1.01 | 1.101 | 0.983 | 8.42E-01 |
| cds.Camellia_sinensis.comp28544_c0_seq2_m.45493 | PREDICTED: histone H1 [Vitis vinifera] | 25.458 | 13.92 | 18.1 | 4 | 6 | 4 | 1.18 | 1.147 | 1.172 | 0.82 | 0.863 | 0.805 | 0.711 | 1.05E-04 |
| cds.Camellia_sinensis.comp28544_c2_seq1_m.42824 | PREDICTED: histone H1 [Vitis vinifera] | 16.262 | 36.331 | 32.9 | 7 | 9 | 7 | 1.099 | 1.122 | 1.151 | 0.81 | 0.863 | 0.921 | 0.769 | 2.60E-03 |
| cds.Camellia_sinensis.comp28548_c0_seq2_m.54773 | PREDICTED: probable NAD(P)H dehydrogenase (quinone) FQR1-like 1 [Eucalyptus grandis] | 15.039 | 3.3033 | 27.9 | 5 | 8 | 1 | 1.024 | 0.974 | 0.934 | 1.048 | 1.038 | 0.996 | 1.051 | 1.78E-01 |
| cds.Camellia_sinensis.comp28551_c0_seq1_m.18183 | PREDICTED: protoporphyrinogen oxidase 1, chloroplastic [Vitis vinifera] | 62.148 | 32.276 | 16.5 | 9 | 13 | 9 | 1.027 | 1.068 | 1.033 | 0.931 | 0.958 | 0.935 | 0.903 | 2.48E-03 |

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| cds.Camellia_sinensis.comp28555_c0_seq5_m.45688 | PREDICTED: 60S ribosomal protein L34-like [Ziziphus jujuba] | 13.737 | 11.453 | 16.7 | 2 | 4 | 2 | 1.03 | 1.027 | 1.063 | 0.958 | 1.006 | 0.916 | 0.923 | 5.09E-02 |
| cds.Camellia_sinensis.comp28560_c0_seq1_m.32994 | PREDICTED: probable caffeoyl-CoA O-methyltransferase At4g26220 [Jatropha curcas] | 26.165 | 37.445 | 25.1 | 4 | 6 | 4 | 1.015 | 1.036 | 0.99 | 0.997 | 1.019 | 0.986 | 0.987 | 4.75E-01 |
| cds.Camellia_sinensis.comp28566_c0_seq1_m.16933 | Allene oxide synthase [Morus notabilis] | 59.022 | 201.04 | 34.5 | 15 | 27 | 15 | 0.98 | 0.983 | 1.013 | 1.019 | 1.073 | 1.004 | 1.04 | 1.60E-01 |
| cds.Camellia_sinensis.comp28567_c0_seq1_m.19821 | PREDICTED: zinc-binding alcohol dehydrogenase domain-containing protein 2 [Vitis vinifera] | 50.739 | 9.2833 | 12.8 | 5 | 6 | 5 | 1.009 | 0.969 | 1.009 | 0.997 | 1.005 | 1.027 | 1.014 | 4.32E-01 |
| cds.Camellia_sinensis.comp28570_c0_seq2_m.15458 | MLO-like protein 1 [Cucumis melo] | 55.148 | 2.5016 | 1.8 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp28571_c0_seq91_m.4622 | PREDICTED: leucine--tRNA ligase, chloroplastic/mitochondrial isoform X1 [Theobroma cacao] | 114.99 | 79.461 | 16.1 | 14 | 23 | 14 | 1.018 | 1.043 | 1.013 | 0.981 | 0.963 | 0.943 | 0.939 | 1.25E-02 |
| cds.Camellia_sinensis.comp28572_c0_seq1_m.34652 | 6,7-dimethyl-8-ribityllumazine synthase [Arabidopsis thaliana] | 28.521 | 32.367 | 5 | 1 | 1 | 1 | 0.985 | 1.09 | 1.112 | 0.99 | 0.904 | 0.92 | 0.883 | 5.70E-02 |
| cds.Camellia_sinensis.comp28574_c0_seq3_m.25434 | PREDICTED: syntaxin-22-like isoform X1 [Jatropha curcas] | 30.301 | 6.8029 | 7 | 2 | 4 | 2 | 1.069 | 0.94 | 0.951 | 1.063 | 1.001 | 0.985 | 1.03 | 5.49E-01 |
| cds.Camellia_sinensis.comp28594_c0_seq1_m.35130 | PREDICTED: probable inactive receptor kinase At2g26730 [Vitis vinifera] | 33.135 | 11.061 | 9.3 | 3 | 4 | 3 | 0.976 | 0.974 | 0.988 | 1.015 | 1.043 | 0.958 | 1.027 | 3.72E-01 |

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| cds.Camellia_sinensis.comp28599_c0_seq1_m.9441 | PREDICTED: fimbrin-1-like [Ipomoea nil] | 82.374 | 1.8909 | 1.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28601_c0_seq1_m.16117 | PREDICTED: alpha,alpha-trehalose-phosphate synthase [UDP-forming] 6 [Vitis vinifera] | 70.966 | 2.2724 | 2.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28607_c0_seq1_m.20197 | PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit isoform X2 [Vitis vinifera] | 48.836 | 10.237 | 6.4 | 3 | 3 | 3 | 0.964 | 0.974 | 0.972 | 1.071 | 1.022 | 1.04 | 1.077 | 6.28E-03 |

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| cds.Camellia_sinensis.comp28614_c0_seq1_m.4055 | PREDICTED: cytochrome b6-f complex iron-sulfur subunit 1, chloroplastic [Vitis vinifera] | 19.905 | 209.27 | 64.3 | 9 | 42 | 9 | 0.99 | 0.97 | 0.994 | 1.014 | 1.019 | 1.01 | 1.03 | 2.04E-02 |
| cds.Camellia_sinensis.comp28615_c0_seq1_m.28385 | PREDICTED: COP9 signalosome complex subunit 6a [Vitis | 34.23 | 2.5372 | 3.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28616_c0_seq1_m.32795 | PREDICTED: nuclear transcription factor Y subunit C-3-like [Cicer arietinum] | 28.057 | 8.0652 | 16.9 | 4 | 4 | 3 | 0.926 | 1.111 | 0.959 | 1.014 | 0.968 | 1.037 | 1.008 | 8.69E-01 |
| cds.Camellia_sinensis.comp28618_c0_seq1_m.22058 | PREDICTED: thiamine thiazole synthase 2, chloroplastic [Nelumbo nucifera] | 38.079 | 87.48 | 24.3 | 7 | 27 | 2 | 1.005 | 0.933 | 0.968 | 1.029 | 1.082 | 1.037 | 1.083 | 3.91E-02 |

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| cds.Camellia_sinensis.comp28618_c0_seq2_m.24583 | PREDICTED: thiamine thiazole synthase 2, chloroplastic [Nelumbo nucifera] | 37.555 | 6.6661 | 23.8 | 6 | 26 | 1 | 1.02 | 0.979 | 0.992 | 1.043 | 1.043 | 0.946 | 1.014 | 7.33E-01 |
| cds.Camellia_sinensis.comp28624_c0_seq1_m.45429 | PREDICTED: cytochrome b5 [Vitis vinifera] | 18.273 | 18.801 | 16.2 | 2 | 2 | 2 | 1.217 | 1.16 | 1.125 | 0.743 | 0.876 | 0.823 | 0.697 | 2.42E-03 |
| cds.Camellia_sinensis.comp28631_c0_seq1_m.3052 | PREDICTED: structural maintenance of chromosomes protein 1 [Vitis vinifera] | 140.04 | 1.511 | 0.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28632_c0_seq1_m.24756 | PREDICTED: cytochrome P450 94A1 [Sesamum indicum] | 46.848 | 2.4849 | 4.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp28635_c0_seq1_m.26795 | PREDICTED: serpin-ZX [Theobroma cacao] | 42.504 | 98.058 | 27.5 | 10 | 15 | 10 | 0.952 | 1.012 | 0.989 | 1.01 | 1.002 | 1.014 | 1.025 | 2.45E-01 |

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| cds.Camellia_sinensis.comp28640_c0_seq80_m.15653 | PREDICTED: serine/threonine-protein kinase STN7, chloroplastic [Juglans regia] | 65.012 | 106.95 | 23.1 | 13 | 21 | 13 | 0.957 | 0.938 | 0.958 | 1.083 | 1.055 | 1.055 | 1.119 | 5.37E-04 |
| cds.Camellia_sinensis.comp28647_c1_seq1_m.46830 | PREDICTED: serine carboxypeptidase-like [Juglans regia] | 14.359 | 2.8562 | 6.4 | 1 | 2 | 1 | 1.034 | 0.942 | 1.046 | 1.013 | 0.958 | 1.012 | 0.987 | 7.63E-01 |
| cds.Camellia_sinensis.comp28649_c0_seq1_m.14486 | PREDICTED: la-related protein 6B [Juglans regia] | 56.159 | 4.4973 | 2 | 1 | 1 | 1 | 1.185 | 1.089 | 1.089 | 0.8 | 0.87 | 0.923 | 0.771 | 6.50E-03 |
| cds.Camellia_sinensis.comp28650_c1_seq2_m.19059 | PREDICTED: probable acyl-activating enzyme 5, peroxisomal isoform X2 [Vitis vinifera] | 61.164 | 6.2333 | 3.9 | 2 | 3 | 2 | 0.838 | 0.928 | 1.006 | 1.173 | 1.046 | 1.059 | 1.183 | 5.78E-02 |

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| cds.Camellia_sinensis.comp28651_c0_seq1_m.27956 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP42 [Theobroma cacao] | 40.853 | 11.602 | 4.8 | 2 | 2 | 2 | 1.015 | 1.035 | 1.006 | 0.971 | 0.997 | 0.978 | 0.964 | 3.35E-02 |
| cds.Camellia_sinensis.comp28652_c0_seq1_m.27184 | PREDICTED: probable protein phosphatase 2C 9 isoform X1 [Vitis vinifera] | 31.107 | 1.8449 | 4.2 | 1 | 1 | 1 | 1.02 | 0.958 | 1.08 | 0.928 | 1.029 | 0.987 | 0.963 | 4.57E-01 |
| cds.Camellia_sinensis.comp28654_c0_seq1_m.17144 | PREDICTED: acetate/butyrate--CoA ligase AAE7, peroxisomal [Vitis vinifera] | 62.339 | 18.957 | 14.5 | 10 | 15 | 10 | 0.964 | 0.933 | 0.945 | 1.061 | 1.062 | 1.06 | 1.12 | 6.98E-03 |
| cds.Camellia_sinensis.comp28660_c0_seq1_m.35924 | PREDICTED: 60S ribosomal protein L8-1-like [Erythranthe guttata] | 29.08 | 36.374 | 23.2 | 6 | 10 | 6 | 1.131 | 1.136 | 1.179 | 0.876 | 0.838 | 0.865 | 0.748 | 1.00E-04 |

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| cds.Camellia_sinensis.comp28662_c0_seq1_m.25855 | PREDICTED: 26S protease regulatory subunit 6B homolog [Juglans regia] | 48.401 | 85.481 | 29.8 | 11 | 18 | 4 | 1.018 | 0.977 | 0.988 | 0.847 | 1.063 | 1.025 | 0.984 | 7.84E-01 |
| cds.Camellia_sinensis.comp28672_c1_seq1_m.6252 | PREDICTED: probable glucan 1,3-alpha-glucosidase [Pyrus x bretschneideri] | 104.89 | 93.033 | 20.5 | 19 | 29 | 19 | 0.997 | 1.001 | 1.03 | 0.975 | 1.033 | 0.987 | 0.989 | 6.13E-01 |
| cds.Camellia_sinensis.comp28680_c0_seq1_m.34192 | plant/F14G9-20 protein [Medicago truncatula] | 42.54 | 12.387 | 7.8 | 3 | 3 | 3 | 1.012 | 1.08 | 0.976 | 0.961 | 0.997 | 0.975 | 0.956 | 2.33E-01 |
| cds.Camellia_sinensis.comp28686_c0_seq1_m.17887 | PREDICTED: mitochondrial phosphate carrier protein 3, mitochondrial [Jatropha curcas] | 46.134 | 2.1466 | 18.9 | 8 | 15 | 1 | 1.045 | 1.137 | 1.022 | 0.898 | 0.966 | 0.919 | 0.869 | 2.28E-02 |

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| cds.Camellia_sinensis.comp28686_c0_seq2_m.19806 | PREDICTED: mitochondrial phosphate carrier protein 3, mitochondrial [Jatropha curcas] | 45.833 | 23.38 | 20.8 | 9 | 17 | 2 | 1.049 | 0.971 | 1.037 | 0.973 | 0.991 | 0.98 | 0.963 | 2.07E-01 |
| cds.Camellia_sinensis.comp28689_c0_seq39_m.12759 | PREDICTED: sodium/pyruvate cotransporter BASS2, chloroplastic [Vitis vinifera] | 28.424 | 2.7041 | 5.2 | 1 | 2 | 1 | 0.976 | 0.858 | 0.916 | 1.07 | 1.151 | 1.062 | 1.194 | 1.70E-02 |
| cds.Camellia_sinensis.comp28691_c0_seq11_m.31137 | PREDICTED: serine/threonine-protein kinase SAPK2-like isoform X1 [Gossypium raimondii] | 20.204 | 2.1693 | 8.5 | 2 | 4 | 1 | 1.013 | 1.06 | 0.949 | 1.001 | 1.033 | 0.951 | 0.988 | 7.82E-01 |
| cds.Camellia_sinensis.comp28692_c0_seq12_m.16119 | PREDICTED: 2-hydroxyacyl-CoA lyase [Ipomoea nil] | 61.941 | 151.18 | 44.6 | 22 | 53 | 22 | 0.976 | 0.956 | 0.978 | 1.031 | 1.034 | 1.018 | 1.059 | 2.68E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp28693_c0_seq2_m.28000 | PREDICTED: golgin subfamily A member 2-like [Nicotiana sylvestris] | 29.593 | 67.315 | 29.2 | 9 | 17 | 9 | 1.04 | 1.031 | 1.048 | 0.96 | 0.964 | 0.939 | 0.918 | 8.16E-04 |
| cds.Camellia_sinensis.comp28699_c0_seq1_m.21392 | PREDICTED: fasciclin-like arabinogalactan protein 10 [Vitis vinifera] | 43.524 | 13.772 | 7.6 | 3 | 3 | 3 | 1.063 | 1.018 | 1.029 | 0.953 | 0.996 | 0.935 | 0.927 | 2.94E-02 |
| cds.Camellia_sinensis.comp28701_c0_seq1_m.31292 | PREDICTED: protein-ribulosamine 3-kinase, chloroplastic [Jatropha curcas] | 39.908 | 7.8604 | 10.7 | 4 | 6 | 4 | 0.948 | 1.009 | 0.955 | 1.01 | 0.979 | 1.066 | 1.049 | 2.07E-01 |
| cds.Camellia_sinensis.comp28704_c0_seq1_m.23471 | PREDICTED: BAHD acyltransferase DCR [Nicotiana attenuata] | 49.995 | 46.095 | 13.4 | 5 | 6 | 5 | 1.335 | 1.368 | 1.341 | 0.636 | 0.605 | 0.629 | 0.462 | 6.90E-07 |

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| cds.Camellia_sinensis.comp28706_c0_seq1_m.43479 | PREDICTED: 40S ribosomal protein S20-2-like isoform X2 [Gossypium hirsutum] | 21.472 | 45.646 | 20.5 | 5 | 10 | 5 | 1.024 | 1.031 | 1.077 | 0.94 | 0.989 | 0.97 | 0.926 | 2.34E-02 |
| cds.Camellia_sinensis.comp28708_c1_seq1_m.31563 | PREDICTED: probable UDP-arabinopyranose mutase 5 isoform X1 [Pyrus x bretschneideri] | 27.822 | 19.632 | 30.2 | 7 | 9 | 6 | 0.894 | 1.036 | 0.978 | 1.139 | 1.043 | 0.946 | 1.076 | 3.54E-01 |
| cds.Camellia_sinensis.comp28708_c1_seq1_m.31564 | PREDICTED: probable UDP-arabinopyranose mutase 5 isoform X1 [Vitis vinifera] | 15.651 | 4.2423 | 9.4 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp28711_c0_seq1_m.30494 | PREDICTED: bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1 [Juglans regia] | 38.909 | 11.005 | 24.3 | 7 | 11 | 6 | 1.012 | 0.986 | 0.983 | 1.034 | 1.015 | 0.963 | 1.01 | 6.89E-01 |
| cds.Camellia_sinensis.comp28715_c0_seq1_m.16881 | PREDICTED: WD-40 repeat-containing protein MSI4-like [Populus euphratica] | 56.68 | 111.44 | 22.5 | 8 | 13 | 3 | 1.078 | 1.073 | 1.142 | 0.913 | 0.892 | 0.883 | 0.816 | 8.20E-04 |
| cds.Camellia_sinensis.comp28715_c0_seq2_m.17799 | PREDICTED: WD-40 repeat-containing protein MSI4-like [Populus euphratica] | 56.594 | 4.3342 | 18.4 | 6 | 12 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28717_c0_seq2_m.31648 | PREDICTED: tryptophan synthase alpha chain-like [Citrus sinensis] | 33.301 | 53.794 | 36.9 | 8 | 11 | 8 | 0.935 | 0.935 | 0.944 | 1.13 | 1.076 | 1.039 | 1.153 | 2.87E-02 |

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| cds.Camellia_sinensis.comp28719_c0_seq1_m.15381 | PREDICTED: suppressor of mec-8 and unc-52 protein homolog 1 isoform X1 [Vitis vinifera] | 60.164 | 10.895 | 10 | 5 | 6 | 5 | 0.954 | 0.918 | 0.929 | 1.016 | 1.09 | 1.125 | 1.154 | 1.16E-02 |
| cds.Camellia_sinensis.comp28721_c0_seq1_m.33393 | PREDICTED: DNA-directed RNA polymerases IV and V subunit 4 [Malus domestica] | 23.06 | 3.4038 | 11.7 | 3 | 3 | 3 | 1.186 | 1.157 | 1.205 | 0.885 | 0.762 | 0.766 | 0.68 | 1.54E-03 |
| cds.Camellia_sinensis.comp28723_c0_seq1_m.811 | PREDICTED: eukaryotic translation initiation factor 4G isoform X2 [Vitis vinifera] | 207.74 | 18.041 | 4.5 | 7 | 9 | 7 | 1.012 | 0.982 | 1.054 | 0.931 | 1.024 | 0.999 | 0.969 | 4.18E-01 |
| cds.Camellia_sinensis.comp28724_c0_seq1_m.17777 | PREDICTED: probable nucleoredoxin 1 isoform X1 [Prunus | 66.378 | 151.68 | 41.5 | 23 | 56 | 22 | 0.892 | 0.899 | 0.881 | 1.113 | 1.114 | 1.112 | 1.25 | 7.01E-04 |

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| cds.Camellia_sinensis.comp28724_c0_seq2_m.18204 | PREDICTED: probable nucleoredoxin 1 [Jatropha curcas] | 66.017 | 13.087 | 10.9 | 6 | 13 | 5 | 1.049 | 1.02 | 1.043 | 0.98 | 0.923 | 0.973 | 0.924 | 1.88E-02 |
| cds.Camellia_sinensis.comp28728_c0_seq1_m.39416 | PREDICTED: probable aminopyrimidine aminohydrolase, mitochondrial isoform X2 [Pyrus x bretschnei | 16.042 | 1.3906 | 11.3 | 2 | 3 | 1 | 0.982 | 0.875 | 0.974 | 0.944 | 1.123 | 1.121 | 1.126 | 1.63E-01 |
| cds.Camellia_sinensis.comp28732_c0_seq1_m.10852 | PREDICTED: acidic repeat-containing protein isoform X1 [Populus euphratica] | 43.497 | -2 | 2.3 | 1 | 1 | 1 | 0.896 | 0.886 | 0.934 | 1.053 | 1.147 | 1.125 | 1.224 | 2.68E-03 |
| cds.Camellia_sinensis.comp28733_c0_seq1_m.10252 | PREDICTED: threonine--tRNA ligase, mitochondrial 1 [Vitis | 84.386 | 60.04 | 27.2 | 22 | 34 | 22 | 0.974 | 0.944 | 0.95 | 1.06 | 1.056 | 1.026 | 1.096 | 2.90E-03 |

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| cds.Camellia_sinensis.comp28738_c0_seq1_m.3615 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 12, chloroplastic [Prunus mume] | 68.108 | 2.4193 | 3.6 | 2 | 2 | 2 | 0.971 | 1.018 | 1.059 | 0.972 | 1.007 | 0.982 | 0.971 | 3.55E-01 |
| cds.Camellia_sinensis.comp28738_c0_seq1_m.3616 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 12, chloroplastic [Gossypium raimondii] | 44.86 | 24.226 | 16.2 | 5 | 5 | 5 | 0.925 | 1.015 | 1.028 | 1.033 | 1.04 | 0.985 | 1.03 | 4.58E-01 |
| cds.Camellia_sinensis.comp28739_c0_seq19_m.32735 | PREDICTED: glutelin type-A 3 isoform X1 [Vitis vinifera] | 37.496 | 38.573 | 19.7 | 6 | 11 | 6 | 0.982 | 0.923 | 0.963 | 1.053 | 1.074 | 1.01 | 1.094 | 2.53E-02 |
| cds.Camellia_sinensis.comp28745_c0_seq2_m.27151 | PREDICTED: mevalonate kinase [Solanum lycopersicum] | 41.914 | 2.2238 | 2.3 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp28748_c0_seq2_m.19166 | PREDICTED: putative G3BP-like protein isoform X4 [Juglans regia] | 46.869 | 7.2712 | 8.4 | 4 | 5 | 4 | 1.013 | 1.046 | 0.996 | 0.946 | 1.023 | 0.974 | 0.963 | 2.35E-01 |
| cds.Camellia_sinensis.comp28749_c0_seq2_m.10694 | PREDICTED: ABC transporter B family member 26, chloroplastic isoform X1 [Vitis vinifera] | 76.502 | 41.596 | 10.1 | 7 | 7 | 7 | 0.965 | 1.036 | 1.011 | 1.031 | 0.947 | 1.023 | 0.996 | 9.13E-01 |
| cds.Camellia_sinensis.comp28751_c0_seq1_m.36414 | PREDICTED: non-specific lipid transfer protein GPI-anchored 1 [Vitis vinifera] | 20.567 | 6.1567 | 5.2 | 1 | 1 | 1 | 1.458 | 1.459 | 1.338 | 0.517 | 0.547 | 0.543 | 0.378 | 4.31E-06 |
| cds.Camellia_sinensis.comp28751_c1_seq1_m.26359 | PREDICTED: metacaspase-4 [Theobroma cacao] | 46.206 | 33.742 | 21.6 | 9 | 13 | 9 | 1.017 | 1.038 | 1.044 | 0.944 | 0.993 | 0.987 | 0.944 | 3.07E-02 |

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| cds.Camellia_sinensis.comp28753_c0_seq1_m.10763 | PREDICTED: probable pectinesterase/pectinesterase inhibitor 61 [Sesamum indicum] | 65.748 | 23.809 | 7.5 | 5 | 9 | 5 | 1.059 | 1.018 | 1.062 | 0.936 | 0.934 | 0.943 | 0.896 | 1.42E-03 |
| cds.Camellia_sinensis.comp28757_c0_seq1_m.27387 | PREDICTED: aldose 1-epimerase [Juglans regia] | 37.045 | 14.618 | 16.8 | 5 | 9 | 5 | 0.949 | 0.96 | 0.988 | 1.036 | 1.057 | 0.989 | 1.064 | 5.55E-02 |
| cds.Camellia_sinensis.comp28762_c0_seq1_m.34011 | PREDICTED: nitrile-specifier protein 5 [Daucus carota subsp. sativus] | 39.845 | 29.873 | 34.7 | 9 | 11 | 9 | 1.038 | 1.038 | 0.982 | 0.976 | 0.998 | 0.927 | 0.949 | 1.39E-01 |
| cds.Camellia_sinensis.comp28768_c0_seq2_m.13174 | plant/F17O14-7 protein [Medicago truncatula] | 32.627 | 3.6145 | 10.7 | 3 | 3 | 3 | 1.013 | 1.008 | 0.964 | 0.977 | 1.012 | 1.032 | 1.012 | 6.22E-01 |
| cds.Camellia_sinensis.comp28770_c0_seq2_m.5558 | PREDICTED: probable endo-1,3(4)-beta-glucanase ARB_01444 [Citrus sinensis] | 17.185 | 17.11 | 23.8 | 3 | 7 | 3 | 0.984 | 0.915 | 0.921 | 1.102 | 1.02 | 1.078 | 1.135 | 1.80E-02 |

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| cds.Camellia_sinensis.comp28780_c0_seq1_m.33527 | PREDICTED: copper chaperone for superoxide dismutase, chloroplastic/cytosolic [Jatropha curcas] | 35.732 | 95.431 | 41.5 | 12 | 21 | 12 | 0.937 | 1.013 | 0.999 | 1.025 | 1.012 | 1.016 | 1.035 | 2.84E-01 |
| cds.Camellia_sinensis.comp28786_c0_seq1_m.32971 | PREDICTED: aspartic proteinase Asp1-like isoform X1 [Citrus sinensis] | 40.28 | 15.436 | 10.9 | 4 | 6 | 4 | 0.943 | 1.008 | 1.006 | 1.043 | 1.016 | 1.005 | 1.036 | 2.17E-01 |
| cds.Camellia_sinensis.comp28791_c0_seq1_m.20293 | PREDICTED: cytochrome P450 704C1 isoform X2 [Populus euphratica] | 60.199 | 5.3799 | 5.2 | 2 | 2 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp28793_c0_seq1_m.14957 | PREDICTED: synaptotagmin-5 [Malus domestica] | 55.874 | 59.912 | 15.3 | 7 | 12 | 7 | 0.944 | 0.946 | 0.979 | 1.051 | 1.075 | 1.067 | 1.113 | 1.38E-03 |

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| cds.Camellia_sinensis.comp28794_c0_seq1_m.19751 | PREDICTED: glutamine synthetase leaf isozyme, chloroplastic [Juglans regia] | 47.936 | 121.11 | 42.4 | 16 | 43 | 16 | 1.067 | 1.037 | 1.03 | 0.946 | 0.954 | 0.95 | 0.909 | 1.02E-03 |
| cds.Camellia_sinensis.comp28797_c0_seq1_m.33679 | PREDICTED: non-specific phospholipase C2 isoform X2 [Citrus sinensis] | 40.953 | 2.1263 | 8.2 | 3 | 4 | 2 | 1.009 | 1.013 | 1.027 | 0.932 | 1.021 | 1 | 0.969 | 3.09E-01 |
| cds.Camellia_sinensis.comp28803_c0_seq1_m.13853 | PREDICTED: xylulose kinase [Vitis vinifera] | 61.118 | 52.011 | 19.4 | 9 | 16 | 9 | 0.961 | 0.979 | 0.963 | 1.067 | 1.035 | 1.017 | 1.074 | 9.24E-03 |
| cds.Camellia_sinensis.comp288099_c0_seq1_m.58829 | PREDICTED: universal stress protein A-like protein isoform X2 [Cucumis sativus] | 11.806 | 1.4107 | 7.7 | 1 | 2 | 1 | 0.991 | 1.044 | 0.926 | 0.975 | 1.043 | 1.03 | 1.029 | 5.03E-01 |

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| cds.Camellia_sinensis.comp28813_c1_seq1_m.29578 | PREDICTED: protein ASPARTIC PROTEASE IN GUARD CELL 2-like [Sesamum indicum] | 40.944 | 4.1554 | 4.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28814_c0_seq1_m.25455 | PREDICTED: probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial isoform X1 [Vitis | 39.572 | 1.3916 | 2.2 | 1 | 1 | 1 | 1.097 | 1.028 | 1.088 | 0.864 | 0.998 | 0.908 | 0.862 | 3.33E-02 |
| cds.Camellia_sinensis.comp28818_c0_seq1_m.28081 | PREDICTED: protein HGH1 homolog [Gossypium hirsutum] | 38.528 | 2.491 | 2.6 | 1 | 1 | 1 | 0.998 | 0.941 | 0.98 | 0.922 | 1.057 | 1.11 | 1.058 | 4.07E-01 |

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| cds.Camellia_sinensis.comp28827_c0_seq7_m.56542 | PREDICTED: probable polygalacturonase isoform X1 [Nicotiana sylvestris] | 13.465 | 3.3225 | 12.2 | 1 | 1 | 1 | 1.043 | 1.039 | 1.043 | 0.966 | 1.068 | 0.841 | 0.92 | 3.31E-01 |
| cds.Camellia_sinensis.comp28828_c0_seq5_m.27283 | photosystem I chlorophyll a/b-binding protein 5, chloroplastic [Cajanus cajan] | 12.144 | 2.6082 | 8.9 | 1 | 2 | 1 | 0.92 | 1.032 | 1.017 | 0.964 | 1.059 | 1.025 | 1.027 | 5.87E-01 |
| cds.Camellia_sinensis.comp28830_c0_seq1_m.25500 | PREDICTED: lys-63-specific deubiquitinase BRCC36-like [Jatropha curcas] | 50.006 | 14.061 | 17.6 | 7 | 7 | 7 | 1.114 | 1.097 | 1.013 | 0.955 | 0.925 | 0.891 | 0.859 | 1.33E-02 |
| cds.Camellia_sinensis.comp28835_c0_seq1_m.35332 | PREDICTED: 14-3-3-like protein A [Theobroma cacao] | 29.421 | 45.168 | 44.8 | 14 | 51 | 9 | 0.951 | 0.969 | 0.937 | 1.019 | 1.058 | 1.037 | 1.09 | 4.10E-03 |

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| cds.Camellia_sinensis.comp28836_c0_seq1_m.11655 | PREDICTED: formate--tetrahydrofolate ligase [Populus euphratica] | 67.527 | 227.29 | 42.5 | 23 | 55 | 23 | 1.008 | 0.974 | 0.987 | 1.017 | 1.031 | 1.017 | 1.032 | 4.39E-02 |
| cds.Camellia_sinensis.comp28844_c0_seq1_m.6125 | PREDICTED: endo-1,4-beta-xylanase A-like [Ziziphus jujuba] | 104.79 | 11.525 | 2.8 | 2 | 2 | 2 | 1.066 | 1.213 | 1.185 | 0.819 | 0.75 | 0.929 | 0.721 | 1.11E-02 |
| cds.Camellia_sinensis.comp28845_c0_seq1_m.28073 | PREDICTED: ubiquinol oxidase, mitochondrial-like [Prunus mume] | 44.246 | 16.262 | 15.4 | 6 | 7 | 6 | 1.004 | 0.952 | 0.995 | 0.997 | 1.013 | 1.008 | 1.023 | 2.55E-01 |
| cds.Camellia_sinensis.comp28846_c0_seq1_m.27141 | PREDICTED: hydroxyphenylpyruvate reductase-like [Nicotiana attenuata] | 34.145 | 17.397 | 20.1 | 6 | 10 | 6 | 1.003 | 0.988 | 1.002 | 1.027 | 1.011 | 1.034 | 1.026 | 3.43E-02 |

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| cds.Camellia_sinensis.comp28853_c0_seq4_m.31738 | PREDICTED: kinesin-like protein KIN-7M, chloroplastic [Camelina sativa] | 31.984 | 15.435 | 20.1 | 6 | 14 | 6 | 1.037 | 1.028 | 1.056 | 0.971 | 0.982 | 0.966 | 0.935 | 1.96E-03 |
| cds.Camellia_sinensis.comp28856_c0_seq1_m.1934 | PREDICTED: transformation/transcription domain-associated protein isoform X4 [Capsicum annuum] | 156.62 | 5.6 | 2.3 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp28856_c1_seq1_m.467 | PREDICTED: transcription-associated protein 1 isoform X1 [Vitis vinifera] | 263.9 | 15.47 | 0.9 | 2 | 2 | 2 | 0.988 | 1.002 | 0.973 | 1.011 | 1.015 | 1.025 | 1.03 | 3.57E-02 |

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| cds.Camellia_sinensis.comp28859_c0_seq6_m.54527 | PREDICTED: NEDD8-conjugating enzyme Ubc12-like isoform X2 [Ziziphus jujuba] | 11.238 | 4.1712 | 17.2 | 3 | 3 | 3 | 0.985 | 0.96 | 0.956 | 1.07 | 0.998 | 1.05 | 1.075 | 3.46E-02 |
| cds.Camellia_sinensis.comp28864_c0_seq1_m.15106 | PREDICTED: SNF1-related protein kinase catalytic subunit alpha KIN10 [Cucumis sativus] | 24.26 | 8.7014 | 13.7 | 3 | 3 | 3 | 0.987 | 1.016 | 0.991 | 1.064 | 0.987 | 1.028 | 1.028 | 3.06E-01 |
| cds.Camellia_sinensis.comp28865_c0_seq1_m.27741 | PREDICTED: 33 kDa ribonucleoprotein, chloroplastic [Erythranthe guttata] | 36.156 | 83.966 | 20 | 4 | 8 | 4 | 1.114 | 1.162 | 1.129 | 0.859 | 0.883 | 0.838 | 0.758 | 1.42E-04 |
| cds.Camellia_sinensis.comp28869_c0_seq1_m.20929 | WSC domain-containing protein ARB_07867 precursor [Ziziphus jujuba] | 60.625 | 4.5543 | 4.4 | 2 | 2 | 2 | 1.071 | 1.133 | 1 | 0.995 | 0.886 | 0.903 | 0.869 | 5.09E-02 |

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| cds.Camellia_sinensis.comp28876_c0_seq2_m.40932 | dynein beta chain, ciliary protein [Arabidopsis thaliana] | 20.927 | 15.71 | 38.2 | 6 | 6 | 6 | 0.979 | 1.016 | 0.957 | 1.078 | 0.899 | 1.085 | 1.037 | 6.32E-01 |
| cds.Camellia_sinensis.comp28877_c0_seq1_m.15313 | PREDICTED: cytosolic enolase 3 [Ipomoea nil] | 39.649 | 5.8113 | 12.5 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp28877_c0_seq1_m.15314 | Cytosolic enolase 3 [Morus notabilis] | 14.166 | 2.1048 | 8.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28885_c0_seq1_m.17355 | PREDICTED: galactinol--sucrose galactosyltransferase-like [Erythranthe guttata] | 69.958 | 41.945 | 16.6 | 12 | 27 | 12 | 1.116 | 1.108 | 1.108 | 0.872 | 0.874 | 0.865 | 0.784 | 2.06E-07 |
| cds.Camellia_sinensis.comp28890_c0_seq2_m.42508 | PREDICTED: zinc finger CCCH domain-containing protein 14-like [Juglans regia] | 16.33 | 16.232 | 25.2 | 3 | 6 | 1 | 0.878 | 1.003 | 1.088 | 1.009 | 0.919 | 1.124 | 1.028 | 7.59E-01 |

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| cds.Camellia_sinensis.comp28891_c0_seq1_m.36773 | RmlC-like cupins superfamily protein [Arabidopsis thaliana] | 19.337 | 28.901 | 33 | 5 | 12 | 5 | 1.031 | 1.043 | 0.989 | 0.968 | 0.982 | 0.982 | 0.957 | 6.12E-02 |
| cds.Camellia_sinensis.comp28901_c0_seq1_m.42012 | potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel protein [Arabidopsis thaliana] | 11.287 | 6.6911 | 24.2 | 3 | 4 | 3 | 0.953 | 1.04 | 1.008 | 0.967 | 1.04 | 0.976 | 0.994 | 8.72E-01 |
| cds.Camellia_sinensis.comp28911_c0_seq2_m.47475 | PREDICTED: 17.3 kDa class I heat shock protein-like [Gossypium raimondii] | 17.116 | 74.141 | 46 | 6 | 16 | 4 | 1.108 | 1.063 | 1.106 | 0.864 | 0.896 | 0.917 | 0.817 | 7.77E-04 |
| cds.Camellia_sinensis.comp28917_c0_seq1_m.11358 | PREDICTED: phosphoenolpyruvate carboxykinase [ATP] [Ziziphus jujuba] | 73.587 | 59.256 | 20.5 | 11 | 18 | 6 | 0.898 | 0.958 | 0.916 | 1.13 | 1.042 | 1.077 | 1.172 | 6.38E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp28917_c0_seq4_m.22810 | PREDICTED: phosphoenolpyruvate carboxykinase [ATP]-like [Sesamum indicum] | 53.101 | 2.0371 | 13.8 | 5 | 6 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28918_c0_seq1_m.15356 | PREDICTED: lysM domain receptor-like kinase 4 [Populus euphratica] | 71.122 | 1.6866 | 1.3 | 1 | 1 | 1 | 1.025 | 1.032 | 0.947 | 1.03 | 0.983 | 0.989 | 0.999 | 9.97E-01 |
| cds.Camellia_sinensis.comp28924_c0_seq8_m.8435 | PREDICTED: protein STRUBBELIG-RECEPTOR FAMILY 6 [Vitis vinifera] | 68.544 | 3.0036 | 1.6 | 1 | 1 | 1 | 1.175 | 1.199 | 1.237 | 0.738 | 0.785 | 0.809 | 0.646 | 1.42E-04 |
| cds.Camellia_sinensis.comp28926_c0_seq16_c0_seq1_m.15424 | PREDICTED: amidophosphoribosyltransferase, chloroplastic [Ricinus communis] | 65.44 | 45.385 | 9.8 | 5 | 8 | 5 | 1.006 | 1.009 | 1.034 | 0.986 | 0.994 | 1.016 | 0.983 | 2.33E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp28927_c0_seq2_m.8142 | PREDICTED: serine/threonine-protein kinase BLUS1 [Theobroma cacao] | 75.838 | 1.8571 | 1.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28928_c0_seq1_m.26817 | PREDICTED: aspartic proteinase nepenthesin-1 [Ziziphus jujuba] | 43.084 | 16.425 | 8.8 | 4 | 6 | 4 | 1.071 | 1.033 | 1.121 | 0.925 | 0.96 | 0.894 | 0.862 | 9.00E-03 |
| cds.Camellia_sinensis.comp28935_c0_seq1_m.36443 | PREDICTED: proteasome subunit alpha type-3 isoform X1 [Gossypium hirsutum] | 28.552 | 35.829 | 45.7 | 11 | 21 | 8 | 0.917 | 1.014 | 0.973 | 1.001 | 1.071 | 1.043 | 1.073 | 1.15E-01 |
| cds.Camellia_sinensis.comp28935_c0_seq2_m.57987 | PREDICTED: proteasome subunit alpha type-3 [Jatropha curcas] | 11.827 | 31.424 | 40 | 4 | 6 | 4 | 0.965 | 0.985 | 0.962 | 1.052 | 1.025 | 1.046 | 1.072 | 2.96E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp28945_c0_seq1_m.36810 | PREDICTED: elongation factor P-like [Nicotiana tabacum] | 25.742 | 1.1763 | 3.4 | 1 | 1 | 1 | 1.06 | 1.012 | 1.134 | 0.964 | 0.871 | 0.949 | 0.868 | 3.67E-02 |
| cds.Camellia_sinensis.comp28948_c0_seq1_m.3320 | PREDICTED: protein CROWDED NUCLEI 1 [Cucumis melo] | 73.4 | 13.392 | 12.9 | 9 | 10 | 8 | 1.124 | 1.066 | 1.07 | 0.893 | 0.884 | 0.886 | 0.817 | 3.15E-04 |
| cds.Camellia_sinensis.comp28948_c0_seq1_m.3321 | PREDICTED: protein CROWDED NUCLEI 1 isoform X2 [Vitis | 58.7 | 3.0255 | 3.6 | 2 | 2 | 2 | 1.003 | 1.094 | 1.167 | 0.913 | 0.953 | 0.862 | 0.836 | 2.76E-02 |
| cds.Camellia_sinensis.comp28953_c0_seq1_m.27824 | PREDICTED: mediator of RNA polymerase II transcription subunit 15a isoform X2 [Fragaria vesca subsp.vesca] | 44.129 | 1.47 | 2 | 1 | 1 | 1 | 1.092 | 1.017 | 1.035 | 0.948 | 0.918 | 0.978 | 0.905 | 2.36E-02 |

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| cds.Camellia_sinensis.comp28957_c0_seq1_m.23027 | PREDICTED: SUPPRESSOR OF ABI3-5 isoform X1 [Theobroma cacao] | 26.673 | 2.5888 | 5.3 | 1 | 1 | 1 | 1.033 | 1.009 | 1.116 | 0.974 | 0.925 | 0.939 | 0.899 | 3.57E-02 |
| cds.Camellia_sinensis.comp28962_c0_seq1_m.23541 | PREDICTED: probable protein disulfide-isomerase A6 [Nicotiana tomentosiformis] | 39.858 | 121.32 | 42.4 | 17 | 38 | 15 | 1.032 | 0.998 | 1.006 | 0.99 | 1.003 | 1.005 | 0.987 | 3.24E-01 |
| cds.Camellia_sinensis.comp28963_c0_seq1_m.29910 | PREDICTED: uroporphyrinogen-III synthase, chloroplastic isoform X2 [Vitis vinifera] | 35.281 | 1.1737 | 4.6 | 2 | 2 | 2 | 1.054 | 1.101 | 0.991 | 0.963 | 0.969 | 0.916 | 0.905 | 4.89E-02 |
| cds.Camellia_sinensis.comp28964_c0_seq1_m.33040 | PREDICTED: TOM1-like protein 2 [Ipomoea nil] | 33.459 | 19.771 | 30.8 | 6 | 10 | 6 | 0.926 | 1.028 | 0.989 | 1.109 | 1.011 | 0.994 | 1.058 | 2.86E-01 |

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| cds.Camellia_sinensis.comp28964_c0_seq3_m.39000 | PREDICTED: target of Myb protein 1 [Vitis vinifera] | 26.211 | 3.372 | 15.6 | 3 | 5 | 3 | 1.046 | 0.926 | 1.007 | 0.949 | 0.992 | 1.013 | 0.992 | 8.63E-01 |
| cds.Camellia_sinensis.comp28967_c0_seq1_m.49180 | PREDICTED: heat shock cognate 70 kDa protein [Solanum lycopersicum] | 22.519 | 4.4789 | 43.5 | 9 | 24 | 1 | 0.977 | 1.067 | 0.924 | 0.972 | 0.957 | 1.11 | 1.024 | 7.32E-01 |
| cds.Camellia_sinensis.comp28968_c0_seq3_m.7600 | PREDICTED: BEL1-like homeodomain protein 1 [Vitis vinifera] | 76.287 | 2.9242 | 3.2 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28969_c0_seq2_m.31057 | PREDICTED: mRNA-decapping enzyme subunit 2 [Daucus carota subsp. sativus] | 36.607 | 6.1684 | 6.5 | 2 | 3 | 2 | 0.864 | 1.052 | 0.985 | 1.151 | 0.964 | 1.021 | 1.081 | 3.71E-01 |
| cds.Camellia_sinensis.comp28971_c0_seq1_m.16528 | PREDICTED: cyclase-associated protein 1 [Vitis vinifera] | 62.147 | 27.245 | 20.5 | 13 | 17 | 13 | 0.973 | 0.956 | 0.998 | 1.009 | 1.019 | 1.024 | 1.043 | 3.37E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp28975_c0_seq1_m.17459 | transcriptional repressor [Arabidopsis lyrata subsp. lyrata] | 67.725 | 143.68 | 29.2 | 16 | 37 | 16 | 1.015 | 1.016 | 1.003 | 0.986 | 0.988 | 0.987 | 0.976 | 2.82E-02 |
| cds.Camellia_sinensis.comp28977_c0_seq3_m.38961 | PREDICTED: putative WEB family protein At1g65010, chloroplastic [Malus domestica] | 23.82 | 1.2572 | 6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp28980_c0_seq40_m.400 | photosystem I P700 chlorophyll A apoprotein A2 (chloroplast) [Camellia crapnelliana] | 82.369 | 264.44 | 20.2 | 11 | 59 | 11 | 1.013 | 1.013 | 1.02 | 0.97 | 0.99 | 0.976 | 0.964 | 4.70E-03 |
| cds.Camellia_sinensis.comp28980_c0_seq40_m.401 | photosystem I P700 chlorophyll A apoprotein A1 (chloroplast) [Camellia crapnelliana] | 56.528 | 40.312 | 15.5 | 9 | 26 | 9 | 1.025 | 0.989 | 1.007 | 0.992 | 1.019 | 0.986 | 0.992 | 6.11E-01 |

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| cds.Camellia_sinensis.comp28980_c0_seq4_m.404 | photosystem I P700 chlorophyll A apoprotein A1 (chloroplast) [Camellia crapnelliana] | 17.031 | 23.712 | 15.9 | 3 | 12 | 3 | 1.012 | 1.018 | 1.054 | 0.938 | 0.999 | 0.954 | 0.937 | 4.61E-02 |
| cds.Camellia_sinensis.comp28981_c0_seq2_m.32966 | PREDICTED: protein trichome birefringence-like 38 [Sesamum indicum] | 44.457 | 26.795 | 14.4 | 4 | 7 | 4 | 1.11 | 1.146 | 1.138 | 0.863 | 0.872 | 0.88 | 0.77 | 2.01E-05 |
| cds.Camellia_sinensis.comp28983_c1_seq1_m.15218 | PREDICTED: selenoprotein O [Jatropha curcas] | 73.473 | 101.58 | 37.3 | 23 | 32 | 23 | 1.022 | 1.006 | 1.004 | 0.96 | 1.014 | 1.007 | 0.983 | 3.95E-01 |
| cds.Camellia_sinensis.comp28984_c0_seq1_m.44429 | PREDICTED: cysteine proteinase inhibitor-like [Populus euphratica] | 13.513 | 76.668 | 33.1 | 6 | 19 | 2 | 1.116 | 1.075 | 1.204 | 0.821 | 0.905 | 0.852 | 0.759 | 3.28E-03 |
| cds.Camellia_sinensis.comp28984_c0_seq2_m.46176 | PREDICTED: cysteine proteinase inhibitor [Ricinus communis] | 11.614 | 63.439 | 36.8 | 5 | 16 | 1 | 0.95 | 0.895 | 0.981 | 1.032 | 1.12 | 1.068 | 1.139 | 2.19E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp28990_c0_seq2_m.47115 | PREDICTED: protein Dr1 homolog isoform X4 [Theobroma cacao] | 16.372 | 12.943 | 24.7 | 3 | 3 | 3 | 0.932 | 0.896 | 0.992 | 1.125 | 1.009 | 1.054 | 1.13 | 4.75E-02 |
| cds.Camellia_sinensis.comp28996_c0_seq1_m.8832 | PREDICTED: protein FAM188A [Theobroma cacao] | 67.43 | 61.132 | 18.6 | 9 | 12 | 9 | 0.89 | 0.973 | 0.89 | 1.108 | 1.026 | 1.132 | 1.186 | 1.54E-02 |
| cds.Camellia_sinensis.comp28997_c0_seq1_m.29127 | PREDICTED: eukaryotic translation initiation factor 3 subunit I [Cucumis sativus] | 35.757 | 68.283 | 35.3 | 11 | 20 | 11 | 0.995 | 0.974 | 0.976 | 1.034 | 1.06 | 1.025 | 1.059 | 9.14E-03 |
| cds.Camellia_sinensis.comp29003_c0_seq1_m.3215 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 26 [Vitis vinifera] | 122.66 | 1.2168 | 0.7 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp29004_c0_seq1_m.28540 | PREDICTED: putative septum site-determining protein minD homolog, chloroplastic [Ziziphus jujuba] | 36.21 | 11.526 | 10.6 | 3 | 3 | 3 | 0.936 | 1.018 | 1.065 | 1.016 | 0.916 | 0.988 | 0.967 | 5.38E-01 |
| cds.Camellia_sinensis.comp29005_c0_seq1_m.10811 | PREDICTED: D-3-phosphoglycerate dehydrogenase 2, chloroplastic-like [Nicotiana attenuata] | 71.371 | 74.516 | 22.4 | 14 | 23 | 12 | 1.084 | 1.108 | 1.082 | 0.881 | 0.888 | 0.901 | 0.816 | 3.75E-05 |
| cds.Camellia_sinensis.comp29007_c0_seq1_m.6485 | PREDICTED: protein GRIP [Juglans regia] | 91.598 | 2.2951 | 1.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29009_c0_seq1_m.6382 | PREDICTED: THO complex subunit 5A isoform X2 [Vitis vinifera] | 58.935 | 1.67 | 1.9 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp29009_c2_seq1_m.33399 | PREDICTED: translation machinery-associated protein 22 [Populus euphratica] | 22.946 | 2.5605 | 11.2 | 2 | 2 | 2 | 1.113 | 1.116 | 0.976 | 0.946 | 0.878 | 0.951 | 0.866 | 4.94E-02 |
| cds.Camellia_sinensis.comp29011_c0_seq1_m.33325 | PREDICTED: ACT domain-containing protein ACR12 [Juglans regia] | 34.168 | 30.961 | 18.8 | 6 | 11 | 6 | 1.015 | 1.012 | 0.996 | 1.004 | 0.995 | 0.99 | 0.989 | 1.90E-01 |
| cds.Camellia_sinensis.comp29013_c0_seq1_m.15937 | PREDICTED: TPR repeat-containing thioredoxin TDX isoform X2 [Malus domestica] | 44.496 | 34.283 | 15.1 | 7 | 9 | 7 | 1.135 | 1.116 | 1.139 | 0.854 | 0.893 | 0.867 | 0.771 | 5.88E-05 |
| cds.Camellia_sinensis.comp29013_c0_seq1_m.15938 | PREDICTED: ubiquitin receptor RAD23c-like [Vigna | 17.285 | 55.608 | 33.7 | 3 | 7 | 3 | 1.072 | 0.946 | 0.963 | 0.979 | 1.035 | 1.003 | 1.012 | 7.69E-01 |

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| cds.Camellia_sinensis.comp29016_c0_seq1_m.12430 | PREDICTED: cysteine--tRNA ligase 2, cytoplasmic [Nelumbo nucifera] | 60.574 | 41.197 | 12 | 6 | 7 | 6 | 0.975 | 1.023 | 0.944 | 1.046 | 0.997 | 0.98 | 1.028 | 4.20E-01 |
| cds.Camellia_sinensis.comp29019_c0_seq1_m.35179 | PREDICTED: U1 small nuclear ribonucleoprotein A-like [Ziziphus jujuba] | 27.341 | 10.732 | 13.9 | 3 | 3 | 3 | 1.056 | 1.003 | 1.117 | 1 | 0.901 | 0.938 | 0.894 | 6.13E-02 |
| cds.Camellia_sinensis.comp29020_c0_seq1_m.11266 | PREDICTED: threonine--tRNA ligase, chloroplastic/mitochondrial 2 [Vitis vinifera] | 77.745 | 25.814 | 13.1 | 8 | 10 | 8 | 0.998 | 0.973 | 0.961 | 1.067 | 1.042 | 1.014 | 1.065 | 2.69E-02 |
| cds.Camellia_sinensis.comp29023_c0_seq3_m.29152 | lipoxygenase [Vitis vinifera] | 52.425 | 1.3242 | 1.7 | 1 | 1 | 1 | 1.107 | 1.124 | 1.06 | 0.901 | 0.935 | 0.85 | 0.816 | 3.44E-03 |

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| cds.Camellia_sinensis.comp29026_c0_seq1_m.42170 | PREDICTED: probable glutathione S-transferase [Populus euphratica] | 25.622 | 1.2231 | 5.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29028_c0_seq1_m.20116 | PREDICTED: ras-related protein Rab11D [Vitis vinifera] | 24.928 | 5.7706 | 26.7 | 6 | 8 | 5 | 0.997 | 1.05 | 1.05 | 0.952 | 0.919 | 0.933 | 0.905 | 7.80E-03 |
| cds.Camellia_sinensis.comp29032_c0_seq1_m.32431 | PREDICTED: proteasome subunit beta type-2-A-like [Jatropha curcas] | 22.685 | 55.433 | 36.6 | 8 | 13 | 3 | 0.979 | 1.024 | 0.987 | 1.011 | 1.035 | 1.032 | 1.029 | 1.36E-01 |
| cds.Camellia_sinensis.comp29032_c0_seq2_m.54937 | PREDICTED: proteasome subunit beta type-2-B [Ipomoea nil] | 15.189 | 3.3625 | 42.8 | 6 | 10 | 1 | 0.94 | 0.96 | 0.989 | 1.01 | 1.104 | 1.022 | 1.085 | 6.12E-02 |
| cds.Camellia_sinensis.comp29039_c0_seq1_m.39236 | PREDICTED: ubiquitin-conjugating enzyme E2 variant 1D [Sesamum indicum] | 16.562 | 77.395 | 58.9 | 8 | 21 | 8 | 1.01 | 0.973 | 0.989 | 1.002 | 1.041 | 1.017 | 1.03 | 1.33E-01 |

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| cds.Camellia_sinensis.comp29046_c0_seq1_m.29078 | PREDICTED: aldo-keto reductase family 4 member C9-like [Gossypium arboreum] | 35.072 | 8.9395 | 14.6 | 6 | 9 | 6 | 1.039 | 0.958 | 0.997 | 1.011 | 1.032 | 0.997 | 1.015 | 5.71E-01 |
| cds.Camellia_sinensis.comp29048_c0_seq1_m.26319 | PREDICTED: myb-related protein Myb4 [Theobroma cacao] | 42.111 | 1.5658 | 3.1 | 1 | 1 | 1 | 1.057 | 0.85 | 0.991 | 1.033 | 1.023 | 1.058 | 1.075 | 3.66E-01 |
| cds.Camellia_sinensis.comp29052_c0_seq1_m.19282 | PREDICTED: cell division control protein 7 [Ziziphus jujuba] | 31.035 | 1.7548 | 4 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29052_c0_seq1_m.19283 | PREDICTED: E3 ubiquitin-protein ligase KEG [Sesamum indicum] | 28.627 | 1.5985 | 5.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29064_c0_seq1_m.4735 | PREDICTED: protein transport protein SEC23 [Vitis vinifera] | 95.394 | 8.4967 | 4.3 | 4 | 4 | 4 | 0.89 | 1.028 | 0.976 | 1.151 | 0.964 | 1.037 | 1.089 | 2.73E-01 |

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| cds.Camellia_sinensis.comp29074_c0_seq1_m.15684 | PREDICTED: enolase-phosphatase E1 [Vitis vinifera] | 54.971 | 3.253 | 2.1 | 1 | 2 | 1 | 1.079 | 0.986 | 0.953 | 0.943 | 1.037 | 0.999 | 0.987 | 8.02E-01 |
| cds.Camellia_sinensis.comp29075_c0_seq1_m.18691 | PREDICTED: inactive dipeptidyl peptidase 10-like isoform X1 [Daucus carota subsp. sativus] | 66.517 | 135.54 | 27.8 | 16 | 24 | 16 | 0.94 | 0.931 | 0.936 | 1.086 | 1.064 | 1.074 | 1.149 | 2.47E-05 |
| cds.Camellia_sinensis.comp29080_c0_seq1_m.18560 | PREDICTED: chorismate synthase 1, chloroplastic [Vitis vinifera] | 47.258 | 9.5773 | 16.5 | 8 | 11 | 8 | 1.056 | 1.116 | 1.071 | 0.878 | 0.891 | 0.921 | 0.829 | 1.02E-03 |
| cds.Camellia_sinensis.comp29085_c0_seq1_m.49093 | PREDICTED: 10 kDa chaperonin-like [Sesamum indicum] | 13.338 | 57.867 | 54.9 | 7 | 23 | 7 | 1.023 | 0.996 | 0.996 | 0.953 | 0.998 | 1.028 | 0.988 | 6.29E-01 |

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| cds.Camellia_sinensis.comp29098_c0_seq1_m.46314 | PREDICTED: 10 kDa chaperonin 1, chloroplastic [Nicotiana attenuata] | 15.39 | 47.222 | 43.7 | 6 | 16 | 6 | 1.008 | 1.03 | 1.047 | 0.972 | 0.982 | 0.956 | 0.943 | 1.24E-02 |
| cds.Camellia_sinensis.comp29099_c0_seq1_m.24039 | alcohol dehydrogenase family protein [Populus trichocarpa] | 41.861 | 21.811 | 10.6 | 4 | 5 | 4 | 1.024 | 1.047 | 1.051 | 0.929 | 0.92 | 0.94 | 0.893 | 3.82E-04 |
| cds.Camellia_sinensis.comp29105_c0_seq1_m.19191 | PREDICTED: probable nucleoredoxin 2 isoform X1 [Ricinus communis] | 34.772 | 2.0821 | 3.3 | 1 | 1 | 1 | 0.962 | 1.009 | 1.003 | 0.955 | 1.02 | 1.062 | 1.021 | 5.88E-01 |
| cds.Camellia_sinensis.comp29108_c0_seq5_m.42787 | PREDICTED: vacuolar protein sorting-associated protein 32 homolog 2 [Cucumis melo] | 23.571 | 20.332 | 38.5 | 8 | 8 | 2 | 1.148 | 1.106 | 1.084 | 0.9 | 0.794 | 0.935 | 0.788 | 9.90E-03 |

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| cds.Camellia_sinensis.comp29111_c0_seq2_m.42119 | PREDICTED: transmembrane emp24 domain-containing protein p24delta9 [Citrus sinensis] | 24.489 | 1.336 | 6.5 | 2 | 3 | 2 | 0.882 | 0.99 | 0.926 | 1.113 | 0.998 | 1.127 | 1.157 | 4.63E-02 |
| cds.Camellia_sinensis.comp29117_c0_seq1_m.25011 | PREDICTED: rhomboid-like protein 15 [Juglans regia] | 46.147 | 5.4179 | 5.9 | 2 | 3 | 2 | 1.003 | 1.025 | 1.072 | 1.061 | 0.947 | 0.901 | 0.938 | 2.77E-01 |
| cds.Camellia_sinensis.comp29118_c0_seq1_m.28793 | PREDICTED: caffeoylshikimate esterase-like isoform X1 [Nicotiana tomentosiformis] | 43.038 | 10.777 | 8.2 | 4 | 4 | 4 | 0.972 | 0.988 | 1.003 | 1.006 | 1.045 | 1.002 | 1.03 | 1.39E-01 |
| cds.Camellia_sinensis.comp29121_c0_seq1_m.33698 | PREDICTED: thioredoxin-like protein AAED1, chloroplastic isoform X2 [Vitis vinifera] | 27.749 | 66.761 | 30.8 | 6 | 13 | 6 | 0.977 | 0.993 | 0.992 | 0.977 | 1.026 | 1.014 | 1.019 | 3.09E-01 |

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| cds.Camellia_sinensis.comp29122_c0_seq1_m.32494 | PREDICTED: bark storage protein A-like [Juglans regia] | 36.404 | 3.7657 | 4.2 | 1 | 1 | 1 | 0.887 | 1.31 | 1.103 | 0.882 | 0.898 | 0.913 | 0.816 | 2.34E-01 |
| cds.Camellia_sinensis.comp29124_c0_seq1_m.29557 | PREDICTED: PI-PLC X domain-containing protein At5g67130 [Arachis duranensis] | 41.926 | 1.7781 | 4.4 | 2 | 2 | 2 | 0.945 | 1.06 | 0.979 | 1.076 | 0.975 | 0.984 | 1.017 | 7.30E-01 |
| cds.Camellia_sinensis.comp29127_c0_seq2_m.27072 | PREDICTED: pyruvate dehydrogenase E1 component subunit beta-2, mitochondrial [Setaria | 18.566 | 34.233 | 49.4 | 8 | 21 | 5 | 0.991 | 1.049 | 1.002 | 0.998 | 0.968 | 0.999 | 0.975 | 2.77E-01 |
| cds.Camellia_sinensis.comp29128_c0_seq1_m.17628 | PREDICTED: homeobox protein knotted-1-like 13 isoform X3 [Vitis vinifera] | 34.562 | 3.8194 | 5.9 | 2 | 2 | 2 | 1.071 | 1.169 | 1.038 | 1.023 | 0.853 | 0.833 | 0.826 | 5.90E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29131_c0_seq1_m.37347 | PREDICTED: photosynthetic NDH subunit of lumenal location 4, chloroplastic [Vitis vinifera] | 25.654 | 33.935 | 26.7 | 5 | 10 | 5 | 0.929 | 1.018 | 1.048 | 0.949 | 0.979 | 1.073 | 1.002 | 9.72E-01 |
| cds.Camellia_sinensis.comp29132_c0_seq2_m.16512 | PREDICTED: molybdopterin biosynthesis protein CNX1 [Jatropha curcas] | 52.017 | 41.384 | 9.2 | 4 | 6 | 4 | 0.975 | 0.933 | 0.92 | 1.051 | 1.043 | 1.1 | 1.129 | 7.24E-03 |
| cds.Camellia_sinensis.comp29136_c0_seq1_m.23393 | PREDICTED: UDP-glucuronic acid decarboxylase 2 [Theobroma cacao] | 48.526 | 6.7826 | 13.7 | 6 | 9 | 4 | 0.921 | 1.08 | 1.061 | 1.062 | 0.997 | 0.899 | 0.966 | 6.49E-01 |
| cds.Camellia_sinensis.comp29143_c0_seq1_m.17411 | Mitochondrial metalloendopeptidase OMA1 [Morus notabilis] | 50.212 | 1.2386 | 1.8 | 1 | 2 | 1 | 0.926 | 1.027 | 0.984 | 1.021 | 1.021 | 1.041 | 1.05 | 1.83E-01 |

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| cds.Camellia_sinensis.comp29144_c0_seq1_m.14277 | PREDICTED: multicopper oxidase LPR1 [Jatropha curcas] | 67.314 | 25.464 | 11.1 | 5 | 9 | 5 | 1 | 1.048 | 0.904 | 1.033 | 0.998 | 0.991 | 1.024 | 6.09E-01 |
| cds.Camellia_sinensis.comp29145_c0_seq1_m.13882 | PREDICTED: L-galactono-1,4-lactone dehydrogenase, mitochondrial [Sesamum indicum] | 50.886 | 100.67 | 23.7 | 9 | 14 | 9 | 1.012 | 1.002 | 1.006 | 0.978 | 1.023 | 0.955 | 0.979 | 3.96E-01 |
| cds.Camellia_sinensis.comp29148_c0_seq1_m.35252 | PREDICTED: chlorophyll a-b binding protein of LHCII type 1-like [Ziziphus jujuba] | 36.449 | 17.289 | 12 | 4 | 5 | 4 | 0.986 | 0.977 | 0.976 | 1.06 | 1.04 | 1.057 | 1.074 | 4.56E-04 |
| cds.Camellia_sinensis.comp29152_c0_seq1_m.21822 | tetratricopeptide repeat-containing protein isoform 2 [Solanum lycopersicum] | 48.627 | 1.5719 | 2.1 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp29155_c0_seq1_m.33111 | transmembrane protein, putative [Medicago truncatula] | 32.567 | 8.9467 | 5.8 | 1 | 2 | 1 | 0.909 | 1.012 | 0.986 | 1.008 | 1.192 | 0.923 | 1.074 | 4.58E-01 |
| cds.Camellia_sinensis.comp29156_c0_seq1_m.32125 | ATP-dependent Clp protease proteolytic subunit 5 [Morus notabilis] | 38.3 | 35.914 | 21.1 | 6 | 15 | 6 | 0.943 | 0.979 | 0.945 | 1.063 | 1.05 | 1.01 | 1.089 | 1.21E-02 |
| cds.Camellia_sinensis.comp29158_c0_seq1_m.36360 | PREDICTED: stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic [Theobroma cacao] | 40.653 | 34.636 | 16 | 5 | 5 | 5 | 0.917 | 0.937 | 0.971 | 1.104 | 1.031 | 1.056 | 1.13 | 9.54E-03 |
| cds.Camellia_sinensis.comp29158_c0_seq2_m.57673 | PREDICTED: stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic isoform X2 [Nelumbo nucifera] | 12.895 | 15.905 | 23.9 | 2 | 2 | 2 | 0.974 | 1.033 | 0.91 | 1.057 | 1.049 | 0.996 | 1.063 | 2.03E-01 |

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| cds.Camellia_sinensis.comp29164_c0_seq1_m.34097 | PREDICTED: chlorophyll a-b binding protein CP26, chloroplastic [Jatropha curcas] | 30.956 | 191.41 | 58.6 | 14 | 89 | 14 | 0.924 | 0.91 | 0.918 | 1.086 | 1.1 | 1.091 | 1.191 | 3.62E-06 |
| cds.Camellia_sinensis.comp29166_c0_seq2_m.33330 | PREDICTED: probable enoyl-CoA hydratase 2, mitochondrial [Juglans regia] | 24.479 | 18.257 | 16.2 | 2 | 2 | 2 | 0.992 | 1.067 | 0.952 | 0.961 | 0.97 | 1.061 | 0.994 | 8.99E-01 |
| cds.Camellia_sinensis.comp29167_c0_seq1_m.10952 | PREDICTED: RNA polymerase II degradation factor 1 [Vitis vinifera] | 76.05 | 43.258 | 7.2 | 4 | 5 | 4 | 1.073 | 1.034 | 1.047 | 0.965 | 0.946 | 1.04 | 0.936 | 9.46E-02 |
| cds.Camellia_sinensis.comp29169_c0_seq1_m.32558 | PREDICTED: fatty acid desaturase 4, chloroplastic [Fragaria vesca subsp. vesca] | 34.715 | 2.8916 | 5.5 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp29172_c0_seq2_m.27857 | PREDICTED: protein FAR1-RELATED SEQUENCE 9 [Vitis | 46.018 | 9.647 | 6.3 | 2 | 2 | 2 | 0.926 | 0.978 | 0.965 | 1.136 | 0.965 | 1.061 | 1.102 | 1.30E-01 |
| cds.Camellia_sinensis.comp29174_c0_seq1_m.31554 | PREDICTED: RNA-binding protein CP29B, chloroplastic [Vitis vinifera] | 37.304 | 54.173 | 19.5 | 6 | 11 | 6 | 1.104 | 1.089 | 1.115 | 0.92 | 0.911 | 0.865 | 0.815 | 5.41E-04 |
| cds.Camellia_sinensis.comp29178_c0_seq1_m.22814 | PREDICTED: thiosulfate/3-mercaptopyruvate sulfurtransferase 1, mitochondrial isoform X1 [Jatropha | 41.559 | 95.763 | 38.3 | 12 | 27 | 12 | 0.948 | 0.96 | 0.974 | 1.029 | 1.071 | 1.031 | 1.086 | 5.52E-03 |
| cds.Camellia_sinensis.comp29182_c0_seq1_m.10746 | PREDICTED: elongation factor G-1, mitochondrial [Theobroma cacao] | 84.612 | 2.5142 | 2.2 | 2 | 2 | 2 | 0.913 | 1.02 | 0.928 | 1.044 | 1.146 | 0.979 | 1.108 | 1.52E-01 |

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| cds.Camellia_sinensis.comp29184_c0_seq2_m.31750 | PH-response transcription factor [Arabidopsis thaliana] | 38.237 | 18.251 | 15.7 | 5 | 8 | 5 | 0.951 | 0.991 | 0.977 | 0.991 | 0.997 | 1.1 | 1.058 | 1.99E-01 |
| cds.Camellia_sinensis.comp29186_c0_seq1_m.24270 | PREDICTED: AP-4 complex subunit mu isoform X1 [Daucus carota subsp. sativus] | 52.844 | 5.2092 | 7.6 | 3 | 4 | 3 | 0.968 | 1.034 | 1.01 | 1.108 | 0.926 | 0.973 | 0.998 | 9.45E-01 |
| cds.Camellia_sinensis.comp29188_c0_seq1_m.28848 | PREDICTED: spermidine synthase 1 [Citrus sinensis] | 39.312 | 25.797 | 11.5 | 3 | 5 | 2 | 0.958 | 1.054 | 1.062 | 0.997 | 0.962 | 1.108 | 0.998 | 9.58E-01 |
| cds.Camellia_sinensis.comp29188_c0_seq2_m.30395 | PREDICTED: spermidine synthase [Theobroma cacao] | 39.351 | 4.1685 | 6.7 | 2 | 3 | 1 | 1.044 | 1.095 | 1.039 | 0.947 | 0.991 | 0.877 | 0.886 | 3.61E-02 |
| cds.Camellia_sinensis.comp29189_c0_seq1_m.26715 | PREDICTED: superoxide dismutase [Mn], mitochondrial [Nicotiana attenuata] | 25.54 | 66.201 | 33.9 | 7 | 37 | 7 | 0.991 | 0.945 | 0.942 | 1.024 | 1.046 | 1.041 | 1.081 | 1.14E-02 |

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| cds.Camellia_sinensis.comp29198_c0_seq1_m.29186 | PREDICTED: quinone oxidoreductase-like protein 2 homolog [Solanum pennellii] | 36.851 | 4.3385 | 8 | 3 | 4 | 3 | 1.03 | 1.099 | 0.984 | 0.913 | 0.943 | 1.022 | 0.925 | 1.66E-01 |
| cds.Camellia_sinensis.comp29200_c0_seq2_m.48153 | PREDICTED: tubulin-folding cofactor A [Gossypium hirsutum] | 12.801 | 54.936 | 41.6 | 5 | 9 | 5 | 0.965 | 0.981 | 0.936 | 1.038 | 1.054 | 1.032 | 1.084 | 5.92E-03 |
| cds.Camellia_sinensis.comp29207_c0_seq2_m.18646 | PREDICTED: protein FREE1 [Vitis vinifera] | 59.644 | 19.187 | 8.7 | 3 | 3 | 3 | 0.981 | 1.031 | 1.082 | 0.994 | 0.917 | 0.998 | 0.94 | 1.94E-01 |
| cds.Camellia_sinensis.comp29208_c0_seq3_m.32955 | PREDICTED: plant UBX domain-containing protein 4 [Eucalyptus grandis] | 34.989 | 16.688 | 17.6 | 4 | 4 | 4 | 0.982 | 1.083 | 0.911 | 0.994 | 1.013 | 1.027 | 1.019 | 6.92E-01 |
| cds.Camellia_sinensis.comp29220_c0_seq1_m.35024 | PREDICTED: tRNA (guanine-N(7)-)-methyltransferase [Citrus sinensis] | 28.754 | 1.9582 | 4.4 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp29221_c0_seq1_m.35565 | PREDICTED: trigger factor-like [Phoenix dactylifera] | 24.688 | 59.672 | 26.9 | 6 | 12 | 6 | 1.036 | 1.028 | 1.079 | 0.953 | 0.94 | 0.939 | 0.901 | 2.72E-03 |
| cds.Camellia_sinensis.comp29223_c0_seq1_m.29121 | PREDICTED: UDP-glucuronic acid decarboxylase 6 [Nelumbo nucifera] | 38.379 | 50.808 | 33.2 | 11 | 21 | 6 | 1.011 | 0.964 | 0.973 | 1.015 | 1.074 | 1.013 | 1.052 | 1.03E-01 |
| cds.Camellia_sinensis.comp29223_c0_seq2_m.37257 | PREDICTED: UDP-glucuronic acid decarboxylase 6 [Arachis ipaensis] | 28.743 | 1.2219 | 20.1 | 6 | 10 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29226_c0_seq2_m.38445 | PREDICTED: endo-1,3;1,4-beta-D-glucanase-like, partial [Nicotiana tomentosiformis] | 18.239 | 8.7447 | 12.2 | 2 | 3 | 2 | 1.075 | 0.946 | 1.011 | 0.996 | 0.983 | 0.989 | 0.979 | 6.44E-01 |

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| cds.Camellia_sinensis.comp29238_c0_seq1_m.38345 | PREDICTED: CBS domain-containing protein CBSX3, mitochondrial [Vitis vinifera] | 22.649 | 35.65 | 50.7 | 9 | 24 | 9 | 0.949 | 0.994 | 0.993 | 1.027 | 1.03 | 1.02 | 1.048 | 3.87E-02 |
| cds.Camellia_sinensis.comp29239_c0_seq1_m.40043 | PREDICTED: probable carboxylesterase 2 [Vitis vinifera] | 19.798 | 4.2994 | 18.5 | 3 | 6 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp29239_c0_seq2_m.40683 | PREDICTED: probable carboxylesterase 2 [Vitis vinifera] | 20.772 | 42.738 | 27 | 5 | 10 | 3 | 0.987 | 0.943 | 0.919 | 1.063 | 1.053 | 1.048 | 1.111 | 7.78E-03 |
| cds.Camellia_sinensis.comp29239_c0_seq3_m.41918 | PREDICTED: probable carboxylesterase 2 [Vitis vinifera] | 28.937 | 2.1282 | 14.8 | 3 | 5 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29242_c0_seq1_m.33354 | Thylakoid lumenal 19 kDa protein [Morus notabilis] | 27.926 | 50.819 | 16.2 | 6 | 15 | 6 | 1.013 | 0.992 | 0.972 | 1.011 | 1.027 | 0.997 | 1.019 | 2.58E-01 |

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| cds.Camellia_sinensis.comp29247_c0_seq2_m.21215 | PREDICTED: alcohol dehydrogenase-like [Nicotiana tabacum] | 47.038 | 152.2 | 23.6 | 8 | 16 | 8 | 0.984 | 0.97 | 0.984 | 1.028 | 1.032 | 1.019 | 1.048 | 1.52E-03 |
| cds.Camellia_sinensis.comp29250_c0_seq1_m.23795 | PREDICTED: probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410 isoform X1[Jatropha curcas] | 48.98 | 12.16 | 13.4 | 5 | 5 | 5 | 1.015 | 1.048 | 1.039 | 0.906 | 0.983 | 1.006 | 0.933 | 1.02E-01 |
| cds.Camellia_sinensis.comp29251_c0_seq1_m.4569 | PREDICTED: NAD(P)H-quinone oxidoreductase subunit N, chloroplastic-like [Nicotiana tabacum] | 19.834 | 4.0794 | 21.5 | 4 | 4 | 4 | 0.953 | 1.026 | 1.036 | 0.981 | 1.102 | 0.918 | 0.995 | 9.14E-01 |
| cds.Camellia_sinensis.comp29256_c0_seq1_m.4724 | PREDICTED: alanine--tRNA ligase [Vitis vinifera] | 112.52 | 207.71 | 28.2 | 28 | 53 | 28 | 0.985 | 0.982 | 0.975 | 1.006 | 1.014 | 1.037 | 1.039 | 1.62E-02 |

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| cds.Camellia_sinensis.comp29258_c0_seq1_m.43491 | PREDICTED: universal stress protein PHOS32 [Pyrus x bretschneideri] | 18.455 | 2.5107 | 18.3 | 4 | 6 | 3 | 0.969 | 0.98 | 0.975 | 1.043 | 1.046 | 1.007 | 1.059 | 1.07E-02 |
| cds.Camellia_sinensis.comp29266_c0_seq1_m.27706 | Dehydration-responsive protein RD22 precursor [Populus trichocarpa] | 12.51 | 42.2 | 31.7 | 5 | 7 | 5 | 1.259 | 1.173 | 1.193 | 0.721 | 0.8 | 0.794 | 0.639 | 3.44E-04 |
| cds.Camellia_sinensis.comp29266_c0_seq2_m.32997 | PREDICTED: BURP domain protein RD22-like, partial [Juglans regia] | 22.294 | 8.7869 | 16.2 | 4 | 4 | 4 | 1.34 | 1.282 | 1.299 | 0.638 | 0.669 | 0.656 | 0.501 | 1.70E-06 |
| cds.Camellia_sinensis.comp29270_c0_seq2_m.14589 | PREDICTED: glucose-6-phosphate isomerase 1, chloroplastic [Ziziphus jujuba] | 68.855 | 197.81 | 49.4 | 29 | 45 | 29 | 1.003 | 0.997 | 1.025 | 0.991 | 0.995 | 1.002 | 0.988 | 2.46E-01 |

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| cds.Camellia_sinensis.comp29274_c0_seq1_m.16753 | PREDICTED: succinate-semialdehyde dehydrogenase, mitochondrial [Prunus | 56.659 | 64.941 | 28.6 | 15 | 32 | 15 | 0.945 | 0.964 | 0.953 | 1.072 | 1.075 | 1.047 | 1.116 | 4.19E-04 |
| cds.Camellia_sinensis.comp29282_c0_seq1_m.45480 | PREDICTED: heparanase-like protein 3 [Vitis vinifera] | 22.451 | 4.1598 | 9 | 2 | 3 | 2 | 1.016 | 1.053 | 1.041 | 1.041 | 0.919 | 0.933 | 0.93 | 1.44E-01 |
| cds.Camellia_sinensis.comp29286_c0_seq2_m.25516 | alpha/beta fold hydrolase [Medicago truncatula] | 41.881 | 29.689 | 17.3 | 6 | 8 | 6 | 1.008 | 0.977 | 1.007 | 0.999 | 1.025 | 0.997 | 1.01 | 5.16E-01 |
| cds.Camellia_sinensis.comp29287_c0_seq6_m.49241 | histone-lysine N-methyltransferase [Arabidopsis thaliana] | 14.982 | 1.9029 | 7.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29290_c0_seq2_m.14601 | PREDICTED: serine/threonine-protein kinase STN8, chloroplastic isoform X1 [Vitis vinifera] | 57.13 | 47.976 | 20.2 | 10 | 10 | 10 | 0.98 | 1.004 | 1.005 | 1.035 | 1.006 | 0.998 | 1.017 | 2.96E-01 |

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| cds.Camellia_sinensis.comp29292_c0_seq4_m.36482 | PREDICTED: TATA-box-binding protein-like [Nicotiana tabacum] | 28.745 | 1.4681 | 4 | 1 | 4 | 1 | 1.088 | 1.087 | 1.061 | 0.93 | 0.914 | 0.948 | 0.863 | 3.82E-04 |
| cds.Camellia_sinensis.comp29295_c0_seq1_m.32773 | PREDICTED: phosphoglucan phosphatase DSP4, amyloplastic [Ziziphus jujuba] | 22.498 | 6.0198 | 19.6 | 3 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp29297_c0_seq2_m.16897 | PREDICTED: NEDD8 ultimate buster 1 [Solanum tuberosum | 61.841 | 12.847 | 10.9 | 6 | 8 | 6 | 1.03 | 0.998 | 1.02 | 0.97 | 1.028 | 0.997 | 0.983 | 4.08E-01 |
| cds.Camellia_sinensis.comp29297_c0_seq3_m.18716 | PREDICTED: aspartic proteinase [Vitis vinifera] | 58.91 | 11.975 | 9.1 | 5 | 7 | 5 | 0.952 | 0.965 | 0.924 | 1.043 | 1.054 | 1.045 | 1.106 | 1.58E-03 |
| cds.Camellia_sinensis.comp29299_c0_seq1_m.33168 | 26S protease regulatory subunit 6B-like protein [Morus notabilis] | 38.558 | 5.1123 | 22.4 | 9 | 14 | 2 | 0.906 | 1.043 | 1.051 | 1.017 | 0.966 | 1.037 | 1.007 | 8.80E-01 |

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| cds.Camellia_sinensis.comp29301_c0_seq1_m.28275 | RNA binding protein [Arabidopsis thaliana] | 45.52 | 6.8912 | 6.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp29307_c0_seq1_m.11343 | PREDICTED: protein SIEVE ELEMENT OCCLUSION B [Ricinus communis] | 48.293 | 53.183 | 32.4 | 14 | 20 | 14 | 0.944 | 0.996 | 0.994 | 1.049 | 1.027 | 1.033 | 1.06 | 3.55E-02 |
| cds.Camellia_sinensis.comp29307_c0_seq1_m.11344 | PREDICTED: protein SIEVE ELEMENT OCCLUSION B [Ricinus communis] | 35.78 | 34.291 | 25.2 | 6 | 9 | 6 | 0.951 | 0.944 | 0.977 | 1.085 | 1.101 | 1.024 | 1.118 | 1.06E-02 |
| cds.Camellia_sinensis.comp29308_c0_seq2_m.24888 | PREDICTED: manganese-dependent ADP-ribose/CDP-alcohol diphosphatase [Vitis vinifera] | 35.925 | 3.4379 | 9.4 | 3 | 3 | 3 | 0.896 | 1.026 | 0.992 | 1.033 | 0.995 | 1.082 | 1.067 | 2.35E-01 |

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| cds.Camellia_sinensis.comp29319_c1_seq1_m.24228 | PREDICTED: alcohol dehydrogenase [Citrus sinensis] | 43.146 | 10.535 | 14.4 | 6 | 11 | 5 | 0.961 | 0.962 | 0.977 | 1.028 | 1.035 | 1.06 | 1.077 | 2.30E-03 |
| cds.Camellia_sinensis.comp29326_c0_seq1_m.19201 | PREDICTED: putative G3BP-like protein [Nelumbo nucifera] | 51.175 | 29.607 | 22.1 | 10 | 13 | 10 | 1.056 | 1.119 | 1.074 | 0.908 | 0.898 | 0.964 | 0.853 | 4.64E-03 |
| cds.Camellia_sinensis.comp29333_c0_seq1_m.15486 | PREDICTED: molybdate-anion transporter [Citrus sinensis] | 50.72 | 1.8137 | 3.5 | 2 | 2 | 2 | 1.067 | 1.125 | 1.108 | 0.881 | 0.899 | 0.898 | 0.812 | 2.58E-04 |
| cds.Camellia_sinensis.comp29334_c0_seq1_m.21420 | EMB2737 [Arabidopsis lyrata subsp. lyrata] | 46.009 | 1.4159 | 2 | 1 | 1 | 1 | 0.997 | 1.055 | 1.005 | 1.064 | 0.927 | 0.962 | 0.966 | 4.67E-01 |
| cds.Camellia_sinensis.comp29337_c0_seq1_m.17938 | Ferredoxin--nitrite reductase [Morus notabilis] | 56.402 | 67.988 | 20.4 | 11 | 17 | 11 | 0.966 | 0.97 | 0.976 | 1.065 | 1.041 | 1.039 | 1.08 | 8.20E-04 |
| cds.Camellia_sinensis.comp29343_c0_seq1_m.39591 | TPR domain protein [Medicago truncatula] | 23.697 | 16.116 | 24.4 | 5 | 7 | 5 | 0.974 | 0.951 | 0.908 | 1.049 | 1.033 | 1.125 | 1.132 | 2.07E-02 |

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| cds.Camellia_sinensis.comp29357_c0_seq1_m.14976 | PREDICTED: asparagine--tRNA ligase, cytoplasmic 1 [Vitis vinifera] | 63.182 | 123.47 | 24.7 | 14 | 31 | 12 | 0.943 | 0.976 | 0.961 | 1.08 | 1.03 | 1.035 | 1.092 | 8.22E-03 |
| cds.Camellia_sinensis.comp29358_c0_seq1_m.36435 | PREDICTED: 60S ribosomal protein L9 [Cucumis melo] | 23.154 | 78.166 | 54.2 | 10 | 22 | 10 | 1.197 | 1.165 | 1.142 | 0.8 | 0.856 | 0.83 | 0.709 | 1.37E-04 |
| cds.Camellia_sinensis.comp29362_c0_seq2_m.33302 | PREDICTED: bifunctional phosphatase IMPL2, chloroplastic-like isoform X1 [Nicotiana tabacum] | 37.645 | 38.799 | 12.9 | 3 | 5 | 3 | 0.922 | 0.963 | 1.034 | 1.094 | 0.996 | 0.977 | 1.051 | 3.65E-01 |
| cds.Camellia_sinensis.comp29363_c0_seq1_m.13525 | PREDICTED: pentatricopeptide repeat-containing protein At2g15690 [Solanum lycopersic | 74.623 | 3.3549 | 3.6 | 2 | 2 | 1 | 0.983 | 1.027 | 1.037 | 0.948 | 0.952 | 1.056 | 0.97 | 4.66E-01 |

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| cds.Camellia_sinensis.comp29363_c0_seq2_m.22606 | PREDICTED: pentatricopeptide repeat-containing protein At2g15690-like [Vitis | 53.849 | 8.2248 | 6.5 | 3 | 3 | 2 | 0.956 | 1.017 | 1.102 | 0.918 | 0.838 | 1.167 | 0.951 | 6.11E-01 |
| cds.Camellia_sinensis.comp29364_c0_seq1_m.23336 | PREDICTED: tyrosine aminotransferase-like [Nicotiana attenuata] | 46.995 | 38.035 | 17.1 | 7 | 9 | 7 | 1.101 | 1.111 | 1.143 | 0.87 | 0.889 | 0.879 | 0.786 | 4.43E-05 |
| cds.Camellia_sinensis.comp29365_c0_seq1_m.8543 | PREDICTED: probable beta-D-xylosidase 7 isoform X2 [Theobroma cacao] | 85.647 | 15.054 | 11 | 8 | 9 | 8 | 1.008 | 1.011 | 1.022 | 1.036 | 0.961 | 0.964 | 0.974 | 3.35E-01 |
| cds.Camellia_sinensis.comp29366_c0_seq1_m.9691 | PREDICTED: WEB family protein At5g55860 [Vitis vinifera] | 71.843 | 33.42 | 18.7 | 12 | 13 | 12 | 0.95 | 0.994 | 0.991 | 0.966 | 1.055 | 1.021 | 1.036 | 2.98E-01 |

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| cds.Camellia_sinensis.comp29370_c0_seq2_m.43077 | PREDICTED: probable xyloglucan endotransglucosylase/hydrolase protein 23 [Vitis vinifera] | 25.9 | 23.438 | 21.6 | 4 | 5 | 3 | 0.809 | 0.877 | 0.874 | 1.182 | 1.085 | 1.234 | 1.368 | 2.48E-03 |
| cds.Camellia_sinensis.comp29371_c0_seq1_m.7891 | PREDICTED: phospholipid:diacylglycerol acyltransferase 1-like [Jatropha curcas] | 74.118 | 25.569 | 5.4 | 4 | 5 | 4 | 0.974 | 0.907 | 1.005 | 0.988 | 1.062 | 1.082 | 1.085 | 1.17E-01 |
| cds.Camellia_sinensis.comp29373_c0_seq2_m.37564 | PREDICTED: vacuolar protein-sorting-associated protein 37 homolog 1-like [Gossypium hirsutum] | 29.518 | 5.9198 | 12.9 | 4 | 8 | 4 | 1.028 | 0.998 | 0.977 | 0.995 | 0.964 | 1.053 | 1.003 | 9.36E-01 |

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| cds.Camellia_sinensis.comp29378_c0_seq1_m.36536 | PREDICTED: mitochondrial outer membrane import complex protein METAXIN [Vitis vinifera] | 38.229 | 2.5981 | 5.3 | 2 | 2 | 2 | 0.982 | 1.057 | 1.013 | 0.999 | 0.953 | 1.004 | 0.969 | 3.05E-01 |
| cds.Camellia_sinensis.comp29380_c0_seq1_m.39114 | PITH domain-containing protein [Morus notabilis] | 20.83 | 18.845 | 11.2 | 2 | 4 | 2 | 0.936 | 0.991 | 0.978 | 1.054 | 1.035 | 1.073 | 1.088 | 1.35E-02 |
| cds.Camellia_sinensis.comp29387_c0_seq1_m.10368 | PREDICTED: acyltransferase-like protein At3g26840, chloroplastic [Vitis vinifera] | 70.567 | 2.2824 | 4 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp29390_c0_seq1_m.22240 | PREDICTED: linolenate hydroperoxide lyase, chloroplastic [Fragaria vesca subsp. vesca] | 54.807 | 56.694 | 22.6 | 11 | 20 | 11 | 1.006 | 0.977 | 0.962 | 1.044 | 1.03 | 1.014 | 1.049 | 3.81E-02 |

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| cds.Camellia_sinensis.comp29392_c1_seq2_m.18187 | PREDICTED: dnaJ protein ERDJ3B [Nelumbo nucifera] | 38.646 | 10.358 | 16.6 | 4 | 6 | 4 | 1.097 | 1.028 | 1.036 | 0.948 | 0.953 | 0.907 | 0.888 | 1.02E-02 |
| cds.Camellia_sinensis.comp29394_c0_seq1_m.5515 | PREDICTED: protein TIC110, chloroplastic isoform X1 [Vitis vinifera] | 69.71 | 143.18 | 33.4 | 18 | 35 | 18 | 0.995 | 1.017 | 1.014 | 0.995 | 0.992 | 1.004 | 0.988 | 2.09E-01 |
| cds.Camellia_sinensis.comp29394_c0_seq1_m.5516 | PREDICTED: protein TIC110, chloroplastic-like, partial [Nicotiana tabacum] | 24.176 | 45.791 | 38.8 | 9 | 17 | 9 | 1 | 1.001 | 1.013 | 0.968 | 1.007 | 0.966 | 0.976 | 1.56E-01 |
| cds.Camellia_sinensis.comp29394_c0_seq1_m.5517 | PREDICTED: protein TIC110, chloroplastic, partial [Ziziphus jujuba] | 22.297 | 90.416 | 42 | 6 | 23 | 6 | 1.001 | 1.011 | 1.008 | 0.994 | 0.99 | 0.991 | 0.985 | 9.24E-03 |

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| cds.Camellia_sinensis.comp29395_c0_seq1_m.21621 | PREDICTED: isocitrate dehydrogenase [NADP], chloroplastic/mitochondrial [Citrus sinensis] | 54.187 | 54.55 | 27.9 | 13 | 16 | 12 | 0.997 | 1.003 | 0.987 | 0.999 | 1.023 | 0.998 | 1.011 | 3.07E-01 |
| cds.Camellia_sinensis.comp29397_c0_seq2_m.33702 | Minor allergen Alt a 7 [Morus notabilis] | 26.511 | 21.708 | 19 | 4 | 6 | 3 | 1.022 | 0.966 | 0.964 | 0.982 | 1.097 | 0.981 | 1.037 | 4.50E-01 |
| cds.Camellia_sinensis.comp29397_c0_seq4_m.45655 | PREDICTED: probable NAD(P)H dehydrogenase (quinone) FQR1-like 2 [Solanum pennellii] | 20.132 | 3.0136 | 13.3 | 2 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29398_c0_seq1_m.19933 | PREDICTED: 26S protease regulatory subunit 6A homolog [Arachis ipaensis] | 47.429 | 269.11 | 64.1 | 24 | 55 | 23 | 0.954 | 0.993 | 0.993 | 1.017 | 1.019 | 1.035 | 1.045 | 3.90E-02 |

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| cds.Camellia_sinensis.comp29403_c0_seq1_m.1874 | PREDICTED: sucrose synthase [Nicotiana tabacum] | 92.452 | 93.255 | 23.2 | 18 | 25 | 15 | 1.152 | 1.168 | 1.246 | 0.763 | 0.812 | 0.824 | 0.673 | 3.01E-04 |
| cds.Camellia_sinensis.comp29417_c0_seq1_m.27919 | PREDICTED: uncharacterized oxidoreductase At4g09670-like [Nicotiana tomentosiformis] | 44.582 | 27.988 | 19.3 | 8 | 16 | 8 | 0.996 | 0.994 | 0.952 | 1.026 | 1.037 | 1.031 | 1.052 | 2.83E-02 |
| cds.Camellia_sinensis.comp29418_c0_seq4_m.30677 | PREDICTED: psbP domain-containing protein 3, chloroplastic [Juglans regia] | 27.62 | 56.251 | 25.5 | 5 | 14 | 5 | 1.02 | 0.995 | 0.968 | 0.983 | 1.016 | 1.029 | 1.015 | 5.02E-01 |
| cds.Camellia_sinensis.comp29420_c0_seq1_m.7741 | PREDICTED: aminopeptidase M1 [Vitis vinifera] | 94.411 | 200.73 | 28.1 | 25 | 44 | 24 | 0.901 | 0.913 | 0.924 | 1.114 | 1.077 | 1.099 | 1.202 | 1.17E-04 |
| cds.Camellia_sinensis.comp29421_c0_seq1_m.26499 | PREDICTED: ornithine carbamoyltransferase, chloroplastic-like [Nicotiana tabacum] | 43.985 | 67.068 | 25.9 | 8 | 19 | 5 | 0.992 | 0.956 | 1.017 | 1.03 | 1.111 | 0.947 | 1.041 | 4.77E-01 |

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| cds.Camellia_sinensis.comp29421_c0_seq2_m.27772 | PREDICTED: ornithine carbamoyltransferase, chloroplastic [Vitis vinifera] | 44.517 | 13.757 | 19.4 | 6 | 18 | 3 | 0.973 | 1.034 | 1.015 | 0.948 | 1.043 | 0.995 | 0.988 | 7.25E-01 |
| cds.Camellia_sinensis.comp29425_c0_seq1_m.27175 | PREDICTED: RNA pseudouridine synthase 7 [Capsicum annuum] | 12.561 | 8.0695 | 10.5 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29426_c0_seq1_m.33534 | PREDICTED: probable protein phosphatase 2C 26 [Juglans regia] | 34.317 | 3.5489 | 7.3 | 2 | 3 | 2 | 0.977 | 1.03 | 1.093 | 1.04 | 0.988 | 0.885 | 0.94 | 3.33E-01 |
| cds.Camellia_sinensis.comp29431_c0_seq1_m.26713 | PREDICTED: ribosome maturation protein SBDS [Nelumbo nucifera] | 40.957 | 11.771 | 5.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp29432_c0_seq1_m.15335 | PREDICTED: eukaryotic translation initiation factor 3 subunit D-like [Vitis vinifera] | 64.853 | 103.17 | 28.6 | 13 | 17 | 13 | 1.026 | 1.02 | 1.046 | 0.984 | 0.977 | 0.952 | 0.942 | 9.06E-03 |

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| cds.Camellia_sinensis.comp29433_c0_seq1_m.8748 | PREDICTED: aldehyde dehydrogenase family 2 member B4, mitochondrial-like [Ziziphus jujuba] | 58.352 | 289.89 | 37.4 | 21 | 66 | 11 | 1.036 | 1.001 | 1.027 | 0.968 | 0.964 | 0.969 | 0.947 | 3.47E-02 |
| cds.Camellia_sinensis.comp29440_c1_seq1_m.13529 | PREDICTED: threonine synthase, chloroplastic [Sesamum indicum] | 59.995 | 113.27 | 23.2 | 12 | 23 | 8 | 0.993 | 0.97 | 0.996 | 1.029 | 1.007 | 1.038 | 1.039 | 3.62E-02 |
| cds.Camellia_sinensis.comp29442_c0_seq1_m.19625 | PREDICTED: 1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic [Vitis vinifera] | 51.292 | 98.423 | 26.9 | 11 | 24 | 11 | 1.008 | 1.022 | 1.02 | 0.982 | 0.976 | 0.976 | 0.962 | 1.24E-03 |
| cds.Camellia_sinensis.comp29445_c0_seq1_m.25904 | PREDICTED: E3 ubiquitin protein ligase RIE1 [Theobroma cacao] | 39.628 | 8.9173 | 8.7 | 3 | 4 | 3 | 0.943 | 0.949 | 1.016 | 1.066 | 1.056 | 0.996 | 1.072 | 9.41E-02 |

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| cds.Camellia_sinensis.comp29449_c0_seq1_m.26166 | PREDICTED: uracil phosphoribosyltransferase [Nelumbo nucifera] | 18.45 | 4.6448 | 18.9 | 4 | 5 | 4 | 0.995 | 1.014 | 0.99 | 1.003 | 0.994 | 1.017 | 1.005 | 6.39E-01 |
| cds.Camellia_sinensis.comp29453_c0_seq1_m.21413 | PREDICTED: ankyrin repeat domain-containing protein 2B-like [Juglans regia] | 38.004 | 5.4048 | 27.8 | 9 | 13 | 3 | 1.054 | 0.981 | 1.013 | 0.989 | 0.994 | 0.982 | 0.973 | 2.66E-01 |
| cds.Camellia_sinensis.comp29453_c0_seq3_m.23364 | PREDICTED: ankyrin repeat domain-containing protein 2B-like [Juglans regia] | 38.658 | 59.736 | 30.4 | 9 | 14 | 3 | 1.119 | 1.054 | 0.992 | 0.913 | 0.927 | 0.943 | 0.879 | 2.40E-02 |
| cds.Camellia_sinensis.comp29463_c0_seq5_m.41542 | PREDICTED: 14 kDa zinc-binding protein isoform X1 [Vitis vinifera] | 23.522 | 9.0624 | 15 | 3 | 3 | 3 | 0.973 | 0.994 | 1.057 | 1.037 | 0.984 | 0.969 | 0.989 | 7.48E-01 |

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| cds.Camellia_sinensis.comp29466_c0_seq1_m.19012 | PREDICTED: lysosomal Pro-X carboxypeptidase [Jatropha curcas] | 50.937 | 51.538 | 16.3 | 7 | 13 | 7 | 1.038 | 1.026 | 1.038 | 0.969 | 0.938 | 0.983 | 0.932 | 7.88E-03 |
| cds.Camellia_sinensis.comp29469_c0_seq1_m.24379 | PREDICTED: D-xylose-proton symporter-like 2 [Jatropha curcas] | 53.585 | 2.0805 | 2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29469_c3_seq1_m.33264 | integral membrane protein [Medicago truncatula] | 31.598 | 8.1923 | 4.8 | 2 | 2 | 2 | 0.906 | 0.954 | 1.01 | 1.051 | 1.09 | 1.02 | 1.101 | 5.74E-02 |
| cds.Camellia_sinensis.comp29470_c0_seq1_m.43811 | PREDICTED: 17.3 kDa class I heat shock protein-like [Nelumbo nucifera] | 18.121 | 7.5093 | 28.3 | 5 | 7 | 3 | 1.459 | 1.406 | 1.484 | 0.488 | 0.5 | 0.509 | 0.344 | 3.76E-07 |
| cds.Camellia_sinensis.comp29472_c0_seq1_m.25608 | PREDICTED: cell division protein FtsY homolog, chloroplastic [Daucus carota subsp. sativus] | 39.021 | 46.233 | 28.3 | 9 | 16 | 9 | 1.019 | 1.053 | 1.025 | 0.966 | 0.979 | 0.956 | 0.937 | 5.92E-03 |

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| cds.Camellia_sinensis.comp29474_c0_seq1_m.21700 | PREDICTED: dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic [Ziziphus jujuba] | 46.268 | 31.135 | 30.1 | 12 | 17 | 12 | 0.987 | 1.003 | 0.972 | 1.003 | 1.013 | 1.039 | 1.031 | 8.99E-02 |
| cds.Camellia_sinensis.comp29477_c0_seq1_m.30956 | thiol-disulfide oxidoreductase DCC [Medicago truncatula] | 25.573 | 7.1022 | 8.9 | 2 | 3 | 2 | 0.944 | 0.935 | 0.963 | 1.095 | 1.068 | 1.042 | 1.128 | 2.00E-03 |
| cds.Camellia_sinensis.comp29485_c0_seq1_m.3324 | PREDICTED: phosphoglucan, water dikinase, chloroplastic isoform X1 [Vitis vinifera] | 132.97 | 225.44 | 32.9 | 33 | 52 | 33 | 1.207 | 1.184 | 1.213 | 0.777 | 0.775 | 0.78 | 0.647 | 2.80E-07 |
| cds.Camellia_sinensis.comp29491_c0_seq1_m.18947 | chloroplast cystathionine beta lyase family protein [Populus trichocarpa] | 50.257 | 25.197 | 11.4 | 5 | 7 | 5 | 1.006 | 1.019 | 1.026 | 1.004 | 0.963 | 0.975 | 0.964 | 5.55E-02 |

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| cds.Camellia_sinensis.comp29492_c0_seq1_m.29823 | PREDICTED: serine racemase isoform X3 [Fragaria vesca subsp. vesca] | 35.804 | 22.85 | 14.4 | 5 | 5 | 5 | 0.99 | 0.997 | 0.946 | 1.04 | 1.012 | 1.047 | 1.057 | 4.70E-02 |
| cds.Camellia_sinensis.comp29499_c1_seq2_m.32075 | survival motor neuron protein [Medicago truncatula] | 26.914 | 2.7838 | 5.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29504_c0_seq1_m.1006 | PREDICTED: brefeldin A-inhibited guanine nucleotide-exchange protein 5 [Vitis vinifera] | 198.79 | 86.639 | 14.9 | 22 | 25 | 22 | 1.021 | 1.038 | 1.022 | 0.962 | 0.964 | 0.971 | 0.94 | 5.22E-04 |
| cds.Camellia_sinensis.comp29507_c0_seq1_m.40448 | PREDICTED: frataxin, mitochondrial [Solanum tuberosum | 22.721 | 4.2534 | 12.7 | 2 | 3 | 2 | 0.919 | 0.99 | 1.08 | 1.101 | 0.975 | 0.961 | 1.016 | 8.11E-01 |

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| cds.Camellia_sinensis.comp29513_c0_seq1_m.28159 | PREDICTED: phosphoribosylglycinamide formyltransferase, chloroplastic [Vitis vinifera] | 33.875 | 55.246 | 9.2 | 2 | 3 | 2 | 0.894 | 1.083 | 0.987 | 1.044 | 0.991 | 1.024 | 1.032 | 5.82E-01 |
| cds.Camellia_sinensis.comp29516_c0_seq1_m.16444 | PREDICTED: leucine aminopeptidase 1-like [Juglans regia] | 60.078 | 323.31 | 53.4 | 23 | 63 | 19 | 0.986 | 0.997 | 0.964 | 1.026 | 1.029 | 1.014 | 1.041 | 2.02E-02 |
| cds.Camellia_sinensis.comp29521_c0_seq1_m.22699 | PREDICTED: COP9 signalosome complex subunit 4 [Ricinus | 45.004 | 32.308 | 21.7 | 8 | 11 | 8 | 0.978 | 0.939 | 1.005 | 1.055 | 1.017 | 0.965 | 1.039 | 3.04E-01 |
| cds.Camellia_sinensis.comp29523_c0_seq1_m.24971 | PREDICTED: serine--glyoxylate aminotransferase [Capsicum annuum] | 44.033 | 290.14 | 47.1 | 15 | 52 | 15 | 1.03 | 0.994 | 1.017 | 0.988 | 0.961 | 0.989 | 0.966 | 7.01E-02 |

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| cds.Camellia_sinensis.comp29527_c0_seq1_m.32348 | PREDICTED: exosome complex component RRP41-like isoform X1 [Nelumbo nucifera] | 27.497 | 2.1137 | 4.7 | 1 | 1 | 1 | 0.971 | 1.026 | 1.086 | 1.014 | 0.975 | 0.938 | 0.949 | 2.62E-01 |
| cds.Camellia_sinensis.comp29532_c0_seq1_m.22729 | PREDICTED: 4-hydroxyphenylpyruvate dioxygenase [Cucumis | 50.965 | 11.36 | 10.2 | 4 | 4 | 4 | 0.979 | 1.005 | 1.014 | 0.99 | 0.992 | 1.022 | 1.002 | 8.98E-01 |
| cds.Camellia_sinensis.comp29535_c0_seq1_m.38228 | PREDICTED: probable plastid-lipid-associated protein 6, chloroplastic [Theobroma cacao] | 29.197 | 159.72 | 40.7 | 10 | 42 | 10 | 0.922 | 0.91 | 0.911 | 1.071 | 1.119 | 1.083 | 1.193 | 2.18E-04 |
| cds.Camellia_sinensis.comp29535_c1_seq2_m.43556 | PREDICTED: nucleoside diphosphate kinase 3-like [Nicotiana tabacum] | 25.9 | 25.72 | 16 | 5 | 11 | 5 | 0.96 | 0.977 | 0.999 | 1.012 | 1.013 | 1.019 | 1.037 | 3.65E-02 |

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| cds.Camellia_sinensis.comp29537_c0_seq1_m.2052 | PREDICTED: DNA-directed RNA polymerase V subunit 1 [Vitis | 102.79 | 6.1456 | 3.6 | 3 | 3 | 3 | 1.066 | 1.337 | 1.053 | 1.011 | 0.759 | 0.748 | 0.729 | 6.26E-02 |
| cds.Camellia_sinensis.comp29537_c0_seq1_m.2053 | PREDICTED: DNA-directed RNA polymerase V subunit 1 isoform X2 [Juglans | 56.261 | 1.3349 | 1.6 | 1 | 1 | 1 | 1.054 | 1.145 | 1.254 | 0.826 | 0.837 | 0.854 | 0.729 | 3.56E-03 |
| cds.Camellia_sinensis.comp29538_c0_seq1_m.25104 | PREDICTED: cysteine synthase [Vitis vinifera] | 34.269 | 187.64 | 50.3 | 13 | 55 | 10 | 0.962 | 0.943 | 0.922 | 1.091 | 1.064 | 1.054 | 1.135 | 1.38E-03 |
| cds.Camellia_sinensis.comp29540_c0_seq1_m.38474 | PREDICTED: adenylate kinase 4 [Jatropha curcas] | 31.07 | 70.014 | 43.7 | 12 | 31 | 8 | 1.008 | 1 | 0.967 | 0.999 | 1.008 | 1.021 | 1.018 | 2.79E-01 |
| cds.Camellia_sinensis.comp29543_c0_seq1_m.4810 | PREDICTED: probable ubiquitin conjugation factor E4 [Nicotiana attenuata] | 117.01 | 25.636 | 7.8 | 8 | 10 | 8 | 0.954 | 0.98 | 0.999 | 1.009 | 1.024 | 1.014 | 1.039 | 5.27E-02 |

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| cds.Camellia_sinensis.comp29545_c0_seq1_m.24783 | PREDICTED: protein ORANGE, chloroplastic [Vitis vinifera] | 28.601 | 2.7335 | 3.5 | 1 | 1 | 1 | 0.986 | 0.99 | 1.111 | 1.007 | 1.028 | 0.889 | 0.947 | 4.13E-01 |
| cds.Camellia_sinensis.comp29546_c0_seq2_m.46414 | PREDICTED: vesicle-associated membrane protein 727-like [Gossypium hirsutum] | 19.514 | 2.0884 | 9.3 | 2 | 2 | 2 | 1.062 | 0.961 | 0.996 | 0.965 | 1.026 | 0.989 | 0.987 | 7.34E-01 |
| cds.Camellia_sinensis.comp29548_c0_seq1_m.22053 | PREDICTED: NPL4-like protein 2 [Ipomoea nil] | 45.936 | 75.533 | 14.4 | 5 | 7 | 5 | 0.998 | 1.036 | 0.957 | 0.988 | 1 | 0.985 | 0.994 | 8.24E-01 |
| cds.Camellia_sinensis.comp29554_c0_seq1_m.19460 | PREDICTED: DEAD-box ATP-dependent RNA helicase 30 [Jatropha curcas] | 16.77 | 9.1415 | 21.5 | 3 | 3 | 3 | 1.024 | 0.965 | 1.013 | 1.022 | 1.059 | 1.002 | 1.027 | 3.35E-01 |

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| cds.Camellia_sinensis.comp29554_c0_seq2_m.22346 | PREDICTED: DEAD-box ATP-dependent RNA helicase 30 [Jatropha curcas] | 46.651 | 49.842 | 34.9 | 13 | 16 | 10 | 0.946 | 1.018 | 1.005 | 1.016 | 1.031 | 1.014 | 1.031 | 2.53E-01 |
| cds.Camellia_sinensis.comp29554_c1_seq1_m.24306 | PREDICTED: protein ELC-like [Nicotiana tomentosiformis] | 47.889 | 6.3077 | 4.2 | 2 | 3 | 2 | 0.881 | 0.966 | 0.995 | 1.129 | 0.989 | 1.076 | 1.124 | 9.39E-02 |
| cds.Camellia_sinensis.comp29555_c0_seq1_m.4214 | PREDICTED: receptor protein kinase TMK1 [Vitis vinifera] | 104.07 | -2 | 1.3 | 1 | 1 | 1 | 1.182 | 0.906 | 0.875 | 1.123 | 1.007 | 0.909 | 1.026 | 7.98E-01 |
| cds.Camellia_sinensis.comp29562_c0_seq1_m.55670 | ubiquitin carboxyl-terminal hydrolase 12-like, partial [Cajanus cajan] | 15.392 | 10.026 | 8.4 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp29569_c1_seq1_m.23928 | PREDICTED: aspartic proteinase nepenthesin-2 [Ziziphus jujuba] | 50.443 | 1.3437 | 2.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29572_c0_seq1_m.23092 | PREDICTED: bifunctional D-cysteine desulfhydrase/1-aminocyclopropane-1-carboxylate deaminase, mitochondrial[Daucus carota subsp. sativus] | 48.828 | 31.608 | 17.6 | 7 | 13 | 7 | 1.016 | 1.004 | 0.967 | 0.996 | 1.02 | 0.963 | 0.997 | 9.08E-01 |
| cds.Camellia_sinensis.comp29574_c0_seq3_m.14046 | PREDICTED: DNA-damage-repair/toleration protein DRT111, chloroplastic [Vitis vinifera] | 21.365 | 4.4728 | 7.5 | 1 | 1 | 1 | 0.934 | 1.01 | 1.141 | 1.021 | 0.895 | 1.012 | 0.949 | 5.22E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29577_c0_seq2_m.34497 | period circadian protein [Arabidopsis thaliana] | 26.274 | 1.5156 | 6.8 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp29581_c0_seq1_m.33141 | PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 3 [Vitis vinifera] | 28.455 | 8.9899 | 15 | 4 | 7 | 4 | 0.983 | 1.021 | 0.995 | 1 | 1.012 | 1.022 | 1.012 | 4.14E-01 |
| cds.Camellia_sinensis.comp29582_c0_seq21_m.33695 | PREDICTED: dehydrogenase/reductase SDR family member 7 isoform X1 [Nelumbo nucifera] | 35.635 | 13.533 | 19 | 5 | 6 | 5 | 0.958 | 1.025 | 0.983 | 1.06 | 1.011 | 1 | 1.035 | 2.60E-01 |
| cds.Camellia_sinensis.comp29586_c0_seq1_m.33130 | PREDICTED: isoeugenol synthase 1-like [Ziziphus jujuba] | 35.935 | 3.5992 | 5.9 | 2 | 2 | 1 | 1.015 | 0.95 | 1.152 | 0.919 | 0.968 | 0.994 | 0.924 | 2.81E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29593_c2_seq1_m.41307 | small GTPase family RAB protein [Medicago truncatula] | 19.166 | 3.1536 | 29.3 | 5 | 7 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp29593_c2_seq2_m.46337 | PREDICTED: ras-related protein RHN1 isoform X2 [Glycine max] | 23.583 | 40.741 | 33.3 | 6 | 9 | 2 | 0.916 | 0.955 | 0.989 | 1.047 | 1.054 | 1.069 | 1.108 | 1.09E-02 |
| cds.Camellia_sinensis.comp29598_c1_seq2_m.44317 | PREDICTED: low molecular weight phosphotyrosine protein phosphatase [Fragaria vesca subsp. vesca] | 18.644 | 21.228 | 34.3 | 5 | 7 | 5 | 1.012 | 1.043 | 0.991 | 1.007 | 0.972 | 0.986 | 0.973 | 2.11E-01 |
| cds.Camellia_sinensis.comp29607_c0_seq1_m.41648 | PREDICTED: dihydroneopterin aldolase-like [Populus euphratica] | 15.261 | 10.109 | 19.4 | 2 | 3 | 2 | 1.037 | 0.912 | 0.986 | 1.011 | 0.968 | 1.095 | 1.047 | 4.23E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29613_c0_seq1_m.38462 | PREDICTED: glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Vitis vinifera] | 35.407 | 79.99 | 47.7 | 15 | 52 | 6 | 1.027 | 0.965 | 0.965 | 1.017 | 1.033 | 0.997 | 1.03 | 2.61E-01 |
| cds.Camellia_sinensis.comp29613_c0_seq2_m.38428 | PREDICTED: glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Vitis vinifera] | 35.561 | 246.38 | 64.4 | 20 | 74 | 11 | 0.945 | 0.946 | 0.946 | 1.061 | 1.084 | 1.063 | 1.131 | 3.10E-03 |
| cds.Camellia_sinensis.comp29615_c0_seq1_m.14327 | PREDICTED: probable pectinesterase/pectinesterase inhibitor 51 [Vitis vinifera] | 64.574 | 19.167 | 5.6 | 3 | 4 | 3 | 0.962 | 1.037 | 0.956 | 1.008 | 1.021 | 1.019 | 1.031 | 3.54E-01 |
| cds.Camellia_sinensis.comp29617_c0_seq1_m.13279 | PREDICTED: L-ascorbate oxidase homolog [Sesamum indicum] | 62.602 | 1.864 | 2.9 | 2 | 2 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29625_c0_seq1_m.18960 | PREDICTED: transmembrane protein 87B-like [Ipomoea nil] | 59.072 | 3.3679 | 5 | 3 | 3 | 3 | 0.99 | 0.974 | 1.023 | 1.033 | 0.976 | 1.016 | 1.013 | 6.01E-01 |
| cds.Camellia_sinensis.comp29628_c0_seq1_m.32748 | PREDICTED: probable ribose-5-phosphate isomerase 3, chloroplastic [Nicotiana tomentosiformis] | 32.504 | 120.75 | 45.8 | 11 | 33 | 11 | 1.03 | 1.007 | 0.991 | 0.974 | 0.987 | 1.002 | 0.979 | 1.94E-01 |
| cds.Camellia_sinensis.comp29631_c0_seq1_m.25884 | PREDICTED: putative glucose-6-phosphate 1-epimerase isoform X2 [Ricinus communis] | 34.535 | 43.535 | 12.8 | 3 | 3 | 3 | 0.971 | 0.968 | 0.995 | 1.029 | 0.967 | 1.085 | 1.05 | 2.36E-01 |
| cds.Camellia_sinensis.comp29636_c0_seq1_m.42298 | PREDICTED: probable glutathione S-transferase [Populus euphratica] | 26.993 | 32.805 | 28.9 | 7 | 11 | 7 | 0.924 | 0.907 | 0.92 | 1.075 | 1.116 | 1.043 | 1.176 | 1.36E-03 |

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| cds.Camellia_sinensis.comp29638_c0_seq3_m.36028 | PREDICTED: ATP synthase subunit delta', mitochondrial [Ipomoea nil] | 23.797 | 6.1642 | 20.9 | 5 | 14 | 0 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp29638_c0_seq4_m.37459 | PREDICTED: ATP synthase subunit delta', mitochondrial [Ipomoea nil] | 23.785 | 22.784 | 20.9 | 5 | 13 | 0 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp29640_c0_seq1_m.16651 | PREDICTED: protein TIC 55, chloroplastic [Theobroma cacao] | 65.698 | 84.884 | 33.5 | 19 | 31 | 12 | 0.988 | 1.011 | 1 | 0.994 | 0.986 | 1.01 | 0.997 | 7.72E-01 |
| cds.Camellia_sinensis.comp29640_c0_seq2_m.26004 | PREDICTED: protein TIC 55, chloroplastic [Vitis vinifera] | 57.381 | 7.5249 | 18.6 | 9 | 15 | 2 | 0.991 | 0.915 | 0.929 | 1.085 | 1.076 | 1.029 | 1.125 | 1.60E-02 |
| cds.Camellia_sinensis.comp29649_c0_seq1_m.4774 | binding protein [Arabidopsis lyrata subsp. lyrata] | 31.408 | 5.1456 | 7 | 2 | 2 | 2 | 1.152 | 1.122 | 1.101 | 0.885 | 0.848 | 0.858 | 0.768 | 1.37E-04 |

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| cds.Camellia_sinensis.comp29649_c0_seq1_m.4775 | TPR domain protein [Medicago truncatula] | 19.568 | 2.0443 | 7.5 | 1 | 1 | 1 | 1.082 | 1.037 | 1.122 | 0.922 | 0.849 | 0.97 | 0.846 | 2.00E-02 |
| cds.Camellia_sinensis.comp29652_c0_seq1_m.21483 | PREDICTED: putative G3BP-like protein isoform X1 [Theobroma cacao] | 52.446 | 40.274 | 16.9 | 7 | 8 | 7 | 1.033 | 1.05 | 1.095 | 0.94 | 0.948 | 0.921 | 0.884 | 3.12E-03 |
| cds.Camellia_sinensis.comp29657_c0_seq1_m.37205 | PREDICTED: eukaryotic translation initiation factor 5A [Eucalyptus grandis] | 17.528 | 43.891 | 43.8 | 7 | 14 | 1 | 1.153 | 1.14 | 0.9 | 0.806 | 0.924 | 1.041 | 0.868 | 2.68E-01 |
| cds.Camellia_sinensis.comp29657_c0_seq2_m.38060 | PREDICTED: eukaryotic translation initiation factor 5A-2-like [Prunus mume] | 17.532 | 21.353 | 31.9 | 5 | 8 | 3 | 1.002 | 1.085 | 1.032 | 0.955 | 0.96 | 0.965 | 0.923 | 7.75E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29657_c0_seq3_m.44557 | eukaryotic translation initiation factor 5A isoform V family protein [Populus trichocarpa] | 14.964 | 14.546 | 19.7 | 3 | 5 | 2 | 1.078 | 1.029 | 1.031 | 0.933 | 0.924 | 0.992 | 0.908 | 2.28E-02 |
| cds.Camellia_sinensis.comp29667_c0_seq1_m.29333 | PREDICTED: DNA-damage-repair/toleration protein DRT100 [Solanum lycopersicum] | 40.354 | 1.8888 | 6 | 2 | 2 | 2 | 0.946 | 0.879 | 0.851 | 1.074 | 1.205 | 1.084 | 1.257 | 9.22E-03 |
| cds.Camellia_sinensis.comp29670_c0_seq1_m.28316 | PREDICTED: uricase-2 isozyme 2 [Juglans regia] | 39.992 | 33.176 | 18.6 | 8 | 10 | 8 | 0.958 | 0.949 | 0.991 | 1.023 | 1.063 | 1.041 | 1.079 | 1.15E-02 |
| cds.Camellia_sinensis.comp29671_c0_seq2_m.15629 | PREDICTED: probable lysine--tRNA ligase, cytoplasmic isoform X2 [Jatropha curcas] | 55.368 | 70.612 | 21.9 | 9 | 11 | 9 | 0.999 | 1.029 | 0.947 | 1.006 | 1.024 | 1.013 | 1.023 | 4.04E-01 |

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| cds.Camellia_sinensis.comp29672_c0_seq1_m.33549 | | 34.169 | 33.488 | 30.8 | 9 | 12 | 8 | 1.161 | 1.081 | 1.123 | 0.852 | 0.855 | 0.886 | 0.771 | 4.19E-04 |
| cds.Camellia_sinensis.comp29672_c0_seq2_m.58600 | | 12.028 | 1.9488 | 17 | 2 | 3 | 1 | 1.154 | 1.063 | 1.111 | 0.875 | 0.898 | 0.868 | 0.794 | 8.76E-04 |
| cds.Camellia_sinensis.comp29679_c0_seq1_m.5887 | PREDICTED: SCY1-like protein 2 [Vitis vinifera] | 81.419 | 4.3922 | 2.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp29680_c0_seq1_m.30435 | PREDICTED: malate dehydrogenase, cytoplasmic-like isoform X1 [Nicotiana tabacum] | 37.838 | 14.158 | 16.7 | 6 | 8 | 5 | 1.057 | 1.035 | 0.992 | 1.017 | 0.954 | 0.968 | 0.953 | 1.48E-01 |
| cds.Camellia_sinensis.comp29682_c0_seq1_m.10171 | PREDICTED: transmembrane 9 superfamily member 11 [Vitis vinifera] | 74.186 | 10.393 | 6.2 | 4 | 6 | 4 | 1.05 | 1.079 | 1.031 | 0.962 | 0.945 | 0.967 | 0.909 | 3.18E-03 |

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| cds.Camellia_sinensis.comp29683_c0_seq1_m.10827 | PREDICTED: protein root UVB sensitive 1, chloroplastic [Vitis vinifera] | 70.893 | 3.5356 | 4.9 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp29686_c0_seq1_m.12915 | PREDICTED: sterol 3-beta-glucosyltransferase UGT80A2-like isoform X1 [Sesamum indicum] | 67.241 | 3.5189 | 4.4 | 2 | 2 | 2 | 0.844 | 1.114 | 1.099 | 0.957 | 1.062 | 0.946 | 0.97 | 8.18E-01 |
| cds.Camellia_sinensis.comp29687_c0_seq1_m.40450 | PREDICTED: probable aldo-keto reductase 2 isoform X2 [Arachis duranensis] | 22.094 | 240.61 | 67.5 | 11 | 30 | 10 | 0.951 | 0.913 | 0.922 | 1.092 | 1.091 | 1.095 | 1.177 | 5.70E-03 |
| cds.Camellia_sinensis.comp29696_c0_seq2_m.22622 | PREDICTED: histidinol-phosphate aminotransferase, chloroplastic-like [Malus domestica] | 47.013 | 5.8874 | 11 | 3 | 4 | 3 | 1.055 | 1.063 | 0.844 | 1.196 | 1.057 | 0.805 | 1.032 | 8.71E-01 |

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| cds.Camellia_sinensis.comp29699_c0_seq1_m.14989 | PREDICTED: bifunctional riboflavin biosynthesis protein RIBA 1, chloroplastic [Vitis vinifera] | 64.091 | 1.3947 | 7.8 | 3 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29699_c0_seq2_m.19920 | PREDICTED: bifunctional riboflavin biosynthesis protein RIBA 1, chloroplastic-like isoform X1 [Populus euphratica] | 61.332 | 31.521 | 13.8 | 6 | 6 | 4 | 0.955 | 0.935 | 0.947 | 1.07 | 1.026 | 1.083 | 1.121 | 2.90E-03 |
| cds.Camellia_sinensis.comp29700_c0_seq2_m.24847 | PREDICTED: histone deacetylase 14 isoform X5 [Juglans regia] | 50.919 | 6.4069 | 6.7 | 3 | 5 | 3 | 1.062 | 1.013 | 0.959 | 0.986 | 0.959 | 1.019 | 0.977 | 5.43E-01 |

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| cds.Camellia_sinensis.comp29703_c0_seq1_m.36163 | PREDICTED: thymidine kinase a isoform X2 [Vitis vinifera] | 31.114 | 1.7459 | 5.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29711_c0_seq1_m.12092 | PREDICTED: uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic [Solanum tuberosum | 75.342 | 62.14 | 18.7 | 11 | 13 | 11 | 0.931 | 0.942 | 1.005 | 1.072 | 1.073 | 1.026 | 1.102 | 2.55E-02 |
| cds.Camellia_sinensis.comp29713_c0_seq1_m.26476 | PREDICTED: probable cinnamyl alcohol dehydrogenase 1 [Ipomoea nil] | 38.949 | 67.689 | 38.4 | 10 | 15 | 10 | 1.012 | 1.005 | 0.982 | 0.988 | 0.998 | 0.995 | 0.994 | 5.68E-01 |
| cds.Camellia_sinensis.comp29714_c0_seq1_m.46746 | 3-oxoacyl-[acyl-carrier-protein] reductase [Populus trichocarpa] | 23.207 | 1.9009 | 7.1 | 2 | 3 | 1 | 1.065 | 1.04 | 0.998 | 0.965 | 0.971 | 0.956 | 0.932 | 2.29E-02 |

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| cds.Camellia_sinensis.comp29714_c0_seq2_m.52145 | PREDICTED: 3-oxoacyl-[acyl-carrier-protein] reductase 4 isoform X2 [Vitis vinifera] | 17.023 | 1.4282 | 9.6 | 2 | 3 | 1 | 0.95 | 1.129 | 0.982 | 0.962 | 1.007 | 0.977 | 0.962 | 5.49E-01 |
| cds.Camellia_sinensis.comp29715_c0_seq1_m.34103 | PREDICTED: inositol-phosphate phosphatase-like [Ziziphus jujuba] | 33.47 | 27.018 | 21.4 | 8 | 11 | 8 | 1.009 | 1.011 | 1.038 | 0.955 | 0.979 | 0.983 | 0.954 | 2.13E-02 |
| cds.Camellia_sinensis.comp29717_c0_seq1_m.55314 | PREDICTED: protein indeterminate-domain 2 isoform X1 [Camelina sativa] | 15.382 | 2.1418 | 6 | 1 | 1 | 1 | 1.058 | 1.049 | 0.916 | 0.88 | 0.955 | 1.131 | 0.981 | 8.10E-01 |
| cds.Camellia_sinensis.comp29718_c0_seq1_m.27494 | PREDICTED: caffeic acid 3-O-methyltransferase isoform X3 [Vitis vinifera] | 42.462 | 39.381 | 28.8 | 9 | 14 | 9 | 1.008 | 0.994 | 1.009 | 1.007 | 1.021 | 0.984 | 1 | 9.85E-01 |

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| cds.Camellia_sinensis.comp29722_c0_seq1_m.57308 | PREDICTED: farnesyl pyrophosphate synthase 1 [Arachis ipaensis] | 13.421 | 10.352 | 19 | 2 | 5 | 1 | 1.075 | 1.062 | 0.836 | 1.064 | 1.005 | 0.963 | 1.02 | 7.85E-01 |
| cds.Camellia_sinensis.comp29727_c0_seq1_m.24095 | SNF1-related kinase regulatory subunit gamma 1 [Medicago truncatula] | 47.636 | 46.988 | 19.6 | 7 | 14 | 7 | 0.934 | 0.952 | 0.996 | 1.075 | 1.09 | 1.023 | 1.106 | 2.04E-02 |
| cds.Camellia_sinensis.comp29728_c0_seq1_m.9789 | PREDICTED: oligopeptide transporter 3 [Nicotiana tabacum] | 83.343 | 45.247 | 1.6 | 1 | 1 | 1 | 1.098 | 1.073 | 1.073 | 0.906 | 0.899 | 0.93 | 0.843 | 1.82E-04 |
| cds.Camellia_sinensis.comp29739_c0_seq2_m.39439 | ATP synthase G subunit family protein [Medicago truncatula] | 14.202 | 2.2604 | 27 | 4 | 5 | 2 | 1.064 | 0.992 | 0.972 | 1.004 | 0.924 | 1.042 | 0.981 | 6.81E-01 |

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| cds.Camellia_sinensis.comp29739_c0_seq39_m.40040 | mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata] | 14.126 | 22.495 | 41.8 | 6 | 10 | 3 | 0.952 | 1.02 | 1.007 | 0.996 | 1.04 | 0.992 | 1.016 | 5.60E-01 |
| cds.Camellia_sinensis.comp29741_c0_seq1_m.17121 | PREDICTED: carbamoyl-phosphate synthase small chain, chloroplastic isoform X2 [Daucus carota subsp. sativus] | 46.573 | 35.812 | 12.4 | 4 | 7 | 4 | 1.015 | 1.043 | 0.997 | 0.98 | 0.994 | 1.014 | 0.978 | 2.50E-01 |
| cds.Camellia_sinensis.comp29742_c0_seq1_m.33840 | PREDICTED: kynurenine formamidase isoform X1 [Solanum tuberosum | 32.454 | 94.718 | 32.2 | 10 | 29 | 10 | 0.897 | 0.92 | 0.935 | 1.104 | 1.073 | 1.078 | 1.183 | 3.59E-04 |
| cds.Camellia_sinensis.comp29756_c0_seq1_m.19956 | calreticulin family protein [Populus trichocarpa] | 47.598 | 62.757 | 41.5 | 15 | 26 | 15 | 0.999 | 1.028 | 0.991 | 0.976 | 0.981 | 1.008 | 0.982 | 3.03E-01 |

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| cds.Camellia_sinensis.comp29771_c0_seq1_m.29964 | PREDICTED: probable 6-phosphogluconolactonase 4, chloroplastic [Nicotiana attenuata] | 40.03 | 28.471 | 23.1 | 9 | 17 | 7 | 0.985 | 1 | 0.973 | 1.086 | 1.027 | 1.038 | 1.065 | 2.89E-02 |
| cds.Camellia_sinensis.comp29771_c0_seq2_m.30189 | PREDICTED: probable 6-phosphogluconolactonase 4, chloroplastic [Nicotiana attenuata] | 28.055 | 7.5369 | 19.8 | 5 | 11 | 3 | 0.921 | 0.908 | 0.825 | 1.089 | 1.143 | 1.11 | 1.259 | 3.44E-03 |
| cds.Camellia_sinensis.comp29773_c0_seq1_m.1135 | PREDICTED: protein NETWORKED 1D [Vitis vinifera] | 141.52 | 3.1113 | 0.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29774_c0_seq2_m.36934 | ribulose-phosphate 3-epimerase, chloroplastic [Solanum lycopersicum] | 30.733 | 119.56 | 26.1 | 5 | 20 | 5 | 1.052 | 1.035 | 1.014 | 0.955 | 0.97 | 0.943 | 0.925 | 4.34E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29780_c0_seq1_m.42303 | Thioredoxin family protein [Arabidopsis thaliana] | 31.601 | 21.099 | 17.1 | 3 | 5 | 3 | 1.043 | 0.965 | 0.937 | 1.091 | 0.926 | 1 | 1.024 | 7.09E-01 |
| cds.Camellia_sinensis.comp29787_c0_seq2_m.12219 | PREDICTED: probable polyol transporter 6 [Eucalyptus grandis] | 54.799 | 12.065 | 5.9 | 3 | 6 | 3 | 0.921 | 0.922 | 0.893 | 1.137 | 1.048 | 1.13 | 1.212 | 2.46E-03 |
| cds.Camellia_sinensis.comp29789_c0_seq1_m.6782 | PREDICTED: scarecrow-like protein 14 [Nicotiana tomentosiformis] | 86.597 | 24.436 | 9.7 | 7 | 9 | 7 | 1.003 | 1.058 | 1.084 | 1.066 | 0.9 | 0.918 | 0.917 | 2.01E-01 |
| cds.Camellia_sinensis.comp29794_c0_seq1_m.35453 | PREDICTED: peroxiredoxin-2F, mitochondrial [Daucus carota subsp. sativus] | 14.118 | 20.617 | 31.5 | 3 | 9 | 3 | 1.005 | 0.975 | 0.97 | 0.979 | 1.038 | 1.009 | 1.026 | 2.79E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29804_c0_seq1_m.27521 | PREDICTED: dnaJ homolog subfamily C member 17 [Nicotiana tomentosiformis] | 32.649 | 6.2867 | 15.1 | 5 | 5 | 5 | 1.093 | 0.981 | 1.043 | 0.925 | 0.988 | 0.947 | 0.918 | 8.08E-02 |
| cds.Camellia_sinensis.comp29810_c0_seq1_m.32455 | PREDICTED: dnaJ homolog subfamily B member 13-like [Nelumbo nucifera] | 35.917 | 1.4394 | 3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp29812_c0_seq1_m.18555 | PREDICTED: 4-coumarate--CoA ligase 2-like [Jatropha curcas] | 60.204 | 4.0311 | 7.8 | 5 | 5 | 2 | 1.142 | 1.254 | 1.239 | 0.822 | 0.723 | 0.767 | 0.636 | 6.62E-04 |
| cds.Camellia_sinensis.comp29815_c0_seq1_m.38712 | PREDICTED: fasciclin-like arabinogalactan protein 7 [Vitis vinifera] | 27.979 | 1.3848 | 3.4 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29820_c0_seq1_m.12786 | PREDICTED: pentatricopeptide repeat-containing protein At1g10270 [Vitis vinifera] | 49.45 | 1.1883 | 3.9 | 2 | 2 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp29828_c0_seq1_m.14841 | PREDICTED: ATP-dependent DNA helicase 2 subunit KU70 [Populus euphratica] | 71.173 | 2.9452 | 3.2 | 2 | 2 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp29836_c0_seq1_m.28714 | PREDICTED: glyoxylate/succinic semialdehyde reductase 2, chloroplastic isoform X2 [Vitis vinifera] | 21.748 | 39.622 | 19 | 3 | 4 | 3 | 1.066 | 1.042 | 1.054 | 0.973 | 0.933 | 1.05 | 0.935 | 1.23E-01 |
| cds.Camellia_sinensis.comp29844_c0_seq3_m.47883 | PREDICTED: ras-related protein RABD1 [Jatropha curcas] | 18.559 | 12.196 | 38.6 | 6 | 7 | 5 | 0.98 | 0.985 | 0.97 | 1.028 | 1.027 | 1.08 | 1.068 | 1.89E-02 |

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| cds.Camellia_sinensis.comp29847_c0_seq1_m.38197 | PREDICTED: cyclic phosphodiesterase-like [Ziziphus jujuba] | 30.663 | 14.943 | 13 | 3 | 4 | 3 | 0.948 | 0.971 | 0.992 | 1.065 | 1.059 | 0.991 | 1.07 | 6.43E-02 |
| cds.Camellia_sinensis.comp29851_c0_seq1_m.42357 | PREDICTED: protochlorophyllide reductase, chloroplastic-like [Malus domestica] | 25.76 | 17.318 | 25.5 | 5 | 10 | 4 | 0.993 | 0.95 | 0.972 | 1.051 | 1.068 | 1.021 | 1.077 | 1.55E-02 |
| cds.Camellia_sinensis.comp29854_c0_seq1_m.26534 | PREDICTED: mitogen-activated protein kinase 3 [Eucalyptus grandis] | 42.755 | 5.427 | 5.1 | 2 | 2 | 2 | 0.948 | 0.961 | 0.989 | 1.044 | 1.078 | 1.006 | 1.079 | 3.19E-02 |
| cds.Camellia_sinensis.comp29855_c0_seq1_m.35040 | PREDICTED: UMP-CMP kinase isoform X1 [Vitis vinifera] | 29.208 | 2.4452 | 10.2 | 3 | 4 | 2 | 1.036 | 0.927 | 0.978 | 1.005 | 1.029 | 1.034 | 1.043 | 2.64E-01 |
| cds.Camellia_sinensis.comp29859_c0_seq1_m.23082 | PREDICTED: COBW domain-containing protein 1-like [Nicotiana tabacum] | 23.858 | 4.4182 | 6.4 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp29859_c0_seq1_m.23083 | PREDICTED: uncharacterized GTP-binding protein YjiA [Ricinus communis] | 20.676 | 31.415 | 32.8 | 5 | 6 | 5 | 1.118 | 1.151 | 1.063 | 0.861 | 0.882 | 0.87 | 0.784 | 5.61E-04 |
| cds.Camellia_sinensis.comp29873_c0_seq13_m.9189 | PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B [Vitis vinifera] | 83.31 | 18.558 | 12 | 10 | 14 | 10 | 0.954 | 0.966 | 0.989 | 0.991 | 1.009 | 1.063 | 1.053 | 9.50E-02 |
| cds.Camellia_sinensis.comp29874_c0_seq1_m.17960 | AP-2 complex subunit mu [Morus notabilis] | 49.362 | 12.564 | 14.2 | 6 | 8 | 6 | 0.979 | 1.007 | 0.991 | 1.008 | 1.007 | 1.012 | 1.017 | 1.14E-01 |
| cds.Camellia_sinensis.comp29888_c0_seq2_m.28666 | PREDICTED: anthocyanidin reductase ((2S)-flavan-3-ol-forming)-like isoform X2 [Vitis vinifera] | 38.354 | 62.24 | 25.1 | 10 | 15 | 10 | 0.984 | 0.97 | 0.967 | 0.999 | 1.048 | 1.032 | 1.054 | 2.54E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29891_c0_seq1_m.28084 | PREDICTED: lanC-like protein GCR2 [Vitis vinifera] | 46.079 | 19.22 | 14.3 | 6 | 8 | 6 | 0.987 | 1.014 | 0.949 | 0.979 | 1.014 | 1.03 | 1.025 | 3.71E-01 |
| cds.Camellia_sinensis.comp29898_c0_seq1_m.36003 | PREDICTED: tropinone reductase homolog [Sesamum indicum] | 28.72 | 29.677 | 21.3 | 6 | 14 | 4 | 0.958 | 1.031 | 1.041 | 0.998 | 1.024 | 0.962 | 0.985 | 6.64E-01 |
| cds.Camellia_sinensis.comp29901_c0_seq1_m.36720 | PREDICTED: 101 kDa malaria antigen [Phoenix dactylifera] | 19.319 | 34.271 | 31.2 | 6 | 13 | 6 | 1.015 | 0.997 | 0.979 | 0.99 | 0.99 | 1.008 | 0.999 | 9.42E-01 |
| cds.Camellia_sinensis.comp29903_c0_seq1_m.17024 | PREDICTED: 6-phosphogluconate dehydrogenase, decarboxylating 1, chloroplastic [Vitis vinifera] | 54.431 | 26.46 | 29.2 | 12 | 20 | 4 | 0.983 | 0.958 | 0.96 | 1.042 | 1.006 | 1.056 | 1.07 | 1.55E-02 |

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| cds.Camellia_sinensis.comp29903_c0_seq2_m.17109 | PREDICTED: 6-phosphogluconate dehydrogenase, decarboxylating 1, chloroplastic [Vitis vinifera] | 54.139 | 120.3 | 37.3 | 16 | 25 | 8 | 0.949 | 0.956 | 0.994 | 1.103 | 1.071 | 1.015 | 1.1 | 2.83E-02 |
| cds.Camellia_sinensis.comp29905_c0_seq1_m.16721 | PREDICTED: probable zinc metallopeptidase EGY3, chloroplastic isoform X1 [Juglans regia] | 67.992 | 28.865 | 11.9 | 8 | 15 | 8 | 1.007 | 0.977 | 1.025 | 0.991 | 0.987 | 1.027 | 0.999 | 9.49E-01 |
| cds.Camellia_sinensis.comp29910_c0_seq1_m.4399 | PREDICTED: probable prolyl 4-hydroxylase 10 [Gossypium raimondii] | 32.219 | 2.5556 | 9.3 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp29915_c0_seq3_m.16355 | PREDICTED: exportin-7 isoform X1 [Nelumbo nucifera] | 62.303 | 1.5927 | 3.7 | 2 | 2 | 2 | 1.019 | 1.074 | 0.928 | 0.971 | 0.995 | 1.015 | 0.987 | 8.06E-01 |

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| cds.Camellia_sinensis.comp29917_c0_seq1_m.18255 | PREDICTED: 4-coumarate--CoA ligase 1 [Nicotiana attenuata] | 58.683 | 20.605 | 9.8 | 5 | 5 | 3 | 1.067 | 1.257 | 1.129 | 0.902 | 0.798 | 0.824 | 0.731 | 6.66E-03 |
| cds.Camellia_sinensis.comp29920_c0_seq1_m.35534 | PREDICTED: uric acid degradation bifunctional protein TTL isoform X1 [Vitis vinifera] | 36.406 | 11.004 | 17.1 | 4 | 5 | 4 | 1.036 | 0.956 | 1.024 | 1.019 | 1.078 | 0.997 | 1.026 | 4.96E-01 |
| cds.Camellia_sinensis.comp29933_c0_seq2_m.34592 | haloacid dehalogenase-like hydrolase family protein [Populus trichocarpa] | 27.33 | 34.643 | 21.8 | 5 | 7 | 5 | 1.12 | 1.088 | 1.097 | 0.883 | 0.875 | 0.859 | 0.792 | 3.95E-05 |
| cds.Camellia_sinensis.comp29934_c0_seq1_m.38024 | alpha/beta hydrolase family protein [Medicago truncatula] | 21.958 | 3.1567 | 6.8 | 1 | 1 | 1 | 1.207 | 0.954 | 1.052 | 0.922 | 0.916 | 0.922 | 0.859 | 1.64E-01 |

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| cds.Camellia_sinensis.comp29934_c1_seq1_m.31287 | PREDICTED: protein CONTINUOUS VASCULAR RING 1 [Vitis vinifera] | 33.118 | 1.744 | 3.3 | 1 | 1 | 1 | | | | | | | | | |
| cds.Camellia_sinensis.comp29935_c0_seq1_m.33952 | PREDICTED: PRA1 family protein A1-like [Populus euphratica] | 30.2 | 2.6212 | 6.5 | 1 | 1 | 1 | | | | | | | | | |
| cds.Camellia_sinensis.comp29937_c0_seq7_m.13219 | PREDICTED: prolycopene isomerase, chloroplastic [Prunus mume] | 33.43 | 3.4696 | 6.3 | 2 | 3 | 2 | 1.016 | 1.012 | 0.962 | 0.941 | 1.039 | 1.033 | 1.008 | 8.59E-01 |
| cds.Camellia_sinensis.comp29939_c0_seq2_m.19375 | PREDICTED: UBP1-associated protein 2C [Nelumbo nucifera] | 40.514 | 19.16 | 12.9 | 5 | 9 | 4 | 0.941 | 0.99 | 0.972 | 1.025 | 1.044 | 0.989 | 1.053 | 7.51E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp29941_c0_seq2_m.29977 | PREDICTED: transcription initiation factor IIB-2 [Daucus carota subsp. sativus] | 34.279 | 27.15 | 9 | 3 | 3 | 3 | 0.834 | 1.003 | 0.986 | 1.099 | 1.044 | 1.093 | 1.146 | 8.41E-02 |
| cds.Camellia_sinensis.comp29944_c0_seq2_m.24140 | Protease HtpX-2-like protein [Morus notabilis] | 27.982 | 13.874 | 15 | 5 | 5 | 5 | 0.934 | 0.939 | 1.011 | 1.065 | 1.046 | 1.017 | 1.085 | 4.74E-02 |
| cds.Camellia_sinensis.comp29947_c0_seq2_m.16040 | PREDICTED: glutamate decarboxylase 1 [Vitis vinifera] | 55.542 | 50.339 | 21.5 | 10 | 20 | 9 | 0.889 | 0.956 | 0.926 | 1.116 | 1.066 | 1.075 | 1.175 | 3.08E-03 |
| cds.Camellia_sinensis.comp29947_c0_seq3_m.35602 | transmembrane protein, putative [Medicago truncatula] | 29.512 | 44.383 | 14.6 | 4 | 4 | 4 | 1.085 | 1.007 | 1.125 | 0.949 | 0.915 | 0.894 | 0.857 | 1.43E-02 |
| cds.Camellia_sinensis.comp29949_c0_seq1_m.28537 | 2-oxoacid dehydrogenases acyltransferase family protein [Arabidopsis thaliana] | 32.796 | 26.088 | 25.2 | 6 | 8 | 5 | 1.066 | 0.939 | 1 | 1.005 | 0.998 | 0.989 | 0.996 | 9.42E-01 |

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| cds.Camellia_sinensis.comp29954_c0_seq2_m.42248 | PREDICTED: 60S ribosomal protein L23-like [Nicotiana tabacum] | 15.061 | 23.705 | 39.3 | 5 | 9 | 5 | 1.179 | 1.179 | 1.152 | 0.831 | 0.825 | 0.813 | 0.703 | 1.99E-06 |
| cds.Camellia_sinensis.comp29955_c0_seq1_m.35485 | PREDICTED: MATH domain and coiled-coil domain-containing protein At2g42460 [Sesamum | 36.878 | 6.313 | 13.2 | 4 | 6 | 4 | 0.93 | 0.967 | 0.917 | 1.142 | 0.981 | 1.056 | 1.13 | 6.15E-02 |
| cds.Camellia_sinensis.comp29957_c0_seq1_m.10883 | sodium/calcium exchanger family protein / calcium-binding EF hand family protein [Arabidopsis thaliana] | 56.8 | 1.5248 | 1.8 | 1 | 1 | 1 | 1.134 | 1.03 | 1.015 | 0.974 | 0.997 | 0.836 | 0.883 | 1.25E-01 |

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| cds.Camellia_sinensis.comp29958_c0_seq2_m.31744 | PREDICTED: cell division protein FtsZ homolog 2-1, chloroplastic [Vitis vinifera] | 34.357 | 85.035 | 26.5 | 6 | 10 | 5 | 1.061 | 1.121 | 1.04 | 0.938 | 0.905 | 0.932 | 0.861 | 3.98E-03 |
| cds.Camellia_sinensis.comp29970_c1_seq5_m.23803 | PREDICTED: heterogeneous nuclear ribonucleoprotein 1 [Vitis vinifera] | 42.742 | 48.218 | 11.2 | 4 | 7 | 4 | 0.922 | 1.008 | 0.931 | 1.032 | 1.075 | 1.036 | 1.099 | 3.83E-02 |
| cds.Camellia_sinensis.comp29972_c0_seq2_m.28176 | PREDICTED: tobamovirus multiplication protein 1 [Prunus mume] | 20.692 | 1.7538 | 3.9 | 1 | 1 | 1 | 0.972 | 0.929 | 0.979 | 1.021 | 1.066 | 1.056 | 1.091 | 1.41E-02 |
| cds.Camellia_sinensis.comp29976_c1_seq26_m.21205 | PREDICTED: protein EARLY-RESPONSIVE TO DEHYDRATION 7, chloroplastic [Vitis vinifera] | 48.502 | 73.778 | 30.1 | 12 | 22 | 12 | 0.967 | 0.961 | 0.983 | 1.029 | 1.041 | 1.049 | 1.071 | 1.40E-03 |

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| cds.Camellia_sinensis.comp29978_c0_seq1_m.26173 | PREDICTED: annexin D3 [Ricinus | 39.548 | 8.9225 | 10.7 | 4 | 4 | 4 | 0.968 | 0.907 | 1.057 | 1.072 | 1.011 | 1.008 | 1.054 | 3.26E-01 |
| cds.Camellia_sinensis.comp29983_c0_seq2_m.38552 | PREDICTED: probable prefoldin subunit 3 isoform X2 [Nelumbo nucifera] | 19.069 | 19.511 | 7.1 | 1 | 1 | 1 | 0.795 | 1.029 | 1.073 | 1.145 | 1.015 | 0.989 | 1.087 | 4.37E-01 |
| cds.Camellia_sinensis.comp29990_c0_seq2_m.8649 | ABC transporter family protein [Populus trichocarpa] | 81.758 | 36.259 | 9.4 | 6 | 10 | 6 | 1.064 | 1.048 | 1.007 | 0.963 | 0.951 | 0.927 | 0.911 | 9.40E-03 |
| cds.Camellia_sinensis.comp30008_c0_seq1_m.29105 | PREDICTED: translocase of chloroplast 34, chloroplastic isoform X2 [Vitis vinifera] | 33.364 | 65.989 | 31 | 9 | 15 | 9 | 0.978 | 0.975 | 1.003 | 1.038 | 1.019 | 1 | 1.034 | 7.48E-02 |
| cds.Camellia_sinensis.comp30008_c0_seq2_m.32150 | PREDICTED: ras-related protein Rab7 [Gossypium arboreum] | 23.072 | 13.996 | 53.9 | 9 | 22 | 4 | 0.983 | 0.97 | 0.984 | 1.039 | 1.029 | 0.974 | 1.036 | 1.68E-01 |

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| cds.Camellia_sinensis.comp30011_c0_seq2_m.23817 | PREDICTED: DUF21 domain-containing protein At4g14240 [Vitis vinifera] | 54.604 | 42.688 | 17.9 | 6 | 6 | 5 | 0.968 | 1.055 | 1.067 | 1.053 | 0.903 | 0.964 | 0.945 | 3.47E-01 |
| cds.Camellia_sinensis.comp30012_c1_seq3_m.27799 | PREDICTED: nuclear pore complex protein NUP88 [Vitis vinifera] | 38.651 | 10.564 | 14.3 | 5 | 6 | 5 | 1.012 | 0.987 | 1.03 | 0.985 | 0.968 | 0.998 | 0.974 | 1.62E-01 |
| cds.Camellia_sinensis.comp30013_c0_seq1_m.29161 | domon-like ligand-binding domain-containing protein precursor [Solanum lycopersicum] | 39.598 | 2.7553 | 9.1 | 3 | 3 | 3 | 0.913 | 1.055 | 1.121 | 0.945 | 1.013 | 0.964 | 0.946 | 4.61E-01 |
| cds.Camellia_sinensis.comp30018_c0_seq1_m.25032 | PREDICTED: protochlorophyllide reductase, chloroplastic [Citrus sinensis] | 43.212 | 39.92 | 25.8 | 10 | 15 | 4 | 0.989 | 0.928 | 0.958 | 1.043 | 1.048 | 1.064 | 1.097 | 8.50E-03 |

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| cds.Camellia_sinensis.comp30018_c0_seq2_m.25602 | PREDICTED: protochlorophyllide reductase, chloroplastic [Citrus sinensis] | 43.243 | 3.1027 | 18.3 | 7 | 8 | 1 | 0.799 | 0.901 | 0.872 | 1.163 | 1.188 | 1.141 | 1.358 | 1.24E-03 |
| cds.Camellia_sinensis.comp30019_c0_seq1_m.15873 | PREDICTED: blue-light photoreceptor PHR2 [Nicotiana tomentosiformis] | 49.656 | 2.6415 | 2.6 | 1 | 1 | 1 | 1.473 | 1.266 | 1.338 | 0.627 | 0.559 | 0.615 | 0.442 | 1.38E-04 |
| cds.Camellia_sinensis.comp30020_c0_seq1_m.23866 | PREDICTED: 40S ribosomal protein SA-like [Ipomoea nil] | 32.087 | 106.39 | 41.2 | 11 | 27 | 11 | 0.974 | 0.974 | 0.964 | 1.063 | 1.028 | 1.046 | 1.077 | 1.92E-03 |
| cds.Camellia_sinensis.comp30027_c0_seq6_m.31289 | peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic isoform X4 [Cajanus cajan] | 17.666 | 11.529 | 35.7 | 5 | 6 | 5 | 1.034 | 1.052 | 1.032 | 0.991 | 0.928 | 0.992 | 0.934 | 3.92E-02 |

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| cds.Camellia_sinensis.comp30027_c0_seq8_m.47951 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic [Jatropha curcas] | 21.909 | 1.3105 | 7.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30040_c0_seq1_m.22474 | PREDICTED: pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic [Vitis vinifera] | 48.213 | 10.307 | 8.5 | 4 | 4 | 2 | 1.029 | 1.012 | 1.017 | 0.97 | 0.981 | 0.992 | 0.962 | 9.24E-03 |
| cds.Camellia_sinensis.comp30040_c0_seq2_m.23034 | PREDICTED: pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic [Vitis vinifera] | 48.065 | 9.6164 | 10.5 | 4 | 6 | 2 | 0.976 | 1.007 | 0.838 | 1.032 | 1.025 | 1.051 | 1.102 | 2.23E-01 |

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| cds.Camellia_sinensis.comp30046_c1_seq7_m.26133 | PREDICTED: bifunctional riboflavin kinase/FMN phosphatase [Daucus carota subsp. sativus] | 43.406 | 9.2158 | 10.4 | 4 | 4 | 4 | 1.066 | 0.99 | 0.996 | 0.955 | 0.981 | 0.973 | 0.953 | 1.30E-01 |
| cds.Camellia_sinensis.comp30049_c0_seq1_m.26651 | PREDICTED: methyl-CpG-binding domain-containing protein 13 isoform X4 [Vitis vinifera] | 45.456 | 14.276 | 10.6 | 3 | 3 | 3 | 1.13 | 1.068 | 1.083 | 0.838 | 0.907 | 0.943 | 0.819 | 6.60E-03 |
| cds.Camellia_sinensis.comp30052_c0_seq1_m.27677 | PREDICTED: histidine--tRNA ligase, cytoplasmic [Jatropha curcas] | 51.362 | 10.188 | 16.6 | 7 | 8 | 7 | 0.977 | 1.018 | 1.022 | 1.009 | 0.987 | 1.037 | 1.005 | 8.07E-01 |

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| cds.Camellia_sinensis.comp30053_c0_seq1_m.25085 | PREDICTED: 15-cis-phytoene desaturase, chloroplastic/chromoplastic-like [Populus euphratica] | 52.942 | 3.8256 | 5.4 | 3 | 3 | 3 | 0.949 | 0.961 | 1.062 | 1.009 | 0.982 | 1.055 | 1.025 | 5.71E-01 |
| cds.Camellia_sinensis.comp30057_c0_seq1_m.29301 | 2-dehydro-3-deoxyphosphoheptonate aldolase family protein [Populus trichocarpa] | 43.241 | 36.368 | 32.1 | 13 | 31 | 7 | 1.294 | 1.258 | 1.324 | 0.676 | 0.671 | 0.673 | 0.521 | 5.23E-04 |
| cds.Camellia_sinensis.comp30057_c1_seq2_m.50785 | PREDICTED: phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic-like [Malus domestica] | 19.615 | 40.349 | 26.9 | 4 | 8 | 4 | 1.335 | 1.244 | 1.382 | 0.642 | 0.668 | 0.639 | 0.492 | 3.57E-05 |

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| cds.Camellia_sinensis.comp30063_c0_seq1_m.13090 | PREDICTED: glutamyl-tRNA reductase 1, chloroplastic-like [Nicotiana tomentosiformis] | 59.838 | 21.126 | 12.1 | 6 | 6 | 6 | 0.994 | 1.005 | 1.066 | 0.966 | 0.983 | 0.998 | 0.962 | 1.76E-01 |
| cds.Camellia_sinensis.comp30068_c0_seq11_m.36320 | PREDICTED: 1,4-dihydroxy-2-naphthoyl-CoA synthase, peroxisomal-like isoform X1 [Nicotiana tabacum] | 32.792 | 6.0648 | 9.9 | 3 | 3 | 3 | 0.979 | 0.927 | 1.011 | 1.047 | 1.027 | 1.029 | 1.064 | 7.47E-02 |
| cds.Camellia_sinensis.comp30070_c0_seq1_m.25428 | PREDICTED: acetylornithine deacetylase [Solanum | 48.944 | 114.87 | 20.3 | 7 | 14 | 7 | 0.963 | 0.992 | 1.006 | 1.03 | 1.006 | 1.008 | 1.028 | 1.37E-01 |
| cds.Camellia_sinensis.comp30073_c0_seq2_m.10486 | PREDICTED: DEAD-box ATP-dependent RNA helicase 8 [Nelumbo nucifera] | 56.587 | 19.491 | 17.5 | 7 | 10 | 2 | 0.866 | 1.006 | 0.956 | 1.06 | 1.1 | 1.05 | 1.135 | 4.99E-02 |

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| cds.Camellia_sinensis.comp30074_c0_seq1_m.11760 | PREDICTED: beta-adaptin-like protein A [Nicotiana tabacum] | 63.034 | 3.4447 | 3 | 1 | 1 | 1 | 0.911 | 1.035 | 0.999 | 0.94 | 1.002 | 1.129 | 1.043 | 5.72E-01 |
| cds.Camellia_sinensis.comp30075_c0_seq1_m.24809 | PREDICTED: malate dehydrogenase, chloroplastic [Solanum tuberosum | 43.67 | 153.91 | 36.9 | 14 | 40 | 14 | 1.01 | 1.001 | 1.018 | 1.001 | 0.985 | 0.971 | 0.976 | 7.43E-02 |
| cds.Camellia_sinensis.comp30077_c0_seq1_m.25826 | PREDICTED: rhomboid-like protein 19 [Juglans regia] | 34.729 | 6.1518 | 5.4 | 1 | 1 | 1 | 0.978 | 0.937 | 1.088 | 0.976 | 1.041 | 0.992 | 1.002 | 9.44E-01 |
| cds.Camellia_sinensis.comp30080_c0_seq1_m.19030 | PREDICTED: glutaredoxin domain-containing cysteine-rich protein 1 [Jatropha curcas] | 37.479 | 49.119 | 27 | 8 | 9 | 8 | 1.016 | 1.028 | 1.015 | 0.949 | 1.006 | 0.979 | 0.959 | 7.26E-02 |
| cds.Camellia_sinensis.comp30085_c0_seq1_m.16810 | PREDICTED: omega-6 fatty acid desaturase, chloroplastic [Vitis vinifera] | 33.054 | 3.818 | 3.6 | 1 | 1 | 1 | 0.967 | 0.99 | 1.088 | 0.952 | 0.985 | 1.026 | 0.973 | 5.63E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30087_c0_seq1_m.47948 | PREDICTED: 2S albumin-like [Ricinus communis] | 17.357 | 37.043 | 33.6 | 6 | 10 | 6 | 1.119 | 1.136 | 1.161 | 0.826 | 0.847 | 0.86 | 0.742 | 4.35E-05 |
| cds.Camellia_sinensis.comp30091_c0_seq1_m.32600 | PREDICTED: protein PPLZ12 [Sesamum indicum] | 32.318 | 39.018 | 36.6 | 10 | 16 | 10 | 0.97 | 1.028 | 1.027 | 0.969 | 0.991 | 0.985 | 0.974 | 2.63E-01 |
| cds.Camellia_sinensis.comp30093_c0_seq1_m.28754 | PREDICTED: polygalacturonase inhibitor-like [Sesamum indicum] | 36.854 | 19.237 | 22 | 7 | 15 | 7 | 0.929 | 0.955 | 0.983 | 1.074 | 1.062 | 1.051 | 1.112 | 3.72E-03 |
| cds.Camellia_sinensis.comp30101_c0_seq1_m.30505 | PREDICTED: 60S ribosomal protein L19-1-like [Cucumis melo] | 24.756 | 34.606 | 20.8 | 4 | 8 | 2 | 0.99 | 1.09 | 1.037 | 0.894 | 0.914 | 0.959 | 0.888 | 2.66E-02 |
| cds.Camellia_sinensis.comp30105_c0_seq1_m.26906 | PREDICTED: indole-3-glycerol phosphate synthase, chloroplastic [Vitis vinifera] | 47.555 | 185.03 | 47.6 | 20 | 51 | 20 | 0.989 | 0.985 | 0.978 | 1.015 | 1.013 | 1.017 | 1.032 | 8.59E-04 |

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| cds.Camellia_sinensis.comp30119_c0_seq2_m.13290 | PREDICTED: probable inactive receptor kinase At1g48480 [Jatropha curcas] | 68.142 | 13.523 | 7 | 5 | 6 | 5 | 1.01 | 0.975 | 0.94 | 0.979 | 1.041 | 1.069 | 1.056 | 1.78E-01 |
| cds.Camellia_sinensis.comp30121_c0_seq1_m.23941 | PREDICTED: homoserine kinase-like [Nicotiana tabacum] | 39.752 | 17.585 | 5.5 | 2 | 4 | 2 | 1.002 | 1.032 | 0.984 | 1.03 | 1.008 | 1.011 | 1.01 | 5.39E-01 |
| cds.Camellia_sinensis.comp30123_c0_seq1_m.21466 | PREDICTED: serine--tRNA ligase, mitochondrial [Jatropha curcas] | 58.997 | 79.008 | 21.6 | 10 | 12 | 10 | 0.967 | 0.971 | 0.979 | 1.049 | 1.047 | 1.017 | 1.067 | 3.66E-03 |
| cds.Camellia_sinensis.comp30125_c1_seq1_m.52105 | PREDICTED: mitogen-activated protein kinase homolog NTF6 [Vitis vinifera] | 19.24 | 1.2801 | 6 | 1 | 1 | 1 | 0.976 | 0.982 | 0.947 | 1.078 | 1.04 | 1 | 1.073 | 4.48E-02 |

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| cds.Camellia_sinensis.comp30126_c0_seq1_m.7663 | PREDICTED: exocyst complex component SEC10 [Ricinus communis] | 96.479 | 63.03 | 10.3 | 9 | 10 | 9 | 1.006 | 0.968 | 1.025 | 1.009 | 1 | 1.057 | 1.022 | 4.11E-01 |
| cds.Camellia_sinensis.comp30127_c0_seq1_m.36678 | immunophilin family protein [Populus trichocarpa] | 23.23 | 5.6207 | 5.3 | 1 | 1 | 1 | 1.103 | 1.137 | 1.175 | 0.783 | 0.891 | 0.874 | 0.746 | 2.64E-03 |
| cds.Camellia_sinensis.comp30127_c1_seq1_m.22508 | PREDICTED: angiomotin-like [Jatropha curcas] | 39.859 | 2.1643 | 2.2 | 1 | 1 | 1 | 0.958 | 0.88 | 0.931 | 1.039 | 1.126 | 1.098 | 1.178 | 8.86E-03 |
| cds.Camellia_sinensis.comp30143_c0_seq1_m.34785 | PREDICTED: secoisolariciresinol dehydrogenase [Vitis vinifera] | 35.948 | 3.5757 | 5.7 | 2 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30143_c0_seq2_m.34793 | PREDICTED: secoisolariciresinol dehydrogenase-like [Nicotiana tabacum] | 36.795 | 15.607 | 13 | 4 | 4 | 3 | 0.985 | 0.824 | 0.93 | 1.013 | 1.188 | 1.089 | 1.201 | 5.82E-02 |

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| cds.Camellia_sinensis.comp30146_c0_seq1_m.21634 | PREDICTED: nuclear pore complex protein NUP50A [Theobroma cacao] | 44.255 | 6.2386 | 12.8 | 4 | 4 | 4 | 1.311 | 1.197 | 1.167 | 0.75 | 0.718 | 0.78 | 0.612 | 3.23E-04 |
| cds.Camellia_sinensis.comp30150_c0_seq1_m.14958 | PREDICTED: putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g14440 [Ipomoea | 38.064 | 1.2569 | 2 | 1 | 1 | 1 | 1.035 | 1.045 | 1.031 | 0.994 | 1.005 | 0.891 | 0.929 | 1.91E-01 |
| cds.Camellia_sinensis.comp30158_c0_seq2_m.35978 | PREDICTED: vesicle-associated protein 1-3 isoform X2 [Nicotiana sylvestris] | 26.985 | 4.2751 | 3.7 | 1 | 1 | 1 | 0.993 | 1.012 | 1.036 | 0.88 | 1.059 | 1.021 | 0.973 | 6.32E-01 |
| cds.Camellia_sinensis.comp30162_c0_seq1_m.16949 | PREDICTED: cytochrome P450 89A2-like [Nicotiana attenuata] | 63.252 | 96.112 | 21 | 11 | 17 | 8 | 1.003 | 0.985 | 0.951 | 1.065 | 0.996 | 0.988 | 1.037 | 2.70E-01 |

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| cds.Camellia_sinensis.comp30163_c0_seq4_m.39095 | glycosyltransferase family protein [Populus trichocarpa] | 31.332 | -2 | 3.8 | 1 | 1 | 1 | 0.975 | 0.976 | 1.074 | 1.047 | 0.906 | 1.034 | 0.987 | 8.20E-01 |
| cds.Camellia_sinensis.comp30177_c0_seq3_m.34348 | PREDICTED: ATP-dependent Clp protease ATP-binding subunit CLPT1, chloroplastic-like [Nicotiana tomentosiformis] | 25.666 | 16.62 | 12.9 | 3 | 8 | 2 | 0.932 | 1.023 | 0.944 | 1.128 | 0.979 | 0.956 | 1.057 | 4.21E-01 |
| cds.Camellia_sinensis.comp30186_c1_seq1_m.34935 | PREDICTED: ER membrane protein complex subunit 3 [Vitis vinifera] | 29.572 | 13.38 | 15.1 | 3 | 3 | 3 | 0.956 | 0.88 | 1.062 | 1.074 | 0.997 | 1.025 | 1.068 | 3.07E-01 |
| cds.Camellia_sinensis.comp30190_c0_seq1_m.10899 | PREDICTED: 30S ribosomal protein 2, chloroplastic [Sesamum indicum] | 28.529 | 50.981 | 23.6 | 7 | 16 | 7 | 1.031 | 1.023 | 1.031 | 0.955 | 0.993 | 0.947 | 0.938 | 1.27E-02 |

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| cds.Camellia_sinensis.comp30197_c0_seq1_m.31887 | beta-glucosidase 44-like [Cajanus cajan] | 45.854 | 18.358 | 17.7 | 8 | 9 | 8 | 1.009 | 1.024 | 0.959 | 0.965 | 0.98 | 1.018 | 0.99 | 7.25E-01 |
| cds.Camellia_sinensis.comp30200_c1_seq1_m.43417 | PREDICTED: 60S ribosomal protein L12-like [Daucus carota subsp. sativus] | 20.286 | 51.749 | 44.2 | 8 | 16 | 8 | 1.126 | 1.074 | 1.046 | 0.918 | 0.898 | 0.951 | 0.852 | 4.26E-03 |
| cds.Camellia_sinensis.comp30206_c0_seq1_m.17707 | PREDICTED: UDP-sulfoquinovose synthase, chloroplastic [Vitis vinifera] | 54.099 | 99.483 | 24.5 | 10 | 25 | 10 | 1.011 | 1.001 | 0.994 | 1.009 | 1.007 | 0.983 | 0.998 | 8.19E-01 |
| cds.Camellia_sinensis.comp30210_c0_seq1_m.20748 | PREDICTED: aspartate aminotransferase [Theobroma cacao] | 43.416 | 112.79 | 38.8 | 14 | 29 | 14 | 0.979 | 1.012 | 1.008 | 1.005 | 1.017 | 0.974 | 0.999 | 9.52E-01 |
| cds.Camellia_sinensis.comp30210_c1_seq1_m.22782 | PREDICTED: la protein 1 [Vitis vinifera] | 53.937 | 15.402 | 9.2 | 4 | 4 | 4 | 1.199 | 1.172 | 1.103 | 0.824 | 0.767 | 0.883 | 0.712 | 2.04E-03 |

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| cds.Camellia_sinensis.comp30212_c0_seq1_m.7102 | PREDICTED: heat shock protein 90-6, mitochondrial-like [Nicotiana tabacum] | 90.064 | 113.73 | 24.8 | 16 | 31 | 12 | 1.062 | 1.061 | 1.058 | 0.96 | 0.951 | 0.974 | 0.907 | 1.58E-04 |
| cds.Camellia_sinensis.comp30214_c0_seq2_m.11773 | PREDICTED: acetyl-coenzyme A synthetase, chloroplastic/glyoxysomal isoform X1 [Juglans regia] | 83.117 | 126.23 | 21.4 | 15 | 24 | 15 | 0.965 | 0.966 | 0.974 | 1.028 | 1.041 | 1.036 | 1.069 | 1.42E-04 |
| cds.Camellia_sinensis.comp30217_c0_seq1_m.14326 | PREDICTED: asparagine--tRNA ligase, cytoplasmic 2 [Sesamum indicum] | 70.297 | 25.048 | 13.6 | 10 | 12 | 9 | 0.963 | 0.922 | 1.002 | 1.015 | 1.079 | 0.997 | 1.071 | 1.14E-01 |
| cds.Camellia_sinensis.comp30219_c0_seq1_m.27886 | PREDICTED: rho-N domain-containing protein 1, chloroplastic [Vitis vinifera] | 40.079 | 4.7068 | 5.3 | 2 | 2 | 2 | 1.265 | 1.217 | 1.338 | 0.742 | 0.683 | 0.678 | 0.551 | 1.18E-04 |

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| cds.Camellia_sinensis.comp30223_c0_seq3_m.43652 | PREDICTED: phospholipase D alpha 1 [Daucus carota subsp. sativus] | 30.004 | 16.354 | 27.7 | 6 | 8 | 2 | 0.986 | 0.991 | 0.989 | 0.964 | 1.041 | 1.04 | 1.027 | 4.20E-01 |
| cds.Camellia_sinensis.comp30236_c0_seq1_m.38327 | PREDICTED: aspartokinase 2, chloroplastic isoform X2 [Vitis vinifera] | 35.829 | 18.546 | 13 | 4 | 5 | 2 | 1.006 | 0.946 | 1.003 | 1.075 | 0.99 | 0.997 | 1.036 | 3.47E-01 |
| cds.Camellia_sinensis.comp30238_c0_seq1_m.38070 | PREDICTED: thylakoid lumenal 17.4 kDa protein, chloroplastic isoform X2 [Populus euphratica] | 25.561 | 53.028 | 35.2 | 7 | 33 | 7 | 0.974 | 0.979 | 0.972 | 1.032 | 1.021 | 1.023 | 1.052 | 2.17E-04 |
| cds.Camellia_sinensis.comp30246_c1_seq1_m.24373 | PREDICTED: natterin-1-like [Zea mays] | 51.883 | 1.7697 | 1.5 | 1 | 2 | 1 | 1.062 | 1.013 | 1.073 | 0.934 | 0.982 | 0.929 | 0.904 | 1.55E-02 |
| cds.Camellia_sinensis.comp30254_c0_seq3_m.19705 | PREDICTED: serine carboxypeptidase-like 27 [Vitis vinifera] | 44.262 | 1.5842 | 4.1 | 2 | 2 | 2 | 1.029 | 1.018 | 0.996 | 0.958 | 1.048 | 0.953 | 0.972 | 4.22E-01 |

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| cds.Camellia_sinensis.comp30266_c0_seq1_m.19323 | PREDICTED: MLO-like protein 10 [Theobroma cacao] | 64.39 | 1.6435 | 1.6 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp30269_c0_seq5_m.34252 | peptidoglycan-binding domain-containing family protein [Populus trichocarpa] | 34.21 | 2.4845 | 13.4 | 4 | 5 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp30271_c0_seq4_m.31584 | PREDICTED: PI-PLC X domain-containing protein At5g67130 [Juglans regia] | 44.351 | 2.7778 | 3 | 1 | 1 | 1 | 0.936 | 1.003 | 0.948 | 1.028 | 1.039 | 1.068 | 1.086 | 2.64E-02 |
| cds.Camellia_sinensis.comp30275_c0_seq1_m.22683 | PREDICTED: UDP-glycosyltransferase 87A1-like [Fragaria vesca subsp. vesca] | 54.242 | 18.609 | 13.3 | 6 | 7 | 6 | 1.011 | 0.996 | 1.016 | 1.04 | 0.947 | 0.975 | 0.98 | 4.97E-01 |

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| cds.Camellia_sinensis.comp30285_c0_seq2_m.40271 | PREDICTED: glycine-rich RNA-binding protein 2-like [Sesamum indicum] | 16.248 | 83.979 | 58.5 | 7 | 25 | 0 |
| cds.Camellia_sinensis.comp30285_c0_seq3_m.43101 | PREDICTED: glycine-rich RNA-binding protein GRP1A-like [Tarenaya hassleriana] | 16.183 | 26.228 | 48.2 | 6 | 23 | 0 |
| cds.Camellia_sinensis.comp30285_c0_seq5_m.48679 | PREDICTED: glycine-rich RNA-binding protein 2-like [Sesamum indicum] | 13.511 | 10.157 | 49.6 | 5 | 16 | 0 |

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| cds.Camellia_sinensis.comp30287_c0_seq1_m.20691 | PREDICTED: probable tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial isoform X2 [Populus | 52.535 | 7.6102 | 5.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp30289_c0_seq2_m.47577 | PREDICTED: acyl-coenzyme A thioesterase 13-like [Pyrus x bretschneideri] | 17.231 | 3.9146 | 6.3 | 1 | 1 | 1 | 1.04 | 1.002 | 0.965 | 1.023 | 0.991 | 0.984 | 0.997 | 9.19E-01 |
| cds.Camellia_sinensis.comp30291_c0_seq1_m.11527 | PREDICTED: primary amine oxidase-like [Juglans regia] | 82.737 | 135.73 | 36.9 | 23 | 47 | 23 | 1.122 | 1.097 | 1.104 | 0.881 | 0.887 | 0.87 | 0.794 | 1.62E-05 |
| cds.Camellia_sinensis.comp30298_c0_seq1_m.9588 | ABC transporter E family member 2 [Morus notabilis] | 68.221 | 32.534 | 14.9 | 10 | 12 | 10 | 1.022 | 1.008 | 1.032 | 0.958 | 0.984 | 1.028 | 0.97 | 2.27E-01 |

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| cds.Camellia_sinensis.comp30299_c1_seq1_m.29581 | PREDICTED: vesicle-associated protein 4-2-like [Gossypium hirsutum] | 29.469 | 9.2212 | 11.4 | 2 | 2 | 2 | 1.005 | 0.982 | 1.037 | 1.053 | 0.973 | 0.961 | 0.988 | 7.14E-01 |
| cds.Camellia_sinensis.comp30303_c0_seq1_m.33137 | PREDICTED: ER membrane protein complex subunit 2 [Ziziphus jujuba] | 21.809 | 5.0825 | 7.6 | 1 | 1 | 1 | 0.984 | 0.979 | 0.882 | 0.958 | 1.118 | 1.094 | 1.114 | 1.49E-01 |
| cds.Camellia_sinensis.comp30312_c0_seq1_m.6452 | PREDICTED: non-lysosomal glucosylceramidase-like isoform X2 [Juglans regia] | 109.58 | 78.849 | 14.8 | 11 | 18 | 11 | 0.983 | 0.993 | 0.985 | 0.997 | 1.009 | 1.031 | 1.026 | 7.01E-02 |
| cds.Camellia_sinensis.comp30313_c0_seq1_m.35730 | PREDICTED: mitochondrial import inner membrane translocase subunit TIM22 [Ziziphus jujuba] | 27.225 | 88.401 | 29.7 | 7 | 17 | 7 | 0.977 | 0.938 | 0.961 | 1.064 | 1.045 | 1.011 | 1.085 | 1.30E-02 |

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| cds.Camellia_sinensis.comp30319_c0_seq2_m.36426 | PREDICTED: protein SYM1 [Erythranthe guttata] | 25.36 | 91.413 | 15.5 | 2 | 5 | 2 | 0.963 | 0.982 | 1.047 | 1.065 | 1.05 | 0.993 | 1.039 | 3.12E-01 |
| cds.Camellia_sinensis.comp30320_c0_seq10_m.24022 | PREDICTED: double-stranded RNA-binding protein 4 isoform X3 [Vitis vinifera] | 39.391 | 5.0646 | 9.5 | 4 | 4 | 2 | 0.987 | 1.095 | 1.143 | 0.917 | 0.922 | 0.93 | 0.859 | 7.50E-02 |
| cds.Camellia_sinensis.comp30323_c0_seq2_m.19870 | PREDICTED: malonyl-CoA decarboxylase, mitochondrial [Vitis vinifera] | 55.948 | 2.2638 | 1.6 | 1 | 1 | 1 | 0.93 | 1.048 | 0.974 | 1.168 | 0.928 | 0.979 | 1.042 | 6.58E-01 |
| cds.Camellia_sinensis.comp30327_c1_seq1_m.25283 | PREDICTED: PCI domain-containing protein 2 isoform X1 [Jatropha curcas] | 48.184 | 2.7586 | 6 | 2 | 2 | 2 | 0.902 | 0.946 | 0.957 | 1.051 | 1.103 | 1.074 | 1.151 | 3.56E-03 |
| cds.Camellia_sinensis.comp30328_c0_seq1_m.33208 | | 27.843 | 16.187 | 17.3 | 4 | 5 | 4 | 1.03 | 1.015 | 0.994 | 1.018 | 0.975 | 0.99 | 0.982 | 3.17E-01 |

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| cds.Camellia_sinensis.comp30329_c0_seq1_m.9005 | PREDICTED: peroxisome biogenesis protein 5 [Sesamum indicum] | 85.257 | 4.4744 | 3.7 | 2 | 2 | 2 | 0.829 | 1.089 | 1.008 | 0.99 | 1.017 | 1.095 | 1.06 | 5.01E-01 |
| cds.Camellia_sinensis.comp30330_c0_seq10_m.44090 | PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 10, mitochondrial [Sesamum indicum] | 17.89 | 3.54 | 9.7 | 2 | 2 | 2 | 0.95 | 1.061 | 0.969 | 1.009 | 0.963 | 1.062 | 1.018 | 7.00E-01 |
| cds.Camellia_sinensis.comp30332_c0_seq12_m.10145 | PREDICTED: acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha, chloroplastic-like [Prunus mume] | 82.43 | 36.28 | 8 | 5 | 6 | 4 | 0.986 | 1.129 | 1.093 | 0.898 | 0.95 | 0.929 | 0.866 | 3.14E-02 |

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| cds.Camellia_sinensis.comp30335_c0_seq1_m.49908 | UDP-glycosyltransferase 73C3 [Morus notabilis] | 19.055 | 1.5191 | 4.7 | 1 | 2 | 1 | 1.077 | 1.043 | 1.093 | 0.939 | 0.94 | 0.897 | 0.864 | 2.12E-03 |
| cds.Camellia_sinensis.comp30337_c0_seq37_m.29088 | PREDICTED: LOW QUALITY PROTEIN: mannosyl-oligosaccharide glucosidase GCS1-like [Malus domestica] | 39.557 | 1.4282 | 2.7 | 1 | 1 | 1 | 0.976 | 1.057 | 1.04 | 0.963 | 0.948 | 1.019 | 0.953 | 2.20E-01 |
| cds.Camellia_sinensis.comp30339_c0_seq1_m.10719 | PREDICTED: beta-glucosidase BoGH3B [Solanum pennellii] | 91.302 | 15.231 | 6 | 5 | 7 | 5 | 1.04 | 1.074 | 1.053 | 0.956 | 0.91 | 0.945 | 0.888 | 2.46E-03 |
| cds.Camellia_sinensis.comp30341_c1_seq1_m.22308 | PREDICTED: fasciclin-like arabinogalactan protein 17 [Vitis vinifera] | 49.243 | 4.6548 | 6.9 | 2 | 2 | 2 | 1.028 | 1.108 | 0.952 | 1.057 | 1.023 | 0.839 | 0.945 | 5.20E-01 |

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| cds.Camellia_sinensis.comp30341_c2_seq9_m.44946 | PREDICTED: D-xylose-proton symporter-like 3, chloroplastic isoform X2 [Ipomoea nil] | 17.358 | 20.362 | 28.9 | 4 | 6 | 4 | 0.995 | 0.977 | 0.985 | 0.99 | 1.084 | 1.013 | 1.044 | 2.02E-01 |
| cds.Camellia_sinensis.comp30342_c0_seq12_m.25365 | adenosine/AMP deaminase family protein [Populus trichocarpa] | 41.05 | 6.0549 | 3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30347_c0_seq37_c0_seq3_m.33116 | PREDICTED: phosphoglucan phosphatase LSF2, chloroplastic isoform X1 [Gossypium raimondii] | 31.254 | 6.7294 | 7.7 | 2 | 3 | 2 | 0.981 | 1.095 | 1.117 | 0.891 | 0.981 | 0.929 | 0.877 | 5.68E-02 |

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| cds.Camellia_sinensis.comp30349_c0_seq1_m.32860 | PREDICTED: isopentenyl-diphosphate Delta-isomerase I [Vigna radiata var. radiata] | 37.08 | 66.205 | 34.5 | 11 | 21 | 11 | 0.994 | 0.977 | 0.993 | 1.015 | 1.014 | 0.994 | 1.02 | 8.91E-02 |
| cds.Camellia_sinensis.comp30350_c0_seq1_m.24392 | PREDICTED: eukaryotic translation initiation factor 3 subunit M [Vitis vinifera] | 46.528 | 69.886 | 27.1 | 8 | 14 | 8 | 0.901 | 0.94 | 1.007 | 1.072 | 1.028 | 1.103 | 1.125 | 3.69E-02 |
| cds.Camellia_sinensis.comp30353_c0_seq1_m.34475 | PREDICTED: chloroplast processing peptidase-like isoform X1 [Nicotiana tabacum] | 34.383 | 30.025 | 25.9 | 5 | 7 | 5 | 1.055 | 0.971 | 1.009 | 0.955 | 1.01 | 1.004 | 0.978 | 5.07E-01 |
| cds.Camellia_sinensis.comp30355_c1_seq2_m.33853 | PREDICTED: F-box protein PP2-A15 [Malus domestica] | 33.364 | 1.3189 | 4 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp30356_c0_seq1_m.13185 | PREDICTED: vacuolar-sorting receptor 6 [Vitis vinifera] | 70.812 | 19.802 | 18.6 | 11 | 12 | 11 | 0.915 | 0.967 | 0.935 | 1.065 | 1.065 | 1.105 | 1.148 | 2.38E-03 |
| cds.Camellia_sinensis.comp30357_c0_seq1_m.16491 | PREDICTED: dihydropyrimidinase [Vitis vinifera] | 58.109 | 56.545 | 18.2 | 12 | 15 | 12 | 0.923 | 0.945 | 0.93 | 1.112 | 1.065 | 1.074 | 1.162 | 5.57E-04 |
| cds.Camellia_sinensis.comp30362_c0_seq1_m.16010 | PREDICTED: probable inositol transporter 2 [Nelumbo nucifera] | 65.018 | 15.409 | 6.5 | 3 | 4 | 3 | 1.077 | 0.954 | 0.899 | 1.153 | 0.862 | 1.065 | 1.051 | 6.79E-01 |
| cds.Camellia_sinensis.comp30363_c0_seq1_m.41907 | PREDICTED: ferredoxin-1 [Gossypium hirsutum] | 22.973 | 3.622 | 5.9 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30366_c0_seq1_m.20288 | PREDICTED: uridine 5'-monophosphate synthase-like [Ipomoea nil] | 57.165 | 14.43 | 6.3 | 3 | 3 | 3 | 1.032 | 1.019 | 0.998 | 0.996 | 0.985 | 0.973 | 0.969 | 5.62E-02 |

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| cds.Camellia_sinensis.comp30367_c0_seq1_m.16928 | PREDICTED: histone deacetylase 19 isoform X1 [Eucalyptus grandis] | 52.827 | 3.5092 | 2.6 | 1 | 1 | 1 | 1.04 | 0.988 | 1.184 | 0.939 | 0.986 | 0.86 | 0.867 | 1.03E-01 |
| cds.Camellia_sinensis.comp30373_c0_seq1_m.9012 | PREDICTED: subtilisin-like protease SBT1.7 [Ricinus communis] | 81.232 | 18.578 | 7.5 | 6 | 7 | 6 | 1.169 | 1.214 | 1.187 | 0.738 | 0.76 | 0.79 | 0.641 | 3.95E-05 |
| cds.Camellia_sinensis.comp30374_c0_seq1_m.36757 | PREDICTED: endo-1,3;1,4-beta-D-glucanase [Ricinus communis] | 28.259 | 9.7754 | 12.7 | 3 | 6 | 3 | 0.939 | 0.945 | 0.91 | 1.067 | 1.115 | 1.075 | 1.166 | 1.02E-03 |
| cds.Camellia_sinensis.comp30380_c0_seq1_m.8250 | PREDICTED: CSC1-like protein ERD4 [Jatropha curcas] | 81.653 | 80.882 | 26.7 | 23 | 41 | 23 | 1.007 | 1.018 | 1.035 | 0.973 | 0.992 | 1.005 | 0.971 | 7.25E-02 |
| cds.Camellia_sinensis.comp30381_c0_seq1_m.28307 | PREDICTED: protein trichome birefringence-like 41 [Ipomoea nil] | 42.034 | 1.4934 | 2.2 | 1 | 1 | 1 | 1.154 | 1.115 | 1.229 | 0.828 | 0.804 | 0.826 | 0.703 | 3.01E-04 |

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| cds.Camellia_sinensis.comp30383_c0_seq1_m.25453 | PREDICTED: guanine nucleotide-binding protein alpha-1 subunit [Jatropha curcas] | 44.776 | 4.853 | 4.9 | 2 | 3 | 2 | 0.924 | 1.009 | 0.938 | 1.122 | 0.989 | 1.048 | 1.1 | 1.05E-01 |
| cds.Camellia_sinensis.comp30386_c0_seq1_m.16307 | PREDICTED: external alternative NAD(P)H-ubiquinone oxidoreductase B1, mitochondrial-like [Ipomoea | 67.612 | 30.735 | 19.9 | 12 | 13 | 11 | 1 | 0.961 | 0.963 | 1.045 | 0.996 | 0.991 | 1.037 | 1.65E-01 |
| cds.Camellia_sinensis.comp30390_c0_seq1_m.29285 | PREDICTED: UPF0160 protein [Ziziphus jujuba] | 41.607 | 21.467 | 13.6 | 4 | 6 | 4 | 0.955 | 1.008 | 1.036 | 0.995 | 1.072 | 1.002 | 1.023 | 5.31E-01 |
| cds.Camellia_sinensis.comp30392_c0_seq1_m.33378 | PREDICTED: RNA-binding protein 2-like isoform X2 [Juglans regia] | 29.17 | 1.4747 | 15.2 | 5 | 6 | 2 | 1.017 | 0.967 | 0.984 | 1.005 | 0.999 | 1.038 | 1.025 | 2.63E-01 |

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| cds.Camellia_sinensis.comp30392_c0_seq2_m.44216 | PREDICTED: RNA-binding protein 2-like isoform X2 [Juglans regia] | 25.007 | 17.497 | 32.5 | 7 | 8 | 4 | 1.006 | 0.987 | 0.997 | 1.012 | 0.951 | 1.052 | 1.008 | 8.14E-01 |
| cds.Camellia_sinensis.comp30396_c0_seq1_m.9383 | PREDICTED: probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 7 isoform X3 [Pyrus x bretschneideri] | 64.982 | 12.424 | 10.2 | 4 | 4 | 4 | 0.819 | 1.012 | 0.864 | 1.12 | 1.017 | 1.214 | 1.243 | 5.47E-02 |
| cds.Camellia_sinensis.comp30396_c0_seq1_m.9384 | PREDICTED: probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 7, partial [Jatropha curcas] | 19.457 | 1.5727 | 5.2 | 1 | 1 | 1 | 0.904 | 0.945 | 0.933 | 1.151 | 1.061 | 1.047 | 1.171 | 8.28E-03 |

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| cds.Camellia_sinensis.comp30398_c0_seq1_m.22768 | PREDICTED: aldehyde dehydrogenase family 2 member C4 [Ricinus communis] | 54.268 | 11.236 | 13.2 | 6 | 6 | 5 | 1.003 | 0.973 | 1.021 | 0.954 | 1.025 | 0.984 | 0.989 | 6.67E-01 |
| cds.Camellia_sinensis.comp30402_c0_seq2_m.38034 | PREDICTED: glycine cleavage system H protein 3, mitochondrial [Juglans regia] | 17.511 | 56.766 | 26.7 | 4 | 22 | 4 | 1.024 | 1.004 | 1.034 | 0.987 | 0.964 | 0.991 | 0.961 | 3.07E-02 |
| cds.Camellia_sinensis.comp30402_c0_seq3_m.46558 | PREDICTED: glycine cleavage system H protein 3, mitochondrial [Pyrus x bretschneideri] | 16.447 | 54.235 | 26.6 | 4 | 18 | 4 | 0.965 | 0.971 | 0.988 | 1.03 | 1.019 | 1.057 | 1.062 | 9.62E-03 |
| cds.Camellia_sinensis.comp30405_c0_seq2_m.5927 | PREDICTED: ubiquinone biosynthesis protein COQ9-B, mitochondrial [Vitis | 35.093 | 63.47 | 19.2 | 6 | 7 | 6 | 0.966 | 0.989 | 0.974 | 1.04 | 1.012 | 0.993 | 1.04 | 6.23E-02 |

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| cds.Camellia_sinensis.comp30409_c1_seq1_m.20071 | PREDICTED: 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic-like [Populus euphratica] | 38.711 | 77.336 | 21.6 | 6 | 17 | 1 | 0.986 | 1.015 | 1.046 | 0.989 | 1.016 | 0.972 | 0.977 | 3.40E-01 |
| cds.Camellia_sinensis.comp30409_c1_seq3_m.41209 | PREDICTED: 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic [Theobroma cacao] | 22.705 | 88.828 | 38.4 | 6 | 11 | 3 | 1.017 | 1.011 | 1.053 | 0.949 | 1.006 | 1.006 | 0.961 | 1.61E-01 |
| cds.Camellia_sinensis.comp30411_c1_seq1_m.31103 | PREDICTED: 60S ribosomal protein L5 [Vitis vinifera] | 35.38 | 30.696 | 16.8 | 6 | 12 | 4 | 0.974 | 0.94 | 0.947 | 1.074 | 1.051 | 1.022 | 1.1 | 6.12E-03 |
| cds.Camellia_sinensis.comp30411_c1_seq2_m.34917 | PREDICTED: 60S ribosomal protein L5 [Populus euphratica] | 34.522 | 3.8403 | 14.6 | 4 | 8 | 2 | 0.95 | 0.961 | 0.961 | 1.139 | 1.002 | 1.017 | 1.1 | 1.49E-01 |

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| cds.Camellia_sinensis.comp30412_c0_seq1_m.51782 | PREDICTED: 17.3 kDa class I heat shock protein-like [Nelumbo nucifera] | 11.746 | 3.7243 | 14.9 | 1 | 1 | 1 | 1.052 | 1.083 | 1.118 | 0.874 | 1.036 | 0.825 | 0.841 | 6.53E-02 |
| cds.Camellia_sinensis.comp30417_c0_seq1_m.20260 | PREDICTED: aspartyl protease family protein At5g10770 [Vitis vinifera] | 50.917 | 84.664 | 21.8 | 9 | 24 | 9 | 1.052 | 1.071 | 1.009 | 0.931 | 0.959 | 0.963 | 0.911 | 1.07E-02 |
| cds.Camellia_sinensis.comp30418_c0_seq1_m.10541 | PREDICTED: ABC transporter F family member 1 [Eucalyptus grandis] | 53.778 | 23.342 | 17.4 | 8 | 9 | 8 | 0.914 | 1.022 | 1.027 | 1.028 | 1.009 | 0.988 | 1.021 | 6.09E-01 |
| cds.Camellia_sinensis.comp30419_c0_seq1_m.29507 | PREDICTED: bifunctional monothiol glutaredoxin-S16, chloroplastic [Prunus mume] | 37.07 | 12.515 | 20.2 | 6 | 8 | 6 | 1.005 | 1.019 | 1.058 | 0.958 | 0.974 | 0.959 | 0.938 | 1.72E-02 |

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| cds.Camellia_sinensis.comp30422_c0_seq1_m.48267 | PREDICTED: dynein light chain 1, cytoplasmic [Jatropha | 14.258 | 3.083 | 17.3 | 2 | 2 | 2 | 0.994 | 0.966 | 0.987 | 0.996 | 1.004 | 1.064 | 1.04 | 1.62E-01 |
| cds.Camellia_sinensis.comp30426_c0_seq1_m.40832 | PREDICTED: ras-related protein RABA2a [Prunus mume] | 23.839 | 89.244 | 49.3 | 9 | 18 | 1 | 1.034 | 0.971 | 1.028 | 0.99 | 0.972 | 1.009 | 0.98 | 4.22E-01 |
| cds.Camellia_sinensis.comp30426_c0_seq2_m.45216 | PREDICTED: ras-related protein RABA2a-like [Gossypium arboreum] | 21.7 | 13.265 | 52.8 | 9 | 14 | 2 | 0.868 | 0.956 | 0.987 | 1.017 | 1.079 | 1.128 | 1.147 | 4.81E-02 |
| cds.Camellia_sinensis.comp30427_c0_seq1_m.28594 | uncharacterized LOC102580903 [Solanum tuberosum | 41.216 | 112.52 | 43.6 | 14 | 32 | 14 | 0.985 | 0.956 | 0.989 | 1.014 | 1.045 | 1.01 | 1.047 | 3.79E-02 |
| cds.Camellia_sinensis.comp30428_c0_seq1_m.32708 | PREDICTED: rhodanese-like/PpiC domain-containing protein 12, chloroplastic [Prunus mume] | 25.507 | 28.719 | 31.7 | 6 | 8 | 6 | 1.002 | 1.031 | 1.042 | 1.004 | 0.963 | 1.003 | 0.966 | 1.26E-01 |

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| cds.Camellia_sinensis.comp30429_c1_seq1_m.31899 | PREDICTED: caffeic acid 3-O-methyltransferase [Vitis vinifera] | 38.272 | 65.214 | 43.7 | 13 | 35 | 13 | 1.045 | 1.036 | 1.039 | 0.965 | 0.956 | 0.945 | 0.919 | 2.03E-04 |
| cds.Camellia_sinensis.comp30431_c0_seq1_m.9052 | PREDICTED: DEAD-box ATP-dependent RNA helicase 3, chloroplastic isoform X1 [Nelumbo nucifera] | 81.033 | 54.478 | 25.5 | 15 | 25 | 10 | 1.105 | 1.116 | 1.145 | 0.889 | 0.847 | 0.886 | 0.779 | 1.84E-04 |
| cds.Camellia_sinensis.comp30431_c0_seq2_m.9474 | PREDICTED: DEAD-box ATP-dependent RNA helicase 3, chloroplastic isoform X1 [Nelumbo nucifera] | 80.434 | 3.4553 | 10.4 | 6 | 10 | 1 | 1.116 | 1.002 | 1.105 | 0.986 | 0.903 | 0.875 | 0.858 | 3.62E-02 |
| cds.Camellia_sinensis.comp30434_c0_seq1_m.24447 | 3-oxoacyl-[acyl-carrier-protein] reductase [Morus notabilis] | 34.44 | 40.791 | 14.8 | 4 | 9 | 3 | 0.997 | 0.931 | 1.03 | 1.048 | 1.098 | 1.041 | 1.077 | 9.27E-02 |

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| cds.Camellia_sinensis.comp30436_c0_seq15_m.2985 | Aquaporin PIP2-7 [Morus notabilis] | 31.629 | 36.815 | 12.5 | 3 | 9 | 3 | 1 | 0.96 | 0.954 | 1.003 | 1.016 | 1.065 | 1.058 | 7.34E-02 |
| cds.Camellia_sinensis.comp30436_c0_seq16_m.31026 | PREDICTED: eukaryotic translation initiation factor 3 subunit F [Daucus carota subsp. sativus] | 31.338 | 12.763 | 25.3 | 8 | 14 | 8 | 0.966 | 1.003 | 0.951 | 1.023 | 1.029 | 1.033 | 1.057 | 2.63E-02 |
| cds.Camellia_sinensis.comp30436_c0_seq28_m.56874 | Histone superfamily protein [Arabidopsis thaliana] | 13.537 | 10.603 | 27.5 | 5 | 14 | 3 | 1.189 | 1.173 | 1.1 | 0.883 | 0.792 | 0.779 | 0.709 | 1.70E-03 |
| cds.Camellia_sinensis.comp30436_c0_seq9_m.19783 | PREDICTED: histone H3.2-like [Nicotiana tabacum] | 15.302 | 1.8199 | 16.9 | 3 | 7 | 1 | 1.087 | 1.076 | 1.122 | 0.816 | 0.96 | 0.914 | 0.819 | 1.54E-02 |
| cds.Camellia_sinensis.comp30436_c2_seq1_m.16118 | PREDICTED: proline iminopeptidase isoform X1 [Prunus | 60.755 | 2.663 | 2 | 1 | 1 | 1 | 1.053 | 0.969 | 1.008 | 1.01 | 0.935 | 1.026 | 0.981 | 6.23E-01 |

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| cds.Camellia_sinensis.comp30439_c0_seq1_m.25477 | PREDICTED: mannose-1-phosphate guanylyltransferase 1 [Daucus carota subsp. sativus] | 39.599 | 17.748 | 13.6 | 4 | 6 | 4 | 1 | 1.008 | 1.066 | 0.949 | 1.004 | 0.95 | 0.944 | 1.05E-01 |
| cds.Camellia_sinensis.comp30443_c0_seq1_m.32367 | PREDICTED: proteasome subunit beta type-3-A [Sesamum indicum] | 22.767 | 5.083 | 6.9 | 1 | 2 | 1 | 0.9 | 0.956 | 0.952 | 1.038 | 1.042 | 1.143 | 1.148 | 2.07E-02 |
| cds.Camellia_sinensis.comp30443_c0_seq2_m.35514 | PREDICTED: proteasome subunit beta type-3-A [Sesamum indicum] | 22.81 | 5.7541 | 6.9 | 1 | 1 | 1 | 0.711 | 1.289 | 0.839 | 1.115 | 0.815 | 1.269 | 1.127 | 5.74E-01 |
| cds.Camellia_sinensis.comp30445_c0_seq1_m.27397 | PREDICTED: splicing factor 3B subunit 4 [Nelumbo nucifera] | 40.257 | 47.242 | 13.9 | 4 | 5 | 4 | 0.957 | 1.011 | 1.042 | 0.967 | 1.046 | 1.06 | 1.021 | 6.18E-01 |

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| cds.Camellia_sinensis.comp30448_c0_seq1_m.13595 | PREDICTED: bifunctional purine biosynthesis protein PurH-like isoform X2 [Gossypium arboreum] | 65.947 | 268.92 | 45.2 | 25 | 67 | 25 | 0.982 | 0.997 | 0.975 | 1.007 | 1.023 | 1.035 | 1.038 | 2.33E-02 |
| cds.Camellia_sinensis.comp30451_c0_seq1_m.44919 | PREDICTED: glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Capsicum annuum] | 14.387 | 2.1733 | 26.7 | 4 | 7 | 2 | 1.06 | 1.052 | 1.072 | 1.028 | 0.891 | 0.892 | 0.883 | 1.17E-01 |
| cds.Camellia_sinensis.comp30452_c0_seq1_m.32345 | PREDICTED: methyl-CpG-binding domain-containing protein 11 [Vitis vinifera] | 34.5 | 18.045 | 16.8 | 5 | 10 | 2 | 1.24 | 1.175 | 1.188 | 0.747 | 0.82 | 0.788 | 0.654 | 1.78E-04 |

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| cds.Camellia_sinensis.comp30452_c0_seq2_m.40812 | PREDICTED: methyl-CpG-binding domain-containing protein 11 [Vitis vinifera] | 29.818 | 34.764 | 28.8 | 6 | 8 | 5 | 1.237 | 1.268 | 1.251 | 0.782 | 0.683 | 0.745 | 0.588 | 1.85E-04 |
| cds.Camellia_sinensis.comp30453_c0_seq1_m.32376 | PREDICTED: bifunctional epoxide hydrolase 2-like [Capsicum annuum] | 37.333 | 3.0489 | 5.2 | 1 | 1 | 1 | 1.016 | 1.276 | 0.888 | 1.011 | 0.692 | 1.102 | 0.882 | 4.94E-01 |
| cds.Camellia_sinensis.comp30453_c1_seq1_m.29710 | PREDICTED: probable 2-oxoglutarate-dependent dioxygenase AOP1 [Vitis vinifera] | 22.474 | 10.463 | 18.7 | 4 | 4 | 4 | 1.142 | 1.146 | 1.222 | 0.804 | 0.807 | 0.834 | 0.697 | 1.36E-04 |
| cds.Camellia_sinensis.comp30454_c1_seq1_m.18257 | PREDICTED: dihydrolipoyl dehydrogenase 1, mitochondrial [Ricinus communis] | 53.812 | 201.3 | 55 | 20 | 60 | 20 | 1.045 | 1.002 | 1.02 | 0.979 | 0.979 | 0.975 | 0.956 | 6.81E-02 |

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| cds.Camellia_sinensis.comp30456_c0_seq1_m.758 | PREDICTED: callose synthase 3-like [Sesamum indicum] | 174.78 | 3.4894 | 1.2 | 2 | 2 | 2 | 0.977 | 1.022 | 0.983 | 1.002 | 1.012 | 1.015 | 1.016 | 3.40E-01 |
| cds.Camellia_sinensis.comp30457_c0_seq1_m.29771 | PREDICTED: syntaxin-71-like [Pyrus x bretschneideri] | 29.915 | 48.741 | 39.1 | 9 | 11 | 9 | 0.998 | 1.02 | 1.065 | 0.971 | 0.981 | 0.966 | 0.946 | 4.95E-02 |
| cds.Camellia_sinensis.comp30462_c1_seq2_m.51610 | PREDICTED: protein FATTY ACID EXPORT 1, chloroplastic [Vitis vinifera] | 17.104 | 36.46 | 17.2 | 2 | 2 | 2 | 0.995 | 1.034 | 0.966 | 0.979 | 1.077 | 0.96 | 1.007 | 8.88E-01 |
| cds.Camellia_sinensis.comp30465_c2_seq2_m.32745 | PREDICTED: enolase [Prunus mume] | 41.332 | 323.31 | 70 | 24 | 68 | 18 | 1.022 | 1.011 | 0.997 | 0.966 | 0.973 | 0.989 | 0.966 | 2.66E-02 |
| cds.Camellia_sinensis.comp30466_c0_seq1_m.19041 | PREDICTED: purple acid phosphatase 18 [Prunus mume] | 48.915 | 16.123 | 8.1 | 3 | 5 | 3 | 0.958 | 1.002 | 0.952 | 1.069 | 0.977 | 1.043 | 1.061 | 1.35E-01 |

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| cds.Camellia_sinensis.comp30467_c1_seq1_m.34326 | PREDICTED: homeobox protein BEL1 homolog [Juglans regia] | 44.679 | 2.0357 | 2.3 | 1 | 1 | 1 | 0.998 | 1.06 | 1.036 | 0.963 | 0.962 | 0.983 | 0.94 | 3.10E-02 |
| cds.Camellia_sinensis.comp30467_c2_seq1_m.40185 | PREDICTED: ATP synthase subunit d, mitochondrial-like [Gossypium hirsutum] | 24.9 | 117.83 | 63.8 | 17 | 42 | 15 | 1.049 | 1.01 | 1.039 | 0.974 | 0.98 | 0.966 | 0.943 | 8.18E-03 |
| cds.Camellia_sinensis.comp30468_c0_seq2_m.34663 | chalcone--flavonone isomerase 2 [Vitis vinifera] | 24.735 | 189.7 | 55.2 | 10 | 24 | 10 | 1.205 | 1.153 | 1.183 | 0.791 | 0.814 | 0.811 | 0.682 | 1.83E-05 |
| cds.Camellia_sinensis.comp30469_c0_seq1_m.14434 | PREDICTED: probable mitochondrial-processing peptidase subunit beta, mitochondrial [Vitis vinifera] | 63.829 | 180.92 | 31.8 | 19 | 46 | 17 | 0.995 | 1.037 | 1.007 | 1.003 | 0.986 | 0.984 | 0.978 | 1.86E-01 |
| cds.Camellia_sinensis.comp30471_c0_seq1_m.40186 | 40S ribosomal protein S19-3 [Cajanus cajan] | 16.159 | 88.633 | 65.5 | 12 | 22 | 12 | 0.93 | 0.957 | 0.91 | 1.074 | 1.071 | 1.064 | 1.147 | 7.56E-04 |

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| cds.Camellia_sinensis.comp30472_c0_seq1_m.38586 | PREDICTED: glutathione S-transferase zeta class-like isoform X1 [Sesamum indicum] | 25.363 | 2.3747 | 4.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30472_c3_seq2_m.23353 | PREDICTED: pectin acetylesterase 8 [Vitis vinifera] | 43.665 | 91.807 | 38.3 | 12 | 19 | 12 | 1.154 | 1.166 | 1.154 | 0.829 | 0.845 | 0.813 | 0.716 | 4.41E-06 |
| cds.Camellia_sinensis.comp30478_c0_seq1_m.35357 | PREDICTED: ribonuclease 2 [Populus euphratica] | 32.03 | 7.2942 | 7.3 | 2 | 3 | 1 | 1.044 | 1.007 | 1.012 | 0.962 | 1.019 | 0.956 | 0.959 | 1.43E-01 |
| cds.Camellia_sinensis.comp30478_c0_seq2_m.35405 | PREDICTED: ribonuclease 2 isoform X1 [Daucus carota subsp. sativus] | 29.591 | 2.0584 | 9 | 2 | 3 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp30479_c0_seq3_m.39564 | PREDICTED: translation initiation factor eIF-2B subunit beta-like, partial [Prunus mume] | 22.195 | 3.7682 | 10.6 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30492_c0_seq4_m.27379 | PREDICTED: photosynthetic NDH subunit of lumenal location 3, chloroplastic [Nelumbo nucifera] | 17.619 | 31.666 | 34.9 | 5 | 6 | 5 | 0.97 | 0.976 | 1.001 | 0.972 | 1.046 | 1.096 | 1.057 | 2.11E-01 |
| cds.Camellia_sinensis.comp30506_c0_seq2_m.33369 | PREDICTED: glucose-induced degradation protein 8 homolog isoform X1 [Citrus sinensis] | 27.493 | 17.758 | 23.6 | 4 | 4 | 4 | 1.032 | 1 | 0.988 | 1.004 | 0.989 | 0.991 | 0.988 | 4.40E-01 |

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| cds.Camellia_sinensis.comp30508_c0_seq2_m.12649 | PREDICTED: methylcrotonoyl-CoA carboxylase beta chain, mitochondrial [Jatropha curcas] | 63.401 | 70.189 | 25.3 | 12 | 14 | 12 | 0.987 | 1.021 | 0.953 | 1.021 | 0.997 | 0.999 | 1.019 | 4.21E-01 |
| cds.Camellia_sinensis.comp30509_c0_seq1_m.20039 | peptidase M50B-like protein [Medicago truncatula] | 25.747 | 9.1807 | 5.2 | 1 | 1 | 1 | 1.114 | 0.956 | 0.87 | 1.027 | 1.086 | 0.952 | 1.043 | 6.07E-01 |
| cds.Camellia_sinensis.comp30517_c0_seq1_m.10671 | PREDICTED: zinc finger BED domain-containing protein DAYSLEEPER-like [Vitis vinifera] | 76.909 | 1.7207 | 6.4 | 4 | 6 | 2 | 1.036 | 0.974 | 1.012 | 0.973 | 0.968 | 0.996 | 0.972 | 2.30E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30525_c0_seq1_m.4935 | PREDICTED: probable inactive ATP-dependent zinc metalloprotease FTSHI 1, chloroplastic [Nicotiana attenuata] | 107.86 | 17.409 | 6.8 | 6 | 7 | 6 | 1.05 | 0.998 | 1.041 | 0.972 | 0.954 | 0.936 | 0.927 | 1.63E-02 |
| cds.Camellia_sinensis.comp30526_c0_seq1_m.17626 | PREDICTED: CDK5RAP3-like protein [Theobroma cacao] | 64.311 | 9.7735 | 9.1 | 6 | 7 | 6 | 0.969 | 0.98 | 0.963 | 1.041 | 1.046 | 0.996 | 1.059 | 2.57E-02 |
| cds.Camellia_sinensis.comp30528_c0_seq1_m.29937 | PREDICTED: E3 ubiquitin-protein ligase At1g63170-like [Ipomoea nil] | 37.631 | 4.0865 | 10.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp30532_c0_seq1_m.22428 | PREDICTED: calcium-transporting ATPase 1, chloroplastic [Solanum pennellii] | 47.557 | 4.5251 | 6.3 | 3 | 4 | 3 | 0.928 | 0.925 | 0.969 | 1.038 | 1.086 | 1.084 | 1.137 | 3.66E-03 |

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| cds.Camellia_sinensis.comp30548_c0_seq1_m.6858 | PREDICTED: death-inducer obliterator 1 [Theobroma cacao] | 98.869 | 3.2742 | 1.4 | 1 | 1 | 1 | 0.734 | 1.097 | 0.944 | 0.92 | 1.228 | 1.121 | 1.178 | 3.05E-01 |
| cds.Camellia_sinensis.comp30551_c0_seq1_m.6176 | PREDICTED: protein KAKU4 isoform X4 [Citrus sinensis] | 38.078 | 1.4118 | 3.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30554_c0_seq4_m.29696 | PREDICTED: protein TIC 22, chloroplastic isoform X1 [Vitis vinifera] | 33.394 | 25.864 | 18.9 | 5 | 10 | 5 | 0.933 | 1 | 0.92 | 1.008 | 1.021 | 0.995 | 1.06 | 9.34E-02 |
| cds.Camellia_sinensis.comp30561_c0_seq1_m.15465 | PREDICTED: alanine aminotransferase 2-like [Nicotiana tabacum] | 56.024 | 236.88 | 30.6 | 12 | 26 | 12 | 0.966 | 0.964 | 0.933 | 1.049 | 1.049 | 1.011 | 1.086 | 7.80E-03 |
| cds.Camellia_sinensis.comp30562_c0_seq1_m.16496 | PREDICTED: ultraviolet-B receptor UVR8 isoform X1 [Ziziphus jujuba] | 65.869 | 4.5542 | 3.6 | 2 | 2 | 2 | 0.974 | 0.974 | 1.01 | 1.031 | 0.974 | 1.053 | 1.034 | 2.79E-01 |

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| cds.Camellia_sinensis.comp30571_c0_seq1_m.31708 | PREDICTED: 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1-like isoform X1 [Juglans | 32.258 | 15.685 | 19.6 | 4 | 7 | 4 | 0.939 | 0.963 | 0.979 | 1.056 | 1.039 | 1.076 | 1.101 | 3.70E-03 |
| cds.Camellia_sinensis.comp30573_c0_seq2_m.39452 | PREDICTED: 30S ribosomal protein S10, chloroplastic [Juglans regia] | 21.737 | 2.0996 | 8.5 | 2 | 5 | 2 | 1.019 | 1.101 | 1.025 | 0.901 | 0.975 | 0.979 | 0.908 | 5.78E-02 |
| cds.Camellia_sinensis.comp30577_c0_seq1_m.21840 | PREDICTED: phenylalanine--tRNA ligase, chloroplastic/mitochondrial [Vitis vinifera] | 52.454 | 61.358 | 32 | 12 | 16 | 12 | 1.008 | 0.998 | 0.985 | 0.986 | 1.021 | 1.003 | 1.006 | 6.31E-01 |
| cds.Camellia_sinensis.comp30579_c0_seq4_m.29219 | Nuclear transport factor 2 (NTF2) family protein [Arabidopsis thaliana] | 32.174 | 11.875 | 11.6 | 3 | 4 | 3 | 1.033 | 1.125 | 0.967 | 0.968 | 0.933 | 1.01 | 0.932 | 2.32E-01 |

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| cds.Camellia_sinensis.comp30587_c0_seq1_m.21326 | PREDICTED: aspartic proteinase PCS1-like [Populus euphratica] | 49.902 | 5.6992 | 5.4 | 2 | 4 | 2 | 0.928 | 0.999 | 0.957 | 1.058 | 1.007 | 1.037 | 1.076 | 4.69E-02 |
| cds.Camellia_sinensis.comp30589_c0_seq1_m.21761 | PREDICTED: diacylglycerol kinase 5-like [Nicotiana tabacum] | 54.002 | 1.2213 | 3.1 | 2 | 2 | 2 | 1.079 | 1.129 | 1.099 | 0.867 | 0.915 | 0.888 | 0.807 | 4.63E-04 |
| cds.Camellia_sinensis.comp30593_c0_seq1_m.41199 | PREDICTED: crocetin glucosyltransferase, chloroplastic-like [Juglans regia] | 26.552 | 3.7718 | 11.3 | 3 | 4 | 3 | 0.928 | 0.956 | 0.981 | 1.061 | 1.04 | 1.072 | 1.108 | 5.08E-03 |
| cds.Camellia_sinensis.comp30601_c0_seq1_m.4143 | PREDICTED: zinc protease PQQL-like isoform X3 [Nicotiana tomentosiformis] | 51.213 | 3.0835 | 3.7 | 2 | 2 | 2 | 0.929 | 0.961 | 1.014 | 0.998 | 1.083 | 1.039 | 1.074 | 1.07E-01 |

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| cds.Camellia_sinensis.comp30604_c1_seq3_m.17421 | PREDICTED: polyadenylate-binding protein RBP45-like [Ipomoea | 39.706 | 17.958 | 7.9 | 3 | 8 | 3 | 0.963 | 0.967 | 1.014 | 1.045 | 1.085 | 0.997 | 1.062 | 1.12E-01 |
| cds.Camellia_sinensis.comp30604_c1_seq5_m.19357 | PREDICTED: polyadenylate-binding protein RBP45 [Daucus carota subsp. | 49.307 | 47.177 | 13.4 | 5 | 10 | 5 | 1.009 | 0.971 | 0.969 | 0.996 | 1.01 | 1.083 | 1.047 | 1.89E-01 |
| cds.Camellia_sinensis.comp30614_c0_seq1_m.48786 | | 13.261 | 8.15 | 23.8 | 3 | 3 | 3 | 1.088 | 1.026 | 1.057 | 0.908 | 0.918 | 0.987 | 0.887 | 1.82E-02 |
| cds.Camellia_sinensis.comp30614_c0_seq2_m.53959 | PREDICTED: inactive protein RESTRICTED TEV MOVEMENT 2 [Solanum tuberosum | 12.797 | 5.5342 | 18.8 | 3 | 3 | 3 | 1.025 | 1.142 | 1.068 | 0.893 | 0.925 | 0.901 | 0.84 | 6.50E-03 |

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| cds.Camellia_sinensis.comp30618_c0_seq3_m.37107 | PREDICTED: 5-formyltetrahydrofolate cyclo-ligase, mitochondrial-like [Nicotiana tabacum] | 26.275 | 4.752 | 11.9 | 2 | 3 | 2 | 0.872 | 0.983 | 0.987 | 1.272 | 0.946 | 0.988 | 1.128 | 3.24E-01 |
| cds.Camellia_sinensis.comp30619_c0_seq1_m.21275 | PREDICTED: pentatricopeptide repeat-containing protein At4g35850, mitochondrial-like [Nicotiana tabacum] | 53.506 | 6.6988 | 8 | 4 | 5 | 4 | 0.95 | 0.981 | 1.036 | 1.033 | 1.011 | 1.009 | 1.029 | 3.31E-01 |
| cds.Camellia_sinensis.comp30621_c0_seq1_m.31503 | zinc finger family protein [Populus trichocarpa] | 34.394 | 1.8312 | 2.4 | 1 | 1 | 1 | 1.091 | 1.105 | 1.078 | 0.962 | 0.868 | 0.876 | 0.827 | 4.68E-03 |
| cds.Camellia_sinensis.comp30622_c0_seq1_m.27600 | PREDICTED: phosphoglycerate mutase-like protein 1 isoform X1 [Sesamum indicum] | 31.245 | 27.202 | 33.3 | 7 | 11 | 7 | 1.02 | 1.006 | 0.963 | 0.979 | 0.953 | 1.062 | 1.002 | 9.82E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30625_c0_seq1_m.28951 | PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic [Sesamum indicum] | 38.227 | 22.256 | 16 | 5 | 5 | 5 | 0.938 | 0.905 | 1.009 | 1.1 | 1.037 | 1.047 | 1.116 | 3.97E-02 |
| cds.Camellia_sinensis.comp30629_c0_seq1_m.29610 | Protein phosphatase 1 regulatory subunit pprA [Morus notabilis] | 40.768 | 1.5357 | 2.2 | 1 | 1 | 1 | 0.951 | 0.878 | 0.966 | 1.148 | 1.066 | 1.028 | 1.16 | 2.80E-02 |
| cds.Camellia_sinensis.comp30630_c0_seq1_m.10372 | PREDICTED: nuclear pore complex protein NUP1 isoform X1 [Vitis vinifera] | 83.744 | 4.1297 | 4.4 | 3 | 3 | 3 | 0.997 | 1.023 | 1.003 | 0.978 | 1.023 | 0.984 | 0.987 | 4.71E-01 |
| cds.Camellia_sinensis.comp30631_c0_seq1_m.33662 | PREDICTED: 2-oxoglutarate-dependent dioxygenase DAO [Vitis vinifera] | 33.894 | 2.4382 | 3.9 | 1 | 1 | 1 | 0.88 | 1.056 | 1.003 | 1.102 | 1.011 | 0.979 | 1.052 | 4.64E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30637_c0_seq6_m.11237 | PREDICTED: 65-kDa microtubule-associated protein 3 [Nelumbo nucifera] | 46.281 | 1.3484 | 1.7 | 1 | 1 | 1 | 1.05 | 1.051 | 0.993 | 0.924 | 0.986 | 0.989 | 0.937 | 8.80E-02 |
| cds.Camellia_sinensis.comp30641_c0_seq2_m.27057 | alanine-tRNA ligase [Arabidopsis thaliana] | 29.894 | 43.331 | 19.8 | 6 | 7 | 6 | 1.043 | 1.031 | 1.012 | 0.982 | 0.951 | 0.962 | 0.938 | 7.64E-03 |
| cds.Camellia_sinensis.comp30651_c0_seq1_m.16356 | PREDICTED: tetratricopeptide repeat protein 7A-like [Juglans regia] | 63.721 | 1.8398 | 1.2 | 1 | 4 | 1 | 0.963 | 0.974 | 0.923 | 1.015 | 1.045 | 1.077 | 1.097 | 1.75E-02 |
| cds.Camellia_sinensis.comp30665_c0_seq1_m.37214 | PREDICTED: nifU-like protein 1, chloroplastic [Juglans regia] | 22.681 | 8.9056 | 18.2 | 3 | 3 | 3 | 0.975 | 0.98 | 1.001 | 1.102 | 1.003 | 0.961 | 1.037 | 4.44E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30675_c0_seq1_m.8779 | PREDICTED: 1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic isoform X1 [Vitis vinifera] | 96.568 | 48.838 | 20.9 | 18 | 20 | 18 | 1.139 | 1.137 | 1.156 | 0.85 | 0.833 | 0.833 | 0.733 | 1.71E-06 |
| cds.Camellia_sinensis.comp30678_c0_seq2_m.27253 | PREDICTED: maltose excess protein 1, chloroplastic isoform X1 [Ricinus communis] | 30.645 | 4.1173 | 4.6 | 1 | 1 | 1 | 1.029 | 1.064 | 1.021 | 0.975 | 0.95 | 0.959 | 0.926 | 6.54E-03 |
| cds.Camellia_sinensis.comp30683_c0_seq1_m.31687 | PREDICTED: peroxidase 72-like [Nelumbo nucifera] | 40.265 | 117.69 | 36.5 | 11 | 24 | 11 | 0.95 | 0.936 | 0.952 | 1.068 | 1.054 | 1.064 | 1.123 | 6.15E-05 |
| cds.Camellia_sinensis.comp30689_c0_seq1_m.27969 | nucleotidyltransferase [Medicago truncatula] | 44.514 | 44.555 | 24.8 | 10 | 14 | 10 | 0.953 | 0.977 | 0.998 | 1.062 | 1.043 | 1.032 | 1.071 | 1.18E-02 |
| cds.Camellia_sinensis.comp30697_c0_seq1_m.25600 | PREDICTED: SEC12-like protein 2 [Nelumbo nucifera] | 31.402 | 4.2576 | 7.3 | 2 | 2 | 2 | 1.072 | 0.954 | 1.009 | 0.943 | 0.956 | 1.06 | 0.975 | 6.35E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30699_c1_seq1_m.13420 | PREDICTED: glutamyl-tRNA(Gln) amidotransferase subunit B, chloroplastic/mitochondrial [Theobrom | 60.706 | 60.371 | 24.5 | 13 | 25 | 13 | 1.018 | 1.011 | 1.024 | 0.965 | 0.989 | 0.981 | 0.961 | 8.26E-03 |
| cds.Camellia_sinensis.comp30702_c0_seq1_m.38848 | PREDICTED: DNA repair RAD52-like protein 1, mitochondrial [Vitis vinifera] | 22.419 | 12.705 | 17.5 | 4 | 6 | 4 | 1.03 | 1.02 | 1.041 | 0.977 | 0.958 | 0.95 | 0.933 | 2.48E-03 |
| cds.Camellia_sinensis.comp30722_c0_seq1_m.25310 | PREDICTED: lecithin-cholesterol acyltransferase-like 1 [Juglans regia] | 33.047 | 3.6446 | 6 | 2 | 3 | 2 | 1.025 | 1.035 | 1.014 | 1.005 | 0.972 | 0.953 | 0.953 | 4.40E-02 |
| cds.Camellia_sinensis.comp30722_c0_seq1_m.25311 | PREDICTED: lecithin-cholesterol acyltransferase-like 1 [Juglans regia] | 18.598 | 5.0967 | 11.8 | 2 | 2 | 2 | 1.057 | 1.122 | 1.026 | 0.973 | 0.915 | 0.896 | 0.869 | 1.76E-02 |

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| cds.Camellia_sinensis.comp30729_c0_seq15_m.47517 | PREDICTED: callose synthase 2-like [Camelina sativa] | 13.925 | 5.806 | 9.1 | 1 | 1 | 1 | 1.057 | 0.946 | 0.948 | 1.035 | 0.961 | 1.06 | 1.036 | 4.93E-01 |
| cds.Camellia_sinensis.comp30732_c0_seq1_m.1325 | PREDICTED: auxin transport protein BIG [Vitis vinifera] | 186.72 | 3.7505 | 1.4 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp30736_c0_seq1_m.27581 | PREDICTED: protein transport protein SEC13 homolog B-like [Malus domestica] | 32.894 | 2.8494 | 12 | 3 | 9 | 1 | 0.938 | 0.92 | 0.977 | 1.051 | 1.127 | 1.018 | 1.127 | 2.68E-02 |
| cds.Camellia_sinensis.comp30740_c0_seq1_m.25588 | PREDICTED: grpE protein homolog, mitochondrial isoform X2 [Sesamum | 26.957 | 25.219 | 9.1 | 2 | 3 | 2 | 1.025 | 1.07 | 1.015 | 0.948 | 0.911 | 0.992 | 0.917 | 4.14E-02 |
| cds.Camellia_sinensis.comp30740_c0_seq1_m.25589 | PREDICTED: protein GrpE-like isoform X2 [Cucumis melo] | 17.072 | 34.481 | 36.4 | 7 | 10 | 7 | 1.034 | 1.038 | 1.083 | 0.966 | 0.925 | 0.953 | 0.901 | 6.12E-03 |

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| cds.Camellia_sinensis.comp30742_c0_seq1_m.24774 | PREDICTED: isovaleryl-CoA dehydrogenase, mitochondrial [Ipomoea nil] | 44.591 | 14.053 | 13.2 | 5 | 5 | 5 | 1.01 | 1.055 | 0.99 | 0.955 | 1.002 | 0.992 | 0.965 | 2.14E-01 |
| cds.Camellia_sinensis.comp30748_c0_seq1_m.15876 | PREDICTED: DEAD-box ATP-dependent RNA helicase 47A [Vitis vinifera] | 32.902 | 2.8592 | 4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30770_c0_seq2_m.37962 | PREDICTED: signal peptide peptidase [Ziziphus jujuba] | 30.063 | 6.6714 | 6.7 | 2 | 2 | 2 | 1.005 | 0.902 | 0.941 | 1.146 | 1.03 | 1.004 | 1.117 | 9.94E-02 |
| cds.Camellia_sinensis.comp30776_c0_seq8_m.41618 | PREDICTED: protein RER1B [Theobroma cacao] | 13.437 | 1.2283 | 8.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30783_c0_seq1_m.21832 | PREDICTED: tafazzin isoform X2 [Vitis vinifera] | 42.042 | 2.0388 | 2.4 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30788_c0_seq1_m.9388 | PREDICTED: uncharacterized aarF domain-containing protein kinase At4g31390, chloroplastic [Vitis vinifera] | 77.309 | 22.392 | 17 | 11 | 13 | 11 | 0.947 | 0.987 | 0.966 | 1.019 | 1.044 | 1.051 | 1.074 | 9.38E-03 |
| cds.Camellia_sinensis.comp30792_c0_seq1_m.34107 | PREDICTED: alkane hydroxylase MAH1-like [Nicotiana tabacum] | 31.537 | 3.2288 | 7 | 2 | 2 | 2 | 0.863 | 0.931 | 0.917 | 1.208 | 1.004 | 1.127 | 1.232 | 2.47E-02 |
| cds.Camellia_sinensis.comp30800_c0_seq1_m.32560 | PREDICTED: phytanoyl-CoA dioxygenase [Prunus mume] | 19.952 | 5.5707 | 11.3 | 3 | 3 | 3 | 0.902 | 0.991 | 1.027 | 1.086 | 1.018 | 1.006 | 1.065 | 2.32E-01 |
| cds.Camellia_sinensis.comp30804_c0_seq1_m.38835 | transcription termination factor family protein [Medicago truncatula] | 24.086 | 21.122 | 18.3 | 5 | 5 | 5 | 1.032 | 1.037 | 1.024 | 0.997 | 0.966 | 0.975 | 0.95 | 6.92E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30816_c0_seq1_m.18539 | PREDICTED: probable sodium/metabolite cotransporter BASS3, chloroplastic [Sesamum indicum] | 45.167 | 3.1264 | 3.7 | 1 | 2 | 1 | 0.994 | 1.088 | 0.887 | 0.884 | 1.09 | 1.058 | 1.021 | 8.29E-01 |
| cds.Camellia_sinensis.comp30825_c0_seq1_m.25138 | PREDICTED: protein MULTIPLE CHLOROPLAST DIVISION SITE 1-like isoform X2 [Nicotiana tabacum] | 16.29 | 5.6382 | 6.9 | 1 | 1 | 1 | 0.936 | 1.197 | 0.989 | 0.886 | 0.978 | 1.012 | 0.921 | 4.08E-01 |
| cds.Camellia_sinensis.comp30830_c0_seq3_m.33258 | PREDICTED: calcineurin B-like protein 3 [Daucus carota subsp. sativus] | 26.259 | 10.221 | 17.3 | 5 | 5 | 5 | 0.972 | 0.958 | 0.981 | 1.032 | 1.041 | 1.043 | 1.07 | 8.77E-04 |

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| cds.Camellia_sinensis.comp30833_c0_seq2_m.38525 | PREDICTED: trafficking protein particle complex subunit 3 [Theobroma cacao] | 20.817 | 11.371 | 40.3 | 7 | 8 | 7 | 0.984 | 0.965 | 0.98 | 1.017 | 0.984 | 1.022 | 1.032 | 7.70E-02 |
| cds.Camellia_sinensis.comp30836_c0_seq2_m.13616 | PREDICTED: calcium-dependent protein kinase 2-like [Nelumbo nucifera] | 59.549 | 7.6811 | 12.7 | 5 | 6 | 4 | 0.953 | 0.929 | 0.95 | 1.043 | 1.09 | 1.076 | 1.133 | 1.24E-03 |
| cds.Camellia_sinensis.comp30836_c0_seq3_m.13814 | PREDICTED: calcium-dependent protein kinase 2-like [Nelumbo nucifera] | 59.134 | 40.29 | 21.1 | 10 | 13 | 4 | 0.995 | 0.985 | 0.986 | 1.001 | 1.047 | 1.004 | 1.029 | 1.29E-01 |
| cds.Camellia_sinensis.comp30836_c0_seq8_m.22506 | PREDICTED: calcium-dependent protein kinase 2-like [Nelumbo nucifera] | 55.148 | 23.117 | 18.4 | 9 | 10 | 4 | 0.99 | 0.991 | 1.023 | 1.008 | 0.98 | 1.003 | 0.996 | 7.72E-01 |

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| cds.Camellia_sinensis.comp30836_c1_seq1_m.24886 | PREDICTED: post-GPI attachment to proteins factor 3 [Jatropha curcas] | 39.38 | 24.268 | 8.5 | 2 | 3 | 2 | 0.93 | 1.096 | 0.927 | 0.997 | 1.045 | 1.022 | 1.038 | 5.23E-01 |
| cds.Camellia_sinensis.comp30842_c0_seq1_m.30149 | PREDICTED: peroxidase N1 [Solanum tuberosum | 38.299 | 17.217 | 14.1 | 4 | 4 | 4 | 0.854 | 0.979 | 0.991 | 1.019 | 1.102 | 1.091 | 1.137 | 7.20E-02 |
| cds.Camellia_sinensis.comp30843_c0_seq1_m.19911 | PREDICTED: COP9 signalosome complex subunit 1 [Vitis | 50.277 | 21.537 | 11.8 | 5 | 5 | 5 | 0.918 | 0.971 | 0.973 | 1.051 | 1.065 | 1.045 | 1.104 | 7.40E-03 |
| cds.Camellia_sinensis.comp30846_c0_seq1_m.36865 | PREDICTED: psbP domain-containing protein 7, chloroplastic [Vitis vinifera] | 30.996 | 41.726 | 37.1 | 9 | 11 | 9 | 0.997 | 1.012 | 0.961 | 0.999 | 0.997 | 1.012 | 1.013 | 4.66E-01 |

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| cds.Camellia_sinensis.comp30851_c0_seq2_m.31785 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 3-like isoform X2 [Gossypium arboreum] | 29.536 | 6.4599 | 13.8 | 4 | 4 | 4 | 0.989 | 0.958 | 0.989 | 1.016 | 0.996 | 1.028 | 1.035 | 6.85E-02 |
| cds.Camellia_sinensis.comp30852_c0_seq2_m.34274 | PREDICTED: protein TONNEAU 1a-like [Juglans regia] | 29.734 | 3.5112 | 5.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30857_c0_seq1_m.28428 | PREDICTED: glutamyl-tRNA reductase-binding protein, chloroplastic [Vitis vinifera] | 41.468 | 19.28 | 9.4 | 2 | 2 | 2 | 1.138 | 1.01 | 1.041 | 0.891 | 0.956 | 0.942 | 0.875 | 3.32E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30876_c0_seq1_m.20229 | PREDICTED: protein PLASTID TRANSCRIPTIONALLY ACTIVE 14 isoform X1 [Ziziphus jujuba] | 38.586 | 1.2437 | 2.1 | 1 | 1 | 1 | 1.046 | 0.969 | 1.023 | 0.957 | 0.968 | 1.037 | 0.975 | 4.94E-01 |
| cds.Camellia_sinensis.comp30878_c1_seq5_m.46877 | PREDICTED: probable histone H2B.1 [Juglans regia] | 16.206 | 31.564 | 48 | 8 | 37 | 8 | 1.153 | 1.132 | 1.096 | 0.844 | 0.846 | 0.882 | 0.761 | 1.83E-04 |
| cds.Camellia_sinensis.comp30879_c0_seq1_m.36130 | PREDICTED: probable carboxylesterase 12 [Populus euphratica] | 14.235 | 7.1361 | 19.5 | 2 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp30894_c0_seq1_m.34389 | PREDICTED: HD domain-containing protein 2 [Jatropha curcas] | 28.86 | 9.9453 | 12.9 | 3 | 4 | 3 | 1.103 | 1.058 | 1.004 | 0.964 | 0.959 | 0.941 | 0.905 | 2.44E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30897_c0_seq1_m.21800 | PREDICTED: phosphoinositide phospholipase C 2 [Vitis vinifera] | 52.253 | 1.1818 | 2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30901_c0_seq13_m.23260 | PREDICTED: leucine-rich repeat extensin-like protein 3 [Populus euphratica] | 42.521 | 1.5575 | 2.4 | 1 | 1 | 1 | 1.1 | 1.021 | 1.041 | 0.955 | 0.924 | 0.946 | 0.893 | 1.00E-02 |
| cds.Camellia_sinensis.comp30902_c0_seq1_m.794 | PREDICTED: callose synthase 10 [Nicotiana attenuata] | 218.2 | 12.501 | 4.2 | 7 | 8 | 6 | 0.999 | 1.005 | 1.06 | 0.975 | 0.936 | 1.065 | 0.971 | 5.16E-01 |
| cds.Camellia_sinensis.comp30907_c0_seq1_m.4244 | PREDICTED: NHL repeat-containing protein 2 [Ziziphus jujuba] | 118.82 | 213.3 | 23.4 | 22 | 38 | 22 | 0.978 | 0.99 | 0.989 | 1 | 1.01 | 1 | 1.018 | 2.57E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30914_c0_seq1_m.13785 | PREDICTED: LOW QUALITY PROTEIN: 65-kDa microtubule-associated protein 1-like [Vitis vinifera] | 65.614 | 19.226 | 10.4 | 5 | 5 | 5 | 1.139 | 1.076 | 1.067 | 0.998 | 0.851 | 0.847 | 0.821 | 2.60E-02 |
| cds.Camellia_sinensis.comp30931_c0_seq5_m.14018 | PREDICTED: protoporphyrinogen oxidase, mitochondrial isoform X1 [Vitis | 62.668 | 34.237 | 14.3 | 7 | 10 | 7 | 1.003 | 0.953 | 0.973 | 1.013 | 1.025 | 1.049 | 1.054 | 4.33E-02 |
| cds.Camellia_sinensis.comp30934_c0_seq1_m.39216 | PREDICTED: late embryogenesis abundant protein D-29-like [Nicotiana tabacum] | 27.878 | 46.336 | 23.3 | 6 | 12 | 6 | 0.961 | 0.896 | 0.888 | 1.058 | 1.099 | 1.129 | 1.197 | 4.50E-03 |
| cds.Camellia_sinensis.comp30939_c0_seq1_m.5098 | PREDICTED: vacuolar protein 8 [Theobroma cacao] | 69.57 | 30.843 | 17 | 10 | 12 | 10 | 0.977 | 0.991 | 0.999 | 0.992 | 1.072 | 1.008 | 1.035 | 2.35E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30939_c0_seq1_m.5099 | PREDICTED: vacuolar protein 8 [Theobroma cacao] | 23.045 | 32.641 | 16.7 | 3 | 4 | 3 | 0.996 | 1.004 | 1.053 | 1.032 | 0.965 | 0.958 | 0.968 | 3.26E-01 |
| cds.Camellia_sinensis.comp30941_c0_seq1_m.40634 | PREDICTED: germin-like protein subfamily 1 member 13 [Theobroma cacao] | 24.269 | 89.566 | 33.9 | 6 | 24 | 6 | 1.022 | 0.994 | 0.984 | 0.989 | 1.022 | 1.003 | 1.005 | 7.67E-01 |
| cds.Camellia_sinensis.comp30943_c0_seq1_m.12978 | PREDICTED: conserved oligomeric Golgi complex subunit 8 isoform X1 [Vitis vinifera] | 63.983 | 1.4449 | 1.6 | 1 | 1 | 1 | 1 | 0.993 | 1.025 | 0.961 | 1.064 | 0.965 | 0.991 | 7.80E-01 |
| cds.Camellia_sinensis.comp30946_c0_seq1_m.27209 | PREDICTED: ribokinase-like [Malus domestica] | 40.011 | 77.722 | 34.7 | 11 | 18 | 11 | 0.974 | 1.029 | 1.012 | 1.051 | 0.985 | 1.003 | 1.008 | 7.72E-01 |

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| cds.Camellia_sinensis.comp30953_c0_seq1_m.24684 | Serine/Threonine-kinase STN7, related protein, putative [Medicago truncatula] | 31.109 | 30.704 | 24.1 | 7 | 11 | 7 | 0.956 | 0.985 | 1.021 | 1.022 | 1.031 | 1 | 1.031 | 2.21E-01 |
| cds.Camellia_sinensis.comp30953_c0_seq1_m.24686 | Protein kinase superfamily protein [Arabidopsis thaliana] | 14.099 | 4.4485 | 7.8 | 1 | 4 | 1 | 1.003 | 1.002 | 0.988 | 0.964 | 1.049 | 1.042 | 1.021 | 5.12E-01 |
| cds.Camellia_sinensis.comp30962_c0_seq4_m.19169 | lipase class 3 family protein [Populus trichocarpa] | 51.044 | 1.8008 | 5.3 | 3 | 3 | 3 | 1.014 | 0.942 | 1.023 | 0.961 | 1.041 | 1.028 | 1.017 | 6.61E-01 |
| cds.Camellia_sinensis.comp30974_c0_seq1_m.26333 | PREDICTED: uncharacterized oxidoreductase At1g06690, chloroplastic [Vitis vinifera] | 26.481 | 135.54 | 31.1 | 6 | 12 | 6 | 1.037 | 1.052 | 1.031 | 0.952 | 0.984 | 0.916 | 0.914 | 1.38E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30974_c0_seq1_m.26334 | uncharacterized oxidoreductase At1g06690, chloroplastic [Ananas comosus] | 18.519 | 51.341 | 40.7 | 7 | 11 | 7 | 1.021 | 1.019 | 1.044 | 0.991 | 0.966 | 0.956 | 0.945 | 1.24E-02 |
| cds.Camellia_sinensis.comp30975_c1_seq2_m.19937 | PREDICTED: flavin-dependent oxidoreductase FOX1-like [Nicotiana tomentosiformis] | 62.388 | 28.149 | 17.7 | 9 | 11 | 9 | 1.033 | 1.058 | 1.102 | 0.94 | 0.921 | 0.89 | 0.862 | 3.82E-03 |
| cds.Camellia_sinensis.comp30979_c1_seq1_m.25752 | PREDICTED: GDP-mannose 3,5-epimerase 2 [Juglans regia] | 42.404 | 114.48 | 42.8 | 16 | 32 | 16 | 1.051 | 1.039 | 1.041 | 0.939 | 0.952 | 0.949 | 0.907 | 5.90E-05 |
| cds.Camellia_sinensis.comp30980_c0_seq20_c0_seq2_m.28639 | PREDICTED: 50S ribosomal protein L24, chloroplastic [Sesamum indicum] | 19.973 | 7.8095 | 12.4 | 2 | 3 | 2 | 1.189 | 1.116 | 1.18 | 0.773 | 0.857 | 0.836 | 0.708 | 7.21E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp30983_c0_seq1_m.12171 | PREDICTED: outer envelope protein 64, mitochondrial [Jatropha curcas] | 66.511 | 3.3038 | 2.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30991_c1_seq3_m.31644 | PREDICTED: HMG-Y-related protein A-like [Raphanus sativus] | 20.266 | 9.7131 | 34.7 | 6 | 13 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp30991_c1_seq6_m.41940 | PREDICTED: HMG-Y-related protein A-like [Raphanus sativus] | 19.574 | 49.648 | 32.3 | 6 | 14 | 1 | 1.251 | 1.197 | 1.148 | 0.771 | 0.811 | 0.758 | 0.651 | 1.80E-04 |
| cds.Camellia_sinensis.comp30992_c0_seq1_m.38770 | PREDICTED: AP-1 complex subunit sigma-1 [Sesamum indicum] | 18.659 | 20.684 | 13.7 | 2 | 3 | 2 | 1.007 | 0.945 | 1.055 | 1.006 | 1.033 | 1.046 | 1.026 | 4.78E-01 |
| cds.Camellia_sinensis.comp31000_c0_seq2_m.33049 | PREDICTED: peptide deformylase 1B, chloroplastic [Vitis vinifera] | 30.703 | 17.829 | 30.4 | 7 | 7 | 7 | 0.99 | 1.057 | 1.01 | 1.054 | 1.01 | 0.926 | 0.978 | 6.16E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31006_c0_seq1_m.35933 | PREDICTED: ras-related protein RABA1d [Vitis vinifera] | 24.186 | 13.307 | 36.2 | 7 | 14 | 2 | 1.068 | 0.952 | 0.925 | 1.016 | 0.998 | 1.045 | 1.039 | 4.35E-01 |
| cds.Camellia_sinensis.comp31013_c0_seq1_m.4933 | PREDICTED: eukaryotic translation initiation factor 3 subunit C [Vitis vinifera] | 107.04 | 35.83 | 10.4 | 10 | 10 | 10 | 1.015 | 1.042 | 0.993 | 0.979 | 0.974 | 1.038 | 0.981 | 4.69E-01 |
| cds.Camellia_sinensis.comp31014_c0_seq1_m.2071 | cytochrome f (chloroplast) [Camellia crapnelliana] | 35.219 | 224.34 | 55.9 | 14 | 74 | 14 | 0.996 | 0.969 | 0.977 | 0.987 | 1.01 | 1.023 | 1.027 | 1.20E-01 |
| cds.Camellia_sinensis.comp31022_c0_seq1_m.26968 | peroxisomal (S)-2-hydroxy-acid oxidase GLO1 isoform X1 [Cajanus cajan] | 40.676 | 271.35 | 60.7 | 18 | 107 | 3 | 0.992 | 0.955 | 0.943 | 1.027 | 1.028 | 1.048 | 1.074 | 1.27E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31022_c0_seq2_m.27008 | peroxisomal (S)-2-hydroxy-acid oxidase GLO1 isoform X1 [Cajanus cajan] | 40.384 | 126.99 | 60.5 | 17 | 103 | 2 | 0.996 | 0.981 | 1.011 | 1.02 | 1.043 | 1.007 | 1.027 | 1.15E-01 |
| cds.Camellia_sinensis.comp31027_c0_seq1_m.11356 | PREDICTED: SNARE-interacting protein KEULE-like isoform X2 [Nicotiana tabacum] | 42.91 | 1.1947 | 1.9 | 1 | 1 | 1 | 1.036 | 1.013 | 0.948 | 0.979 | 1.038 | 0.99 | 1.003 | 9.14E-01 |
| cds.Camellia_sinensis.comp31031_c0_seq1_m.9294 | PREDICTED: alpha-N-acetylglucosaminidase isoform X1 [Vitis vinifera] | 92.124 | 39.215 | 12.5 | 9 | 9 | 9 | 1.024 | 0.952 | 1.009 | 0.974 | 0.998 | 0.991 | 0.993 | 7.81E-01 |
| cds.Camellia_sinensis.comp31035_c0_seq1_m.19017 | PREDICTED: probable lactoylglutathione lyase, chloroplastic [Nelumbo nucifera] | 41.181 | 32.549 | 30.7 | 11 | 48 | 2 | 1.006 | 0.905 | 0.946 | 1.075 | 1.092 | 1.05 | 1.126 | 2.17E-02 |

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| cds.Camellia_sinensis.comp31035_c0_seq2_m.20044 | PREDICTED: probable lactoylglutathione lyase, chloroplastic [Prunus mume] | 40.353 | 11.947 | 31.3 | 11 | 45 | 2 | 1.025 | 0.971 | 0.919 | 0.972 | 1.032 | 1.089 | 1.061 | 2.63E-01 |
| cds.Camellia_sinensis.comp31050_c0_seq20_m.27451 | PREDICTED: probable isoaspartyl peptidase/L-asparaginase 3 isoform X2 [Vitis vinifera] | 27.187 | 6.2571 | 4.8 | 1 | 1 | 1 | 1.092 | 1.078 | 1.017 | 0.899 | 0.988 | 0.91 | 0.878 | 2.37E-02 |
| cds.Camellia_sinensis.comp31052_c0_seq1_m.33192 | trigger factor [Arabidopsis thaliana] | 23.356 | 7.5921 | 9.9 | 2 | 4 | 2 | 0.865 | 0.911 | 0.937 | 1.09 | 1.216 | 1.03 | 1.23 | 1.93E-02 |
| cds.Camellia_sinensis.comp31054_c0_seq1_m.44381 | PREDICTED: glutathione S-transferase L3 isoform X1 [Vitis vinifera] | 18.406 | 10.927 | 22.6 | 5 | 8 | 5 | 1.12 | 1.064 | 1.083 | 0.907 | 0.894 | 0.899 | 0.826 | 2.60E-04 |
| cds.Camellia_sinensis.comp31058_c0_seq1_m.3937 | PREDICTED: aconitate hydratase, cytoplasmic [Citrus sinensis] | 108.76 | 145.83 | 32.1 | 30 | 67 | 15 | 0.971 | 0.989 | 0.963 | 1.013 | 1.024 | 1.054 | 1.057 | 1.72E-02 |

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| cds.Camellia_sinensis.comp31058_c0_seq2_m.10105 | PREDICTED: aconitate hydratase, cytoplasmic [Nelumbo nucifera] | 73.651 | 146.52 | 36.5 | 21 | 58 | 14 | 0.978 | 0.999 | 0.946 | 1.015 | 1.034 | 1.039 | 1.056 | 3.39E-02 |
| cds.Camellia_sinensis.comp31060_c0_seq1_m.3230 | PREDICTED: pentatricopeptide repeat-containing protein MRL1, chloroplastic isoform X1 [Vitis vinifera] | 126.72 | 4.6739 | 2.4 | 3 | 3 | 3 | 1.072 | 1.052 | 1.033 | 1.009 | 0.888 | 0.939 | 0.898 | 4.79E-02 |
| cds.Camellia_sinensis.comp31061_c0_seq1_m.10833 | PREDICTED: serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' theta isoform isoform X1 [Vitis vinifera] | 58.796 | 2.6477 | 3.5 | 2 | 2 | 2 | 0.975 | 0.946 | 0.938 | 1.009 | 1.079 | 1.072 | 1.105 | 1.49E-02 |

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| cds.Camellia_sinensis.comp31062_c0_seq1_m.26787 | PREDICTED: 3-dehydroquinate synthase homolog isoform X4 [Ziziphus jujuba] | 39.34 | 12.504 | 14.3 | 5 | 5 | 5 | 0.971 | 1.007 | 1.007 | 0.984 | 1.01 | 0.954 | 0.988 | 5.72E-01 |
| cds.Camellia_sinensis.comp31066_c0_seq1_m.29752 | PREDICTED: alanine--tRNA ligase isoform X1 [Citrus sinensis] | 29.293 | 1.5211 | 3.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31068_c0_seq1_m.13277 | DCD (development and cell death) domain protein [Medicago truncatula] | 44.829 | 3.814 | 2.5 | 1 | 1 | 1 | 1.041 | 1.134 | 1.183 | 0.824 | 0.838 | 0.951 | 0.778 | 1.29E-02 |
| cds.Camellia_sinensis.comp31069_c0_seq1_m.10638 | PREDICTED: protein S-acyltransferase 8 [Ricinus communis] | 48.481 | 7.3907 | 7.8 | 3 | 4 | 3 | 1.141 | 1.07 | 1.152 | 0.877 | 0.871 | 0.876 | 0.78 | 8.72E-03 |
| cds.Camellia_sinensis.comp31074_c0_seq1_m.17913 | PREDICTED: diacylglycerol kinase 7-like [Citrus sinensis] | 53.405 | 14.843 | 10.4 | 4 | 4 | 2 | 0.903 | 1.018 | 0.989 | 0.948 | 1.053 | 1.108 | 1.068 | 3.26E-01 |

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| cds.Camellia_sinensis.comp31074_c0_seq2_m.26304 | PREDICTED: diacylglycerol kinase 7-like [Citrus sinensis] | 54.448 | 13.571 | 11.6 | 5 | 6 | 3 | 0.94 | 0.996 | 0.976 | 1.01 | 1.036 | 1.07 | 1.07 | 4.66E-02 |
| cds.Camellia_sinensis.comp31076_c0_seq16_m.8629 | Delta(24)-sterol reductase [Morus notabilis] | 72.586 | 13.681 | 6.2 | 4 | 4 | 4 | 1.123 | 1.1 | 1.117 | 0.892 | 0.895 | 0.852 | 0.79 | 1.59E-04 |
| cds.Camellia_sinensis.comp31084_c0_seq84_m.39802 | universal stress family protein [Medicago truncatula] | 25.319 | 17.318 | 12.6 | 3 | 8 | 3 | 0.965 | 1.014 | 0.921 | 1.048 | 1.016 | 1.03 | 1.067 | 8.84E-02 |
| cds.Camellia_sinensis.comp31085_c0_seq15_m.15362 | PREDICTED: D-3-phosphoglycerate dehydrogenase 1, chloroplastic-like [Daucus carota subsp. sativus] | 63.01 | 123.93 | 19.9 | 11 | 24 | 8 | 0.966 | 0.976 | 0.992 | 1.018 | 0.999 | 1.028 | 1.038 | 3.13E-02 |
| cds.Camellia_sinensis.comp31085_c0_seq3_m.50077 | PREDICTED: keratin, type I cytoskeletal 9 isoform X1 [Arachis ipaensis] | 21.85 | 3.3421 | 13.2 | 3 | 4 | 3 | 0.969 | 1.037 | 0.978 | 1.035 | 0.964 | 1.049 | 1.021 | 5.68E-01 |

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| cds.Camellia_sinensis.comp31090_c0_seq1_m.34311 | catalytic/coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] | 30.637 | 14.714 | 6.4 | 2 | 3 | 2 | 0.938 | 1.047 | 1.023 | 1.031 | 1.009 | 0.97 | 1.001 | 9.71E-01 |
| cds.Camellia_sinensis.comp31091_c0_seq2_m.31417 | hydroxyproline-rich glycoprotein [Populus trichocarpa] | 15.83 | 1.7763 | 7.5 | 1 | 1 | 1 | 0.924 | 1.084 | 0.997 | 0.967 | 0.89 | 1.147 | 1 | 9.67E-01 |
| cds.Camellia_sinensis.comp31095_c0_seq1_m.26137 | WRKY transcription factor 11-2, putative [Medicago truncatula] | 45.815 | 9.9485 | 10.2 | 4 | 7 | 4 | 1.004 | 0.972 | 1.034 | 1.028 | 1.039 | 1.012 | 1.023 | 3.03E-01 |
| cds.Camellia_sinensis.comp31096_c0_seq2_m.15188 | | 14.195 | -2 | 6.6 | 1 | 1 | 1 | 0.984 | 0.925 | 0.958 | 1.083 | 0.988 | 1.084 | 1.1 | 5.57E-02 |
| cds.Camellia_sinensis.comp31098_c1_seq1_m.15559 | PREDICTED: violaxanthin de-epoxidase, chloroplastic-like [Populus euphratica] | 61.45 | 9.9885 | 3.7 | 2 | 2 | 2 | 0.996 | 1.079 | 1.107 | 0.959 | 0.967 | 0.892 | 0.886 | 4.14E-02 |

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| cds.Camellia_sinensis.comp31113_c0_seq1_m.22495 | PREDICTED: ureidoglycolate hydrolase [Juglans regia] | 53.52 | 66.838 | 17.6 | 7 | 19 | 7 | 0.949 | 0.934 | 0.92 | 1.065 | 1.08 | 1.052 | 1.141 | 3.61E-04 |
| cds.Camellia_sinensis.comp31119_c0_seq1_m.23072 | PREDICTED: UDP-glycosyltransferase 74E2-like isoform X1 [Juglans regia] | 54.517 | 2.6303 | 3.7 | 2 | 2 | 2 | 1.212 | 1.119 | 1.041 | 0.838 | 0.855 | 0.89 | 0.766 | 5.00E-03 |
| cds.Camellia_sinensis.comp31127_c0_seq1_m.6174 | PREDICTED: chaperone protein ClpB1 [Nicotiana tabacum] | 101.46 | 225.87 | 36.4 | 30 | 39 | 28 | 0.994 | 1.028 | 1.024 | 0.973 | 0.984 | 0.988 | 0.967 | 4.38E-02 |
| cds.Camellia_sinensis.comp31129_c0_seq1_m.4353 | PREDICTED: intracellular protein transport protein USO1 [Nicotiana attenuata] | 75.838 | 43.291 | 20.8 | 15 | 17 | 15 | 0.999 | 1.031 | 1.047 | 0.988 | 0.962 | 0.979 | 0.952 | 3.63E-02 |
| cds.Camellia_sinensis.comp31133_c0_seq1_m.12936 | PREDICTED: pyruvate decarboxylase 1 [Gossypium arboreum] | 63.495 | 25.612 | 13.4 | 7 | 10 | 5 | 0.861 | 0.93 | 0.89 | 1.157 | 1.064 | 1.105 | 1.241 | 2.82E-03 |

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| cds.Camellia_sinensis.comp31135_c1_seq1_m.30434 | PREDICTED: methyl-CpG-binding domain-containing protein 11 isoform X1 [Vitis vinifera] | 37.597 | 159.77 | 62.2 | 20 | 32 | 18 | 1.134 | 1.121 | 1.096 | 0.874 | 0.866 | 0.889 | 0.785 | 4.15E-05 |
| cds.Camellia_sinensis.comp31135_c2_seq2_m.13406 | PREDICTED: long chain acyl-CoA synthetase 1 [Sesamum indicum] | 74.769 | 7.8079 | 7.4 | 5 | 5 | 5 | 1.103 | 1.245 | 1.211 | 0.907 | 0.831 | 0.668 | 0.676 | 1.53E-02 |
| cds.Camellia_sinensis.comp31136_c0_seq1_m.35724 | PREDICTED: 30S ribosomal protein S6 alpha, chloroplastic [Vitis vinifera] | 28.105 | 9.1059 | 10.6 | 2 | 7 | 2 | 1.021 | 1.028 | 1.015 | 0.974 | 0.953 | 0.984 | 0.95 | 7.16E-03 |
| cds.Camellia_sinensis.comp31139_c0_seq6_m.36886 | PREDICTED: putative RNA-binding protein YlmH [Theobroma cacao] | 17.281 | 2.0955 | 4.3 | 1 | 1 | 1 | 0.978 | 1.015 | 0.99 | 1.004 | 1.037 | 0.989 | 1.016 | 4.30E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31140_c0_seq1_m.7027 | PREDICTED: zinc finger protein VAR3, chloroplastic [Vitis vinifera] | 100.83 | 106.3 | 17.1 | 12 | 14 | 12 | 0.98 | 1.041 | 1.017 | 1.023 | 0.963 | 1.013 | 0.987 | 6.40E-01 |
| cds.Camellia_sinensis.comp31147_c0_seq4_m.40318 | PREDICTED: ras-related protein RABA5b-like [Nicotiana tabacum] | 25.402 | 7.0492 | 15.4 | 4 | 5 | 3 | 1.007 | 1.069 | 1.028 | 0.924 | 1.015 | 0.955 | 0.932 | 9.67E-02 |
| cds.Camellia_sinensis.comp31148_c0_seq2_m.31105 | PREDICTED: protein trichome birefringence-like 39 [Ziziphus jujuba] | 43.425 | 12.607 | 18 | 6 | 6 | 6 | 1.058 | 1.061 | 1.011 | 0.888 | 0.98 | 0.973 | 0.908 | 5.09E-02 |
| cds.Camellia_sinensis.comp31154_c0_seq1_m.28476 | PREDICTED: (S)-ureidoglycine aminohydrolase [Solanum lycopersicum] | 34.597 | 1.5063 | 4.5 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31170_c0_seq2_m.13451 | PREDICTED: D-2-hydroxyglutarate dehydrogenase, mitochondrial [Vitis vinifera] | 65.442 | 13.703 | 10.3 | 7 | 11 | 7 | 1.014 | 1.014 | 1.069 | 0.983 | 0.986 | 0.959 | 0.945 | 4.69E-02 |
| cds.Camellia_sinensis.comp31171_c0_seq1_m.26823 | PREDICTED: IST1 homolog [Solanum pennellii] | 36.274 | 44.124 | 27.6 | 8 | 12 | 8 | 0.96 | 0.977 | 1.004 | 1.063 | 0.971 | 1.047 | 1.048 | 2.11E-01 |
| cds.Camellia_sinensis.comp31172_c0_seq1_m.3334 | PREDICTED: exocyst complex component SEC8 [Vitis vinifera] | 119.3 | 55.8 | 12.2 | 10 | 10 | 10 | 1.028 | 0.971 | 0.988 | 1.004 | 1.03 | 0.96 | 1.002 | 9.38E-01 |
| cds.Camellia_sinensis.comp31173_c0_seq2_m.31664 | PREDICTED: sanguinarine reductase isoform X1 [Citrus sinensis] | 36.914 | 92.17 | 32.4 | 11 | 17 | 11 | 1.033 | 0.987 | 1.018 | 1.022 | 0.977 | 0.966 | 0.976 | 3.26E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31176_c0_seq1_m.25007 | PREDICTED: probable dual-specificity RNA methyltransferase RlmN isoform X1 [Daucus carota subsp. sativus] | 42.547 | 1.5601 | 2.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31178_c0_seq1_m.31701 | PREDICTED: protein WHI4 isoform X2 [Malus domestica] | 35.668 | 2.185 | 2.1 | 1 | 1 | 1 | 1.06 | 1 | 1.08 | 0.98 | 0.933 | 0.941 | 0.909 | 2.64E-02 |
| cds.Camellia_sinensis.comp31183_c0_seq1_m.26990 | Putative arsenical pump-driving ATPase [Morus notabilis] | 45.86 | 22.449 | 16.5 | 6 | 9 | 6 | 1.054 | 1.092 | 1.023 | 0.969 | 0.904 | 0.93 | 0.885 | 1.13E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31186_c0_seq1_m.26570 | PREDICTED: magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic isoform X2[Ziziphus jujuba] | 48.864 | 61.529 | 33.6 | 15 | 25 | 15 | 1.044 | 1.044 | 1.018 | 0.971 | 0.951 | 0.937 | 0.92 | 3.40E-03 |
| cds.Camellia_sinensis.comp31186_c1_seq1_m.18514 | PREDICTED: UDP-glucose 6-dehydrogenase 1 [Vitis vinifera] | 52.995 | 134.97 | 41 | 16 | 30 | 16 | 1.022 | 1.017 | 0.996 | 0.99 | 0.985 | 0.991 | 0.977 | 4.76E-02 |
| cds.Camellia_sinensis.comp31187_c0_seq1_m.29494 | PREDICTED: vesicle-associated protein 1-2 [Theobroma cacao] | 35.307 | 21.629 | 14.9 | 5 | 9 | 4 | 1.03 | 0.993 | 1.02 | 1.071 | 0.976 | 0.968 | 0.991 | 7.81E-01 |
| cds.Camellia_sinensis.comp31187_c0_seq2_m.31271 | PREDICTED: vesicle-associated protein 1-2 [Theobroma cacao] | 35.21 | 26.434 | 15.2 | 6 | 10 | 5 | 0.963 | 1.094 | 0.937 | 0.963 | 1.004 | 1.025 | 0.999 | 9.81E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31188_c0_seq2_m.28517 | PREDICTED: pyruvate kinase isozyme A, chloroplastic [Theobrom | 41.4 | 21.026 | 21.5 | 7 | 10 | 7 | 0.956 | 1.014 | 1.011 | 1.006 | 0.999 | 1.039 | 1.021 | 4.04E-01 |
| cds.Camellia_sinensis.comp31188_c1_seq1_m.39043 | PREDICTED: pyruvate kinase isozyme A, chloroplastic [Vitis | 35.505 | 35.286 | 3.7 | 1 | 3 | 1 | 0.98 | 1.029 | 1.028 | 1.033 | 0.986 | 0.956 | 0.98 | 4.93E-01 |
| cds.Camellia_sinensis.comp31191_c0_seq3_m.14179 | PREDICTED: electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial isoform | 68.67 | 5.0429 | 5.2 | 3 | 3 | 3 | 0.891 | 0.913 | 1.024 | 1.01 | 1.097 | 1.097 | 1.133 | 6.89E-02 |
| cds.Camellia_sinensis.comp31194_c0_seq1_m.23449 | PREDICTED: probable protein phosphatase 2C 76 [Ziziphus jujuba] | 43.058 | 3.2678 | 4.9 | 2 | 2 | 2 | 0.969 | 1.052 | 1.101 | 0.949 | 0.875 | 1.054 | 0.922 | 2.75E-01 |

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| cds.Camellia_sinensis.comp31198_c0_seq1_m.17489 | PREDICTED: UPF0051 protein ABCI8, chloroplastic [Vitis vinifera] | 62.134 | 74.416 | 31 | 14 | 19 | 14 | 0.995 | 0.998 | 1.041 | 0.986 | 1.013 | 0.993 | 0.986 | 4.55E-01 |
| cds.Camellia_sinensis.comp31199_c0_seq1_m.41911 | short-chain dehydrogenase/reductase family protein [Populus trichocarpa] | 30.046 | 9.8716 | 14.4 | 5 | 7 | 5 | 0.986 | 0.961 | 0.919 | 1.029 | 1.064 | 1.048 | 1.096 | 1.55E-02 |
| cds.Camellia_sinensis.comp31205_c0_seq1_m.15992 | PREDICTED: glutathione reductase, chloroplastic [Vitis vinifera] | 60.57 | 129.02 | 35.5 | 16 | 36 | 16 | 0.986 | 0.994 | 0.959 | 1.01 | 1.033 | 1.037 | 1.048 | 2.62E-02 |
| cds.Camellia_sinensis.comp31205_c1_seq1_m.18720 | PREDICTED: pectinesterase-like [Populus euphratica] | 31.464 | 43.178 | 17.8 | 6 | 14 | 6 | 0.879 | 0.869 | 0.912 | 1.126 | 1.143 | 1.141 | 1.282 | 8.22E-05 |
| cds.Camellia_sinensis.comp31207_c0_seq1_m.21467 | PREDICTED: actin-depolymerizing factor 2 [Ricinus | 16.07 | 11.403 | 41.7 | 4 | 9 | 3 | 1.038 | 1.01 | 1.004 | 0.974 | 0.955 | 1.008 | 0.962 | 1.10E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31210_c0_seq1_m.18091 | PREDICTED: elongation factor 1-gamma [Vitis vinifera] | 48.228 | 64.061 | 30.3 | 14 | 41 | 14 | 1.068 | 1.034 | 1.035 | 0.942 | 0.956 | 0.954 | 0.909 | 1.20E-03 |
| cds.Camellia_sinensis.comp31217_c0_seq1_m.33570 | PREDICTED: protein CDI-like [Nicotiana attenuata] | 32.291 | 5.705 | 3.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31218_c1_seq1_m.20508 | PREDICTED: tryptophan--tRNA ligase, chloroplastic/mitochondrial isoform X1 [Theobroma cacao] | 46.381 | 34.901 | 15.7 | 6 | 7 | 6 | 0.913 | 1.069 | 1.047 | 1.008 | 1.007 | 0.986 | 0.991 | 9.02E-01 |
| cds.Camellia_sinensis.comp31222_c1_seq1_m.35525 | PREDICTED: ran-binding protein 1 homolog c-like [Ipomoea nil] | 24.654 | 58.526 | 29.2 | 5 | 7 | 4 | 1.088 | 1.07 | 1.083 | 0.873 | 0.903 | 0.922 | 0.832 | 3.83E-04 |

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| cds.Camellia_sinensis.comp31222_c2_seq1_m.42949 | PREDICTED: nucleoside diphosphate kinase B-like [Nelumbo nucifera] | 16.432 | 46.385 | 28.4 | 5 | 10 | 5 | 0.944 | 0.98 | 0.95 | 1.056 | 1.043 | 1.058 | 1.098 | 1.62E-03 |
| cds.Camellia_sinensis.comp31222_c4_seq1_m.33714 | 14-3-3 protein [Vitis vinifera] | 29.408 | 102.49 | 54 | 14 | 51 | 8 | 1.049 | 0.983 | 0.995 | 0.977 | 1.014 | 0.999 | 0.988 | 6.24E-01 |
| cds.Camellia_sinensis.comp31226_c0_seq1_m.36088 | plant/F21F14-40 protein [Medicago truncatula] | 30.12 | 41.57 | 15 | 4 | 11 | 4 | 0.896 | 0.887 | 0.927 | 1.101 | 1.103 | 1.084 | 1.213 | 1.80E-04 |
| cds.Camellia_sinensis.comp31226_c1_seq1_m.33340 | PREDICTED: farnesyl pyrophosphate synthase 1 [Arachis duranensis] | 40.387 | 17.961 | 15.4 | 7 | 13 | 6 | 0.991 | 0.971 | 1.042 | 1.014 | 0.984 | 0.997 | 0.997 | 9.13E-01 |
| cds.Camellia_sinensis.comp31236_c0_seq1_m.32178 | PREDICTED: xanthoxin dehydrogenase-like isoform X1 [Juglans regia] | 30.617 | 120.71 | 24 | 6 | 17 | 6 | 0.978 | 0.95 | 0.979 | 1.058 | 1.059 | 1.016 | 1.078 | 1.13E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31237_c0_seq1_m.31685 | mitochondrial outer membrane protein porin of 36 kDa [Solanum tuberosum | 29.437 | 102.2 | 46.7 | 11 | 23 | 8 | 1.02 | 1.019 | 1.048 | 0.985 | 0.95 | 0.958 | 0.937 | 1.05E-02 |
| cds.Camellia_sinensis.comp31237_c0_seq2_m.40792 | PREDICTED: mitochondrial outer membrane protein porin of 36 kDa [Eucalyptus grandis] | 22.999 | 3.1935 | 16.4 | 4 | 10 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31239_c0_seq1_m.8873 | PREDICTED: eukaryotic translation initiation factor 3 subunit B [Vitis vinifera] | 85.203 | 15.558 | 7 | 5 | 8 | 5 | 0.984 | 1.141 | 1.168 | 0.946 | 0.856 | 0.904 | 0.822 | 3.33E-02 |
| cds.Camellia_sinensis.comp31241_c0_seq2_m.19977 | PREDICTED: mitochondrial import inner membrane translocase subunit TIM44-2 [Theobroma cacao] | 61.556 | 3.8747 | 4.3 | 3 | 4 | 3 | 1.075 | 1.121 | 1.119 | 0.872 | 0.902 | 0.916 | 0.811 | 4.75E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31244_c0_seq1_m.20382 | PREDICTED: biotin carboxylase 1, chloroplastic [Theobroma cacao] | 58.6 | 56.384 | 32.6 | 16 | 32 | 16 | 1.005 | 1.029 | 1.034 | 0.963 | 0.96 | 0.984 | 0.948 | 1.01E-02 |
| cds.Camellia_sinensis.comp31250_c0_seq1_m.34626 | PREDICTED: proteasome subunit beta type-5 [Gossypium hirsutum] | 29.132 | 41.095 | 19.4 | 6 | 17 | 6 | 0.956 | 0.957 | 0.928 | 1.067 | 1.02 | 1.046 | 1.103 | 4.04E-03 |
| cds.Camellia_sinensis.comp31251_c0_seq1_m.15866 | PREDICTED: alternative NAD(P)H-ubiquinone oxidoreductase C1, chloroplastic/mitochondrial [Vitis | 21.814 | 19.284 | 15.5 | 2 | 3 | 2 | 0.946 | 0.915 | 0.965 | 1.103 | 1.091 | 1.01 | 1.134 | 1.70E-02 |
| cds.Camellia_sinensis.comp31251_c0_seq2_m.17301 | PREDICTED: alternative NAD(P)H-ubiquinone oxidoreductase C1, chloroplastic/mitochondrial [Vitis | 24.758 | 13.339 | 16.7 | 3 | 4 | 3 | 0.94 | 0.911 | 1.003 | 1.125 | 1.072 | 1.087 | 1.151 | 1.13E-02 |

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| cds.Camellia_sinensis.comp31251_c0_seq3_m.45793 | NADH dehydrogenase [Medicago truncatula] | 12.58 | 35.996 | 37.7 | 3 | 5 | 3 | 0.921 | 0.981 | 0.958 | 1.061 | 1.109 | 1.021 | 1.116 | 2.23E-02 |
| cds.Camellia_sinensis.comp31254_c0_seq1_m.27350 | PREDICTED: geraniol 8-hydroxylase-like [Sesamum indicum] | 49.485 | 16.739 | 23 | 10 | 14 | 8 | 0.937 | 0.948 | 0.904 | 1.079 | 1.04 | 1.08 | 1.147 | 1.92E-03 |
| cds.Camellia_sinensis.comp31257_c1_seq1_m.25709 | PREDICTED: malate dehydrogenase [Sesamum indicum] | 36.913 | 98.661 | 34.6 | 11 | 33 | 5 | 0.964 | 0.965 | 0.954 | 1.047 | 1.067 | 1.046 | 1.096 | 2.44E-04 |
| cds.Camellia_sinensis.comp31257_c1_seq2_m.37787 | PREDICTED: malate dehydrogenase [Sesamum indicum] | 28.109 | 53.868 | 34.6 | 10 | 27 | 4 | 1.023 | 0.978 | 0.974 | 0.987 | 1.047 | 1.013 | 1.024 | 3.62E-01 |
| cds.Camellia_sinensis.comp31261_c0_seq1_m.13115 | PREDICTED: signal recognition particle 54 kDa protein, chloroplastic [Solanum pennellii] | 63.501 | 151.5 | 41.2 | 23 | 45 | 23 | 1.042 | 1.049 | 1.021 | 0.95 | 0.952 | 0.963 | 0.921 | 8.39E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31263_c3_seq1_m.49060 | PREDICTED: ubiquitin-related modifier 1 homolog 2 [Ricinus communis] | 13.822 | 1.8869 | 12 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31269_c0_seq1_m.26183 | plant/T7N9-9 protein [Medicago truncatula] | 41.753 | 37.484 | 23.9 | 8 | 9 | 8 | 1.011 | 0.978 | 0.977 | 0.968 | 1.033 | 1.019 | 1.018 | 4.78E-01 |
| cds.Camellia_sinensis.comp31270_c0_seq20_m.16661 | PREDICTED: folylpolyglutamate synthase isoform X2 [Vitis vinifera] | 28.549 | 5.1992 | 6.7 | 2 | 2 | 2 | 0.987 | 0.988 | 1.025 | 1.007 | 1.003 | 1.002 | 1.004 | 7.72E-01 |
| cds.Camellia_sinensis.comp31270_c0_seq20_m.16662 | PREDICTED: folylpolyglutamate synthase-like isoform X1 [Capsicum annuum] | 15.334 | 1.3912 | 7.5 | 1 | 2 | 1 | 0.952 | 1.044 | 1.103 | 1.065 | 0.84 | 1.005 | 0.939 | 4.72E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31273_c0_seq1_m.15035 | PREDICTED: 15-cis-phytoene desaturase, chloroplastic/chromoplastic isoform X1 [Vitis vinifera] | 64.9 | 45.321 | 23 | 11 | 14 | 11 | 1.035 | 1.039 | 1.065 | 0.956 | 0.925 | 0.965 | 0.907 | 3.30E-03 |
| cds.Camellia_sinensis.comp31275_c0_seq1_m.19312 | PREDICTED: beta-galactosidase-like [Sesamum indicum] | 68.686 | 54.92 | 18.7 | 10 | 21 | 8 | 0.842 | 0.827 | 0.809 | 1.198 | 1.198 | 1.19 | 1.447 | 3.07E-06 |
| cds.Camellia_sinensis.comp31276_c0_seq1_m.31390 | PREDICTED: 2-Cys peroxiredoxin BAS1, chloroplastic [Juglans regia] | 30.692 | 96.646 | 45.7 | 11 | 43 | 3 | 0.918 | 0.934 | 0.963 | 1.084 | 1.069 | 1.023 | 1.128 | 5.74E-03 |
| cds.Camellia_sinensis.comp31276_c0_seq2_m.31885 | PREDICTED: 2-Cys peroxiredoxin BAS1, chloroplastic [Juglans regia] | 29.991 | 20.276 | 31.4 | 9 | 40 | 1 | 1.007 | 0.976 | 1.091 | 0.988 | 0.954 | 0.935 | 0.936 | 1.51E-01 |
| cds.Camellia_sinensis.comp31277_c0_seq2_m.35600 | PREDICTED: mitochondrial import receptor subunit TOM20 [Vitis vinifera] | 21.758 | 12.61 | 24.7 | 4 | 4 | 4 | 0.984 | 0.994 | 0.996 | 1.028 | 1.061 | 0.953 | 1.023 | 5.70E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31278_c0_seq3_m.47850 | PREDICTED: probable NAD(P)H dehydrogenase subunit CRR3, chloroplastic [Capsicum annuum] | 20.739 | 7.3951 | 17.4 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp31279_c0_seq2_m.10195 | PREDICTED: IAA-amino acid hydrolase ILR1-like isoform X2 [Ziziphus jujuba] | 46.935 | 1.2403 | 3.7 | 2 | 2 | 1 | 1.018 | 0.947 | 1.026 | 0.972 | 0.969 | 1.073 | 1.008 | 8.73E-01 |
| cds.Camellia_sinensis.comp31280_c0_seq1_m.12848 | dihydroxy-acid dehydratase-like [Solanum lycopersicum] | 65.943 | 41.388 | 23.3 | 13 | 21 | 13 | 0.943 | 0.96 | 0.949 | 1.064 | 1.065 | 1.035 | 1.109 | 6.40E-04 |
| cds.Camellia_sinensis.comp31287_c0_seq12_m.42513 | PREDICTED: IST1-like protein isoform X1 [Jatropha curcas] | 27.878 | 20.126 | 7.7 | 2 | 2 | 2 | 0.91 | 1.275 | 1.033 | 0.94 | 0.858 | 0.98 | 0.863 | 2.60E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31288_c0_seq1_m.17314 | PREDICTED: polypyrimidine tract-binding protein homolog 1 isoform X1 [Vitis vinifera] | 36.182 | 1.5279 | 4.3 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp31289_c0_seq1_m.5138 | PREDICTED: elongation factor 2 [Juglans regia] | 93.649 | 323.31 | 36.7 | 33 | 99 | 33 | 0.976 | 0.975 | 0.976 | 1.011 | 1.039 | 1.014 | 1.047 | 3.41E-02 |
| cds.Camellia_sinensis.comp31295_c0_seq1_m.4827 | PREDICTED: 4-coumarate--CoA ligase 2 [Theobroma cacao] | 61.529 | 11.529 | 4.7 | 3 | 3 | 2 | 1.387 | 1.367 | 1.352 | 0.531 | 0.651 | 0.592 | 0.432 | 4.92E-03 |
| cds.Camellia_sinensis.comp31296_c0_seq1_m.16184 | PREDICTED: pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta-like [Daucus carota subsp. sativus] | 61.663 | 171.18 | 37.8 | 18 | 38 | 18 | 1.006 | 1.001 | 0.995 | 0.983 | 0.999 | 1.002 | 0.994 | 4.21E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31298_c0_seq3_m.21813 | PREDICTED: SH3 domain-containing protein 2-like [Gossypium hirsutum] | 41.041 | 1.7475 | 2.4 | 1 | 1 | 1 | 1.104 | 0.991 | 0.948 | 0.998 | 0.978 | 0.975 | 0.97 | 5.65E-01 |
| cds.Camellia_sinensis.comp31298_c0_seq6_m.27802 | PREDICTED: SH3 domain-containing protein 2-like [Ipomoea nil] | 27.96 | 20.749 | 12.4 | 3 | 3 | 3 | 0.998 | 0.954 | 1.006 | 1.123 | 0.948 | 1.002 | 1.039 | 5.32E-01 |
| cds.Camellia_sinensis.comp31305_c0_seq1_m.16175 | PREDICTED: synaptotagmin-5-like [Ziziphus jujuba] | 26.531 | 2.5374 | 4.2 | 1 | 2 | 1 | 0.933 | 0.946 | 1 | 1.045 | 1.057 | 1.046 | 1.093 | 1.40E-02 |
| cds.Camellia_sinensis.comp31306_c0_seq1_m.29350 | PREDICTED: ferritin isoform X1 [Solanum tuberosum | 28.521 | 42.039 | 24.7 | 4 | 10 | 3 | 1.078 | 1.054 | 1.083 | 0.869 | 0.916 | 0.939 | 0.847 | 2.40E-03 |
| cds.Camellia_sinensis.comp31308_c0_seq2_m.19470 | PREDICTED: protein HASTY 1 isoform X4 [Nelumbo nucifera] | 18.847 | 1.2204 | 12.1 | 2 | 2 | 2 | 1.046 | 0.964 | 1.067 | 0.964 | 1.006 | 0.954 | 0.95 | 2.24E-01 |

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| cds.Camellia_sinensis.comp31310_c0_seq1_m.36302 | PREDICTED: carbonic anhydrase 2-like [Citrus sinensis] | 26.853 | 54.121 | 33.1 | 7 | 14 | 7 | 0.915 | 0.928 | 0.912 | 1.128 | 1.092 | 1.135 | 1.218 | 1.17E-04 |
| cds.Camellia_sinensis.comp31313_c0_seq13_c0_seq1_m.16545 | PREDICTED: alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic [Vitis vinifera] | 68.013 | 63.367 | 17.4 | 10 | 17 | 8 | 1.002 | 1.002 | 0.999 | 0.975 | 0.976 | 0.987 | 0.978 | 5.64E-03 |
| cds.Camellia_sinensis.comp31313_c0_seq4_m.26743 | PREDICTED: alpha-1,4 glucan phosphorylase L-1 isozyme, chloroplastic/amyloplastic isoform X2 [Nicotiana tabacum] | 56.271 | 2.0705 | 5.1 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31317_c0_seq3_m.29906 | PREDICTED: sorbitol dehydrogenase [Juglans regia] | 39.421 | 127.55 | 52.3 | 13 | 23 | 12 | 0.927 | 0.972 | 0.953 | 1.046 | 1.044 | 1.03 | 1.094 | 3.50E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31322_c0_seq2_m.13542 | PREDICTED: glucose-6-phosphate 1-dehydrogenase 4, chloroplastic isoform X1 [Vitis vinifera] | 79.095 | 9.3664 | 6.6 | 5 | 5 | 5 | 0.939 | 0.962 | 0.945 | 1.03 | 1.087 | 1.064 | 1.118 | 3.00E-03 |
| cds.Camellia_sinensis.comp31330_c0_seq1_m.4335 | Chaperone protein [Morus notabilis] | 55.673 | 8.39 | 12.7 | 6 | 10 | 5 | 0.979 | 1.002 | 0.985 | 1.012 | 1.032 | 1.005 | 1.028 | 5.91E-02 |
| cds.Camellia_sinensis.comp31342_c0_seq2_m.33632 | PREDICTED: probable plastid-lipid-associated protein 7, chloroplastic [Vitis vinifera] | 24.522 | 12.484 | 21.6 | 4 | 5 | 4 | 0.864 | 0.967 | 1.212 | 1.118 | 0.916 | 0.953 | 0.982 | 9.21E-01 |
| cds.Camellia_sinensis.comp31345_c0_seq1_m.17042 | PREDICTED: protein NLRC3 isoform X2 [Vitis vinifera] | 66.19 | 39.41 | 10.7 | 6 | 7 | 6 | 0.981 | 1.005 | 1.05 | 1 | 0.991 | 1.016 | 0.99 | 6.85E-01 |
| cds.Camellia_sinensis.comp31351_c0_seq1_m.37134 | PREDICTED: ras-related protein RABH1e [Ipomoea nil] | 23.131 | 1.6546 | 19.8 | 4 | 8 | 0 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31351_c0_seq2_m.50012 | PREDICTED: ras-related protein RABH1e [Ipomoea nil] | 11.804 | 1.9129 | 26.6 | 3 | 3 | 1 | 1.025 | 1.049 | 1.066 | 0.957 | 0.941 | 0.958 | 0.91 | 1.76E-03 |
| cds.Camellia_sinensis.comp31353_c0_seq4_m.6311 | PREDICTED: structural maintenance of chromosomes protein 2-1-like [Ziziphus jujuba] | 33.556 | 18.796 | 19.6 | 7 | 9 | 7 | 1.084 | 1.044 | 1.017 | 0.937 | 0.925 | 0.957 | 0.896 | 6.52E-03 |
| cds.Camellia_sinensis.comp31353_c0_seq4_m.6313 | DNA repair ATPase-related family protein [Populus trichocarpa] | 19.049 | 4.5979 | 17.8 | 2 | 2 | 2 | 1.032 | 1.089 | 1.029 | 1.023 | 0.886 | 0.939 | 0.904 | 8.87E-02 |
| cds.Camellia_sinensis.comp31354_c0_seq14_c0_seq1_m.36920 | DUF2996 family protein [Medicago truncatula] | 22.698 | 7.1573 | 22.7 | 4 | 5 | 4 | 1.04 | 1.03 | 0.988 | 0.951 | 1.008 | 1.024 | 0.975 | 4.12E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31357_c0_seq1_m.18229 | PREDICTED: arginine biosynthesis bifunctional protein ArgJ, chloroplastic isoform X1 [Solanum tuberosum | 24.199 | 11.721 | 12.4 | 3 | 4 | 3 | 0.99 | 0.974 | 0.967 | 1.018 | 1.028 | 1.044 | 1.054 | 6.40E-03 |
| cds.Camellia_sinensis.comp31357_c0_seq1_m.18230 | PREDICTED: arginine biosynthesis bifunctional protein ArgJ, chloroplastic [Ricinus communis] | 18.399 | 2.6 | 11.1 | 2 | 3 | 2 | 1.003 | 1.043 | 1.032 | 0.965 | 0.97 | 0.99 | 0.95 | 2.23E-02 |
| cds.Camellia_sinensis.comp31361_c0_seq4_m.23466 | PREDICTED: pyruvate dehydrogenase E1 component subunit beta-1, mitochondrial [Nelumbo nucifera] | 40.379 | 73.312 | 29.4 | 10 | 26 | 7 | 1.013 | 0.981 | 0.981 | 1 | 1.006 | 0.966 | 0.999 | 9.52E-01 |

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| cds.Camellia_sinensis.comp31366_c0_seq2_m.41934 | PREDICTED: isocitrate dehydrogenase [NADP] isoform X2 [Sesamum indicum] | 17.381 | 3.7374 | 29.2 | 4 | 10 | 2 | 1.005 | 1.039 | 1.077 | 0.963 | 1.018 | 0.901 | 0.923 | 1.18E-01 |
| cds.Camellia_sinensis.comp31374_c0_seq6_m.6902 | PREDICTED: clathrin interactor EPSIN 2 [Sesamum indicum] | 94.053 | 7.0501 | 1.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31378_c0_seq1_m.15382 | PREDICTED: LIMR family protein At5g01460 [Citrus sinensis] | 56.249 | 2.9756 | 2 | 1 | 2 | 1 | 0.979 | 1.284 | 1.059 | 1.016 | 0.766 | 0.885 | 0.803 | 1.28E-01 |
| cds.Camellia_sinensis.comp31393_c0_seq1_m.18843 | PREDICTED: uncharacterized membrane protein At1g16860-like [Solanum tuberosum | 50.551 | 2.071 | 3.8 | 2 | 2 | 2 | 1.107 | 1.091 | 1.101 | 0.915 | 0.837 | 0.924 | 0.811 | 2.20E-02 |

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| cds.Camellia_sinensis.comp31395_c0_seq4_m.41708 | PREDICTED: oxysterol-binding protein-related protein 1C-like isoform X1 [Gossypium arboreum] | 29.284 | 2.2174 | 2.8 | 1 | 2 | 1 | 0.97 | 0.989 | 1.017 | 0.991 | 1.026 | 1.021 | 1.021 | 3.03E-01 |
| cds.Camellia_sinensis.comp31397_c0_seq1_m.2604 | PREDICTED: probable manganese-transporting ATPase PDR2 [Vitis vinifera] | 134.73 | 32.351 | 8.3 | 10 | 10 | 10 | 1.025 | 1.043 | 1.108 | 0.899 | 0.942 | 0.953 | 0.88 | 1.24E-02 |
| cds.Camellia_sinensis.comp31398_c0_seq4_m.4052 | PREDICTED: peroxisome biogenesis protein 1 isoform X3 [Vitis vinifera] | 34.006 | -2 | 2.3 | 1 | 2 | 1 | 1.02 | 1.007 | 1.085 | 0.973 | 0.972 | 0.945 | 0.929 | 4.20E-02 |
| cds.Camellia_sinensis.comp31401_c0_seq1_m.25465 | isopentenyl-diphosphate delta-isomerase [Arabidopsis thaliana] | 36.582 | 14.071 | 7.8 | 2 | 3 | 2 | 0.95 | 0.941 | 0.961 | 1.065 | 1.064 | 1.048 | 1.114 | 1.78E-04 |

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| cds.Camellia_sinensis.comp31402_c0_seq1_m.31439 | PREDICTED: syntaxin-61 [Vitis vinifera] | 28.189 | 2.1049 | 4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31409_c0_seq1_m.27497 | PREDICTED: GDP-mannose 4,6 dehydratase 1 [Ipomoea nil] | 41.322 | 5.6067 | 11.1 | 5 | 7 | 5 | 1.032 | 1.015 | 1.027 | 0.945 | 0.987 | 0.994 | 0.952 | 4.02E-02 |
| cds.Camellia_sinensis.comp31413_c1_seq2_m.24829 | PREDICTED: macrophage erythroblast attacher [Nelumbo nucifera] | 27.524 | 1.8941 | 3.8 | 1 | 1 | 1 | 0.96 | 0.956 | 0.927 | 1.057 | 1.079 | 1.048 | 1.12 | 1.28E-03 |
| cds.Camellia_sinensis.comp31413_c1_seq2_m.24830 | PREDICTED: macrophage erythroblast attacher [Glycine max] | 23.826 | 6.2066 | 15 | 4 | 5 | 4 | 0.955 | 0.987 | 0.987 | 1.026 | 0.989 | 1.055 | 1.048 | 9.73E-02 |
| cds.Camellia_sinensis.comp31417_c0_seq1_m.11793 | PREDICTED: acyl-CoA-binding domain-containing protein 4 isoform X1 [Vitis vinifera] | 73.396 | 23.176 | 13.7 | 9 | 9 | 8 | 1.014 | 1.056 | 1.016 | 0.981 | 0.913 | 0.984 | 0.933 | 6.51E-02 |

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| cds.Camellia_sinensis.comp31420_c0_seq2_m.37281 | PREDICTED: UMP-CMP kinase 3-like [Sesamum indicum] | 23.194 | 6.134 | 12.4 | 3 | 5 | 2 | 1.037 | 1.039 | 1.016 | 1.021 | 0.889 | 0.996 | 0.94 | 2.14E-01 |
| cds.Camellia_sinensis.comp31421_c0_seq2_m.20836 | PREDICTED: ACT domain-containing protein ACR10 [Prunus mume] | 46.488 | 2.2599 | 3.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31423_c0_seq1_m.8048 | PREDICTED: eukaryotic translation initiation factor 3 subunit L-like [Juglans regia] | 60.856 | 45.063 | 18 | 8 | 11 | 8 | 0.966 | 0.974 | 0.973 | 1.034 | 1.066 | 1.073 | 1.089 | 1.88E-03 |
| cds.Camellia_sinensis.comp31428_c0_seq1_m.16859 | PREDICTED: gamma aminobutyrate transaminase 3, chloroplastic-like [Gossypium hirsutum] | 57.364 | 112.21 | 29.7 | 11 | 26 | 11 | 0.966 | 0.963 | 0.987 | 0.993 | 1.035 | 1.032 | 1.049 | 3.57E-02 |

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| cds.Camellia_sinensis.comp31428_c1_seq1_m.4646 | NADH-plastoquinone oxidoreductase chain 4L (chloroplast) [Camellia crapnelliana] | 11.258 | 2.2505 | 8.9 | 1 | 2 | 1 | 0.863 | 0.912 | 0.946 | 1.126 | 1.077 | 1.123 | 1.222 | 2.68E-03 |
| cds.Camellia_sinensis.comp31430_c0_seq1_m.17258 | PREDICTED: glutamate--glyoxylate aminotransferase 2 [Jatropha curcas] | 53.544 | 251.89 | 47 | 21 | 58 | 15 | 1.039 | 1.015 | 1.007 | 0.962 | 1.001 | 0.954 | 0.953 | 5.13E-02 |
| cds.Camellia_sinensis.comp31430_c0_seq2_m.40957 | PREDICTED: glutamate--glyoxylate aminotransferase 2-like [Juglans regia] | 18.454 | 39.85 | 53 | 6 | 16 | 4 | 1.097 | 1.002 | 1.001 | 0.977 | 0.984 | 0.96 | 0.942 | 1.34E-01 |
| cds.Camellia_sinensis.comp31435_c0_seq1_m.13980 | transmembrane protein [Arabidopsis thaliana] | 73.9 | 6.3432 | 5 | 3 | 3 | 3 | 1.055 | 1.041 | 0.982 | 0.971 | 0.931 | 1.016 | 0.948 | 1.85E-01 |

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| cds.Camellia_sinensis.comp31436_c0_seq1_m.14855 | PREDICTED: germinal center kinase 1 isoform X3 [Vitis vinifera] | 72.963 | 1.2564 | 1.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31439_c0_seq1_m.17754 | PREDICTED: uncharacterized aarF domain-containing protein kinase At5g05200, chloroplastic [Vitis vinifera] | 59.251 | 71.329 | 25.7 | 12 | 19 | 12 | 1.008 | 1.021 | 1.012 | 0.998 | 0.983 | 1.004 | 0.982 | 6.43E-02 |
| cds.Camellia_sinensis.comp31443_c0_seq1_m.4815 | PREDICTED: phototropin-2 [Vitis vinifera] | 31.198 | 7.1811 | 13.1 | 3 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp31443_c0_seq2_m.5583 | PREDICTED: phototropin-2 [Vitis vinifera] | 31.112 | 7.2338 | 8.2 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31443_c0_seq2_m.5584 | PREDICTED: phototropin-2-like [Malus domestica] | 22.588 | 31.686 | 28.9 | 5 | 5 | 4 | 1.233 | 1.126 | 1.186 | 0.789 | 0.788 | 0.877 | 0.692 | 1.12E-03 |

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| cds.Camellia_sinensis.comp31443_c0_seq2_m.5585 | PREDICTED: phototropin-2 [Nelumbo nucifera] | 11.501 | 1.6787 | 14.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31446_c1_seq1_m.31776 | PREDICTED: COP9 signalosome complex subunit 7-like isoform X2 [Nicotiana | 28.105 | 2.1067 | 7.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp31451_c0_seq1_m.18500 | PREDICTED: cytochrome P450 86B1-like [Sesamum indicum] | 57.848 | 5.5293 | 6.8 | 3 | 3 | 3 | 1.404 | 1.26 | 1.295 | 0.609 | 0.584 | 0.735 | 0.487 | 7.42E-04 |
| cds.Camellia_sinensis.comp31454_c0_seq1_m.4100 | PREDICTED: vam6/Vps39-like protein [Vitis vinifera] | 112.57 | 4.5719 | 2.1 | 2 | 2 | 2 | 1.039 | 1.009 | 0.96 | 0.918 | 1.023 | 1.05 | 0.994 | 8.92E-01 |
| cds.Camellia_sinensis.comp31457_c0_seq1_m.2138 | ATPase family AAA domain-containing protein 1 [Morus notabilis] | 137.34 | 12.061 | 2.6 | 2 | 2 | 1 | 1.045 | 1.157 | 1.127 | 0.934 | 0.79 | 0.926 | 0.796 | 2.11E-02 |

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| cds.Camellia_sinensis.comp31459_c0_seq2_m.9376 | PREDICTED: acyltransferase-like protein At1g54570, chloroplastic isoform X1 [Vitis vinifera] | 63.915 | 5.6143 | 5.1 | 3 | 3 | 3 | 1.04 | 0.937 | 1.084 | 1.027 | 1.017 | 0.903 | 0.963 | 5.63E-01 |
| cds.Camellia_sinensis.comp31464_c0_seq1_m.19989 | PREDICTED: leucine-rich repeat extensin-like protein 6 [Daucus carota subsp. sativus] | 50.99 | 50.07 | 21.6 | 10 | 21 | 10 | 1.003 | 1.008 | 0.977 | 1.014 | 0.981 | 1.011 | 1.006 | 6.98E-01 |
| cds.Camellia_sinensis.comp31465_c0_seq3_m.12731 | PREDICTED: fasciclin-like arabinogalactan protein 1 [Sesamum indicum] | 43.379 | 8.6034 | 7.6 | 2 | 3 | 2 | 1.057 | 1.047 | 0.934 | 0.88 | 1.178 | 0.902 | 0.974 | 7.58E-01 |
| cds.Camellia_sinensis.comp31465_c0_seq5_m.13544 | PREDICTED: fasciclin-like arabinogalactan protein 2 [Theobroma cacao] | 20.53 | 1.8199 | 4.6 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp31474_c0_seq3_m.1857 | PREDICTED: stromal processing peptidase, chloroplastic [Vitis vinifera] | 143.42 | 164.03 | 19 | 21 | 30 | 21 | 0.993 | 1.008 | 1.033 | 0.98 | 0.98 | 0.987 | 0.971 | 6.93E-02 |
| cds.Camellia_sinensis.comp31475_c0_seq1_m.12049 | PREDICTED: glucan endo-1,3-beta-glucosidase 6 [Juglans | 40.907 | 3.3748 | 9 | 3 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp31476_c0_seq1_m.29022 | PREDICTED: COP9 signalosome complex subunit 8 [Vitis | 21.739 | 14.877 | 10.6 | 2 | 2 | 2 | 0.948 | 0.976 | 1.114 | 0.943 | 1.053 | 0.979 | 0.979 | 7.59E-01 |
| cds.Camellia_sinensis.comp31481_c1_seq1_m.17674 | PREDICTED: glucose-6-phosphate/phosphate translocator 1, chloroplastic isoform X2 [Populus euphratica] | 43.511 | 7.5853 | 4.8 | 2 | 2 | 2 | 1.056 | 1.015 | 1.02 | 0.946 | 0.982 | 0.976 | 0.94 | 2.14E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31483_c0_seq1_m.35630 | PREDICTED: 17.8 kDa class II heat shock protein [Theobroma cacao] | 30.257 | 43.625 | 19.8 | 4 | 9 | 4 | 1.002 | 0.953 | 1.007 | 1.053 | 1.028 | 0.954 | 1.025 | 5.29E-01 |
| cds.Camellia_sinensis.comp31489_c0_seq1_m.25731 | PREDICTED: probable indole-3-pyruvate monooxygenase YUCCA10 isoform X1 [Nelumbo nucifera] | 42.664 | 29.008 | 31.4 | 10 | 15 | 10 | 0.989 | 1.075 | 1.016 | 0.965 | 0.962 | 0.928 | 0.927 | 5.22E-02 |
| cds.Camellia_sinensis.comp31491_c0_seq1_m.14592 | PREDICTED: vacuolar protein-sorting-associated protein 33 homolog isoform X2 [Solanum tuberosum | 67.853 | 7.7812 | 4.2 | 3 | 3 | 3 | 0.949 | 0.927 | 0.974 | 1.001 | 1.038 | 1.016 | 1.072 | 1.73E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31494_c0_seq1_m.11585 | PREDICTED: phosphatidylserine decarboxylase proenzyme 3-like [Malus domestica] | 73.368 | 38.291 | 22 | 14 | 19 | 11 | 1.014 | 1.032 | 1.039 | 0.968 | 0.978 | 0.981 | 0.949 | 3.20E-03 |
| cds.Camellia_sinensis.comp31494_c0_seq2_m.28102 | PREDICTED: phosphatidylserine decarboxylase proenzyme 2 [Vitis vinifera] | 42.343 | 4.6582 | 16.1 | 7 | 8 | 4 | 1.131 | 1.097 | 1.212 | 0.871 | 0.84 | 0.815 | 0.734 | 9.38E-04 |
| cds.Camellia_sinensis.comp31503_c0_seq1_m.23563 | SOUL heme-binding family protein [Medicago truncatula] | 44.862 | 6.5765 | 8.4 | 4 | 6 | 4 | 1.042 | 1.039 | 0.987 | 0.944 | 0.98 | 0.985 | 0.948 | 7.45E-02 |
| cds.Camellia_sinensis.comp31504_c0_seq1_m.40828 | PREDICTED: glutathione S-transferase zeta class-like [Fragaria vesca subsp. vesca] | 26.492 | 9.6859 | 27.5 | 5 | 7 | 5 | 0.973 | 0.965 | 0.967 | 1.062 | 1.034 | 1.045 | 1.081 | 6.63E-04 |

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| cds.Camellia_sinensis.comp31513_c0_seq2_m.27050 | PREDICTED: beta-ureidopropionase [Ipomoea nil] | 48.626 | 11.128 | 9.9 | 3 | 4 | 3 | 1.018 | 1.153 | 0.937 | 1.132 | 0.891 | 0.875 | 0.932 | 5.14E-01 |
| cds.Camellia_sinensis.comp31528_c0_seq1_m.9279 | PREDICTED: probable methionine--tRNA ligase [Daucus carota subsp. sativus] | 90.978 | 147.32 | 36.3 | 25 | 35 | 23 | 1.045 | 1.031 | 1.051 | 0.942 | 0.982 | 0.95 | 0.919 | 3.70E-03 |
| cds.Camellia_sinensis.comp31534_c0_seq1_m.24580 | PREDICTED: UDP-glycosyltransferase 73C2 [Vitis vinifera] | 55.675 | 39.703 | 16.2 | 7 | 12 | 7 | 0.979 | 0.955 | 0.958 | 1.056 | 1.107 | 0.975 | 1.085 | 1.01E-01 |
| cds.Camellia_sinensis.comp31534_c0_seq2_m.50624 | PREDICTED: UDP-glycosyltransferase 73C2 [Vitis vinifera] | 21.076 | 13.456 | 10.9 | 1 | 1 | 1 | 0.813 | 0.988 | 1.096 | 1.098 | 0.989 | 1.058 | 1.086 | 3.93E-01 |
| cds.Camellia_sinensis.comp31546_c0_seq2_m.19660 | GYF domain-containing family protein [Populus trichocarpa] | 23.868 | 9.4244 | 10.1 | 1 | 1 | 1 | 1.225 | 1.025 | 1.072 | 0.856 | 0.832 | 0.947 | 0.793 | 2.56E-02 |

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| cds.Camellia_sinensis.comp31546_c0_seq2_m.19661 | GYF domain-containing protein [Arabidopsis thaliana] | 21.29 | 1.659 | 4.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31549_c0_seq5_m.7432 | PREDICTED: dipeptidyl aminopeptidase 4 [Malus domestica] | 87.835 | 10.998 | 3.7 | 3 | 3 | 3 | 0.921 | 0.972 | 1.032 | 0.983 | 1.053 | 1.059 | 1.058 | 2.34E-01 |
| cds.Camellia_sinensis.comp31550_c0_seq1_m.16059 | PREDICTED: probably inactive leucine-rich repeat receptor-like protein kinase IMK2 [Citrus sinensis] | 65.384 | 2.0964 | 2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31551_c0_seq7_m.41104 | PREDICTED: tobamovirus multiplication protein 2A-like [Gossypium hirsutum] | 17.528 | 4.4109 | 8.4 | 1 | 1 | 1 | 1.077 | 1.024 | 1.104 | 0.891 | 0.753 | 1.127 | 0.865 | 2.53E-01 |

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| cds.Camellia_sinensis.comp31558_c0_seq1_m.19170 | PREDICTED: squalene synthase [Vitis vinifera] | 47.269 | 5.8641 | 6 | 2 | 2 | 2 | 1.199 | 0.979 | 0.679 | 1.216 | 1.272 | 0.674 | 1.107 | 7.51E-01 |
| cds.Camellia_sinensis.comp31559_c0_seq3_m.32145 | PREDICTED: vesicle-associated membrane protein 722-like [Vigna radiata var. radiata] | 24.815 | -2 | 10.9 | 4 | 11 | 1 | 1.011 | 1.104 | 1.103 | 0.939 | 0.901 | 0.934 | 0.862 | 9.82E-03 |
| cds.Camellia_sinensis.comp31559_c0_seq5_m.33305 | Putative vesicle-associated membrane protein 726 [Morus notabilis] | 24.779 | 59.748 | 29.5 | 8 | 19 | 5 | 0.972 | 0.961 | 1.008 | 1.051 | 1.015 | 1.001 | 1.043 | 1.09E-01 |
| cds.Camellia_sinensis.comp31560_c0_seq1_m.23697 | PREDICTED: PGR5-like protein 1A, chloroplastic [Ziziphus jujuba] | 35.181 | 28.184 | 19.4 | 7 | 10 | 7 | 1.04 | 1.004 | 1.015 | 0.992 | 0.978 | 0.976 | 0.963 | 3.18E-02 |

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| cds.Camellia_sinensis.comp31572_c0_seq2_m.39642 | PREDICTED: protein LURP-one-related 12-like [Nicotiana tabacum] | 23.361 | 3.1983 | 9 | 2 | 2 | 2 | 0.993 | 0.962 | 1.039 | 1.004 | 1.009 | 1.006 | 1.008 | 7.32E-01 |
| cds.Camellia_sinensis.comp31577_c0_seq1_m.18209 | iron-sulfur cluster biosynthesis family protein [Medicago truncatula] | 59.811 | 108.51 | 16.2 | 8 | 13 | 8 | 0.98 | 0.981 | 1.035 | 0.99 | 1.02 | 0.991 | 1.002 | 9.31E-01 |
| cds.Camellia_sinensis.comp31578_c0_seq2_m.37745 | SNF7 family protein [Populus trichocarpa] | 27.134 | 10.817 | 15.2 | 4 | 4 | 4 | 1.216 | 1.204 | 1.226 | 0.72 | 0.775 | 0.776 | 0.623 | 4.39E-05 |
| cds.Camellia_sinensis.comp31580_c0_seq1_m.19204 | BSD domain-containing family protein [Populus trichocarpa] | 53.407 | 2.1591 | 2.1 | 1 | 1 | 1 | 1.177 | 1.197 | 1.132 | 0.935 | 0.786 | 0.732 | 0.7 | 8.28E-03 |
| cds.Camellia_sinensis.comp31581_c0_seq1_m.13417 | Dynamin-related protein 1E [Morus notabilis] | 68.627 | 15.202 | 27.3 | 15 | 19 | 4 | 1.056 | 1.049 | 1.081 | 0.876 | 0.931 | 0.933 | 0.86 | 2.60E-03 |
| cds.Camellia_sinensis.comp31581_c0_seq2_m.13831 | Dynamin-related protein 1E [Morus notabilis] | 69.077 | 83.96 | 30.4 | 16 | 21 | 4 | 0.916 | 0.945 | 0.933 | 1.093 | 1.074 | 1.104 | 1.171 | 2.00E-04 |

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| cds.Camellia_sinensis.comp31585_c0_seq1_m.34323 | PREDICTED: serine/threonine-protein phosphatase 4 regulatory subunit 2 isoform X1 [Ziziphus jujuba] | 27.935 | 5.7844 | 13.5 | 4 | 5 | 4 | 0.935 | 1.07 | 1.075 | 1.019 | 0.945 | 0.969 | 0.952 | 4.05E-01 |
| cds.Camellia_sinensis.comp31586_c1_seq5_m.40052 | PREDICTED: probable prefoldin subunit 2 [Juglans regia] | 16.257 | 21.523 | 54.4 | 9 | 11 | 9 | 0.962 | 0.971 | 0.954 | 1.056 | 1.026 | 1.051 | 1.085 | 1.36E-03 |
| cds.Camellia_sinensis.comp31587_c0_seq1_m.32497 | PREDICTED: HD domain-containing protein 2 [Vitis vinifera] | 30.043 | 1.5811 | 7.1 | 2 | 2 | 2 | 0.997 | 1.031 | 1.09 | 0.98 | 0.957 | 0.948 | 0.925 | 5.03E-02 |
| cds.Camellia_sinensis.comp31592_c0_seq1_m.13329 | propionyl-CoA carboxylase, putative [Medicago truncatula] | 74.98 | 2.3327 | 1.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31599_c0_seq1_m.8884 | 40S ribosomal protein S14-3 [Morus notabilis] | 16.325 | 78.275 | 46 | 6 | 12 | 6 | 1.159 | 1.168 | 1.142 | 0.814 | 0.835 | 0.827 | 0.714 | 2.25E-06 |

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| cds.Camellia_sinensis.comp31609_c0_seq1_m.1993 | PREDICTED: magnesium-chelatase subunit ChlH, chloroplastic [Gossypium | 156.47 | 42.581 | 7.5 | 9 | 9 | 9 | 0.978 | 1.019 | 1.104 | 0.953 | 0.984 | 1.009 | 0.95 | 2.69E-01 |
| cds.Camellia_sinensis.comp31610_c0_seq1_m.25962 | PREDICTED: insulin-degrading enzyme-like 1, peroxisomal [Theobroma cacao] | 46.134 | 12.081 | 8.2 | 3 | 4 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp31614_c1_seq1_m.20028 | PREDICTED: vacuolar-processing enzyme-like [Jatropha curcas] | 44.625 | 3.3268 | 4 | 2 | 4 | 2 | 1.088 | 1.068 | 1.084 | 0.886 | 0.934 | 0.932 | 0.849 | 8.40E-04 |
| cds.Camellia_sinensis.comp31617_c0_seq1_m.20299 | PREDICTED: cytochrome P450 98A2 [Citrus sinensis] | 59.852 | 9.0653 | 5.9 | 4 | 4 | 4 | 1.173 | 1.061 | 1.04 | 0.875 | 0.884 | 0.883 | 0.807 | 2.94E-02 |

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| cds.Camellia_sinensis.comp31628_c0_seq1_m.23367 | PREDICTED: ubiquitin-activating enzyme E1 1-like [Ziziphus jujuba] | 47.768 | 13.454 | 14.7 | 8 | 15 | 3 | 0.979 | 0.953 | 0.989 | 1.028 | 1.022 | 0.977 | 1.036 | 1.43E-01 |
| cds.Camellia_sinensis.comp31628_c1_seq1_m.44607 | PREDICTED: ubiquitin-activating enzyme E1 1-like [Ziziphus jujuba] | 28.047 | 4.959 | 8.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp31629_c2_seq1_m.24972 | PREDICTED: ABC transporter G family member 11 [Vitis vinifera] | 47.276 | 9.734 | 2.4 | 1 | 1 | 1 | 1.233 | 1.228 | 1.006 | 0.775 | 0.805 | 0.893 | 0.713 | 1.34E-02 |
| cds.Camellia_sinensis.comp31633_c0_seq1_m.23576 | PREDICTED: crocetin glucosyltransferase, chloroplastic-like [Nicotiana sylvestris] | 51.15 | 35.256 | 10 | 4 | 5 | 2 | 0.953 | 0.953 | 0.981 | 1.011 | 1.053 | 1.071 | 1.086 | 1.39E-02 |

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| cds.Camellia_sinensis.comp31633_c0_seq2_m.35544 | PREDICTED: crocetin glucosyltransferase, chloroplastic-like, partial [Sesamum indicum] | 35.64 | 15.347 | 10.8 | 3 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31634_c0_seq3_m.15811 | PREDICTED: protein MON2 homolog isoform X2 [Juglans regia] | 24.093 | 1.4044 | 4.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31636_c0_seq2_m.39904 | PREDICTED: ADP-ribosylation factor 1 [Prunus mume] | 20.231 | 15.529 | 14.8 | 2 | 4 | 2 | 1.059 | 1.031 | 1.004 | 1.073 | 0.97 | 0.999 | 0.983 | 6.29E-01 |
| cds.Camellia_sinensis.comp31638_c0_seq1_m.17824 | PREDICTED: protein TRIGALACTOSYLDIACYLGLYCEROL 3, chloroplastic isoform X1 [Sesamum indicum] | 37.986 | 2.9666 | 5.1 | 2 | 3 | 2 | 1.023 | 1.055 | 1.013 | 0.916 | 0.989 | 1.001 | 0.94 | 1.09E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31639_c0_seq2_m.22265 | PREDICTED: tubulin alpha-3 chain [Gossypium raimondii] | 49.711 | 18.069 | 24.7 | 10 | 19 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp31642_c0_seq2_m.42606 | PREDICTED: probable mediator of RNA polymerase II transcription subunit 37c, partial [Eucalyptus grandis] | 22.778 | 7.1212 | 15.1 | 3 | 5 | 1 | 0.995 | 1.033 | 1.054 | 0.869 | 1.08 | 0.97 | 0.947 | 4.23E-01 |
| cds.Camellia_sinensis.comp31646_c0_seq1_m.28973 | alpha/beta-Hydrolases superfamily protein [Arabidopsis thaliana] | 36.259 | 2.725 | 4.8 | 2 | 2 | 2 | 1.048 | 1.074 | 1.042 | 0.816 | 0.997 | 1.008 | 0.892 | 2.27E-01 |
| cds.Camellia_sinensis.comp31652_c0_seq1_m.6916 | PREDICTED: protein EXORDIUM-like 2 [Theobroma cacao] | 36.343 | 21.274 | 14 | 4 | 6 | 4 | 1.017 | 1.015 | 1.047 | 0.973 | 0.951 | 0.964 | 0.938 | 6.02E-03 |

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| cds.Camellia_sinensis.comp31652_c0_seq1_m.6917 | PREDICTED: fumarate hydratase 1, mitochondrial isoform X2 [Gossypium | 29.957 | 99.173 | 43.3 | 10 | 20 | 10 | 1.016 | 1.063 | 1.049 | 0.916 | 0.958 | 0.973 | 0.91 | 1.39E-02 |
| cds.Camellia_sinensis.comp31652_c0_seq1_m.6918 | Fumarate hydratase 1 family protein [Populus trichocarpa] | 18.7 | 11.413 | 16.5 | 3 | 3 | 3 | 1.045 | 1.051 | 1.043 | 0.934 | 0.95 | 0.953 | 0.904 | 1.05E-04 |
| cds.Camellia_sinensis.comp31653_c0_seq1_m.14478 | PREDICTED: CLP protease regulatory subunit CLPX1, mitochondrial-like [Solanum pennellii] | 68.927 | 4.6876 | 4.7 | 3 | 4 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31654_c0_seq2_m.30801 | PREDICTED: fatty-acid-binding protein 3, chloroplastic [Vitis vinifera] | 30.251 | 18.353 | 9.8 | 2 | 4 | 2 | 0.996 | 1.063 | 1.06 | 0.958 | 0.945 | 0.969 | 0.921 | 2.16E-02 |

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| cds.Camellia_sinensis.comp31662_c0_seq1_m.30500 | PREDICTED: putative glucose-6-phosphate 1-epimerase [Nelumbo nucifera] | 35.501 | 10.983 | 29.6 | 7 | 13 | 2 | 1.013 | 0.912 | 1.038 | 0.918 | 1.066 | 1.06 | 1.027 | 6.99E-01 |
| cds.Camellia_sinensis.comp31676_c0_seq1_m.23298 | PREDICTED: OTU domain-containing protein 6B [Cucumis melo] | 27.75 | 1.7361 | 4.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31678_c1_seq1_m.16965 | zinc ion-binding protein, putative [Medicago truncatula] | 40.757 | 5.25 | 8.9 | 4 | 4 | 4 | 0.936 | 0.951 | 0.945 | 1.04 | 1.091 | 1.055 | 1.125 | 1.40E-03 |
| cds.Camellia_sinensis.comp31687_c0_seq2_m.32126 | PREDICTED: proteasome subunit beta type-7-A [Sesamum indicum] | 29.52 | 11.415 | 9.2 | 3 | 10 | 3 | 1.02 | 1.003 | 1.023 | 1.01 | 0.983 | 0.976 | 0.975 | 1.01E-01 |
| cds.Camellia_sinensis.comp31690_c0_seq1_m.13753 | PREDICTED: plant UBX domain-containing protein 11 isoform X1 [Vitis vinifera] | 62.219 | 4.5695 | 6.2 | 4 | 4 | 4 | 0.986 | 0.992 | 1.043 | 0.955 | 0.949 | 1.028 | 0.971 | 3.88E-01 |

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| cds.Camellia_sinensis.comp31693_c0_seq1_m.36890 | PREDICTED: vesicle-associated membrane protein 714 [Prunus mume] | 26.479 | 2.1048 | 3.9 | 1 | 1 | 1 | 0.992 | 0.992 | 0.959 | 1.058 | 1.034 | 0.983 | 1.045 | 1.50E-01 |
| cds.Camellia_sinensis.comp31694_c0_seq1_m.25248 | PREDICTED: 3-oxo-Delta(4,5)-steroid 5-beta-reductase-like [Nicotiana attenuata] | 30.526 | 9.7601 | 21.9 | 6 | 9 | 6 | 0.933 | 1.028 | 1.023 | 0.994 | 1.011 | 0.984 | 1.002 | 9.40E-01 |
| cds.Camellia_sinensis.comp31694_c0_seq6_m.38692 | PREDICTED: universal stress protein A-like protein [Ziziphus jujuba] | 18.521 | 7.9883 | 16 | 4 | 6 | 4 | 1.011 | 1.011 | 0.968 | 0.979 | 0.995 | 1.027 | 1.004 | 8.64E-01 |
| cds.Camellia_sinensis.comp31696_c0_seq1_m.8121 | aleurone layer morphogenesis protein [Medicago truncatula] | 85.151 | 5.347 | 4.5 | 4 | 4 | 4 | 1.041 | 1.02 | 0.991 | 0.958 | 0.969 | 1.02 | 0.966 | 2.17E-01 |

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| cds.Camellia_sinensis.comp31697_c0_seq1_m.20650 | PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial [Ziziphus jujuba] | 38.682 | 67.922 | 32.1 | 10 | 14 | 10 | 1.011 | 1.023 | 0.975 | 1.006 | 0.982 | 1.017 | 0.999 | 9.48E-01 |
| cds.Camellia_sinensis.comp31714_c0_seq2_m.17445 | PREDICTED: renalase isoform X1 [Citrus sinensis] | 27.415 | 7.0843 | 12 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp31715_c0_seq1_m.21131 | PREDICTED: 2-methylbutanal oxime monooxygenase [Theobroma cacao] | 58.791 | 22.417 | 12.4 | 7 | 9 | 7 | 0.901 | 0.932 | 0.946 | 1.118 | 1.094 | 1.082 | 1.185 | 6.02E-04 |
| cds.Camellia_sinensis.comp31721_c0_seq1_m.24824 | PREDICTED: mitogen-activated protein kinase homolog MMK1 [Vigna angularis] | 45.454 | 11.166 | 15.8 | 6 | 7 | 5 | 0.977 | 0.971 | 1.026 | 1.006 | 1.024 | 1.056 | 1.038 | 1.74E-01 |

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| cds.Camellia_sinensis.comp31721_c0_seq21_m.41791 | PREDICTED: mitogen-activated protein kinase homolog MMK2 isoform X2 [Glycine max] | 20.964 | 1.6928 | 9.8 | 2 | 3 | 1 | 0.989 | 1.038 | 0.905 | 1.015 | 1.021 | 1.044 | 1.05 | 2.84E-01 |
| cds.Camellia_sinensis.comp31721_c0_seq31_m.44147 | PREDICTED: mitogen-activated protein kinase homolog MMK2 [Pyrus x bretschneideri] | 29.242 | 11.143 | 14.3 | 4 | 6 | 3 | 0.976 | 1.093 | 1.055 | 0.986 | 0.979 | 0.917 | 0.923 | 1.20E-01 |
| cds.Camellia_sinensis.comp31721_c1_seq11_m.40504 | PREDICTED: mitogen-activated protein kinase homolog MMK2 [Vitis vinifera] | 22.169 | 86.288 | 28.1 | 4 | 6 | 3 | 1.037 | 0.962 | 0.93 | 1.104 | 0.964 | 1.007 | 1.05 | 4.02E-01 |
| cds.Camellia_sinensis.comp31723_c0_seq13_c0_seq1_m.25436 | PREDICTED: trithorax group protein osa [Ziziphus jujuba] | 54.091 | 127.87 | 33.2 | 12 | 24 | 11 | 1.007 | 1.02 | 0.958 | 0.998 | 1.003 | 0.994 | 1.003 | 8.66E-01 |

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| cds.Camellia_sinensis.comp31731_c0_seq1_m.2028 | PREDICTED: xanthine dehydrogenase 1 [Vitis vinifera] | 91.284 | 3.3731 | 2.3 | 2 | 3 | 2 | 0.989 | 0.931 | 1.086 | 1.014 | 0.971 | 1.022 | 1 | 9.67E-01 |
| cds.Camellia_sinensis.comp31764_c0_seq2_m.44977 | PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial [Ipomoea nil] | 14.225 | 2.4462 | 17.7 | 2 | 3 | 2 | 1.091 | 0.917 | 1.018 | 0.871 | 0.808 | 1.277 | 0.977 | 7.95E-01 |
| cds.Camellia_sinensis.comp31766_c0_seq1_m.39689 | PREDICTED: dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial-like [Juglans regia] | 30.695 | 2.9499 | 3.5 | 1 | 3 | 1 | 1.095 | 0.941 | 1.002 | 0.947 | 0.974 | 1.034 | 0.973 | 6.32E-01 |

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| cds.Camellia_sinensis.comp31767_c1_seq1_m.31627 | PREDICTED: 60S ribosomal protein L14-2-like [Nelumbo nucifera] | 15.416 | 10.763 | 35.8 | 5 | 14 | 2 | 1.11 | 1.113 | 1.124 | 0.877 | 0.831 | 0.87 | 0.77 | 1.05E-04 |
| cds.Camellia_sinensis.comp31769_c0_seq1_m.36107 | PREDICTED: protein N-terminal glutamine amidohydrolase [Citrus sinensis] | 25.432 | 5.083 | 6.2 | 1 | 1 | 1 | 0.93 | 0.916 | 1.072 | 1.067 | 0.995 | 1.047 | 1.065 | 2.94E-01 |
| cds.Camellia_sinensis.comp31776_c0_seq1_m.23439 | PREDICTED: dolichyl-phosphate beta-glucosyltransferase [Ricinus communis] | 20.68 | 5.9004 | 14.3 | 2 | 2 | 2 | 0.986 | 0.956 | 0.995 | 1.052 | 1.019 | 1.01 | 1.049 | 5.06E-02 |
| cds.Camellia_sinensis.comp31779_c0_seq1_m.1001 | PREDICTED: proteasome-associated protein ECM29 homolog [Vitis vinifera] | 187.43 | 7.8071 | 2.5 | 4 | 4 | 4 | 0.972 | 1.023 | 0.996 | 1.007 | 1.026 | 0.99 | 1.011 | 5.83E-01 |

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| cds.Camellia_sinensis.comp31781_c0_seq1_m.40000 | PREDICTED: 39S ribosomal protein L47, mitochondrial [Cucumis sativus] | 16.537 | 7.9898 | 28.7 | 3 | 3 | 3 | 0.927 | 1.03 | 0.905 | 1.07 | 0.989 | 1.103 | 1.105 | 1.23E-01 |
| cds.Camellia_sinensis.comp31787_c0_seq1_m.11219 | PREDICTED: YTH domain-containing family protein 1-like [Sesamum indicum] | 79.591 | 31.73 | 13.4 | 11 | 15 | 11 | 0.928 | 0.975 | 1 | 1.028 | 1.071 | 1.04 | 1.081 | 3.53E-02 |
| cds.Camellia_sinensis.comp31788_c0_seq1_m.5572 | PREDICTED: probable receptor-like protein kinase At5g47070 isoform X2 [Nelumbo nucifera] | 46.778 | 22.622 | 8.6 | 4 | 5 | 3 | 1.011 | 1.069 | 1.01 | 0.982 | 0.962 | 0.975 | 0.945 | 4.53E-02 |
| cds.Camellia_sinensis.comp31789_c0_seq1_m.20372 | PREDICTED: cytochrome P450 76C2-like [Vitis vinifera] | 63.468 | 14.003 | 13.3 | 7 | 9 | 6 | 0.999 | 1.05 | 1.025 | 0.975 | 0.969 | 0.986 | 0.953 | 3.50E-02 |

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| cds.Camellia_sinensis.comp31792_c2_seq1_m.12491 | PREDICTED: uncharacterized membrane protein At3g27390 [Sesamum | 28.132 | 4.0855 | 4 | 1 | 1 | 1 | 1.181 | 1.031 | 1.169 | 0.807 | 0.868 | 0.903 | 0.762 | 7.80E-03 |
| cds.Camellia_sinensis.comp31806_c0_seq1_m.4333 | PREDICTED: protein argonaute 4-like isoform X2 [Juglans regia] | 102.18 | 81.51 | 23.8 | 20 | 28 | 11 | 1.142 | 1.186 | 1.174 | 0.82 | 0.825 | 0.795 | 0.697 | 2.17E-05 |
| cds.Camellia_sinensis.comp31809_c0_seq1_m.5522 | PREDICTED: pyruvate, phosphate dikinase, chloroplastic [Malus domestica] | 107 | 165.23 | 25.8 | 26 | 55 | 26 | 0.974 | 1.006 | 0.998 | 1.019 | 1 | 0.987 | 1.009 | 5.24E-01 |
| cds.Camellia_sinensis.comp31810_c0_seq2_m.6849 | PREDICTED: probable linoleate 9S-lipoxygenase 5 [Juglans regia] | 86.42 | 141.24 | 37.1 | 30 | 59 | 27 | 0.991 | 0.966 | 0.985 | 1.018 | 1.019 | 1.024 | 1.04 | 7.42E-03 |

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| cds.Camellia_sinensis.comp31810_c0_seq2_m.6850 | PREDICTED: probable linoleate 9S-lipoxygenase 5 [Eucalyptus grandis] | 21.445 | 48.311 | 30.2 | 6 | 11 | 6 | 0.992 | 1.009 | 0.953 | 1.049 | 1.03 | 1.003 | 1.043 | 1.17E-01 |
| cds.Camellia_sinensis.comp31816_c1_seq3_m.30019 | PREDICTED: acyl-CoA-binding domain-containing protein 1 [Vitis vinifera] | 40.747 | 3.3527 | 3.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31817_c0_seq1_m.7018 | PREDICTED: polyadenylate-binding protein 8-like isoform X2 [Nicotiana | 44.482 | 2.2016 | 18.1 | 8 | 13 | 1 | 1 | 1.024 | 0.914 | 1.019 | 1.022 | 1.034 | 1.047 | 3.12E-01 |
| cds.Camellia_sinensis.comp31817_c0_seq2_m.7904 | PREDICTED: polyadenylate-binding protein 8-like isoform X2 [Nicotiana | 44.471 | 57.432 | 23.6 | 9 | 15 | 2 | 0.926 | 0.951 | 0.998 | 1.05 | 0.977 | 0.973 | 1.043 | 2.69E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31817_c0_seq2_m.7905 | polyadenylate-binding family protein [Populus trichocarpa | 29.29 | 66.505 | 41.5 | 10 | 12 | 10 | 0.976 | 0.982 | 1 | 1.03 | 0.991 | 1.019 | 1.028 | 1.16E-01 |
| cds.Camellia_sinensis.comp31819_c0_seq1_m.19399 | PREDICTED: sphingosine-1-phosphate lyase [Jatropha curcas] | 62.296 | 7.6452 | 8.9 | 5 | 5 | 5 | 0.961 | 1.051 | 1.025 | 1.055 | 0.95 | 1.056 | 1.008 | 8.76E-01 |
| cds.Camellia_sinensis.comp31821_c0_seq13_m.22182 | PREDICTED: protein indeterminate-domain 5, chloroplastic isoform X1 [Theobroma cacao] | 20.883 | 1.7351 | 4.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31826_c0_seq1_m.17816 | PREDICTED: nicotinate phosphoribosyltransferase 2 [Daucus carota subsp. sativus] | 62.797 | 7.4605 | 6.4 | 3 | 4 | 3 | 1.008 | 1.019 | 1.024 | 0.964 | 1.002 | 0.982 | 0.966 | 4.65E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31827_c0_seq1_m.11455 | calcium ion-binding protein [Medicago truncatula] | 64.054 | 1.5508 | 1.6 | 1 | 1 | 1 | 0.992 | 0.961 | 1.005 | 1.115 | 0.969 | 0.979 | 1.035 | 5.22E-01 |
| cds.Camellia_sinensis.comp31830_c0_seq1_m.18863 | PREDICTED: serine carboxypeptidase-like [Eucalyptus grandis] | 25.392 | 34.376 | 34.1 | 6 | 17 | 6 | 1.069 | 1.043 | 0.985 | 0.949 | 0.986 | 0.975 | 0.94 | 8.21E-02 |
| cds.Camellia_sinensis.comp31831_c0_seq2_m.20143 | PREDICTED: plasminogen activator inhibitor 1 RNA-binding protein [Vitis vinifera] | 40.744 | 35.755 | 13.6 | 4 | 5 | 3 | 1.107 | 1.144 | 1.206 | 0.882 | 0.789 | 0.839 | 0.726 | 1.42E-03 |
| cds.Camellia_sinensis.comp31831_c0_seq3_m.20572 | PREDICTED: U3 small nucleolar RNA-associated protein 25 [Jatropha curcas] | 40.236 | 48.52 | 19.8 | 6 | 13 | 4 | 1.308 | 1.202 | 1.239 | 0.708 | 0.658 | 0.781 | 0.573 | 5.42E-04 |

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| cds.Camellia_sinensis.comp31831_c0_seq7_m.23621 | PREDICTED: plasminogen activator inhibitor 1 RNA-binding protein [Vitis vinifera] | 38.619 | 114.14 | 26 | 7 | 15 | 6 | 1.16 | 1.134 | 1.089 | 0.834 | 0.844 | 0.838 | 0.744 | 9.76E-05 |
| cds.Camellia_sinensis.comp31838_c0_seq18_m.38193 | PREDICTED: probable glutathione peroxidase 2 [Citrus sinensis] | 22.177 | 11.021 | 34.7 | 8 | 15 | 8 | 0.942 | 0.961 | 0.922 | 1.092 | 1.091 | 1.02 | 1.134 | 8.04E-03 |
| cds.Camellia_sinensis.comp31839_c1_seq12_m.43599 | PREDICTED: 40S ribosomal protein S26-1 [Musa acuminata subsp. malaccensis] | 17.653 | 21.35 | 33.5 | 5 | 9 | 1 | 1.042 | 1.055 | 1.118 | 0.901 | 0.977 | 0.897 | 0.863 | 1.39E-02 |
| cds.Camellia_sinensis.comp31839_c1_seq13_m.43609 | PREDICTED: 40S ribosomal protein S26-3 [Vitis vinifera] | 17.755 | 3.7895 | 33.3 | 5 | 10 | 1 | 1.119 | 1.083 | 1.08 | 0.801 | 0.958 | 0.929 | 0.819 | 2.30E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp31839_c1_seq9_m.41622 | PREDICTED: mavicyanin [Theobroma cacao] | 24.512 | 15.908 | 10.1 | 2 | 3 | 2 | 1.019 | 1.029 | 1.017 | 0.986 | 1.005 | 0.97 | 0.966 | 3.34E-02 |
| cds.Camellia_sinensis.comp31852_c0_seq1_m.12704 | PREDICTED: probable pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH9 isoform X1 [Theobroma cacao] | 77.817 | 2.6793 | 1.7 | 1 | 1 | 1 | 0.879 | 1.08 | 0.907 | 1.091 | 1.075 | 1.003 | 1.106 | 2.07E-01 |
| cds.Camellia_sinensis.comp31855_c0_seq25_c0_seq2_m.30542 | PREDICTED: putative hydrolase C777.06c [Citrus sinensis] | 36.191 | 6.6618 | 4 | 1 | 1 | 1 | 1.089 | 0.959 | 1.129 | 0.927 | 0.979 | 0.906 | 0.885 | 9.25E-02 |

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| cds.Camellia_sinensis.comp31857_c0_seq5_m.17877 | PREDICTED: putative E3 ubiquitin-protein ligase XBAT35 isoform X2 [Nicotiana sylvestris] | 58.081 | 6.101 | 3 | 1 | 1 | 1 | 1.047 | 1.043 | 0.986 | 0.787 | 1.044 | 1.078 | 0.946 | 5.57E-01 |
| cds.Camellia_sinensis.comp31860_c0_seq10_c0_seq1_m.5968 | PREDICTED: ubiquitin-conjugating enzyme E2 36 [Theobroma cacao] | 22.288 | 59.801 | 34.8 | 7 | 21 | 7 | 0.998 | 1.024 | 0.979 | 0.998 | 1.018 | 1.008 | 1.008 | 6.14E-01 |
| cds.Camellia_sinensis.comp31866_c0_seq1_m.8702 | PREDICTED: pentatricopeptide repeat-containing protein At1g74850, chloroplastic [Vitis vinifera] | 91.798 | 5.3669 | 3.7 | 3 | 3 | 3 | 0.975 | 1.001 | 1.035 | 0.994 | 0.977 | 1.03 | 0.997 | 8.95E-01 |

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| cds.Camellia_sinensis.comp31868_c0_seq1_m.13263 | PREDICTED: soluble starch synthase 1, chloroplastic/amyloplastic [Ricinus communis] | 71.693 | 31.484 | 15.4 | 7 | 7 | 7 | 0.937 | 0.982 | 0.963 | 0.985 | 1.056 | 1.098 | 1.089 | 7.06E-02 |
| cds.Camellia_sinensis.comp31870_c0_seq1_m.10965 | PREDICTED: probable cadmium/zinc-transporting ATPase HMA1, chloroplastic [Sesamum indicum] | 44.186 | 2.7391 | 3.8 | 2 | 2 | 2 | 1.133 | 1.079 | 1.109 | 0.849 | 0.934 | 0.867 | 0.798 | 2.16E-03 |
| cds.Camellia_sinensis.comp31872_c0_seq1_m.4416 | PREDICTED: 4-alpha-glucanotransferase DPE2-like [Populus euphratica] | 54.165 | 26.595 | 19.2 | 7 | 9 | 7 | 1 | 1.006 | 1.047 | 0.957 | 0.966 | 0.988 | 0.953 | 5.11E-02 |
| cds.Camellia_sinensis.comp31872_c0_seq1_m.4417 | PREDICTED: 4-alpha-glucanotransferase DPE2 [Prunus mume] | 45.813 | 31.861 | 23.6 | 8 | 15 | 8 | 1.068 | 1.019 | 1.001 | 0.939 | 0.975 | 0.989 | 0.94 | 6.75E-02 |

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| cds.Camellia_sinensis.comp31876_c1_seq9_m.17023 | PREDICTED: protein TRANSPARENT TESTA 12 [Jatropha curcas] | 52.1 | 3.0324 | 5.4 | 3 | 3 | 3 | 0.986 | 0.974 | 1.029 | 0.976 | 1.015 | 1.03 | 1.011 | 6.69E-01 |
| cds.Camellia_sinensis.comp31879_c0_seq1_m.17822 | PREDICTED: transcription factor HBP-1b(c38)-like [Sesamum indicum] | 20.744 | 2.0083 | 7.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31879_c0_seq3_m.23557 | PREDICTED: transcription factor HBP-1b(c1)-like isoform X1 [Sesamum indicum] | 36.731 | 2.0037 | 2.1 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp31884_c0_seq1_m.15173 | PREDICTED: mitochondrial-processing peptidase subunit alpha [Musa acuminata subsp. malaccensis] | 54.485 | 182.83 | 44 | 17 | 41 | 17 | 1.019 | 0.985 | 0.996 | 0.991 | 1.019 | 0.994 | 1.001 | 9.24E-01 |
| cds.Camellia_sinensis.comp31888_c0_seq4_m.43428 | Metal-dependent phosphohydrolase [Arabidopsis thaliana] | 25.147 | 12.217 | 16.6 | 3 | 3 | 3 | 1.163 | 1.175 | 1.164 | 0.81 | 0.803 | 0.837 | 0.7 | 1.53E-05 |
| cds.Camellia_sinensis.comp31892_c0_seq1_m.18682 | PREDICTED: 3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial isoform X1 [Vitis | 50.769 | 27.358 | 7.2 | 2 | 2 | 2 | 0.822 | 1.18 | 1.104 | 1.109 | 0.873 | 0.938 | 0.94 | 6.98E-01 |

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| cds.Camellia_sinensis.comp31896_c0_seq2_m.899 | PREDICTED: nuclear pore complex protein NUP205 isoform X1 [Vitis vinifera] | 210.18 | 8.8411 | 2.8 | 6 | 6 | 6 | 0.925 | 1.003 | 0.967 | 1.055 | 0.962 | 0.985 | 1.037 | 3.76E-01 |
| cds.Camellia_sinensis.comp31897_c0_seq5_m.20303 | PREDICTED: adenylate kinase 5, chloroplastic isoform X9 [Eucalyptus grandis] | 37.035 | 116.82 | 49.5 | 15 | 35 | 14 | 0.979 | 0.964 | 0.933 | 1.077 | 1.011 | 1.036 | 1.086 | 2.37E-02 |
| cds.Camellia_sinensis.comp31897_c0_seq5_m.20304 | PREDICTED: adenylate kinase 5, chloroplastic [Prunus mume] | 24.94 | 63.793 | 35.3 | 6 | 15 | 6 | 0.943 | 0.978 | 0.944 | 1.045 | 1.045 | 1.03 | 1.089 | 2.70E-03 |
| cds.Camellia_sinensis.comp31900_c0_seq10_c0_seq1_m.9317 | PREDICTED: UPF0261 protein mll9388 [Daucus carota subsp. sativus] | 81.029 | 18.749 | 7.8 | 6 | 6 | 6 | 0.964 | 0.974 | 0.964 | 1.041 | 1.062 | 0.999 | 1.069 | 2.24E-02 |

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| cds.Camellia_sinensis.comp31905_c0_seq4_m.29858 | PREDICTED: gamma-soluble NSF attachment protein [Citrus sinensis] | 25.122 | 34.24 | 21.8 | 5 | 5 | 5 | 0.96 | 1.033 | 1.027 | 1.025 | 1.017 | 1.003 | 1.008 | 7.38E-01 |
| cds.Camellia_sinensis.comp31906_c0_seq7_m.42862 | PREDICTED: probable protein phosphatase 2C 11 [Nicotiana tabacum] | 11.134 | 16.463 | 19 | 1 | 1 | 1 | 1.142 | 1.056 | 0.829 | 1.074 | 0.885 | 1.006 | 0.98 | 9.01E-01 |
| cds.Camellia_sinensis.comp31907_c0_seq4_m.34738 | PREDICTED: protein STRICTOSIDINE SYNTHASE-LIKE 10 [Prunus mume] | 31.691 | 5.4191 | 8.3 | 2 | 3 | 2 | 0.89 | 1.042 | 0.947 | 1.012 | 0.997 | 1.135 | 1.092 | 2.24E-01 |
| cds.Camellia_sinensis.comp31908_c0_seq1_m.34676 | PREDICTED: UDP-glycosyltransferase 88A1 [Vitis vinifera] | 41.835 | 5.5749 | 8.2 | 3 | 3 | 3 | 0.9 | 1.003 | 0.938 | 1.047 | 1.021 | 1.05 | 1.098 | 4.57E-02 |
| cds.Camellia_sinensis.comp31908_c1_seq1_m.55064 | PREDICTED: UDP-glycosyltransferase 88A1-like [Vitis vinifera] | 12.391 | 18.292 | 26.1 | 2 | 4 | 2 | 0.962 | 1.028 | 0.935 | 1.014 | 1.097 | 0.982 | 1.057 | 2.68E-01 |

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| cds.Camellia_sinensis.comp31909_c0_seq1_m.17647 | PREDICTED: 26S proteasome regulatory subunit 4 homolog A [Sesamum | 49.555 | 81.331 | 42.7 | 19 | 25 | 19 | 1.173 | 1.171 | 1.16 | 0.817 | 0.807 | 0.794 | 0.69 | 1.02E-06 |
| cds.Camellia_sinensis.comp31910_c0_seq2_m.21802 | PREDICTED: guanosine nucleotide diphosphate dissociation inhibitor 2 isoform X2 [Ziziphus jujuba] | 49.602 | 192.48 | 39.2 | 16 | 42 | 16 | 0.99 | 0.963 | 0.968 | 0.998 | 1.038 | 1.035 | 1.051 | 3.04E-02 |
| cds.Camellia_sinensis.comp31911_c0_seq1_m.1537 | PREDICTED: clustered mitochondria protein [Vitis vinifera] | 155.82 | 19.682 | 4.4 | 5 | 5 | 5 | 1.089 | 1.12 | 1.113 | 0.854 | 0.846 | 0.942 | 0.795 | 2.88E-03 |
| cds.Camellia_sinensis.comp31913_c0_seq1_m.21576 | PREDICTED: peroxiredoxin Q, chloroplastic [Ricinus communis] | 24.214 | 134.98 | 46.8 | 9 | 34 | 9 | 1.061 | 1.015 | 1.024 | 0.961 | 0.953 | 0.963 | 0.928 | 5.88E-03 |

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| cds.Camellia_sinensis.comp31916_c0_seq1_m.9389 | PREDICTED: calcium-dependent protein kinase 1 [Theobroma cacao] | 64.326 | 3.4849 | 3.3 | 2 | 4 | 2 | 0.96 | 0.964 | 0.955 | 1.057 | 1.049 | 1.056 | 1.098 | 1.66E-05 |
| cds.Camellia_sinensis.comp31922_c0_seq2_m.26835 | PREDICTED: ATP-citrate synthase alpha chain protein 2 [Nicotiana attenuata] | 48.023 | 1.21 | 10.3 | 5 | 9 | 2 | 1.348 | 1.238 | 1.215 | 0.647 | 0.688 | 0.769 | 0.554 | 5.81E-04 |
| cds.Camellia_sinensis.comp31929_c0_seq3_m.23533 | PREDICTED: lysophospholipid acyltransferase LPEAT1 isoform X1 [Nelumbo nucifera] | 43.816 | 1.6855 | 2.1 | 1 | 1 | 1 | 1.046 | 1.001 | 0.87 | 0.987 | 1.048 | 1.054 | 1.059 | 3.70E-01 |
| cds.Camellia_sinensis.comp31929_c0_seq8_m.42956 | PREDICTED: probable protein phosphatase 2C 62 isoform X1 [Sesamum indicum] | 18.358 | 1.8239 | 7.1 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp31931_c0_seq1_m.7532 | PREDICTED: pyrophosphate-energized vacuolar membrane proton pump-like [Ipomoea nil] | 80.572 | 120.24 | 18.5 | 13 | 34 | 7 | 1.026 | 0.969 | 0.994 | 0.979 | 1.019 | 0.993 | 1.001 | 9.70E-01 |
| cds.Camellia_sinensis.comp31936_c0_seq1_m.9484 | PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Vitis vinifera] | 85.11 | 1.8695 | 3.4 | 3 | 6 | 1 | 1.056 | 1.036 | 1.008 | 0.968 | 1.01 | 0.92 | 0.935 | 8.75E-02 |
| cds.Camellia_sinensis.comp31946_c0_seq1_m.19079 | PREDICTED: DEAD-box ATP-dependent RNA helicase 38 [Ipomoea nil] | 54.44 | 94.859 | 29.7 | 13 | 22 | 13 | 0.954 | 0.977 | 0.968 | 1.009 | 1.061 | 1.053 | 1.077 | 1.23E-02 |
| cds.Camellia_sinensis.comp31950_c0_seq1_m.31380 | PREDICTED: probable proteasome inhibitor [Ziziphus jujuba] | 31.92 | 19.493 | 14.5 | 4 | 7 | 4 | 1.01 | 0.957 | 0.935 | 1.046 | 0.995 | 1.094 | 1.08 | 9.71E-02 |

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| cds.Camellia_sinensis.comp31952_c0_seq2_m.12569 | PREDICTED: pentatricopeptide repeat-containing protein At1g26460, mitochondrial [Nelumbo nucifera] | 69.016 | 6.5756 | 2.7 | 2 | 2 | 2 | 1.055 | 0.92 | 1.033 | 0.969 | 1.006 | 1.02 | 0.996 | 9.54E-01 |
| cds.Camellia_sinensis.comp31955_c0_seq7_m.21954 | PREDICTED: nicotinate-nucleotide pyrophosphorylase [carboxylating], chloroplastic [Jatropha curcas] | 35.621 | 37.042 | 17.9 | 6 | 7 | 6 | 0.985 | 1.022 | 0.98 | 1.009 | 0.994 | 1.04 | 1.019 | 3.78E-01 |
| cds.Camellia_sinensis.comp31956_c0_seq1_m.37546 | PREDICTED: granule-bound starch synthase 1, chloroplastic/amyloplastic-like [Ziziphus jujuba] | 27.177 | 33.057 | 17.9 | 4 | 6 | 3 | 0.901 | 0.945 | 0.903 | 1.053 | 1.082 | 1.13 | 1.188 | 2.62E-03 |

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| cds.Camellia_sinensis.comp31956_c1_seq1_m.27245 | PREDICTED: granule-bound starch synthase 1, chloroplastic/amyloplastic-like isoform X1 [Juglans regia] | 41.147 | 12.727 | 14.3 | 5 | 6 | 5 | 0.908 | 0.914 | 0.968 | 1.063 | 1.099 | 1.083 | 1.163 | 2.54E-03 |
| cds.Camellia_sinensis.comp31957_c0_seq1_m.21585 | PREDICTED: ATP sulfurylase 1, chloroplastic [Vitis vinifera] | 52.087 | 2.2585 | 3.9 | 2 | 3 | 1 | 1.021 | 1.154 | 1.015 | 0.905 | 0.935 | 0.957 | 0.877 | 4.43E-02 |
| cds.Camellia_sinensis.comp31970_c0_seq1_m.27609 | PREDICTED: GDSL esterase/lipase At5g55050 [Vitis vinifera] | 40.373 | 3.1195 | 5.6 | 2 | 3 | 2 | 0.959 | 1.106 | 1.098 | 0.953 | 0.948 | 0.937 | 0.897 | 1.50E-01 |
| cds.Camellia_sinensis.comp31972_c0_seq3_m.32434 | PREDICTED: LOW QUALITY PROTEIN: ammonium transporter 1 member 2 [Citrus | 28.097 | 58.859 | 18.9 | 4 | 8 | 4 | 1.054 | 0.997 | 0.98 | 0.995 | 1.003 | 1.001 | 0.989 | 6.92E-01 |

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| cds.Camellia_sinensis.comp31973_c2_seq4_m.32928 | PREDICTED: protein-lysine N-methyltransferase Mettl10-like [Daucus carota subsp. sativus] | 37.398 | 3.0913 | 20.8 | 6 | 6 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp31973_c2_seq5_m.36078 | PREDICTED: protein-lysine N-methyltransferase Mettl10 [Vitis vinifera] | 37.447 | 24.782 | 25.8 | 7 | 7 | 2 | 0.927 | 1.001 | 1.04 | 1.037 | 0.881 | 1.131 | 1.027 | 7.92E-01 |
| cds.Camellia_sinensis.comp31974_c0_seq2_m.16924 | PREDICTED: T-complex protein 1 subunit delta [Cucumis melo] | 57.783 | 97.147 | 30.5 | 18 | 31 | 18 | 0.918 | 0.958 | 0.941 | 1.069 | 1.049 | 1.063 | 1.129 | 8.59E-04 |
| cds.Camellia_sinensis.comp31976_c1_seq1_m.38493 | PREDICTED: ferritin-3, chloroplastic [Theobroma cacao] | 28.646 | 153.31 | 42.4 | 10 | 88 | 10 | 0.948 | 0.949 | 0.974 | 1.061 | 1.06 | 1.043 | 1.102 | 7.41E-04 |

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| cds.Camellia_sinensis.comp31977_c0_seq1_m.18004 | PREDICTED: serine/threonine-protein kinase STY46-like [Gossypium arboreum] | 48.339 | 12.914 | 18.6 | 9 | 10 | 8 | 0.954 | 0.977 | 1.045 | 1.007 | 1.025 | 1.02 | 1.026 | 4.03E-01 |
| cds.Camellia_sinensis.comp31981_c0_seq1_m.2451 | PREDICTED: structural maintenance of chromosomes protein 3 [Daucus carota subsp. sativus] | 76.744 | 7.1283 | 5.5 | 4 | 4 | 4 | 1.098 | 1.138 | 1.051 | 0.902 | 0.943 | 0.927 | 0.843 | 2.98E-03 |
| cds.Camellia_sinensis.comp31981_c0_seq1_m.2452 | PREDICTED: structural maintenance of chromosomes protein 3 [Vitis vinifera] | 63.56 | 8.4056 | 5.8 | 4 | 5 | 4 | 1.059 | 1.108 | 1.146 | 0.873 | 0.884 | 0.886 | 0.798 | 6.41E-04 |
| cds.Camellia_sinensis.comp31984_c0_seq1_m.21525 | PREDICTED: arabinosyltransferase RRA3-like [Nelumbo nucifera] | 48.963 | 2.9882 | 2.3 | 1 | 1 | 1 | 1.008 | 1.028 | 0.895 | 1.044 | 1.011 | 1.027 | 1.052 | 3.05E-01 |

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| cds.Camellia_sinensis.comp31984_c1_seq4_m.33674 | adaptin ear-binding coat-associated protein 1 [Medicago truncatula] | 30.531 | 24.374 | 13.4 | 3 | 3 | 3 | 1.054 | 0.976 | 1.056 | 0.934 | 0.981 | 0.956 | 0.93 | 7.23E-02 |
| cds.Camellia_sinensis.comp31984_c2_seq1_m.13214 | peptidyl-prolyl cis-trans isomerase CYP71 [Cajanus cajan] | 37.666 | 3.5294 | 9.6 | 3 | 3 | 3 | 0.934 | 1.01 | 0.976 | 1.054 | 1.005 | 1.044 | 1.063 | 8.57E-02 |
| cds.Camellia_sinensis.comp31984_c2_seq1_m.13215 | PREDICTED: peptidyl-prolyl cis-trans isomerase CYP71-like [Gossypium hirsutum] | 17.258 | 2.6346 | 11.8 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp31990_c0_seq1_m.12729 | PREDICTED: CSC1-like protein HYP1 isoform X2 [Vitis vinifera] | 57.491 | 7.3314 | 8.3 | 4 | 4 | 4 | 1.006 | 0.99 | 0.945 | 0.949 | 1.049 | 1.068 | 1.043 | 3.80E-01 |

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| cds.Camellia_sinensis.comp32000_c0_seq1_m.11354 | PREDICTED: FRIGIDA-like protein 3 [Vitis vinifera] | 42.698 | 42.802 | 25.6 | 9 | 12 | 9 | 1.019 | 1.051 | 1.03 | 0.958 | 1.015 | 0.938 | 0.939 | 6.61E-02 |
| cds.Camellia_sinensis.comp32006_c0_seq1_m.11509 | PREDICTED: thylakoid lumenal 17.9 kDa protein, chloroplastic [Nelumbo nucifera] | 25.818 | 42.195 | 33.6 | 6 | 10 | 6 | 0.963 | 0.909 | 0.946 | 1.04 | 1.013 | 1.094 | 1.117 | 1.76E-02 |
| cds.Camellia_sinensis.comp32007_c0_seq2_m.24766 | PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase 2 [Vigna angularis] | 28.159 | 10.727 | 11.2 | 3 | 3 | 3 | 0.97 | 1.011 | 1.117 | 0.977 | 0.966 | 0.966 | 0.939 | 2.83E-01 |
| cds.Camellia_sinensis.comp32009_c0_seq1_m.9085 | PREDICTED: ABC transporter D family member 2, chloroplastic [Nelumbo nucifera] | 20.86 | 1.9763 | 5.3 | 1 | 1 | 1 | 0.958 | 0.969 | 1.042 | 0.934 | 1.027 | 1.08 | 1.024 | 6.72E-01 |

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| cds.Camellia_sinensis.comp32011_c0_seq1_m.24958 | PREDICTED: mitochondrial import inner membrane translocase subunit TIM17-2-like [Daucus carota subsp.sativus] | 24.116 | 1.8303 | 3.8 | 1 | 1 | 1 | 0.979 | 1.004 | 0.995 | 1.009 | 0.993 | 1.031 | 1.018 | 2.38E-01 |
| cds.Camellia_sinensis.comp32013_c0_seq2_m.11407 | PREDICTED: pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha [Sesamum indicum] | 67.174 | 6.2866 | 23.2 | 11 | 15 | 2 | 1.004 | 1.058 | 0.981 | 0.907 | 0.936 | 0.948 | 0.917 | 2.93E-02 |
| cds.Camellia_sinensis.comp32013_c0_seq3_m.12719 | PREDICTED: pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha [Sesamum indicum] | 67.297 | 59.581 | 27.7 | 13 | 17 | 4 | 0.945 | 0.966 | 0.949 | 1.029 | 1.048 | 1.087 | 1.106 | 4.48E-03 |

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| cds.Camellia_sinensis.comp32014_c0_seq2_m.20692 | PREDICTED: methylthioribose kinase [Vitis vinifera] | 47.734 | 74.525 | 32.5 | 13 | 21 | 13 | 0.935 | 0.963 | 0.936 | 1.055 | 1.064 | 1.059 | 1.121 | 3.23E-04 |
| cds.Camellia_sinensis.comp32016_c1_seq1_m.16328 | PREDICTED: probable leucine-rich repeat receptor-like protein kinase At5g49770 [Capsicum | 74.639 | 3.6044 | 3.5 | 3 | 3 | 2 | 0.934 | 0.952 | 0.973 | 1.086 | 1.025 | 1.058 | 1.108 | 7.38E-03 |
| cds.Camellia_sinensis.comp32023_c0_seq13_m.7956 | PREDICTED: conserved oligomeric Golgi complex subunit 4 [Erythranthe guttata] | 65.246 | 1.7826 | 2 | 1 | 1 | 1 | 0.951 | 1.026 | 1.126 | 1.021 | 0.96 | 0.929 | 0.938 | 3.27E-01 |
| cds.Camellia_sinensis.comp32026_c0_seq16_m.14730 | PREDICTED: glucosidase 2 subunit beta isoform X1 [Vitis vinifera] | 69.482 | 2.4058 | 3.4 | 2 | 2 | 2 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32027_c0_seq1_m.3932 | PREDICTED: ATPase 10, plasma membrane-type [Eucalyptus grandis] | 104.46 | 196.46 | 38.8 | 32 | 80 | 22 | 0.998 | 0.988 | 1.01 | 1 | 1.012 | 1.004 | 1.007 | 4.10E-01 |
| cds.Camellia_sinensis.comp32027_c0_seq4_m.14972 | transmembrane protein, putative [Medicago truncatula] | 26.309 | 8.107 | 15.8 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp32029_c0_seq1_m.29689 | PREDICTED: photosynthetic NDH subunit of subcomplex B 2, chloroplastic [Juglans regia] | 40.599 | 58.33 | 20.1 | 6 | 7 | 6 | 0.994 | 0.986 | 1.012 | 1.022 | 1.015 | 0.985 | 1.01 | 5.09E-01 |
| cds.Camellia_sinensis.comp32030_c0_seq3_m.42437 | PREDICTED: thymidylate kinase isoform X2 [Sesamum indicum] | 15.97 | 2.9187 | 7.6 | 1 | 1 | 1 | 0.96 | 1.085 | 0.955 | 1 | 0.97 | 1.04 | 1.003 | 9.24E-01 |
| cds.Camellia_sinensis.comp32031_c0_seq1_m.16650 | PREDICTED: citrate synthase, glyoxysomal [Sesamum indicum] | 56.278 | 49.115 | 21.5 | 10 | 16 | 10 | 0.965 | 0.967 | 0.984 | 1.059 | 1.029 | 1.02 | 1.066 | 7.86E-03 |

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| cds.Camellia_sinensis.comp32035_c0_seq3_m.19627 | PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit isoform X3 [Vitis vinifera] | 48.95 | 14.938 | 13.5 | 6 | 11 | 6 | 1.002 | 0.987 | 0.955 | 1.01 | 1.043 | 1.016 | 1.042 | 7.34E-02 |
| cds.Camellia_sinensis.comp32035_c0_seq4_m.21981 | PREDICTED: scopoletin glucosyltransferase [Theobroma cacao] | 52.919 | 24.768 | 18.4 | 9 | 15 | 9 | 0.93 | 0.978 | 0.96 | 1.067 | 1.072 | 1.033 | 1.106 | 5.78E-03 |
| cds.Camellia_sinensis.comp32036_c0_seq1_m.17656 | PREDICTED: probable solanesyl-diphosphate synthase 3, chloroplastic [Ricinus communis] | 46.323 | 4.6719 | 6.7 | 3 | 4 | 3 | 0.974 | 0.973 | 1.02 | 0.968 | 0.957 | 1.118 | 1.026 | 6.83E-01 |

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| cds.Camellia_sinensis.comp32037_c2_seq4_m.5633 | PREDICTED: KH domain-containing protein At4g18375 isoform X2 [Eucalyptus grandis] | 58.48 | 97.132 | 40.2 | 19 | 24 | 17 | 1.022 | 1.04 | 1.04 | 0.996 | 0.956 | 0.946 | 0.934 | 1.52E-02 |
| cds.Camellia_sinensis.comp32037_c2_seq5_m.11381 | PREDICTED: KH domain-containing protein At4g18375-like isoform X1 [Nicotiana tabacum] | 57.174 | 128.33 | 26.6 | 14 | 18 | 13 | 1.042 | 1.059 | 1.049 | 0.933 | 0.963 | 0.957 | 0.906 | 7.76E-04 |
| cds.Camellia_sinensis.comp32038_c0_seq1_m.13087 | PREDICTED: auxilin-related protein 2 [Vitis vinifera] | 84.421 | 4.8131 | 2.6 | 2 | 3 | 2 | 1.144 | 1.224 | 1.125 | 0.693 | 0.791 | 0.966 | 0.701 | 2.20E-02 |
| cds.Camellia_sinensis.comp32040_c0_seq90_m.9512 | PREDICTED: probable lactoylglutathione lyase, chloroplastic [Citrus sinensis] | 38.267 | 65.407 | 36.8 | 12 | 46 | 6 | 0.962 | 0.95 | 0.983 | 1.04 | 1.031 | 1.032 | 1.072 | 2.56E-03 |

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| cds.Camellia_sinensis.comp32041_c0_seq1_m.33904 | PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 3 [Vitis vinifera] | 32.839 | 6.4579 | 16.1 | 4 | 4 | 4 | 0.873 | 0.955 | 0.922 | 1.136 | 1.104 | 1.056 | 1.199 | 5.74E-03 |
| cds.Camellia_sinensis.comp32054_c0_seq1_m.4386 | PREDICTED: exportin-2 [Daucus carota subsp. sativus] | 81.504 | 18.972 | 4.5 | 4 | 4 | 4 | 0.947 | 0.99 | 0.937 | 1.035 | 1.026 | 1.053 | 1.084 | 1.22E-02 |
| cds.Camellia_sinensis.comp32054_c0_seq1_m.4387 | PREDICTED: exportin-2 [Vitis vinifera] | 27.506 | 24.096 | 16.3 | 3 | 5 | 3 | 0.942 | 0.992 | 0.977 | 1.06 | 1.05 | 1.003 | 1.069 | 4.32E-02 |
| cds.Camellia_sinensis.comp32055_c0_seq13_m.33899 | PREDICTED: inositol-pentakisphosphate 2-kinase [Vitis vinifera] | 26.37 | 1.2853 | 3.8 | 1 | 1 | 1 | 0.99 | 0.996 | 1.065 | 0.997 | 0.987 | 0.973 | 0.969 | 2.76E-01 |
| cds.Camellia_sinensis.comp32062_c0_seq4_m.10927 | PREDICTED: putative clathrin assembly protein At2g25430 [Sesamum | 71.016 | 22.404 | 9.9 | 5 | 7 | 5 | 1.228 | 1.063 | 0.947 | 0.863 | 0.938 | 0.969 | 0.855 | 1.41E-01 |

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| cds.Camellia_sinensis.comp32072_c0_seq1_m.9129 | PREDICTED: zinc finger BED domain-containing protein DAYSLEEPER-like [Nicotiana tabacum] | 77.118 | 22.41 | 9.1 | 5 | 6 | 2 | 0.963 | 0.992 | 0.979 | 1.004 | 1.009 | 1.069 | 1.05 | 8.93E-02 |
| cds.Camellia_sinensis.comp32072_c0_seq2_m.9179 | PREDICTED: zinc finger BED domain-containing protein DAYSLEEPER-like [Nicotiana tabacum] | 77.498 | 1.802 | 6.5 | 4 | 5 | 1 | 0.955 | 1.09 | 0.989 | 0.98 | 0.971 | 1.023 | 0.98 | 6.85E-01 |
| cds.Camellia_sinensis.comp32081_c0_seq1_m.30822 | PREDICTED: omega-amidase, chloroplastic [Nicotiana attenuata] | 40.89 | 120.55 | 28.6 | 9 | 25 | 9 | 0.927 | 0.948 | 0.965 | 1.075 | 1.034 | 1.05 | 1.112 | 2.78E-03 |

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| cds.Camellia_sinensis.comp32088_c0_seq1_m.18859 | PREDICTED: 2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxononatrienedioate hydrolase isoform X1 [Vigna radiata var. radiata] | 54.271 | 2.0886 | 2.2 | 1 | 1 | 1 | 1.099 | 0.987 | 0.957 | 0.952 | 0.924 | 1.071 | 0.968 | 6.27E-01 |
| cds.Camellia_sinensis.comp32093_c0_seq1_m.17441 | PREDICTED: pentatricopeptide repeat-containing protein At5g13770, chloroplastic [Nicotiana tomentosiformis] | 72.428 | 1.2708 | 1.4 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32094_c0_seq1_m.5391 | PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase 4, plasma membrane-type-like [Ziziphus jujuba] | 116.18 | 23.398 | 7.9 | 8 | 12 | 6 | 0.962 | 0.94 | 0.921 | 1.069 | 1.051 | 1.076 | 1.132 | 9.97E-04 |
| cds.Camellia_sinensis.comp32095_c0_seq1_m.21396 | PREDICTED: fructose-1,6-bisphosphatase, cytosolic [Jatropha curcas] | 51.329 | 79.64 | 28.3 | 10 | 11 | 10 | 0.93 | 0.945 | 0.944 | 1.054 | 1.088 | 1.084 | 1.144 | 2.80E-04 |
| cds.Camellia_sinensis.comp32098_c0_seq3_m.35699 | PREDICTED: glycine-rich RNA-binding protein 2, mitochondrial-like isoform X2 [Nicotiana tomentosiformis] | 28.961 | 134.76 | 21.5 | 4 | 8 | 1 | 1.077 | 0.956 | 0.998 | 1.046 | 0.977 | 0.95 | 0.981 | 6.96E-01 |

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| cds.Camellia_sinensis.comp32098_c0_seq8_m.39893 | PREDICTED: glycine-rich RNA-binding protein blt801 [Vitis vinifera] | 16.541 | 1.8011 | 37.3 | 4 | 9 | 1 | 0.976 | 1.014 | 0.973 | 0.989 | 1.062 | 1 | 1.03 | 3.25E-01 |
| cds.Camellia_sinensis.comp32098_c1_seq1_m.2920 | PREDICTED: RNA-binding protein Musashi homolog 2 [Vitis vinifera] | 40.367 | 43.45 | 22.1 | 7 | 9 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp32098_c1_seq4_m.23978 | PREDICTED: heterogeneous nuclear ribonucleoprotein A/B [Ziziphus jujuba] | 39.804 | 2.5328 | 19.4 | 6 | 9 | 1 | 0.941 | 0.985 | 0.967 | 1.033 | 1.057 | 1.041 | 1.082 | 6.02E-03 |
| cds.Camellia_sinensis.comp32098_c3_seq1_m.36836 | PREDICTED: calmodulin-7 isoform X1 [Vitis vinifera] | 16.848 | 125.03 | 55 | 11 | 46 | 11 | 1.001 | 0.967 | 0.97 | 1.004 | 1.046 | 1.034 | 1.05 | 4.21E-02 |

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| cds.Camellia_sinensis.comp32107_c0_seq1_m.31113 | PREDICTED: probable inactive purple acid phosphatase 27 [Juglans regia] | 48.189 | 9.3346 | 9.5 | 4 | 4 | 3 | 0.796 | 0.991 | 0.916 | 1.18 | 1.131 | 1.045 | 1.242 | 4.03E-02 |
| cds.Camellia_sinensis.comp32112_c0_seq2_m.32185 | PREDICTED: N-(5'-phosphoribosyl)anthranilate isomerase 1, chloroplastic isoform X2 [Ricinus communis] | 29.997 | 8.5974 | 13.8 | 3 | 3 | 3 | 1.093 | 1.044 | 1.048 | 0.919 | 0.943 | 0.937 | 0.879 | 1.48E-03 |
| cds.Camellia_sinensis.comp32115_c0_seq1_m.13747 | PREDICTED: transcription initiation factor IIF subunit alpha-like isoform X1 [Juglans regia] | 59.741 | 1.9279 | 3.3 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp32116_c0_seq3_m.15155 | PREDICTED: probable protein phosphatase 2C 60 isoform X1 [Nelumbo nucifera] | 25.977 | 6.0133 | 15.8 | 5 | 7 | 4 | 0.942 | 0.946 | 0.993 | 1.05 | 1.035 | 1.039 | 1.084 | 9.62E-03 |
| cds.Camellia_sinensis.comp32116_c0_seq6_m.22215 | PREDICTED: probable protein phosphatase 2C 60 [Pyrus x bretschneideri] | 10.92 | 1.3693 | 8.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32119_c0_seq1_m.26230 | PREDICTED: protein FLX-like 1 [Nelumbo nucifera] | 33.426 | 4.9706 | 9.1 | 3 | 3 | 2 | 1.008 | 0.99 | 0.988 | 1.048 | 0.932 | 1.044 | 1.013 | 7.88E-01 |
| cds.Camellia_sinensis.comp32127_c0_seq1_m.30393 | PREDICTED: short-chain dehydrogenase TIC 32, chloroplastic [Vitis vinifera] | 34.14 | 63.954 | 16.8 | 3 | 4 | 3 | 0.975 | 1.035 | 0.968 | 0.963 | 1.018 | 1.009 | 1.004 | 8.86E-01 |
| cds.Camellia_sinensis.comp32128_c0_seq1_m.17622 | PREDICTED: fumarylacetoacetase [Jatropha curcas] | 42.157 | 52.045 | 16.7 | 6 | 8 | 6 | 1.05 | 1.03 | 1.052 | 0.945 | 0.963 | 0.949 | 0.912 | 4.82E-04 |

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| cds.Camellia_sinensis.comp32129_c0_seq4_m.28333 | PREDICTED: sugar transporter ERD6-like 5 isoform X1 [Daucus carota subsp. sativus] | 47.497 | 8.9092 | 5.9 | 4 | 5 | 4 | 0.946 | 0.972 | 0.988 | 1.05 | 1.076 | 1.023 | 1.084 | 1.42E-02 |
| cds.Camellia_sinensis.comp32129_c0_seq5_m.28757 | PREDICTED: syntaxin-121-like [Juglans regia] | 22.938 | 17.293 | 15.2 | 3 | 4 | 3 | 0.917 | 0.925 | 0.976 | 1.062 | 1.087 | 1.093 | 1.15 | 2.78E-03 |
| cds.Camellia_sinensis.comp32133_c0_seq2_m.52215 | PREDICTED: purple acid phosphatase 2-like [Nicotiana tabacum] | 15.569 | 1.7413 | 5 | 1 | 3 | 1 | 0.961 | 0.997 | 1.046 | 0.994 | 1.051 | 0.967 | 1.003 | 9.43E-01 |
| cds.Camellia_sinensis.comp32134_c0_seq1_m.14166 | PREDICTED: sorcin [Eucalyptus grandis] | 19.439 | 1.9488 | 5.9 | 1 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32141_c1_seq1_m.28717 | PREDICTED: phosphoglucan phosphatase DSP4, amyloplastic-like isoform X2 [Juglans regia] | 44.121 | 17.365 | 10.4 | 4 | 4 | 3 | 0.996 | 0.986 | 1.045 | 1.004 | 1.028 | 0.952 | 0.986 | 6.43E-01 |

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| cds.Camellia_sinensis.comp32142_c0_seq1_m.26960 | oxidoreductase family protein [Populus trichocarpa] | 34.503 | 52.481 | 31.7 | 10 | 22 | 10 | 0.977 | 0.967 | 0.991 | 1.015 | 1.03 | 1.025 | 1.046 | 5.64E-03 |
| cds.Camellia_sinensis.comp32145_c0_seq15_m.12715 | PREDICTED: UDP-sugar pyrophosphorylase [Ziziphus jujuba] | 68.995 | 43.801 | 24.8 | 17 | 23 | 17 | 1.005 | 1.001 | 1.021 | 0.995 | 0.975 | 1 | 0.981 | 1.25E-01 |
| cds.Camellia_sinensis.comp32151_c0_seq1_m.30264 | PREDICTED: anamorsin homolog isoform X3 [Vitis vinifera] | 29.862 | 15.633 | 20.7 | 4 | 5 | 4 | 0.942 | 1.075 | 1.001 | 0.989 | 1.053 | 0.946 | 0.99 | 8.56E-01 |
| cds.Camellia_sinensis.comp32152_c0_seq1_m.21546 | PREDICTED: D-glycerate 3-kinase, chloroplastic [Juglans regia] | 51.891 | 37.865 | 20.8 | 8 | 16 | 8 | 1.01 | 1.004 | 0.986 | 0.992 | 0.999 | 0.972 | 0.988 | 3.20E-01 |
| cds.Camellia_sinensis.comp32154_c0_seq34_m.14388 | lycopene beta/epsilon cyclase [Medicago truncatula] | 24.114 | 7.3996 | 11.3 | 2 | 2 | 2 | 1.033 | 0.972 | 1.046 | 1.046 | 0.927 | 0.981 | 0.968 | 4.72E-01 |

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| cds.Camellia_sinensis.comp32155_c0_seq1_m.31991 | PREDICTED: succinate dehydrogenase subunit 5, mitochondrial [Vitis vinifera] | 29.706 | 125.41 | 42.7 | 9 | 19 | 9 | 0.999 | 1.017 | 0.985 | 1.024 | 0.981 | 0.982 | 0.995 | 7.91E-01 |
| cds.Camellia_sinensis.comp32158_c0_seq2_m.17123 | PREDICTED: protein ASPARTIC PROTEASE IN GUARD CELL 1-like [Nicotiana tabacum] | 49.376 | 62.233 | 20.3 | 6 | 6 | 6 | 1.008 | 1.064 | 1.095 | 0.967 | 0.916 | 0.89 | 0.876 | 1.80E-02 |
| cds.Camellia_sinensis.comp32158_c1_seq1_m.14727 | PREDICTED: patellin-3 [Populus euphratica] | 57.719 | 176.63 | 40.6 | 19 | 45 | 18 | 0.947 | 0.92 | 0.95 | 1.073 | 1.078 | 1.059 | 1.14 | 3.42E-04 |
| cds.Camellia_sinensis.comp32162_c0_seq1_m.28224 | PREDICTED: 3-hydroxyisobutyryl-CoA hydrolase 1-like [Juglans regia] | 43.603 | 12.381 | 15 | 5 | 7 | 3 | 0.961 | 1.047 | 1.022 | 1.007 | 0.951 | 1.023 | 0.984 | 6.58E-01 |

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| cds.Camellia_sinensis.comp32162_c0_seq3_m.43558 | PREDICTED: 3-hydroxyisobutyryl-CoA hydrolase 1 isoform X1 [Vitis vinifera] | 28.973 | 48.369 | 24.2 | 5 | 8 | 3 | 0.887 | 1.06 | 0.997 | 1.046 | 0.959 | 1.075 | 1.046 | 4.97E-01 |
| cds.Camellia_sinensis.comp32168_c0_seq1_m.16101 | PREDICTED: regulation of nuclear pre-mRNA domain-containing protein 2 isoform X2 [Theobroma cacao] | 55.617 | 1.8075 | 2 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp32175_c0_seq1_m.9849 | PREDICTED: trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1 [Vitis vinifera] | 75.906 | 22.214 | 13.8 | 10 | 10 | 9 | 1.053 | 1.043 | 1.016 | 0.959 | 0.985 | 0.962 | 0.934 | 7.36E-03 |
| cds.Camellia_sinensis.comp32183_c0_seq1_m.8166 | PREDICTED: UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase-like [Nicotiana tabacum] | 86.924 | 2.953 | 2 | 2 | 2 | 2 | 1.063 | 1.098 | 1.123 | 0.872 | 0.914 | 0.91 | 0.821 | 8.40E-04 |

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| cds.Camellia_sinensis.comp32188_c0_seq1_m.41118 | PREDICTED: mitochondrial outer membrane protein porin 2-like [Nicotiana attenuata] | 29.782 | 17.572 | 37.4 | 11 | 26 | 5 | 1.023 | 1.018 | 0.985 | 0.97 | 1.018 | 1.027 | 0.996 | 8.67E-01 |
| cds.Camellia_sinensis.comp32188_c0_seq2_m.46109 | PREDICTED: mitochondrial outer membrane protein porin 2-like [Nicotiana attenuata] | 24.947 | 54.364 | 41.7 | 11 | 29 | 5 | 0.971 | 0.999 | 0.988 | 1.003 | 1.022 | 1.023 | 1.03 | 4.57E-02 |
| cds.Camellia_sinensis.comp32189_c0_seq1_m.16263 | PREDICTED: inosine-5'-monophosphate dehydrogenase 2-like isoform X1 [Nelumbo nucifera] | 53.517 | 95.67 | 30.2 | 12 | 22 | 12 | 0.948 | 0.921 | 0.941 | 1.064 | 1.07 | 1.062 | 1.137 | 1.38E-04 |
| cds.Camellia_sinensis.comp32202_c0_seq1_m.40220 | PREDICTED: 40S ribosomal protein S24-1 [Sesamum indicum] | 15.8 | 2.504 | 11.7 | 2 | 5 | 2 | 1.108 | 1.129 | 1.076 | 0.859 | 0.894 | 0.928 | 0.809 | 1.30E-03 |

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| cds.Camellia_sinensis.comp32203_c0_seq1_m.3830 | PREDICTED: presequence protease 1, chloroplastic/mitochondrial-like isoform X1 [Ipomoea nil] | 134.51 | 323.31 | 47.1 | 54 | 133 | 54 | 0.998 | 0.993 | 0.99 | 1.008 | 1.01 | 1.013 | 1.017 | 3.78E-03 |
| cds.Camellia_sinensis.comp32205_c0_seq1_m.13071 | PREDICTED: outer envelope protein 64, chloroplastic-like [Nelumbo nucifera] | 64.388 | 4.7647 | 10.5 | 7 | 7 | 4 | 1.043 | 1.014 | 0.95 | 0.946 | 0.967 | 1.078 | 0.995 | 9.05E-01 |
| cds.Camellia_sinensis.comp32205_c0_seq2_m.13339 | PREDICTED: outer envelope protein 64, chloroplastic-like [Nelumbo nucifera] | 64.334 | 48.641 | 24.2 | 13 | 16 | 10 | 0.953 | 0.969 | 0.959 | 1.043 | 1.078 | 1.052 | 1.101 | 9.38E-04 |
| cds.Camellia_sinensis.comp32207_c0_seq1_m.13675 | PREDICTED: phosphomannomutase/phosphoglucomutase isoform X1 [Prunus | 69.24 | 40.24 | 20.3 | 11 | 18 | 11 | 0.976 | 0.954 | 0.971 | 1.026 | 1.018 | 1.048 | 1.066 | 4.54E-03 |

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| cds.Camellia_sinensis.comp32209_c0_seq1_m.29095 | arginase 1 [Solanum lycopersicum] | 41.886 | 86.806 | 30.4 | 10 | 21 | 9 | 1.041 | 1.117 | 1.08 | 0.938 | 0.922 | 0.914 | 0.857 | 2.08E-03 |
| cds.Camellia_sinensis.comp32212_c1_seq1_m.2978 | PREDICTED: pumilio homolog 2 [Theobroma cacao] | 113.63 | 30.888 | 5.8 | 4 | 4 | 4 | 1.041 | 1.014 | 1.017 | 1.067 | 0.957 | 1.009 | 0.987 | 6.95E-01 |
| cds.Camellia_sinensis.comp32212_c2_seq1_m.2678 | PREDICTED: ABC transporter B family member 1 [Ipomoea nil] | 147.41 | 7.0531 | 5.1 | 5 | 6 | 4 | 1.104 | 0.98 | 1.126 | 0.895 | 0.952 | 0.927 | 0.864 | 3.70E-02 |
| cds.Camellia_sinensis.comp32214_c0_seq1_m.34384 | PREDICTED: 14-3-3-like protein GF14 kappa [Daucus carota subsp. sativus] | 28.611 | 80.223 | 53.8 | 13 | 33 | 6 | 0.951 | 0.953 | 0.881 | 1.108 | 1.104 | 1.051 | 1.172 | 6.84E-03 |
| cds.Camellia_sinensis.comp32214_c0_seq3_m.43656 | PREDICTED: 14-3-3-like protein GF14 kappa [Daucus carota subsp. sativus] | 20.201 | 56.274 | 47.5 | 6 | 20 | 3 | 1.017 | 1.01 | 0.953 | 0.984 | 1.083 | 0.993 | 1.027 | 5.20E-01 |

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| cds.Camellia_sinensis.comp32220_c0_seq1_m.15769 | PREDICTED: trigger factor-like protein TIG, Chloroplastic [Vitis vinifera] | 61.406 | 133.2 | 35.8 | 18 | 30 | 18 | 1.011 | 0.999 | 0.997 | 1.006 | 1.009 | 0.993 | 1 | 9.63E-01 |
| cds.Camellia_sinensis.comp32222_c0_seq1_m.16474 | PREDICTED: BTB/POZ domain-containing protein At5g48800 isoform X1 [Vitis vinifera] | 69.478 | 1.2464 | 3.6 | 3 | 3 | 2 | 0.997 | 0.975 | 1.051 | 0.99 | 1.012 | 0.985 | 0.988 | 6.52E-01 |
| cds.Camellia_sinensis.comp32225_c0_seq2_m.10673 | PREDICTED: sulfite reductase [ferredoxin], chloroplastic [Citrus sinensis] | 72.426 | 78.367 | 30.8 | 19 | 39 | 19 | 0.989 | 0.978 | 0.971 | 1.021 | 1.028 | 1.014 | 1.043 | 3.30E-03 |
| cds.Camellia_sinensis.comp32228_c0_seq1_m.50575 | PREDICTED: putative lipid-binding protein At4g00165 [Juglans regia] | 12.894 | 1.3554 | 6.5 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp32229_c0_seq1_m.3901 | PREDICTED: phosphoenolpyruvate carboxylase 4 [Eucalyptus grandis] | 119.31 | 126.11 | 26.4 | 27 | 37 | 27 | 1.02 | 1.004 | 1.029 | 0.978 | 0.983 | 0.978 | 0.963 | 6.80E-03 |
| cds.Camellia_sinensis.comp32232_c0_seq1_m.2058 | PREDICTED: ABC transporter C family member 10-like [Populus euphratica] | 147.83 | 11.382 | 2.9 | 3 | 5 | 1 | 1.162 | 0.973 | 0.83 | 1.012 | 0.99 | 1.025 | 1.021 | 7.88E-01 |
| cds.Camellia_sinensis.comp32233_c0_seq3_m.16588 | PREDICTED: serine/threonine-protein phosphatase 5 isoform X2 [Jatropha curcas] | 54.998 | 3.4471 | 6.2 | 3 | 4 | 3 | 0.982 | 0.994 | 0.988 | 1.076 | 1.031 | 0.949 | 1.031 | 5.13E-01 |
| cds.Camellia_sinensis.comp32237_c0_seq1_m.38904 | | 13.007 | 32.337 | 42.6 | 6 | 14 | 6 | 1.102 | 0.986 | 0.994 | 0.902 | 0.995 | 1.025 | 0.948 | 3.67E-01 |

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| cds.Camellia_sinensis.comp32238_c0_seq2_m.1501 | PREDICTED: nuclear pore complex protein NUP160 [Vitis vinifera] | 168.45 | 2.9997 | 1.5 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp32239_c0_seq1_m.9961 | PREDICTED: prolyl endopeptidase [Jatropha curcas] | 88.772 | 55.459 | 10.9 | 10 | 23 | 8 | 1.001 | 1.003 | 0.995 | 0.988 | 1.024 | 1.02 | 1.011 | 4.03E-01 |
| cds.Camellia_sinensis.comp32240_c0_seq10_c0_seq1_m.17125 | PREDICTED: pre-mRNA-processing factor 19 [Vitis vinifera] | 56.825 | 13.909 | 13.5 | 7 | 9 | 6 | 0.929 | 0.973 | 1.006 | 1.044 | 0.963 | 1.003 | 1.035 | 3.53E-01 |
| cds.Camellia_sinensis.comp32240_c0_seq30_c0_seq3_m.46763 | PREDICTED: pre-mRNA-processing factor 19 [Vitis vinifera] | 13.225 | 4.1548 | 30.8 | 4 | 6 | 3 | 0.879 | 0.953 | 1.001 | 0.981 | 1.141 | 1.077 | 1.129 | 1.06E-01 |
| cds.Camellia_sinensis.comp32243_c0_seq1_m.3211 | PREDICTED: paladin [Vitis vinifera] | 142.95 | 1.5251 | 0.8 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp32245_c0_seq1_m.4096 | PREDICTED: probable 26S protease regulatory subunit 10B isoform X2 [Juglans regia] | 50.495 | 1.3175 | 2.4 | 1 | 1 | 1 | 0.943 | 1.114 | 0.957 | 0.963 | 0.997 | 1.034 | 0.993 | 9.45E-01 |
| cds.Camellia_sinensis.comp32245_c0_seq1_m.4098 | PREDICTED: probable 26S protease regulatory subunit 10B isoform X1 [Juglans regia] | 19.299 | 2.4147 | 13.5 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp32254_c0_seq1_m.30872 | PREDICTED: strigolactone esterase D14 [Juglans regia] | 32.449 | 36.651 | 21.9 | 6 | 12 | 6 | 1.024 | 1.049 | 1.055 | 0.945 | 0.961 | 0.941 | 0.91 | 1.08E-03 |
| cds.Camellia_sinensis.comp32262_c0_seq1_m.19868 | PREDICTED: actin-7 [Prunus mume] | 41.695 | 253.54 | 47.5 | 17 | 120 | 2 | 0.991 | 1.021 | 1.004 | 1.015 | 0.98 | 0.988 | 0.989 | 4.65E-01 |

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| cds.Camellia_sinensis.comp32262_c1_seq1_m.35881 | PREDICTED: 60S ribosomal protein L10a [Phoenix dactylifera] | 24.516 | 24.037 | 32.4 | 7 | 17 | 7 | 1.039 | 1.037 | 1.029 | 0.962 | 1 | 0.974 | 0.946 | 8.94E-03 |
| cds.Camellia_sinensis.comp32271_c0_seq1_m.19075 | PREDICTED: glutathione synthetase, chloroplastic isoform X1 [Vitis vinifera] | 62.209 | 15.9 | 11.7 | 7 | 9 | 6 | 0.895 | 0.94 | 0.939 | 1.102 | 1.042 | 1.085 | 1.164 | 2.84E-03 |
| cds.Camellia_sinensis.comp32271_c0_seq2_m.46601 | PREDICTED: glutathione synthetase, chloroplastic isoform X3 [Vitis vinifera] | 25.792 | 8.9201 | 13.5 | 3 | 4 | 2 | 0.995 | 1.015 | 0.993 | 1.079 | 1.005 | 0.929 | 1.003 | 9.74E-01 |
| cds.Camellia_sinensis.comp32272_c0_seq3_m.2750 | PREDICTED: protein MODIFIER OF SNC1 1 [Vitis vinifera] | 99.007 | 2.2957 | 2.2 | 2 | 2 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp32275_c0_seq1_m.40576 | PREDICTED: germin-like protein subfamily T member 1 [Juglans regia] | 22.619 | 29.867 | 27.2 | 5 | 13 | 5 | 0.898 | 0.901 | 0.932 | 1.133 | 1.14 | 1.091 | 1.232 | 3.24E-04 |
| cds.Camellia_sinensis.comp32284_c0_seq1_m.945 | PREDICTED: protein SHOOT GRAVITROPISM 6 isoform X2 [Vitis vinifera] | 62.846 | 5.9657 | 2.1 | 1 | 1 | 1 | 0.959 | 0.981 | 1.025 | 1.146 | 0.988 | 0.928 | 1.033 | 6.85E-01 |
| cds.Camellia_sinensis.comp32284_c0_seq3_m.1022 | PREDICTED: protein SHOOT GRAVITROPISM 6 isoform X4 [Vitis vinifera] | 68.995 | 5.3556 | 5.5 | 3 | 3 | 3 | 0.979 | 0.993 | 0.957 | 1.167 | 0.976 | 0.952 | 1.057 | 4.76E-01 |
| cds.Camellia_sinensis.comp32285_c1_seq7_m.22791 | PREDICTED: serine/threonine-protein kinase HT1-like [Sesamum indicum] | 41.091 | 8.8736 | 6.5 | 2 | 3 | 2 | 0.88 | 0.876 | 0.964 | 1.122 | 1.048 | 1.162 | 1.225 | 9.54E-03 |

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| cds.Camellia_sinensis.comp32288_c0_seq1_m.43494 | peroxidase P7 precursor [Capsicum annuum] | 25.098 | 45.347 | 31.4 | 7 | 15 | 5 | 0.933 | 0.878 | 0.927 | 1.108 | 1.105 | 1.064 | 1.197 | 1.52E-03 |
| cds.Camellia_sinensis.comp32293_c1_seq1_m.24238 | thioredoxin family protein [Populus trichocarpa] | 47.782 | 6.649 | 10.6 | 4 | 5 | 2 | 1.013 | 1.113 | 1.093 | 0.949 | 0.916 | 0.909 | 0.862 | 9.54E-03 |
| cds.Camellia_sinensis.comp32293_c1_seq2_m.25320 | PREDICTED: protein disulfide isomerase-like 2-3 [Juglans regia] | 48.101 | 12.993 | 10.2 | 4 | 5 | 2 | 1.065 | 1.008 | 1.05 | 1.006 | 0.907 | 0.988 | 0.929 | 1.07E-01 |
| cds.Camellia_sinensis.comp32304_c0_seq1_m.3254 | phenylalanine ammonia-lyase family protein [Populus trichocarpa] | 77.185 | 5.9738 | 28.2 | 19 | 41 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32304_c0_seq3_m.11225 | PREDICTED: phenylalanine ammonia-lyase [Vitis vinifera] | 77.077 | 118.08 | 37.8 | 25 | 54 | 6 | 1.375 | 1.378 | 1.392 | 0.561 | 0.579 | 0.587 | 0.417 | 1.92E-07 |

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| cds.Camellia_sinensis.comp32304_c0_seq5_m.38144 | PREDICTED: phenylalanine ammonia-lyase [Vitis vinifera] | 30.151 | 2.475 | 15.7 | 5 | 10 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp32311_c0_seq1_m.42109 | NADPH:QUINONE OXIDOREDUCTASE family protein [Populus trichocarpa] | 22.987 | 38.035 | 31.2 | 4 | 4 | 4 | 0.963 | 1.054 | 1.012 | 1.034 | 0.953 | 0.968 | 0.976 | 5.32E-01 |
| cds.Camellia_sinensis.comp32313_c0_seq1_m.11206 | PREDICTED: protein BONZAI 1-like [Juglans regia] | 65.25 | 1.3509 | 3 | 2 | 2 | 2 | 0.897 | 1.011 | 0.889 | 1.173 | 1.085 | 0.988 | 1.161 | 8.37E-02 |
| cds.Camellia_sinensis.comp32314_c0_seq2_m.7150 | PREDICTED: guanine nucleotide-binding protein subunit beta-2 [Citrus sinensis] | 41.112 | 10.711 | 8 | 3 | 4 | 3 | 0.98 | 0.951 | 0.963 | 1.03 | 1.067 | 1.045 | 1.086 | 3.62E-03 |

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| cds.Camellia_sinensis.comp32315_c0_seq4_m.34834 | PREDICTED: protein LUTEIN DEFICIENT 5, chloroplastic [Ipomoea nil] | 34.82 | 1.8687 | 2.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32321_c0_seq1_m.22581 | PREDICTED: V-type proton ATPase subunit H [Theobrom | 55.987 | 59.034 | 15.4 | 7 | 11 | 7 | 0.967 | 0.959 | 0.974 | 1.044 | 1.077 | 1.006 | 1.078 | 2.07E-02 |
| cds.Camellia_sinensis.comp32323_c0_seq1_m.26511 | PREDICTED: pyruvate dehydrogenase (acetyl-transferring) kinase, mitochondrial-like [Nicotiana attenuata] | 41.962 | 1.5816 | 4.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32324_c0_seq8_m.30857 | PREDICTED: probable polyamine aminopropyl transferase [Malus domestica] | 18.543 | 3.8695 | 5.9 | 1 | 1 | 1 | 1.069 | 1.053 | 0.972 | 0.993 | 0.927 | 0.979 | 0.937 | 1.49E-01 |

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| cds.Camellia_sinensis.comp32335_c0_seq1_m.14824 | PREDICTED: putative 3,4-dihydroxy-2-butanone kinase [Malus | 53.565 | 109.98 | 36.3 | 15 | 25 | 15 | 0.959 | 0.946 | 0.938 | 1.088 | 1.029 | 1.044 | 1.112 | 4.10E-03 |
| cds.Camellia_sinensis.comp32336_c2_seq3_m.47894 | PREDICTED: transmembrane protein 33 homolog [Juglans regia] | 17.468 | 42.018 | 19.9 | 2 | 3 | 2 | 0.934 | 0.938 | 0.954 | 1.032 | 1.099 | 1.026 | 1.117 | 8.58E-03 |
| cds.Camellia_sinensis.comp32341_c1_seq1_m.31959 | PREDICTED: glutamate dehydrogenase 2 [Gossypium raimondii] | 32.818 | 18.896 | 24.3 | 6 | 9 | 4 | 0.973 | 0.965 | 0.942 | 1.122 | 1.015 | 1.075 | 1.115 | 2.40E-02 |
| cds.Camellia_sinensis.comp32343_c1_seq1_m.13967 | PREDICTED: fatty acid amide hydrolase-like [Sesamum indicum] | 66.642 | 2.9938 | 3.3 | 2 | 2 | 2 | 1.191 | 1.182 | 1.254 | 0.774 | 0.74 | 0.799 | 0.638 | 1.00E-04 |

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| cds.Camellia_sinensis.comp32345_c0_seq1_m.37112 | PREDICTED: proteasome subunit alpha type-2-A [Daucus carota subsp. sativus] | 25.65 | 87.343 | 46 | 9 | 18 | 9 | 1.002 | 0.975 | 0.992 | 1.01 | 1.021 | 1.002 | 1.022 | 9.14E-02 |
| cds.Camellia_sinensis.comp32347_c1_seq1_m.26020 | PREDICTED: phosphoribulokinase, chloroplastic-like [Populus | 46.592 | 236.37 | 47.6 | 18 | 105 | 17 | 1.02 | 1.02 | 1 | 0.979 | 1 | 0.978 | 0.973 | 4.76E-02 |
| cds.Camellia_sinensis.comp32348_c0_seq1_m.12333 | PREDICTED: flowering time control protein FCA isoform X3 [Vitis vinifera] | 65.426 | 6.3868 | 3.1 | 2 | 2 | 2 | 1.011 | 1 | 0.995 | 0.996 | 1.037 | 0.969 | 0.999 | 9.37E-01 |
| cds.Camellia_sinensis.comp32356_c0_seq5_m.37866 | PREDICTED: 50S ribosomal protein HLP, mitochondrial isoform X3 [Nelumbo | 13.333 | 1.8762 | 8.1 | 1 | 1 | 1 | 0.887 | 1.035 | 1.109 | 1.084 | 0.889 | 1.019 | 0.987 | 8.98E-01 |

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| cds.Camellia_sinensis.comp32360_c0_seq1_m.22186 | PREDICTED: 30S ribosomal protein S1-like [Nicotiana tabacum] | 46.85 | 41.834 | 15.2 | 5 | 7 | 5 | 0.992 | 1.057 | 0.939 | 1.001 | 1.055 | 0.968 | 1.012 | 7.82E-01 |
| cds.Camellia_sinensis.comp32362_c0_seq1_m.5696 | PREDICTED: alpha-xylosidase 1-like [Juglans regia] | 102.92 | 96.953 | 21 | 18 | 27 | 16 | 0.97 | 0.92 | 0.93 | 1.066 | 1.08 | 1.046 | 1.132 | 2.64E-03 |
| cds.Camellia_sinensis.comp32362_c0_seq2_m.6011 | PREDICTED: alpha-xylosidase 1-like [Juglans regia] | 103 | 20.166 | 10.2 | 9 | 13 | 7 | 1.017 | 1.009 | 1.028 | 1.01 | 0.951 | 1.002 | 0.97 | 1.94E-01 |
| cds.Camellia_sinensis.comp32367_c0_seq1_m.5385 | PREDICTED: protein translocase subunit SecA, chloroplastic [Vitis vinifera] | 107.75 | 232.29 | 41.8 | 35 | 48 | 35 | 1.002 | 1.017 | 1.01 | 0.994 | 0.977 | 0.992 | 0.978 | 3.36E-02 |
| cds.Camellia_sinensis.comp32368_c0_seq1_m.6891 | PREDICTED: linoleate 13S-lipoxygenase 3-1, chloroplastic [Nicotiana tabacum] | 102.78 | 21.33 | 9.8 | 8 | 9 | 8 | 0.952 | 0.997 | 1.062 | 1.009 | 0.98 | 1.023 | 1 | 9.74E-01 |

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| cds.Camellia_sinensis.comp32370_c0_seq3_m.44534 | PREDICTED: superoxide dismutase [Fe] 3, chloroplastic [Juglans regia] | 27.666 | 1.2639 | 3.3 | 1 | 1 | 1 | 0.897 | 0.99 | 0.959 | 1.069 | 1.065 | 1.053 | 1.12 | 6.06E-02 |
| cds.Camellia_sinensis.comp32371_c0_seq1_m.8400 | PREDICTED: nucleolin 2 [Prunus mume] | 79.316 | 3.9865 | 2 | 1 | 1 | 1 | 1.251 | 1.248 | 1.228 | 0.744 | 0.722 | 0.735 | 0.591 | 4.70E-07 |
| cds.Camellia_sinensis.comp32375_c0_seq2_m.21212 | PREDICTED: oxysterol-binding protein-related protein 3C-like [Nelumbo nucifera] | 51.934 | 11.64 | 9.9 | 4 | 4 | 3 | 1.034 | 1.021 | 1.122 | 1.041 | 0.847 | 0.933 | 0.888 | 1.42E-01 |
| cds.Camellia_sinensis.comp32378_c0_seq1_m.4555 | PREDICTED: phosphatidylinositol 4-phosphate 5-kinase 9-like [Sesamum indicum] | 92.934 | 1.9421 | 1 | 1 | 1 | 1 | 1.22 | 1.184 | 1.215 | 0.769 | 0.804 | 0.747 | 0.641 | 4.23E-05 |
| cds.Camellia_sinensis.comp32382_c0_seq1_m.25543 | PREDICTED: 60S ribosomal protein L7-2-like [Ipomoea nil] | 28.589 | 51.596 | 44.7 | 10 | 14 | 10 | 1.139 | 1.172 | 1.166 | 0.796 | 0.863 | 0.82 | 0.713 | 1.78E-04 |

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| cds.Camellia_sinensis.comp32384_c0_seq1_m.22206 | PREDICTED: sucrose-phosphatase 2-like [Sesamum indicum] | 48.112 | 162.33 | 31.6 | 12 | 24 | 12 | 1.037 | 1.053 | 0.985 | 0.955 | 0.963 | 0.961 | 0.936 | 8.45E-02 |
| cds.Camellia_sinensis.comp32386_c0_seq1_m.26881 | PREDICTED: translation initiation factor eIF-2B subunit beta-like [Nicotiana tabacum] | 44.049 | 6.7722 | 6.7 | 3 | 3 | 2 | 0.934 | 1.001 | 1.034 | 0.992 | 1.041 | 1.016 | 1.027 | 4.56E-01 |
| cds.Camellia_sinensis.comp32387_c0_seq1_m.7300 | PREDICTED: eukaryotic translation initiation factor [Vitis vinifera] | 87.118 | 109.52 | 29.4 | 23 | 32 | 23 | 0.961 | 0.96 | 0.949 | 1.038 | 1.055 | 1.073 | 1.103 | 7.01E-04 |
| cds.Camellia_sinensis.comp32388_c0_seq1_m.31024 | PREDICTED: perakine reductase-like [Populus euphratica] | 30.224 | 5.9833 | 7.4 | 2 | 3 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp32393_c0_seq1_m.22641 | PREDICTED: probable N-acetyl-gamma-glutamyl-phosphate reductase, chloroplastic [Vitis vinifera] | 44.074 | 49.966 | 23.1 | 9 | 11 | 9 | 0.979 | 1.021 | 0.954 | 0.971 | 0.998 | 1.054 | 1.023 | 5.03E-01 |
| cds.Camellia_sinensis.comp32394_c0_seq74_m.10219 | PREDICTED: probable acyl-activating enzyme 18, peroxisomal [Ziziphus | 81.183 | 52.494 | 14.9 | 9 | 10 | 9 | 1.289 | 1.404 | 1.323 | 0.588 | 0.58 | 0.607 | 0.442 | 4.53E-06 |
| cds.Camellia_sinensis.comp32394_c0_seq9_m.12860 | PREDICTED: 15.7 kDa heat shock protein, peroxisomal [Solanum tuberosum | 18.83 | 5.4027 | 22.5 | 4 | 4 | 4 | 1.029 | 1.041 | 1.035 | 0.945 | 0.941 | 1.004 | 0.931 | 7.65E-02 |
| cds.Camellia_sinensis.comp32397_c0_seq17_m.21879 | PREDICTED: V-type proton ATPase subunit d2-like [Daucus carota subsp. | 40.616 | 10.037 | 15.1 | 6 | 8 | 6 | 0.987 | 1.007 | 0.965 | 0.985 | 1.045 | 1.018 | 1.03 | 2.34E-01 |

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| cds.Camellia_sinensis.comp32401_c0_seq1_m.44336 | PREDICTED: uroporphyrinogen decarboxylase, chloroplastic [Ipomoea nil] | 21.735 | 14.659 | 23.2 | 3 | 6 | 3 | 1.009 | 0.978 | 0.893 | 1.062 | 1.023 | 1.042 | 1.086 | 9.41E-02 |
| cds.Camellia_sinensis.comp32402_c0_seq1_m.10103 | PREDICTED: zeaxanthin epoxidase, chloroplastic [Juglans regia] | 73.508 | 66.786 | 27.4 | 18 | 32 | 18 | 1.015 | 0.997 | 1.005 | 0.979 | 1 | 1.004 | 0.989 | 2.92E-01 |
| cds.Camellia_sinensis.comp32410_c0_seq1_m.12637 | PREDICTED: protein TOPLESS-like, partial [Juglans regia] | 48.81 | 27.386 | 15 | 6 | 7 | 5 | 0.903 | 0.905 | 0.938 | 1.074 | 1.108 | 1.074 | 1.186 | 4.56E-04 |
| cds.Camellia_sinensis.comp32413_c0_seq1_m.18086 | P-loop nucleoside triphosphate hydrolase superfamily protein [Medicago truncatula] | 57.784 | 12.969 | 10.1 | 5 | 6 | 5 | 1.01 | 1.027 | 1.059 | 0.983 | 0.948 | 0.97 | 0.937 | 2.04E-02 |

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| cds.Camellia_sinensis.comp32419_c0_seq1_m.20477 | PREDICTED: serine/threonine-protein kinase SRK2A [Vitis vinifera] | 41.231 | 4.688 | 14 | 5 | 6 | 3 | 1.09 | 1.077 | 1.077 | 0.917 | 0.909 | 0.911 | 0.844 | 1.88E-06 |
| cds.Camellia_sinensis.comp32429_c0_seq3_m.4590 | PREDICTED: putative late blight resistance protein homolog R1B-14 [Solanum pennellii] | 96.321 | 7.4915 | 5.7 | 5 | 6 | 5 | 0.957 | 0.96 | 1.03 | 1.042 | 1.049 | 0.973 | 1.04 | 3.15E-01 |
| cds.Camellia_sinensis.comp32432_c0_seq1_m.18622 | PREDICTED: calcium-dependent protein kinase 1-like [Nelumbo nucifera] | 57.26 | 45.757 | 23.2 | 10 | 12 | 6 | 1.045 | 0.991 | 0.994 | 0.949 | 1.067 | 1.02 | 1.002 | 9.78E-01 |

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| cds.Camellia_sinensis.comp32434_c0_seq1_m.25833 | PREDICTED: 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic/chromoplastic [Nicotiana attenuata] | 45.215 | 21.832 | 11.5 | 4 | 6 | 4 | 1.005 | 1.017 | 1.029 | 1.034 | 0.972 | 1.019 | 0.991 | 6.79E-01 |
| cds.Camellia_sinensis.comp32434_c0_seq3_m.38079 | PREDICTED: 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic/chromoplastic isoform X2[Vitis vinifera] | 28.668 | 3.2328 | 8.4 | 2 | 4 | 2 | 1.011 | 0.979 | 1.027 | 1.09 | 0.986 | 0.923 | 0.994 | 8.80E-01 |
| cds.Camellia_sinensis.comp32437_c0_seq1_m.8865 | PREDICTED: acyl-CoA dehydrogenase family member 10 [Jatropha | 92.395 | 40.355 | 15.3 | 12 | 19 | 12 | 0.955 | 1.01 | 0.96 | 1.005 | 1.036 | 1.01 | 1.043 | 1.04E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32440_c0_seq1_m.1590 | PREDICTED: cleavage and polyadenylation specificity factor subunit 1 isoform X1 [Theobroma cacao] | 164.58 | 12.974 | 4.5 | 6 | 6 | 6 | 0.954 | 0.963 | 0.953 | 1.087 | 1.035 | 1.035 | 1.1 | 4.68E-03 |
| cds.Camellia_sinensis.comp32443_c0_seq1_m.34125 | PREDICTED: peptide methionine sulfoxide reductase A1 [Ricinus communis] | 29.217 | 39.908 | 21.9 | 7 | 22 | 7 | 1.027 | 1.02 | 0.984 | 0.963 | 0.986 | 1.012 | 0.977 | 2.97E-01 |
| cds.Camellia_sinensis.comp32444_c0_seq1_m.4295 | PREDICTED: multiple C2 and transmembrane domain-containing protein 1-like [Jatropha curcas] | 116.26 | 70.831 | 16.4 | 15 | 23 | 15 | 0.957 | 0.971 | 0.982 | 1.042 | 1.039 | 1.028 | 1.068 | 1.48E-03 |

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| cds.Camellia_sinensis.comp32448_c0_seq2_m.29251 | PREDICTED: 3-hydroxyisobutyryl-CoA hydrolase-like protein 3, mitochondrial isoform X1 [Juglans | 32.919 | 23.432 | 24.5 | 7 | 12 | 7 | 1.008 | 0.958 | 1.016 | 1.01 | 0.955 | 1.026 | 1.003 | 9.24E-01 |
| cds.Camellia_sinensis.comp32451_c0_seq1_m.37243 | phosphoglycerate mutase family protein [Medicago truncatula] | 30.907 | 12.848 | 13.6 | 3 | 3 | 3 | 1.068 | 0.956 | 1 | 1.01 | 1.01 | 0.959 | 0.985 | 7.16E-01 |
| cds.Camellia_sinensis.comp32453_c0_seq1_m.12949 | PREDICTED: lysine--tRNA ligase, cytoplasmic-like [Gossypium hirsutum] | 69.931 | 94.876 | 37.2 | 25 | 36 | 25 | 0.965 | 0.953 | 0.947 | 1.038 | 1.037 | 1.042 | 1.088 | 1.22E-04 |
| cds.Camellia_sinensis.comp32458_c0_seq1_m.14581 | PREDICTED: probable galactinol--sucrose galactosyltransferase 2 [Eucalyptus grandis] | 64.87 | 86.998 | 19.5 | 12 | 20 | 12 | 1.139 | 1.189 | 1.21 | 0.835 | 0.79 | 0.795 | 0.684 | 1.15E-04 |

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| cds.Camellia_sinensis.comp32458_c1_seq1_m.45032 | PREDICTED: probable galactinol--sucrose galactosyltransferase 2 [Citrus sinensis] | 18.413 | 46.075 | 30.8 | 3 | 6 | 2 | 1.227 | 1.145 | 1.162 | 0.755 | 0.835 | 0.805 | 0.678 | 4.21E-04 |
| cds.Camellia_sinensis.comp32458_c1_seq2_m.46697 | PREDICTED: probable galactinol--sucrose galactosyltransferase 2 [Sesamum indicum] | 18.472 | 1.2074 | 20.1 | 2 | 4 | 1 | 1.028 | 1.013 | 0.985 | 1.112 | 0.727 | 1.138 | 0.984 | 8.27E-01 |
| cds.Camellia_sinensis.comp32459_c1_seq1_m.24665 | PREDICTED: serine carboxypeptidase-like 18 [Jatropha curcas] | 52.937 | 11.819 | 17.6 | 6 | 9 | 4 | 0.94 | 0.965 | 0.954 | 1.05 | 1.027 | 1.088 | 1.107 | 5.32E-03 |
| cds.Camellia_sinensis.comp32460_c0_seq1_m.14509 | PREDICTED: reticuline oxidase-like protein [Eucalyptus grandis] | 46.143 | 17.56 | 16.8 | 8 | 12 | 7 | 1.006 | 1.009 | 1.015 | 0.989 | 0.941 | 1.05 | 0.983 | 6.35E-01 |

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| cds.Camellia_sinensis.comp32467_c0_seq1_m.27579 | PREDICTED: 2-methylene-furan-3-one reductase [Theobroma cacao] | 42.717 | 279.91 | 52.5 | 19 | 66 | 19 | 1.057 | 1.017 | 1.004 | 0.964 | 0.964 | 0.978 | 0.944 | 2.40E-02 |
| cds.Camellia_sinensis.comp32471_c0_seq4_m.12264 | PREDICTED: NEDD8-activating enzyme E1 regulatory subunit AXR1 isoform X1 [Vitis vinifera] | 64.292 | 42.122 | 16 | 8 | 10 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp32475_c0_seq1_m.12477 | PREDICTED: vacuolar-sorting receptor 3 [Theobroma cacao] | 69.884 | 4.3057 | 14.4 | 7 | 8 | 1 | 1.015 | 0.979 | 1.027 | 1.031 | 1.013 | 0.947 | 0.99 | 7.42E-01 |
| cds.Camellia_sinensis.comp32475_c0_seq2_m.12762 | PREDICTED: vacuolar-sorting receptor 3-like [Juglans regia] | 69.568 | 58.183 | 18 | 9 | 10 | 3 | 1.016 | 1.044 | 1.106 | 0.998 | 0.971 | 0.867 | 0.896 | 8.92E-02 |

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| cds.Camellia_sinensis.comp32485_c0_seq3_m.14868 | PREDICTED: 70 kDa peptidyl-prolyl isomerase-like [Prunus mume] | 64.493 | 1.6608 | 4.5 | 3 | 6 | 1 | 1.094 | 1.105 | 1.146 | 0.914 | 0.829 | 0.887 | 0.786 | 1.68E-03 |
| cds.Camellia_sinensis.comp32494_c0_seq2_m.1383 | PREDICTED: protein transport protein SEC16B homolog [Prunus mume] | 114.8 | 3.7918 | 0.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32494_c0_seq2_m.1384 | PREDICTED: protein transport protein SEC16B homolog [Solanum tuberosum | 29.447 | 2.1614 | 3.8 | 1 | 1 | 1 | 1.053 | 1.15 | 1.037 | 0.957 | 0.78 | 1.004 | 0.846 | 1.09E-01 |
| cds.Camellia_sinensis.comp32495_c1_seq8_m.32998 | PREDICTED: derlin-2.2 [Ipomoea nil] | 28.292 | 4.2017 | 13.5 | 3 | 3 | 2 | 0.948 | 0.95 | 1.086 | 1.016 | 1.099 | 0.924 | 1.018 | 8.05E-01 |
| cds.Camellia_sinensis.comp32495_c1_seq9_m.33127 | PREDICTED: derlin-2.2 [Ipomoea nil] | 28.151 | 8.5652 | 8.2 | 2 | 2 | 1 | 1.003 | 0.875 | 0.927 | 1.032 | 1.107 | 1.079 | 1.147 | 3.59E-02 |

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| cds.Camellia_sinensis.comp32501_c0_seq3_m.20794 | PREDICTED: kelch domain-containing protein 3 isoform X3 [Vitis vinifera] | 57.433 | 3.2848 | 1.9 | 1 | 1 | 1 | 1.087 | 0.824 | 1.134 | 0.947 | 1.06 | 0.948 | 0.97 | 8.49E-01 |
| cds.Camellia_sinensis.comp32502_c1_seq1_m.40785 | PREDICTED: glutamyl-tRNA(Gln) amidotransferase subunit C, chloroplastic/mitochondrial-like [Vitis | 17.402 | 11.111 | 9.2 | 1 | 3 | 1 | 1.059 | 1.001 | 1.004 | 0.992 | 0.994 | 0.95 | 0.958 | 1.45E-01 |
| cds.Camellia_sinensis.comp32506_c0_seq2_m.22896 | PREDICTED: peptide chain release factor PrfB1, chloroplastic [Sesamum indicum] | 27.069 | 11.607 | 22.2 | 6 | 9 | 6 | 0.987 | 1.028 | 1.067 | 1.025 | 0.99 | 0.95 | 0.962 | 2.86E-01 |

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| cds.Camellia_sinensis.comp32506_c0_seq2_m.22897 | PREDICTED: peptide chain release factor PrfB1, chloroplastic [Vitis vinifera] | 17.521 | 14.814 | 26.8 | 3 | 4 | 3 | 0.873 | 1.122 | 0.938 | 1.061 | 1.084 | 0.952 | 1.056 | 5.28E-01 |
| cds.Camellia_sinensis.comp32513_c0_seq4_m.40033 | PREDICTED: putative F-box protein At3g23950 [Daucus carota subsp. sativus] | 30.028 | 2.1194 | 3.4 | 1 | 1 | 1 | 0.895 | 1.058 | 1.032 | 1.031 | 1.004 | 1.003 | 1.018 | 7.22E-01 |
| cds.Camellia_sinensis.comp32522_c2_seq1_m.14114 | PREDICTED: peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A-like [Nicotiana | 71.676 | 20.114 | 6.4 | 4 | 9 | 3 | 0.964 | 1.002 | 1.043 | 1.006 | 1.041 | 0.979 | 1.006 | 8.50E-01 |

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| cds.Camellia_sinensis.comp32522_c2_seq3_m.15766 | PREDICTED: peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A [Prunus | 65.729 | 17.41 | 6.6 | 4 | 5 | 1 | 1.027 | 1.06 | 1.009 | 1.061 | 0.896 | 0.95 | 0.939 | 2.75E-01 |
| cds.Camellia_sinensis.comp32523_c0_seq2_m.19658 | PREDICTED: tubulin beta-1 chain [Ipomoea nil] | 50.754 | 48.789 | 30.2 | 9 | 19 | 2 | 1.252 | 1.157 | 1.144 | 0.734 | 0.777 | 0.869 | 0.67 | 2.14E-03 |
| cds.Camellia_sinensis.comp32523_c0_seq3_m.20537 | PREDICTED: tubulin beta-1 chain [Oryza brachyantha] | 54.973 | 54.033 | 29.5 | 10 | 23 | 3 | 1.169 | 1.162 | 1.091 | 0.838 | 0.866 | 0.867 | 0.751 | 3.21E-04 |
| cds.Camellia_sinensis.comp32523_c0_seq4_m.21036 | PREDICTED: tubulin beta-2 chain [Nelumbo nucifera] | 53.579 | 82.705 | 36.1 | 12 | 24 | 3 | | | | | | | | |

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| cds.Camellia_sinensis.comp32523_c1_seq1_m.11627 | PREDICTED: WPP domain-interacting tail-anchored protein 1 [Vitis vinifera] | 77.162 | 1.5994 | 3.6 | 3 | 3 | 3 | 0.867 | 1.042 | 1.107 | 1.051 | 0.962 | 0.998 | 0.998 | 9.71E-01 |
| cds.Camellia_sinensis.comp32526_c0_seq1_m.7405 | PREDICTED: nuclear pore complex protein NUP85 [Vitis vinifera] | 80.37 | 27.331 | 8.4 | 4 | 5 | 4 | 0.952 | 1.008 | 1.105 | 1.148 | 0.877 | 0.965 | 0.976 | 7.62E-01 |
| cds.Camellia_sinensis.comp32528_c0_seq1_m.20398 | PREDICTED: hydroxymethylglutaryl-CoA synthase-like [Gossypium arboreum] | 51.699 | 6.5554 | 8.9 | 4 | 5 | 3 | 1.009 | 1.014 | 0.913 | 1.081 | 1.04 | 1.026 | 1.072 | 1.35E-01 |
| cds.Camellia_sinensis.comp32528_c0_seq2_m.21516 | PREDICTED: hydroxymethylglutaryl-CoA synthase [Theobroma cacao] | 51.561 | 21.405 | 8.1 | 4 | 5 | 3 | 0.949 | 0.98 | 0.939 | 1.052 | 1.022 | 1.121 | 1.114 | 2.36E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32536_c0_seq3_m.1041 | Heterogeneous nuclear ribonucleoprotein Q [Morus notabilis] | 90.479 | 19.33 | 10.4 | 8 | 8 | 8 | 0.994 | 1.047 | 0.999 | 0.953 | 0.95 | 1.022 | 0.962 | 2.52E-01 |
| cds.Camellia_sinensis.comp32537_c0_seq1_m.2620 | tolB protein-like protein [Arabidopsis thaliana] | 73.827 | 107.67 | 25.8 | 13 | 18 | 11 | 0.93 | 0.914 | 0.902 | 1.133 | 1.074 | 1.06 | 1.19 | 1.46E-03 |
| cds.Camellia_sinensis.comp32537_c0_seq3_m.13950 | tolB protein-like protein [Arabidopsis thaliana] | 77.657 | 55.919 | 22.6 | 12 | 18 | 10 | 0.902 | 0.933 | 0.928 | 1.114 | 1.1 | 1.066 | 1.187 | 5.18E-04 |
| cds.Camellia_sinensis.comp32537_c0_seq5_m.16986 | PREDICTED: topless-related protein 1 isoform X1 [Vigna radiata var. radiata] | 62.321 | 20.338 | 15 | 8 | 11 | 4 | 0.965 | 0.974 | 1.044 | 0.983 | 0.957 | 1.089 | 1.015 | 7.73E-01 |

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| cds.Camellia_sinensis.comp32538_c0_seq1_m.33174 | PREDICTED: probable 2-oxoglutarate-dependent dioxygenase At3g49630 isoform X1 [Theobroma cacao] | 37.605 | 3.4332 | 10.4 | 3 | 3 | 3 | 0.984 | 0.909 | 0.962 | 1.131 | 1.029 | 1.013 | 1.111 | 6.56E-02 |
| cds.Camellia_sinensis.comp32542_c0_seq2_m.8482 | PREDICTED: vacuolar protein sorting-associated protein 51 homolog [Vitis vinifera] | 89.96 | 10.538 | 4 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp32546_c0_seq1_m.9615 | PREDICTED: heat shock 70 kDa protein, mitochondrial-like [Sesamum indicum] | 72.905 | 306.64 | 41.2 | 29 | 84 | 23 | 0.993 | 0.97 | 0.969 | 1.025 | 1.015 | 1.017 | 1.043 | 8.04E-03 |

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| cds.Camellia_sinensis.comp32554_c0_seq1_m.10016 | PREDICTED: nuclear pore complex protein NUP62 [Vitis vinifera] | 74.947 | 13.645 | 7.3 | 6 | 6 | 6 | 0.929 | 1.02 | 1.003 | 1.014 | 1.004 | 0.99 | 1.019 | 5.45E-01 |
| cds.Camellia_sinensis.comp32556_c0_seq1_m.17665 | PREDICTED: pyridoxine/pyridoxamine 5'-phosphate oxidase 1, chloroplastic [Vitis vinifera] | 53.413 | 25.09 | 16.8 | 6 | 7 | 6 | 0.951 | 1.04 | 0.976 | 1.155 | 0.932 | 0.969 | 1.03 | 7.35E-01 |
| cds.Camellia_sinensis.comp32557_c2_seq3_m.24353 | type 2A protein phosphatase-3 [Populus trichocarpa] | 35.665 | 67.883 | 26.8 | 6 | 8 | 4 | 0.986 | 0.972 | 0.973 | 1.119 | 1.126 | 0.852 | 1.057 | 6.61E-01 |

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| cds.Camellia_sinensis.comp32557_c2_seq6_m.32119 | PREDICTED: probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 1[Nicotiana attenuata] | 45.532 | 33.579 | 19.6 | 9 | 12 | 9 | 0.991 | 0.994 | 0.989 | 1.084 | 0.983 | 1.027 | 1.04 | 3.05E-01 |
| cds.Camellia_sinensis.comp32559_c0_seq1_m.23940 | PREDICTED: 30S ribosomal protein S1 isoform X1 [Theobroma cacao] | 43.965 | 7.4792 | 5.8 | 2 | 4 | 2 | 0.951 | 0.99 | 1.079 | 0.985 | 1.059 | 0.958 | 0.994 | 9.14E-01 |
| cds.Camellia_sinensis.comp32561_c0_seq9_m.47671 | 39S ribosomal protein L53/MRP-L53 [Medicago truncatula] | 18.602 | -2 | 6.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32565_c0_seq1_m.19595 | PREDICTED: chaperone protein dnaJ GFA2, mitochondrial [Vitis vinifera] | 44.78 | 3.3611 | 4.9 | 2 | 2 | 2 | 0.988 | 0.973 | 0.894 | 1.045 | 1.031 | 1.088 | 1.108 | 4.19E-02 |

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| cds.Camellia_sinensis.comp32566_c0_seq2_m.24088 | PREDICTED: ERBB-3 BINDING PROTEIN 1 [Theobroma cacao] | 43.52 | 52.548 | 30.6 | 11 | 13 | 8 | 1.199 | 1.148 | 1.055 | 0.862 | 0.882 | 0.855 | 0.764 | 2.28E-03 |
| cds.Camellia_sinensis.comp32566_c0_seq3_m.24185 | PREDICTED: EBP1 isoform X1 [Solanum tuberosum | 19.199 | 12.455 | 29.7 | 5 | 6 | 2 | 1.039 | 1.412 | 0.889 | 0.911 | 0.806 | 0.914 | 0.788 | 1.94E-01 |
| cds.Camellia_sinensis.comp32567_c0_seq1_m.20559 | PREDICTED: casein kinase I isoform delta-like [Ziziphus jujuba] | 53.237 | 3.3561 | 5.5 | 3 | 4 | 3 | 0.998 | 1.074 | 1.095 | 0.936 | 0.901 | 0.964 | 0.884 | 2.35E-02 |
| cds.Camellia_sinensis.comp32575_c0_seq1_m.12281 | PREDICTED: 2-isopropylmalate synthase A [Vitis vinifera] | 66.102 | 92.444 | 29.2 | 15 | 23 | 11 | 0.99 | 0.962 | 0.961 | 1.035 | 1.012 | 0.991 | 1.043 | 5.75E-02 |
| cds.Camellia_sinensis.comp32575_c0_seq3_m.14832 | PREDICTED: 2-isopropylmalate synthase A [Vitis vinifera] | 65.888 | 6.956 | 15.3 | 9 | 11 | 5 | 0.923 | 1.057 | 0.958 | 1.022 | 1.02 | 1.041 | 1.049 | 2.91E-01 |

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| cds.Camellia_sinensis.comp32577_c0_seq1_m.48543 | PREDICTED: pentatricopeptide repeat-containing protein At4g38150-like [Malus domestica] | 22.736 | 8.6434 | 22.2 | 5 | 5 | 5 | 0.996 | 1.065 | 1.074 | 0.95 | 0.94 | 0.973 | 0.913 | 2.53E-02 |
| cds.Camellia_sinensis.comp32577_c1_seq1_m.18933 | PREDICTED: argininosuccinate lyase, chloroplastic [Vitis vinifera] | 59.026 | 22.933 | 14.3 | 7 | 8 | 7 | 1.013 | 0.98 | 0.94 | 1.024 | 1.053 | 0.994 | 1.047 | 1.66E-01 |
| cds.Camellia_sinensis.comp32578_c0_seq1_m.37624 | PREDICTED: vacuolar protein sorting-associated protein 26A [Ziziphus jujuba] | 25.996 | 27.362 | 13.1 | 3 | 3 | 2 | 0.913 | 0.948 | 1.042 | 1.026 | 1.048 | 1.049 | 1.076 | 1.36E-01 |
| cds.Camellia_sinensis.comp32581_c1_seq3_m.881 | PREDICTED: heat shock protein 90-5, chloroplastic [Ziziphus jujuba] | 91.123 | 323.31 | 41.9 | 26 | 55 | 22 | 1.194 | 1.155 | 1.172 | 0.807 | 0.787 | 0.827 | 0.688 | 2.33E-05 |

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| cds.Camellia_sinensis.comp32581_c1_seq51_m.2176 | PREDICTED: trafficking protein particle complex II-specific subunit 130 homolog [Vitis vinifera] | 140.11 | 8.0215 | 4.3 | 5 | 5 | 5 | 0.959 | 1.078 | 0.976 | 1.009 | 0.967 | 1.023 | 0.995 | 9.33E-01 |
| cds.Camellia_sinensis.comp32581_c1_seq91_c1_seq9 _m.24298 | PREDICTED: probable protein phosphatase 2C 60 [Nelumbo nucifera] | 49.565 | 3.2527 | 5.1 | 2 | 2 | 2 | 0.96 | 1.001 | 1.034 | 0.985 | 1.031 | 1.004 | 1.008 | 7.51E-01 |
| cds.Camellia_sinensis.comp32585_c0_seq1_m.4306 | PREDICTED: 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [Ziziphus jujuba] | 71.439 | 46.35 | 26.5 | 17 | 46 | 11 | 0.985 | 0.973 | 0.987 | 1.022 | 1.027 | 1.017 | 1.041 | 1.58E-03 |

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| cds.Camellia_sinensis.comp32586_c0_seq1_m.27262 | PREDICTED: triosephosphate isomerase, chloroplastic [Solanum pennellii] | 34.474 | 155.35 | 37.8 | 11 | 40 | 11 | 1.054 | 0.998 | 1.036 | 0.948 | 0.971 | 0.969 | 0.935 | 2.01E-02 |
| cds.Camellia_sinensis.comp325875_c0_seq1_m.52540 | PREDICTED: trans-resveratrol di-O-methyltransferase-like [Capsicum annuum] | 18.308 | 3.3564 | 6.7 | 1 | 1 | 1 | 0.827 | 0.94 | 0.8 | 1.074 | 1.207 | 1.205 | 1.358 | 8.00E-03 |
| cds.Camellia_sinensis.comp32591_c0_seq1_m.18528 | PREDICTED: anthranilate phosphoribosyltransferase, chloroplastic [Jatropha curcas] | 44.465 | 35.223 | 17 | 6 | 11 | 6 | 1.007 | 0.99 | 1.044 | 0.94 | 1.022 | 1.044 | 0.988 | 7.47E-01 |
| cds.Camellia_sinensis.comp32592_c3_seq4_m.29222 | PREDICTED: arogenate dehydratase 3, chloroplastic [Vitis vinifera] | 45.948 | 3.0291 | 4.3 | 2 | 2 | 1 | 1.331 | 1.137 | 1.271 | 0.663 | 0.842 | 0.675 | 0.583 | 3.78E-03 |

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| cds.Camellia_sinensis.comp32594_c0_seq1_m.2005 | PREDICTED: translocase of chloroplast 159, chloroplastic [Nicotiana attenuata] | 145.19 | 169.24 | 17.4 | 19 | 26 | 19 | 1.093 | 1.091 | 1.089 | 0.9 | 0.863 | 0.894 | 0.812 | 3.90E-03 |
| cds.Camellia_sinensis.comp32595_c0_seq1_m.5552 | PREDICTED: tubulin--tyrosine ligase-like protein 12 isoform X2 [Vitis vinifera] | 102.33 | 1.3778 | 0.9 | 1 | 1 | 1 | 1.037 | 0.888 | 1.004 | 0.848 | 1.055 | 1.167 | 1.048 | 7.20E-01 |
| cds.Camellia_sinensis.comp32596_c0_seq2_m.1710 | PREDICTED: CLIP-associated protein isoform X1 [Vitis vinifera] | 161.78 | 3.2754 | 1.6 | 2 | 2 | 2 | 0.835 | 1.039 | 1.221 | 1.007 | 1.037 | 0.888 | 0.947 | 7.30E-01 |
| cds.Camellia_sinensis.comp32598_c0_seq1_m.32571 | PREDICTED: nifU-like protein 4, mitochondrial [Citrus sinensis] | 20.076 | 20.747 | 38.9 | 6 | 9 | 6 | 0.963 | 1.038 | 0.964 | 0.988 | 1.013 | 0.964 | 1 | 9.89E-01 |

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| cds.Camellia_sinensis.comp32599_c0_seq1_m.31879 | PREDICTED: gamma carbonic anhydrase 1, mitochondrial [Ziziphus jujuba] | 29.459 | 79.989 | 38.4 | 10 | 17 | 4 | 1.018 | 1.026 | 0.977 | 0.992 | 0.976 | 0.986 | 0.978 | 2.35E-01 |
| cds.Camellia_sinensis.comp32599_c0_seq3_m.34004 | PREDICTED: gamma carbonic anhydrase 1, mitochondrial-like [Gossypium hirsutum] | 29.493 | 23.55 | 32.8 | 9 | 16 | 3 | 0.987 | 0.959 | 0.931 | 1.048 | 1.042 | 1.008 | 1.077 | 2.34E-02 |
| cds.Camellia_sinensis.comp32604_c0_seq2_m.38380 | PREDICTED: ER membrane protein complex subunit 4-like [Gossypium raimondii] | 19.751 | 3.5857 | 17.8 | 3 | 4 | 3 | 0.998 | 0.908 | 1.104 | 0.93 | 1.013 | 1.053 | 0.995 | 9.69E-01 |
| cds.Camellia_sinensis.comp32608_c0_seq2_m.39213 | PREDICTED: proteasome subunit alpha type-7 [Vitis vinifera] | 27.457 | 64.161 | 48.8 | 13 | 26 | 13 | 1.003 | 0.967 | 0.963 | 1.011 | 1.025 | 1.043 | 1.05 | 3.67E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32611_c0_seq2_m.7606 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 8 homolog A [Sesamum | 26.899 | 75.183 | 45.3 | 9 | 14 | 9 | 1.012 | 0.992 | 0.996 | 0.954 | 0.984 | 1.015 | 0.984 | 4.43E-01 |
| cds.Camellia_sinensis.comp32611_c0_seq5_m.9822 | PREDICTED: eukaryotic translation initiation factor 5B isoform X2 [Prunus | 49.752 | 2.1091 | 4.1 | 1 | 1 | 1 | 0.883 | 0.94 | 1.151 | 1.074 | 1.077 | 0.91 | 1.029 | 7.57E-01 |
| cds.Camellia_sinensis.comp32612_c0_seq1_m.44258 | PREDICTED: small ubiquitin-related modifier 1 [Eucalyptus grandis] | 11.644 | 63.404 | 33.3 | 4 | 8 | 1 | 1.095 | 1.016 | 1.17 | 0.962 | 0.784 | 0.954 | 0.823 | 6.51E-02 |
| cds.Camellia_sinensis.comp32612_c1_seq1_m.15867 | transaldolase family protein [Populus trichocarpa] | 48.347 | 172.31 | 32.3 | 13 | 33 | 13 | 1.061 | 1.018 | 1.054 | 0.946 | 0.961 | 0.966 | 0.917 | 3.76E-03 |

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| cds.Camellia_sinensis.comp32613_c0_seq1_m.19293 | PREDICTED: phenylalanine--tRNA ligase alpha subunit, cytoplasmic [Vitis vinifera] | 59.46 | 7.2012 | 8.2 | 5 | 6 | 5 | 0.961 | 0.985 | 0.953 | 1.038 | 1.038 | 1.011 | 1.065 | 9.00E-03 |
| cds.Camellia_sinensis.comp32614_c0_seq24_m.32059 | plastid transcriptionally active 6 [Arabidopsis thaliana] | 39.691 | 1.67 | 4.9 | 2 | 2 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp32619_c1_seq1_m.30469 | Tetratricopeptide repeat (TPR)-like superfamily protein [Arabidopsis thaliana] | 21.115 | 2.1993 | 6.2 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp32624_c0_seq18_m.48943 | PREDICTED: organellar oligopeptidase A, chloroplastic/mitochondrial [Vitis vinifera] | 20.667 | 1.6392 | 11.2 | 2 | 2 | 2 |  |  |  |  |  |  |  |  |

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| cds.Camellia_sinensis.comp32624_c0_seq1_m.4750 | PREDICTED: probable ADP-ribosylation factor GTPase-activating protein AGD14 isoform X2 [Theobroma cacao] | 34.441 | 2.1163 | 2.9 | 1 | 1 | 1 | 1.061 | 1.021 | 1.007 | 1.042 | 0.96 | 0.91 | 0.943 | 2.28E-01 |
| cds.Camellia_sinensis.comp32625_c0_seq1_m.1156 | ribulose-1 (chloroplast) [Carpinus putoensis] | 53.444 | 323.31 | 55.6 | 31 | 631 | 31 | 1 | 1.022 | 1.005 | 0.992 | 0.971 | 0.971 | 0.969 | 3.24E-02 |
| cds.Camellia_sinensis.comp32625_c0_seq1_m.1157 | ATP synthase CF1 beta subunit (chloroplast) [Camellia leptophylla] | 49.355 | 323.31 | 72.1 | 22 | 234 | 21 | 1.005 | 1.007 | 0.995 | 1.001 | 1.012 | 0.988 | 0.998 | 8.09E-01 |
| cds.Camellia_sinensis.comp32625_c0_seq1_m.1158 | ATP synthase CF1 epsilon subunit (chloroplast) [Camellia leptophylla] | 14.685 | 149.91 | 66.9 | 7 | 28 | 7 | 0.992 | 0.98 | 0.977 | 1.056 | 0.995 | 1.015 | 1.04 | 9.97E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32626_c0_seq3_m.34857 | Thioredoxin-like protein [Morus notabilis] | 28.957 | 87.929 | 42.5 | 11 | 20 | 11 | 1.013 | 1.035 | 0.985 | 0.992 | 0.988 | 0.985 | 0.978 | 2.61E-01 |
| cds.Camellia_sinensis.comp32626_c2_seq1_m.40398 | TATA BINDING protein ASSOCIATED FACTOR 21KDA SUBUNIT [Populus trichocarpa] | 23.413 | 1.9244 | 4.8 | 1 | 2 | 1 | 1.021 | 0.954 | 1.054 | 0.961 | 0.98 | 1.034 | 0.982 | 6.56E-01 |
| cds.Camellia_sinensis.comp32626_c3_seq1_m.19050 | PREDICTED: FRIGIDA-like protein 4a [Nicotiana tabacum] | 63.348 | 24.606 | 14.5 | 8 | 13 | 8 | 1.011 | 1.075 | 1.095 | 0.942 | 0.92 | 0.906 | 0.87 | 6.52E-03 |
| cds.Camellia_sinensis.comp32628_c0_seq6_m.1529 | PREDICTED: chromatin modification-related protein eaf-1 [Vitis vinifera] | 102.17 | 17.366 | 9.1 | 8 | 8 | 8 | 1.033 | 1.073 | 1.076 | 0.932 | 0.897 | 0.962 | 0.877 | 5.52E-03 |
| cds.Camellia_sinensis.comp32629_c0_seq1_m.13549 | PREDICTED: T-complex protein 1 subunit alpha [Jatropha curcas] | 41.847 | 70.735 | 33.3 | 11 | 18 | 11 | 0.955 | 0.977 | 0.935 | 1.051 | 1.054 | 1.035 | 1.095 | 2.80E-03 |

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| cds.Camellia_sinensis.comp32629_c0_seq1_m.13550 | PREDICTED: T-complex protein 1 subunit alpha [Jatropha curcas] | 17.331 | 9.7863 | 16.2 | 3 | 6 | 3 | 0.938 | 1.002 | 1.025 | 1.035 | 1.017 | 1.043 | 1.044 | 1.90E-01 |
| cds.Camellia_sinensis.comp32632_c0_seq1_m.2349 | SH3 domain protein [Medicago truncatula] | 116.34 | 3.2732 | 2.1 | 3 | 3 | 3 | 1.072 | 1.098 | 1.151 | 0.881 | 0.887 | 0.889 | 0.8 | 8.84E-03 |
| cds.Camellia_sinensis.comp32633_c0_seq1_m.37141 | PREDICTED: secoisolariciresinol dehydrogenase [Malus domestica] | 32.062 | 11.239 | 15.1 | 5 | 7 | 5 | 0.965 | 0.962 | 0.996 | 1.059 | 1.015 | 1.017 | 1.057 | 3.46E-02 |
| cds.Camellia_sinensis.comp32635_c0_seq1_m.17640 | PREDICTED: phospholipase SGR2 isoform X4 [Ziziphus jujuba] | 53.979 | 12.173 | 8.2 | 3 | 3 | 3 | 0.926 | 1.056 | 1.078 | 0.999 | 1.007 | 0.938 | 0.962 | 5.22E-01 |
| cds.Camellia_sinensis.comp32637_c0_seq1_m.12436 | PREDICTED: protein MLP1 isoform X2 [Vitis vinifera] | 76.674 | 11.268 | 7.2 | 5 | 6 | 4 | 1.065 | 1.144 | 1.081 | 0.882 | 0.892 | 0.929 | 0.822 | 1.88E-03 |

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| cds.Camellia_sinensis.comp32637_c0_seq6_m.41238 | PREDICTED: protein MLP1 isoform X2 [Vitis vinifera] | 31.347 | 1.7717 | 3.9 | 1 | 1 | 1 | 0.959 | 0.948 | 1.147 | 1.045 | 0.978 | 0.94 | 0.97 | 7.12E-01 |
| cds.Camellia_sinensis.comp32640_c0_seq1_m.17669 | PREDICTED: haloalkane dehalogenase [Theobroma cacao] | 44.878 | 124.04 | 39.3 | 12 | 30 | 12 | 1.066 | 1.059 | 1.003 | 0.937 | 0.945 | 0.943 | 0.903 | 3.49E-02 |
| cds.Camellia_sinensis.comp32640_c0_seq10_c0_seq1_m.17671 | PREDICTED: U6 snRNA-associated Sm-like protein LSm3 [Populus euphratica] | 16.597 | 2.7429 | 12.9 | 2 | 3 | 2 | 0.871 | 1.01 | 0.981 | 1.179 | 1.031 | 0.97 | 1.111 | 2.29E-01 |
| cds.Camellia_sinensis.comp32641_c0_seq11_c0_seq1_m.1177 | PREDICTED: transcription elongation factor SPT6 homolog [Vitis vinifera] | 189.38 | 8.921 | 0.9 | 2 | 2 | 2 | 1.068 | 1.138 | 1.129 | 0.893 | 0.843 | 0.905 | 0.792 | 1.38E-03 |

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| cds.Camellia_sinensis.comp32645_c0_seq1_m.1618 | PREDICTED: enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic [Vitis vinifera] | 41.544 | 94.606 | 27 | 9 | 25 | 3 | 0.993 | 0.945 | 0.972 | 1.035 | 1.052 | 1.015 | 1.066 | 2.24E-02 |
| cds.Camellia_sinensis.comp32654_c0_seq1_m.12782 | PREDICTED: peptidyl-prolyl cis-trans isomerase PASTICCINO1 isoform X1 [Vitis vinifera] | 70.005 | 10.659 | 6.1 | 3 | 3 | 3 | 1.04 | 1.116 | 1.044 | 0.911 | 0.851 | 0.864 | 0.821 | 3.04E-03 |
| cds.Camellia_sinensis.comp32659_c0_seq6_m.10945 | PREDICTED: probable glutamate carboxypeptidase 2 isoform X1 [Sesamum indicum] | 39.017 | 27.07 | 19 | 6 | 9 | 6 | 0.946 | 0.987 | 0.949 | 1.033 | 1.045 | 1.092 | 1.1 | 1.19E-02 |
| cds.Camellia_sinensis.comp32659_c0_seq6_m.10946 | PREDICTED: probable glutamate carboxypeptidase 2 [Vitis vinifera] | 22.959 | 16.231 | 18.2 | 4 | 5 | 4 | 0.942 | 0.956 | 0.966 | 1.069 | 1.068 | 1.029 | 1.105 | 2.32E-03 |

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| cds.Camellia_sinensis.comp32660_c0_seq1_m.8080 | PREDICTED: pyrophosphate-energized vacuolar membrane proton pump [Theobroma cacao] | 40.823 | 29.981 | 12.9 | 4 | 13 | 2 | 0.96 | 1.022 | 1.056 | 0.987 | 1.058 | 1.032 | 1.013 | 7.24E-01 |
| cds.Camellia_sinensis.comp32660_c0_seq1_m.8081 | PREDICTED: pyrophosphate-energized vacuolar membrane proton pump 1-like isoform X2 [Nicotiana tomentosiformis] | 22.99 | 3.1325 | 30.8 | 6 | 15 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32669_c0_seq1_m.22867 | PREDICTED: stomatin-like protein 2, mitochondrial [Capsicum annuum] | 44.407 | 84.708 | 43.7 | 16 | 26 | 16 | 0.994 | 1.043 | 0.988 | 0.995 | 0.991 | 1.012 | 0.991 | 6.59E-01 |

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| cds.Camellia_sinensis.comp32675_c0_seq1_m.32022 | PREDICTED: DCN1-like protein 1 [Theobroma cacao] | 30.045 | 2.5435 | 7.4 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp32685_c0_seq1_m.26863 | PREDICTED: acidic mammalian chitinase [Vitis vinifera] | 47.12 | 24.795 | 5.4 | 2 | 2 | 2 | 1.015 | 1.091 | 1.018 | 1.056 | 0.949 | 0.875 | 0.922 | 2.31E-01 |
| cds.Camellia_sinensis.comp32690_c0_seq1_m.15967 | PREDICTED: ectonucleotide pyrophosphatase/phosphodiesterase family member 3-like [Nicotiana tomentosiformis] | 55.646 | 14.376 | 11 | 6 | 7 | 5 | 1.039 | 1.054 | 1.042 | 0.974 | 0.931 | 0.943 | 0.908 | 2.44E-03 |

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| cds.Camellia_sinensis.comp32691_c0_seq2_m.17320 | PREDICTED: lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex,mitochondrial [Vitis vinifera] | 62.031 | 24.979 | 5.9 | 2 | 2 | 2 | 0.976 | 0.967 | 1.171 | 0.967 | 0.964 | 0.962 | 0.929 | 3.80E-01 |
| cds.Camellia_sinensis.comp32694_c0_seq3_m.27655 | alpha/beta-hydrolases superfamily protein precursor [Solanum lycopersicum] | 22.834 | 1.7437 | 4 | 1 | 2 | 1 | 1.019 | 1.017 | 1.02 | 0.972 | 0.99 | 0.984 | 0.964 | 2.56E-03 |
| cds.Camellia_sinensis.comp32696_c0_seq3_m.41222 | PREDICTED: aladin isoform X1 [Vitis vinifera] | 27.84 | 5.1003 | 14.9 | 4 | 4 | 4 | 0.992 | 0.924 | 0.958 | 1.055 | 1.023 | 1.086 | 1.101 | 2.29E-02 |
| cds.Camellia_sinensis.comp32699_c0_seq1_m.25218 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 13 homolog A [Vitis vinifera] | 47.41 | 46.294 | 22.8 | 9 | 16 | 9 | 0.961 | 0.964 | 0.993 | 1.031 | 1.033 | 0.99 | 1.047 | 5.88E-02 |

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| cds.Camellia_sinensis.comp32701_c0_seq1_m.13827 | PREDICTED: ATPase family AAA domain-containing protein 3-B [Nelumbo nucifera] | 74.452 | 28.859 | 11.9 | 9 | 12 | 8 | 0.923 | 0.975 | 0.939 | 1.035 | 1.042 | 1.027 | 1.094 | 5.72E-03 |
| cds.Camellia_sinensis.comp32702_c0_seq14_m.38973 | PREDICTED: profilin-2 [Gossypium hirsutum] | 14.14 | 34.761 | 38.9 | 5 | 19 | 4 | 1.041 | 0.993 | 0.974 | 0.99 | 1.006 | 1.022 | 1.003 | 8.76E-01 |
| cds.Camellia_sinensis.comp32707_c0_seq1_m.33071 | PREDICTED: probable diphthine methyl ester synthase [Vitis vinifera] | 30.465 | 6.7062 | 6.9 | 2 | 2 | 2 | 0.917 | 0.959 | 0.997 | 1.095 | 1.017 | 1.045 | 1.099 | 4.35E-02 |
| cds.Camellia_sinensis.comp32709_c0_seq2_m.50782 | PREDICTED: (+)-neomenthol dehydrogenase [Vitis vinifera] | 17.282 | 59.453 | 40.4 | 7 | 17 | 7 | 0.983 | 1.005 | 0.997 | 1.013 | 1.008 | 1.024 | 1.02 | 6.68E-02 |

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| cds.Camellia_sinensis.comp32709_c3_seq1_m.49004 | PREDICTED: (+)-neomenthol dehydrogenase [Theobroma cacao] | 17.639 | 47.85 | 48.1 | 7 | 15 | 7 | 0.997 | 0.979 | 1 | 1.011 | 0.995 | 0.985 | 1.005 | 6.45E-01 |
| cds.Camellia_sinensis.comp32710_c0_seq50_m.19068 | PREDICTED: endoplasmic reticulum-Golgi intermediate compartment protein 3 isoform X1 [Juglans regia] | 40.331 | 1.9355 | 2.3 | 1 | 1 | 1 | 1.016 | 0.985 | 1.082 | 0.972 | 1.012 | 0.936 | 0.947 | 2.04E-01 |
| cds.Camellia_sinensis.comp32716_c0_seq1_m.13905 | PREDICTED: phosphoglucomutase, chloroplastic-like [Populus | 68.529 | 116.97 | 29 | 15 | 37 | 15 | 0.968 | 0.976 | 0.97 | 1.055 | 1.05 | 1.022 | 1.073 | 2.30E-03 |
| cds.Camellia_sinensis.comp32716_c0_seq2_m.17812 | PREDICTED: phosphoglucomutase, cytoplasmic [Daucus carota subsp. | 63.336 | 295.75 | 42.7 | 23 | 62 | 12 | 0.957 | 0.956 | 0.966 | 1.033 | 1.061 | 1.042 | 1.089 | 5.61E-04 |

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| cds.Camellia_sinensis.comp32716_c0_seq3_m.17919 | PREDICTED: phosphoglucomutase, cytoplasmic [Daucus carota subsp. | 63.559 | 70.773 | 34.3 | 18 | 50 | 7 | 1.038 | 1.026 | 1.01 | 0.945 | 0.993 | 0.969 | 0.946 | 2.67E-02 |
| cds.Camellia_sinensis.comp32716_c3_seq1_m.24652 | PREDICTED: desiccation-related protein At2g46140 [Ziziphus | 34.969 | 57.56 | 30.8 | 11 | 18 | 11 | 1.162 | 1.127 | 1.143 | 0.854 | 0.848 | 0.842 | 0.741 | 3.33E-06 |
| cds.Camellia_sinensis.comp32717_c0_seq1_m.34599 | PREDICTED: glutathione S-transferase U17-like [Malus domestica] | 25.892 | 29.821 | 32.2 | 7 | 15 | 7 | 1.337 | 1.307 | 1.346 | 0.645 | 0.642 | 0.635 | 0.482 | 1.07E-07 |
| cds.Camellia_sinensis.comp32721_c2_seq17_m.22610 | PREDICTED: multiple inositol polyphosphate phosphatase 1 [Vitis vinifera] | 57.393 | 5.2379 | 8.9 | 5 | 6 | 2 | 1.016 | 0.9 | 0.964 | 1.147 | 0.985 | 1.011 | 1.091 | 2.15E-01 |

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| cds.Camellia_sinensis.comp32721_c3_seq1_m.7620 | PREDICTED: DNA-binding protein SMUBP-2 [Theobroma cacao] | 97.559 | 4.3756 | 3.9 | 4 | 4 | 4 | 1.046 | 1.138 | 1.098 | 0.916 | 0.933 | 0.853 | 0.823 | 6.06E-03 |
| cds.Camellia_sinensis.comp32724_c0_seq9_m.38007 | PREDICTED: PHD finger-like domain-containing protein 5B [Brassica oleracea var. oleracea] | 12.414 | 2.0466 | 8.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32724_c1_seq1_m.8232 | PREDICTED: importin subunit beta-1 [Vitis vinifera] | 91.958 | 9.8643 | 3.4 | 2 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp32730_c0_seq1_m.23155 | PREDICTED: ADP,ATP carrier protein, mitochondrial-like [Ipomoea nil] | 49.552 | 68.861 | 20.8 | 11 | 52 | 6 | 1.023 | 0.997 | 1.007 | 1.002 | 1 | 1.018 | 0.998 | 8.19E-01 |

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| cds.Camellia_sinensis.comp32730_c0_seq2_m.54520 | PREDICTED: ADP,ATP carrier protein 1, mitochondrial, partial [Cucumis melo] | 15.292 | 28.758 | 28.9 | 4 | 30 | 2 | 1.006 | 0.999 | 0.985 | 1.042 | 0.998 | 0.966 | 1.005 | 8.41E-01 |
| cds.Camellia_sinensis.comp32732_c0_seq5_m.39027 | PREDICTED: thiosulfate sulfurtransferase 16, chloroplastic-like [Nicotiana tabacum] | 20.187 | 20.809 | 13.9 | 2 | 4 | 2 | 0.708 | 0.694 | 0.783 | 1.411 | 1.215 | 1.441 | 1.861 | 6.96E-04 |
| cds.Camellia_sinensis.comp32733_c0_seq2_m.7870 | PREDICTED: nucleolin 2 isoform X2 [Populus euphratica] | 43.038 | 2.5127 | 4.2 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp32733_c0_seq2_m.7871 | PREDICTED: nucleolin 2 isoform X5 [Theobroma cacao] | 37.571 | 11.486 | 14.8 | 5 | 5 | 5 | 1.064 | 1.012 | 1.042 | 0.982 | 0.947 | 0.949 | 0.923 | 1.28E-02 |
| cds.Camellia_sinensis.comp32734_c0_seq1_m.19033 | PREDICTED: serine/threonine-protein kinase rio1 [Theobroma cacao] | 55.265 | -2 | 1.8 | 1 | 1 | 1 | 1.053 | 1.091 | 1.133 | 0.923 | 0.905 | 0.88 | 0.826 | 1.66E-03 |

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| cds.Camellia_sinensis.comp32736_c2_seq9_m.26887 | PREDICTED: ATP-dependent Clp protease proteolytic subunit-related protein 3, chloroplastic [Daucus carota subsp. sativus] | 36.507 | 21.394 | 18.6 | 6 | 11 | 6 | 0.995 | 1.011 | 1.016 | 0.987 | 0.968 | 0.965 | 0.966 | 2.21E-02 |
| cds.Camellia_sinensis.comp32737_c1_seq27_m.36809 | PREDICTED: putative pterin-4-alpha-carbinolamine dehydratase [Theobroma cacao] | 21.022 | 2.0391 | 8.6 | 2 | 2 | 2 | 0.984 | 0.976 | 1.038 | 0.926 | 1.052 | 1.031 | 1.004 | 9.58E-01 |
| cds.Camellia_sinensis.comp32739_c0_seq3_m.16599 | PREDICTED: protein disulfide-isomerase [Nelumbo nucifera] | 59.466 | 136.03 | 39.8 | 21 | 52 | 18 | 1.023 | 0.994 | 1.017 | 0.972 | 0.985 | 0.993 | 0.972 | 5.97E-02 |
| cds.Camellia_sinensis.comp32739_c0_seq5_m.46232 | PREDICTED: protein disulfide-isomerase [Nelumbo nucifera] | 11.563 | 58.865 | 46.1 | 5 | 10 | 4 | 0.939 | 0.987 | 0.981 | 1.022 | 1.079 | 1.039 | 1.08 | 2.65E-02 |

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| cds.Camellia_sinensis.comp32742_c1_seq1_m.45933 | PREDICTED: MLP-like protein 329 [Malus domestica] | 15.84 | 14.108 | 29.2 | 6 | 19 | 6 | 1.096 | 1.026 | 1.02 | 0.923 | 0.96 | 0.956 | 0.904 | 1.82E-02 |
| cds.Camellia_sinensis.comp32743_c0_seq1_m.18298 | PREDICTED: pheophorbide a oxygenase, chloroplastic [Citrus sinensis] | 64.511 | 31.615 | 17 | 10 | 16 | 9 | 0.959 | 1.004 | 0.983 | 1.025 | 1.03 | 1.004 | 1.038 | 7.03E-02 |
| cds.Camellia_sinensis.comp32746_c0_seq4_m.1832 | PREDICTED: cell division cycle and apoptosis regulator protein 1 [Citrus sinensis] | 91.223 | 21.677 | 3.3 | 2 | 2 | 2 | 1.115 | 1.082 | 0.999 | 0.971 | 0.852 | 0.963 | 0.872 | 6.13E-02 |
| cds.Camellia_sinensis.comp32746_c0_seq4_m.1833 | PREDICTED: cell division cycle and apoptosis regulator protein 1-like [Juglans regia] | 73.066 | 17.17 | 6.1 | 3 | 3 | 3 | 0.897 | 0.978 | 0.977 | 1.069 | 1.05 | 1.061 | 1.115 | 1.97E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32750_c0_seq1_m.2788 | PREDICTED: heat shock 70 kDa protein 14-like [Sesamum indicum] | 93.302 | 139 | 33 | 29 | 58 | 19 | 1.054 | 1.044 | 1.031 | 0.947 | 0.968 | 0.976 | 0.924 | 2.00E-03 |
| cds.Camellia_sinensis.comp32750_c0_seq40_m.29864 | PREDICTED: heat shock 70 kDa protein 14-like [Sesamum indicum] | 39.488 | 36.472 | 29.4 | 11 | 23 | 6 | 1.041 | 1.012 | 1.026 | 1.021 | 0.958 | 0.935 | 0.946 | 1.13E-01 |
| cds.Camellia_sinensis.comp32759_c0_seq3_m.33575 | PREDICTED: erlin-2-B [Juglans regia] | 26.825 | 10.511 | 22.8 | 6 | 7 | 6 | 0.98 | 0.992 | 0.996 | 0.983 | 1.023 | 1.02 | 1.02 | 2.34E-01 |
| cds.Camellia_sinensis.comp32762_c0_seq1_m.10285 | PREDICTED: ABC transporter G family member 11 [Ricinus | 79.525 | 7.4286 | 2.7 | 2 | 2 | 2 | 1.174 | 1.224 | 1.243 | 0.792 | 0.761 | 0.749 | 0.632 | 4.14E-05 |
| cds.Camellia_sinensis.comp32762_c0_seq5_m.23908 | carboxyl-terminal peptidase, putative (DUF239) [Arabidopsis thaliana] | 46.737 | 12.397 | 7.1 | 2 | 2 | 2 | 0.969 | 1.075 | 0.98 | 0.999 | 1.041 | 0.948 | 0.988 | 7.99E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32762_c1_seq32_m.42855 | polyketide cyclase/dehydrase and lipid transporter [Medicago truncatula] | 20.26 | 3.243 | 9.5 | 2 | 5 | 2 | 1.011 | 1.035 | 1.009 | 1.045 | 0.944 | 0.964 | 0.967 | 3.38E-01 |
| cds.Camellia_sinensis.comp32765_c1_seq25_m.35449 | RAP release 2, galactose-binding-like domain protein, putative (DUF1997) [Arabidopsis thaliana] | 30.745 | 19.69 | 6.9 | 2 | 2 | 2 | 0.997 | 0.985 | 0.947 | 1.05 | 0.973 | 1.063 | 1.054 | 1.79E-01 |
| cds.Camellia_sinensis.comp32769_c0_seq19_m.42882 | PREDICTED: microtubule-associated protein 70-2 [Vitis vinifera] | 24.68 | 3.264 | 4.9 | 1 | 1 | 1 | 0.977 | 1.006 | 1.07 | 1 | 1.003 | 0.955 | 0.969 | 3.74E-01 |
| cds.Camellia_sinensis.comp32769_c1_seq29_m.20869 | PREDICTED: microtubule-associated protein 70-2-like isoform X1 [Jatropha curcas] | 45.149 | 3.4536 | 6.7 | 2 | 2 | 2 | 1.013 | 0.982 | 1.004 | 1.019 | 1 | 0.992 | 1.004 | 7.58E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32771_c0_seq3_m.18310 | PREDICTED: protein NRT1/PTR FAMILY 8.3-like [Nicotiana tabacum] | 64.9 | 2.7966 | 3.1 | 2 | 2 | 2 | 1.13 | 1.079 | 1.049 | 0.929 | 0.84 | 0.948 | 0.834 | 1.35E-02 |
| cds.Camellia_sinensis.comp32800_c0_seq1_m.3897 | PREDICTED: phospholipase A-2-activating protein [Prunus mume] | 84.033 | 86.378 | 22.6 | 14 | 19 | 14 | 0.982 | 0.973 | 0.977 | 1.022 | 1.016 | 1.007 | 1.039 | 1.72E-03 |
| cds.Camellia_sinensis.comp32800_c0_seq1_m.3898 | PREDICTED: succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial [Juglans regia] | 41.711 | 150.34 | 27.6 | 9 | 18 | 9 | 1.011 | 0.992 | 1.011 | 1.021 | 1.001 | 0.992 | 1 | 9.98E-01 |

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| cds.Camellia_sinensis.comp32800_c0_seq3_m.35099 | PREDICTED: LOW QUALITY PROTEIN: succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial-like[Sesamum indicum] | 28.478 | 7.2209 | 25.7 | 6 | 14 | 3 | 1.026 | 0.927 | 0.997 | 0.967 | 1.032 | 1.06 | 1.037 | 4.21E-01 |
| cds.Camellia_sinensis.comp32800_c0_seq5_m.39195 | PREDICTED: LOW QUALITY PROTEIN: succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial-like[Sesamum indicum] | 28.503 | 82.298 | 34 | 7 | 20 | 4 | 1.021 | 1.039 | 1.024 | 0.954 | 1.007 | 0.982 | 0.954 | 4.67E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32801_c0_seq3_m.30883 | PREDICTED: V-type proton ATPase subunit D [Theobrom | 29.117 | 57.583 | 48.7 | 14 | 21 | 14 | 0.955 | 0.986 | 0.972 | 1.06 | 1.05 | 1.033 | 1.079 | 3.10E-03 |
| cds.Camellia_sinensis.comp32802_c0_seq1_m.10798 | PREDICTED: endoglucanase 25-like [Solanum | 68.121 | 1.4024 | 1.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32806_c0_seq1_m.28386 | PREDICTED: beta-glucosidase BoGH3B [Theobroma cacao] | 46.413 | 22.959 | 8.8 | 3 | 4 | 3 | 0.903 | 0.981 | 0.907 | 1.103 | 1.071 | 1.039 | 1.151 | 1.15E-02 |
| cds.Camellia_sinensis.comp32806_c0_seq3_m.55090 | PREDICTED: beta-glucosidase BoGH3B [Theobroma cacao] | 10.718 | 3.3033 | 11.1 | 1 | 3 | 1 | 0.868 | 0.925 | 0.97 | 1.043 | 1.103 | 1.13 | 1.186 | 1.29E-02 |
| cds.Camellia_sinensis.comp32809_c0_seq9_m.17983 | PREDICTED: eukaryotic translation initiation factor 6-2 [Juglans regia] | 26.483 | 24.118 | 18 | 4 | 6 | 4 | 0.967 | 0.914 | 0.958 | 1.065 | 1.032 | 1.114 | 1.131 | 1.21E-02 |

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| cds.Camellia_sinensis.comp32812_c0_seq1_m.9893 | PREDICTED: acylamino-acid-releasing enzyme isoform X2 [Juglans regia] | 90.165 | 101.05 | 20.3 | 13 | 27 | 13 | 0.951 | 0.959 | 0.952 | 1.065 | 1.038 | 1.077 | 1.111 | 7.21E-04 |
| cds.Camellia_sinensis.comp32814_c0_seq17_m.3754 | RanBP1 domain protein [Medicago truncatula] | 29.525 | 4.9083 | 12.4 | 3 | 3 | 3 | 1.06 | 1.048 | 0.954 | 0.964 | 1.019 | 0.953 | 0.959 | 3.52E-01 |
| cds.Camellia_sinensis.comp32818_c0_seq3_m.31143 | PREDICTED: short-chain type dehydrogenase/reductase isoform X2 [Jatropha curcas] | 27.946 | 6.6083 | 9 | 2 | 3 | 2 | 0.92 | 0.974 | 0.922 | 1.123 | 1.068 | 1.03 | 1.144 | 1.27E-02 |
| cds.Camellia_sinensis.comp32818_c0_seq3_m.31144 | transmembrane protein [Arabidopsis thaliana] | 14.878 | 6.5071 | 9.6 | 1 | 2 | 1 | 0.95 | 1.016 | 1.006 | 0.988 | 0.973 | 1.08 | 1.023 | 5.95E-01 |
| cds.Camellia_sinensis.comp32820_c0_seq1_m.30501 | S-adenosyl-L-methionine-dependent methyltransferase [Medicago truncatula] | 17.397 | 21.181 | 19.4 | 3 | 4 | 3 | 0.967 | 1.062 | 0.984 | 1.076 | 0.977 | 0.996 | 1.012 | 7.88E-01 |

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| cds.Camellia_sinensis.comp32820_c0_seq4_m.31281 | S-adenosyl-L-methionine-dependent methyltransferase [Medicago truncatula] | 11.507 | 36.026 | 52.9 | 4 | 9 | 4 | 0.991 | 0.996 | 1.038 | 1.018 | 0.983 | 0.966 | 0.981 | 4.14E-01 |
| cds.Camellia_sinensis.comp32825_c0_seq15_c0_seq1_m.3789 | PREDICTED: nuclear pore complex protein GP210 [Vitis vinifera] | 89.918 | 11.104 | 1.5 | 1 | 1 | 1 | 0.991 | 1.061 | 1.044 | 1.063 | 0.924 | 0.926 | 0.941 | 2.84E-01 |
| cds.Camellia_sinensis.comp32825_c0_seq3_m.9245 | PREDICTED: nuclear pore complex protein GP210 [Vitis vinifera] | 92.267 | 11.033 | 3.6 | 3 | 3 | 3 | 0.961 | 1.018 | 1.062 | 1.009 | 0.967 | 0.995 | 0.977 | 5.13E-01 |
| cds.Camellia_sinensis.comp32827_c0_seq1_m.7451 | PREDICTED: granule-bound starch synthase 2, chloroplastic/amyloplastic isoform X2 [Vitis vinifera] | 83.244 | 17.404 | 6 | 5 | 6 | 5 | 0.986 | 1.003 | 1.04 | 0.965 | 1.035 | 1.009 | 0.993 | 8.05E-01 |

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| cds.Camellia_sinensis.comp32828_c0_seq1_m.1768 | PREDICTED: enhancer of mRNA-decapping protein 4-like [Sesamum indicum] | 110.09 | 107.56 | 13.2 | 13 | 16 | 13 | 0.966 | 0.997 | 0.996 | 1.006 | 1.02 | 1.037 | 1.035 | 6.36E-02 |
| cds.Camellia_sinensis.comp32828_c0_seq1_m.1769 | PREDICTED: enhancer of mRNA-decapping protein 4 [Vitis vinifera] | 29.879 | 2.5966 | 5.8 | 1 | 2 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp32831_c0_seq1_m.10962 | PREDICTED: long chain acyl-CoA synthetase 2 [Ipomoea nil] | 49.022 | 1.6066 | 1.6 | 1 | 2 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp32836_c0_seq2_m.19349 | PREDICTED: protein SSUH2 homolog [Ricinus communis] | 48.317 | 72.251 | 40.8 | 16 | 28 | 16 | 0.947 | 0.95 | 0.941 | 1.088 | 1.057 | 1.054 | 1.127 | 3.41E-04 |
| cds.Camellia_sinensis.comp32846_c0_seq1_m.32656 | PREDICTED: cinnamoyl-CoA reductase 2-like [Nicotiana attenuata] | 35.4 | 73.272 | 36.4 | 12 | 18 | 12 | 1.001 | 0.981 | 1.008 | 1.008 | 0.986 | 1.031 | 1.012 | 4.91E-01 |

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| cds.Camellia_sinensis.comp32847_c0_seq1_m.24332 | PREDICTED: RNA-binding KH domain-containing protein PEPPER [Vitis vinifera] | 49.479 | 37.144 | 23.6 | 11 | 15 | 6 | 0.972 | 0.927 | 0.928 | 1.025 | 1.082 | 1.017 | 1.105 | 1.62E-02 |
| cds.Camellia_sinensis.comp32847_c0_seq2_m.26434 | RNA-binding KH domain-containing protein PEPPER-like [Cajanus cajan] | 48.055 | 79.058 | 26.5 | 12 | 16 | 7 | 0.971 | 0.968 | 0.965 | 1.025 | 1.035 | 1.009 | 1.057 | 1.94E-03 |
| cds.Camellia_sinensis.comp32850_c0_seq2_m.6603 | PREDICTED: alpha-glucosidase-like [Vitis vinifera] | 102.68 | 24.61 | 10.1 | 9 | 16 | 7 | 0.927 | 0.924 | 0.919 | 1.098 | 1.069 | 1.111 | 1.183 | 1.37E-04 |
| cds.Camellia_sinensis.comp32850_c0_seq3_m.7253 | PREDICTED: alpha-glucosidase [Juglans regia] | 103.12 | 9.0077 | 5.3 | 5 | 10 | 3 | 0.914 | 0.921 | 0.901 | 1.118 | 1.092 | 1.103 | 1.211 | 3.70E-05 |
| cds.Camellia_sinensis.comp32851_c0_seq1_m.13429 | PREDICTED: peroxisomal membrane protein PEX14 [Juglans regia] | 37.63 | 18.71 | 11.5 | 5 | 5 | 5 | 0.983 | 0.989 | 0.992 | 0.994 | 0.986 | 1.043 | 1.02 | 3.88E-01 |

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| cds.Camellia_sinensis.comp32851_c0_seq1_m.13430 | PREDICTED: peroxisomal membrane protein PEX14 [Jatropha curcas] | 31.968 | 14.919 | 18.5 | 4 | 5 | 4 | 1.081 | 0.977 | 0.977 | 0.992 | 1.032 | 0.936 | 0.975 | 6.05E-01 |
| cds.Camellia_sinensis.comp32857_c0_seq2_m.10287 | PREDICTED: somatic embryogenesis receptor kinase 2 [Vitis vinifera] | 68.949 | 1.5451 | 2.7 | 2 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp32863_c1_seq1_m.3632 | PREDICTED: phototropin-1 isoform X2 [Vitis vinifera] | 114.58 | 1.435 | 2.5 | 3 | 3 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp32865_c0_seq1_m.13403 | PREDICTED: probable aspartyl aminopeptidase [Juglans regia] | 53.372 | 60.294 | 23.3 | 10 | 14 | 10 | 0.937 | 0.953 | 0.975 | 1.042 | 1.076 | 1.055 | 1.108 | 2.34E-03 |

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| cds.Camellia_sinensis.comp32867_c1_seq2_m.38138 | PREDICTED: ubiquitin-conjugating enzyme E2 2 isoform X1 [Gossypium hirsutum] | 17.334 | 1.7217 | 15.8 | 2 | 2 | 1 | 0.995 | 1.102 | 0.964 | 0.943 | 0.956 | 1.039 | 0.96 | 4.69E-01 |
| cds.Camellia_sinensis.comp32867_c2_seq1_m.1279 | PREDICTED: nucleolin 2-like isoform X1 [Juglans regia] | 101.17 | 1.6245 | 1.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32867_c2_seq2_m.8329 | PREDICTED: exocyst complex component EXO70A1 [Vitis vinifera] | 74.002 | -2 | 1.5 | 1 | 1 | 1 | 1.068 | 1.022 | 1.13 | 0.954 | 0.917 | 0.899 | 0.86 | 1.15E-02 |
| cds.Camellia_sinensis.comp32869_c0_seq59_m.46979 | PREDICTED: V-type proton ATPase subunit F [Sesamum | 14.523 | 15.556 | 21.5 | 3 | 4 | 3 | 1.01 | 0.97 | 0.926 | 1.066 | 1.053 | 0.993 | 1.071 | 1.08E-01 |

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| cds.Camellia_sinensis.comp32871_c0_seq1_m.5864 | PREDICTED: exocyst complex component SEC3A [Theobroma cacao] | 100.12 | 11.192 | 3.3 | 3 | 3 | 3 | 0.99 | 0.984 | 1.068 | 0.981 | 0.953 | 1.048 | 0.98 | 6.31E-01 |
| cds.Camellia_sinensis.comp32872_c0_seq11_m.40246 | PREDICTED: photosynthetic NDH subunit of lumenal location 1, chloroplastic isoform X1 [Nelumbo nucifera] | 23.951 | 35.807 | 43.3 | 9 | 17 | 9 | 0.97 | 0.988 | 1.014 | 0.976 | 1.025 | 0.998 | 1.009 | 6.62E-01 |
| cds.Camellia_sinensis.comp32872_c0_seq5_m.2326 | PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1B [Jatropha curcas] | 52.023 | 18.148 | 14.7 | 8 | 9 | 8 | 1.006 | 0.972 | 0.992 | 1.007 | 0.992 | 1.047 | 1.026 | 2.55E-01 |
| cds.Camellia_sinensis.comp32875_c0_seq1_m.22914 | PREDICTED: elongation factor Ts, mitochondrial [Ricinus communis] | 21.138 | 2.5364 | 13.3 | 3 | 3 | 3 | 1.024 | 0.921 | 1.041 | 1.022 | 1.003 | 1 | 1.013 | 7.31E-01 |

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| cds.Camellia_sinensis.comp32876_c0_seq9_m.20024 | histidine phosphatase family (branch 1) protein [Medicago truncatula] | 26.609 | 11.541 | 15.8 | 4 | 6 | 4 | 0.972 | 0.981 | 0.94 | 1.01 | 1.056 | 1.062 | 1.081 | 1.90E-02 |
| cds.Camellia_sinensis.comp32880_c0_seq2_m.10056 | PREDICTED: topless-related protein 3-like [Sesamum indicum] | 82.193 | 10.865 | 7.5 | 6 | 7 | 6 | 0.917 | 0.938 | 0.951 | 1.073 | 1.118 | 1.053 | 1.156 | 2.16E-03 |
| cds.Camellia_sinensis.comp32891_c1_seq3_m.39628 | PREDICTED: protein CREG1 isoform X1 [Sesamum indicum] | 22.324 | 5.7675 | 10 | 2 | 3 | 2 | 1.033 | 1.019 | 0.927 | 0.949 | 1.024 | 1.05 | 1.015 | 7.61E-01 |
| cds.Camellia_sinensis.comp32896_c0_seq2_m.3153 | PREDICTED: protein transport protein Sec24-like At4g32640 isoform X1 [Vitis vinifera] | 101.38 | 14.385 | 5.5 | 5 | 5 | 5 | 0.988 | 0.984 | 1.019 | 0.983 | 1.032 | 1.004 | 1.009 | 6.33E-01 |

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| cds.Camellia_sinensis.comp32898_c0_seq1_m.8011 | PREDICTED: NADPH--cytochrome P450 reductase [Theobroma cacao] | 76.867 | 30.958 | 13.4 | 10 | 13 | 10 | 1.009 | 1.127 | 1.058 | 0.968 | 0.919 | 0.92 | 0.879 | 2.41E-02 |
| cds.Camellia_sinensis.comp32899_c0_seq1_m.5712 | PREDICTED: polyribonucleotide nucleotidyltransferase 2, mitochondrial [Vitis vinifera] | 103.65 | 4.9102 | 4.3 | 5 | 5 | 5 | 0.922 | 1.009 | 1.024 | 1.056 | 1.02 | 0.995 | 1.039 | 3.49E-01 |
| cds.Camellia_sinensis.comp32900_c0_seq2_m.8385 | PREDICTED: exocyst complex component EXO84B [Vitis vinifera] | 85.674 | 10.938 | 2.7 | 2 | 3 | 2 | 1.068 | 1.074 | 0.915 | 1.052 | 0.914 | 0.976 | 0.962 | 6.04E-01 |
| cds.Camellia_sinensis.comp32901_c0_seq1_m.18562 | PREDICTED: low-temperature-induced cysteine proteinase [Vitis vinifera] | 55.425 | 53.097 | 11 | 5 | 16 | 4 | 1.038 | 1.007 | 0.973 | 0.984 | 0.982 | 0.967 | 0.972 | 2.20E-01 |

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| cds.Camellia_sinensis.comp32902_c0_seq1_m.22717 | PREDICTED: cytochrome P450 81E8-like [Fragaria vesca subsp. vesca] | 56.736 | 6.5762 | 6.4 | 3 | 3 | 1 | 1.005 | 1.139 | 1.048 | 0.969 | 0.936 | 0.898 | 0.878 | 3.95E-02 |
| cds.Camellia_sinensis.comp32903_c0_seq1_m.28618 | PREDICTED: short-chain dehydrogenase TIC 32, chloroplastic [Eucalyptus grandis] | 35.246 | 1.6557 | 2.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32905_c0_seq2_m.23124 | PREDICTED: rab escort protein 1 [Vitis vinifera] | 21.926 | 1.1978 | 3.5 | 1 | 1 | 1 | 0.936 | 0.937 | 1.07 | 1 | 1.009 | 1.069 | 1.046 | 3.98E-01 |
| cds.Camellia_sinensis.comp32908_c0_seq1_m.21148 | PREDICTED: beta-glucosidase-like SFR2, chloroplastic isoform X2 [Vitis vinifera] | 66.04 | 32.834 | 13.5 | 8 | 11 | 8 | 0.982 | 1.025 | 1.031 | 0.989 | 0.991 | 1.016 | 0.986 | 4.79E-01 |
| cds.Camellia_sinensis.comp32914_c0_seq1_m.2641 | PREDICTED: myosin-9-like [Populus euphratica] | 139.41 | 177.1 | 31.8 | 36 | 48 | 36 | 1.02 | 1.015 | 1.016 | 0.966 | 0.962 | 0.99 | 0.956 | 7.94E-03 |

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| cds.Camellia_sinensis.comp32917_c0_seq4_m.31727 | PREDICTED: chorismate mutase 1, chloroplastic-like isoform X1 [Nelumbo nucifera] | 36.759 | 20.297 | 23.6 | 7 | 7 | 5 | 1.255 | 0.89 | 1.197 | 0.779 | 0.974 | 0.861 | 0.782 | 1.30E-01 |
| cds.Camellia_sinensis.comp32917_c0_seq5_m.34127 | PREDICTED: chorismate mutase 3, chloroplastic [Prunus mume] | 37.031 | 2.032 | 12.7 | 4 | 4 | 2 | 0.983 | 1.096 | 0.644 | 0.883 | 1.121 | 1.283 | 1.207 | 3.61E-01 |
| cds.Camellia_sinensis.comp32919_c0_seq1_m.35142 | PREDICTED: shootin-1-like [Juglans regia] | 30.589 | 1.7725 | 4 | 1 | 1 | 1 | 0.956 | 1.057 | 1.04 | 0.983 | 1.033 | 0.944 | 0.97 | 4.92E-01 |
| cds.Camellia_sinensis.comp32921_c0_seq3_m.29082 | PREDICTED: ATP-dependent (S)-NAD(P)H-hydrate dehydratase isoform X2 [Juglans regia] | 39.62 | 24.919 | 31.9 | 9 | 11 | 7 | 0.939 | 0.969 | 0.979 | 1.046 | 1.083 | 1.011 | 1.088 | 2.35E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32921_c0_seq51_m.30515 | PREDICTED: ATP-dependent (S)-NAD(P)H-hydrate dehydratase isoform X2 [Juglans regia] | 39.752 | 5.2957 | 11.2 | 4 | 5 | 2 | 0.906 | 0.925 | 0.962 | 1.063 | 1.14 | 1.041 | 1.161 | 1.02E-02 |
| cds.Camellia_sinensis.comp32922_c0_seq8_m.5477 | COP1-interacting-like protein [Medicago truncatula] | 91.503 | -2 | 1.2 | 1 | 1 | 1 | 0.896 | 0.955 | 1.058 | 1.035 | 1.033 | 1.051 | 1.072 | 2.77E-01 |
| cds.Camellia_sinensis.comp32929_c0_seq19_m.26024 | PREDICTED: IAA-amino acid hydrolase ILR1-like 4 [Vitis vinifera] | 46.508 | 43.968 | 30.8 | 11 | 20 | 11 | 0.977 | 0.977 | 0.971 | 1.025 | 1.044 | 1.009 | 1.052 | 7.20E-03 |
| cds.Camellia_sinensis.comp32936_c1_seq16_m.15922 | PREDICTED: methyl-CpG-binding domain-containing protein 11-like [Nelumbo nucifera] | 17.779 | 1.9602 | 7.5 | 1 | 1 | 1 | 1.15 | 1.065 | 1.133 | 0.835 | 0.955 | 0.83 | 0.783 | 8.68E-03 |
| cds.Camellia_sinensis.comp32936_c1_seq16_m.15923 |  | 17.216 | 2.7012 | 12.8 | 2 | 2 | 2 | 1.235 | 1.101 | 1.145 | 0.778 | 0.783 | 0.902 | 0.708 | 4.14E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp32938_c0_seq1_m.2560 | PREDICTED: ABC transporter B family member 27-like [Juglans regia] | 69.361 | 9.9672 | 8.1 | 6 | 8 | 6 | 0.991 | 1.023 | 1.068 | 1.025 | 0.953 | 1.032 | 0.977 | 5.16E-01 |
| cds.Camellia_sinensis.comp32939_c0_seq1_m.21635 | PREDICTED: probable protein phosphatase 2C 59 isoform X3 [Ziziphus jujuba] | 33.229 | 16.795 | 20.6 | 6 | 7 | 4 | 1.019 | 0.94 | 0.931 | 1.031 | 1.035 | 1.031 | 1.072 | 1.35E-01 |
| cds.Camellia_sinensis.comp32940_c0_seq1_m.6630 | PREDICTED: receptor-like protein kinase FERONIA [Eucalyptus grandis] | 97.286 | 3.5028 | 2 | 2 | 2 | 1 | 1.034 | 0.994 | 0.975 | 1.016 | 0.975 | 1.011 | 1 | 9.93E-01 |
| cds.Camellia_sinensis.comp32944_c0_seq2_m.12177 | PREDICTED: phosphoribosylaminoimidazole carboxylase, chloroplastic isoform X1 [Vitis vinifera] | 63.85 | 67.56 | 21.8 | 10 | 12 | 10 | 0.963 | 0.957 | 0.979 | 1.063 | 0.97 | 1.037 | 1.059 | 1.15E-01 |

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| cds.Camellia_sinensis.comp32948_c0_seq1_m.27404 | PREDICTED: early nodulin-93-like isoform X1 [Cucumis sativus] | 12.508 | 1.3107 | 8.6 | 1 | 3 | 1 | 0.938 | 1.017 | 0.848 | 1.08 | 0.968 | 1.175 | 1.15 | 1.44E-01 |
| cds.Camellia_sinensis.comp32951_c0_seq41_m.5915 | PREDICTED: probable fructokinase-6, chloroplastic [Prunus mume] | 42.152 | 140.47 | 35.2 | 11 | 26 | 10 | 1.039 | 1.025 | 1.034 | 0.958 | 0.961 | 1.011 | 0.946 | 3.51E-02 |
| cds.Camellia_sinensis.comp32954_c0_seq1_m.19253 | PREDICTED: tocopherol cyclase, chloroplastic-like [Juglans regia] | 57.86 | 69.003 | 30.9 | 14 | 22 | 14 | 0.996 | 1.002 | 0.997 | 0.983 | 0.986 | 1.035 | 1.003 | 8.86E-01 |
| cds.Camellia_sinensis.comp32955_c1_seq2_m.24660 | spermine synthase-like [Pyrus x bretschneideri] | 17.418 | 2.7036 | 9 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp32956_c0_seq1_m.16454 | PREDICTED: proline--tRNA ligase, chloroplastic/mitochondrial [Vitis vinifera] | 41.292 | 38.907 | 32.7 | 11 | 13 | 11 | 0.982 | 0.983 | 0.998 | 1.002 | 0.996 | 1.009 | 1.015 | 8.34E-02 |

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| cds.Camellia_sinensis.comp32956_c0_seq1_m.16455 | PREDICTED: proline--tRNA ligase, chloroplastic/mitochondrial-like [Ziziphus jujuba] | 21.203 | 19.885 | 6.8 | 1 | 2 | 1 | 1.017 | 0.983 | 1.017 | 0.892 | 1.013 | 1.076 | 0.988 | 8.05E-01 |
| cds.Camellia_sinensis.comp32958_c0_seq1_m.15709 | PREDICTED: protein disulfide isomerase-like 1-6 [Juglans regia] | 69.483 | 34.066 | 17.8 | 10 | 15 | 10 | 0.946 | 0.985 | 0.997 | 1.04 | 1.068 | 1.033 | 1.073 | 2.03E-02 |
| cds.Camellia_sinensis.comp32960_c0_seq25_m.26509 | PREDICTED: ubiquitin thioesterase otubain-like [Prunus mume] | 34.039 | 10.643 | 8.9 | 3 | 4 | 3 | 0.966 | 0.948 | 1.032 | 0.979 | 0.98 | 1.018 | 1.011 | 7.22E-01 |
| cds.Camellia_sinensis.comp32962_c0_seq4_m.49070 | PREDICTED: probable complex I intermediate-associated protein 30 [Eucalyptus grandis] | 15.347 | 12.445 | 11.1 | 1 | 2 | 1 | 0.956 | 1.038 | 0.977 | 0.961 | 1.041 | 1.04 | 1.024 | 5.51E-01 |

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| cds.Camellia_sinensis.comp32965_c0_seq10_m.29424 | PREDICTED: 15-cis-phytoene desaturase-like [Citrus sinensis] | 25.462 | 10.155 | 10.1 | 2 | 2 | 2 | 0.848 | 0.931 | 0.922 | 1.172 | 1.143 | 1.038 | 1.241 | 1.04E-02 |
| cds.Camellia_sinensis.comp32965_c0_seq6_m.16402 | Phytoene dehydrogenase [Morus notabilis] | 14.666 | 17.376 | 38.9 | 4 | 4 | 4 | 0.87 | 0.907 | 0.997 | 1.173 | 0.931 | 1.081 | 1.148 | 1.61E-01 |
| cds.Camellia_sinensis.comp32966_c0_seq4_m.46913 | Uncharacterized RNA-binding protein [Morus notabilis] | 21.176 | 28.295 | 34.6 | 5 | 13 | 4 | 0.971 | 0.973 | 0.966 | 1.049 | 1.028 | 1.051 | 1.075 | 6.19E-04 |
| cds.Camellia_sinensis.comp32966_c1_seq1_m.3138 | PREDICTED: beta-xylosidase/alpha-L-arabinofuranosidase 2 [Theobroma cacao] | 85.23 | 89.468 | 21.5 | 14 | 39 | 13 | 0.986 | 0.96 | 0.945 | 1.025 | 1.033 | 1.043 | 1.073 | 6.30E-03 |
| cds.Camellia_sinensis.comp32970_c0_seq1_m.25443 | PREDICTED: 26S protease regulatory subunit 8 homolog A-like [Nelumbo nucifera] | 47.343 | 16.414 | 43.8 | 16 | 36 | 1 | 1.079 | 0.963 | 1.092 | 0.988 | 0.91 | 0.963 | 0.913 | 1.27E-01 |

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| cds.Camellia_sinensis.comp32970_c0_seq2_m.28918 | PREDICTED: 26S protease regulatory subunit 8 homolog A [Elaeis guineensis | 47.36 | 113.48 | 48.3 | 18 | 38 | 3 | 0.964 | 0.962 | 1.009 | 1 | 1.06 | 0.988 | 1.039 | 2.33E-01 |
| cds.Camellia_sinensis.comp32974_c0_seq1_m.6813 | PREDICTED: protein VACUOLELESS1 [Ziziphus jujuba] | 29.532 | 2.8655 | 3.8 | 1 | 1 | 1 | 1.05 | 1.13 | 0.945 | 0.921 | 0.866 | 1.073 | 0.915 | 3.35E-01 |
| cds.Camellia_sinensis.comp32978_c1_seq1_m.3957 | DUF1680 domain protein [Medicago truncatula] | 96.576 | 123.37 | 22.1 | 17 | 35 | 17 | 1.033 | 1.019 | 1.025 | 0.962 | 0.959 | 0.958 | 0.936 | 8.42E-05 |
| cds.Camellia_sinensis.comp32978_c2_seq3_m.35595 | PREDICTED: thioredoxin-like 2, chloroplastic [Juglans regia] | 24.845 | 2.7549 | 5.3 | 1 | 2 | 1 | 1.085 | 0.933 | 0.968 | 1.065 | 1.012 | 0.944 | 1.012 | 8.38E-01 |
| cds.Camellia_sinensis.comp32979_c0_seq7_m.19787 | PREDICTED: starch synthase VI isoform X1 [Vitis vinifera] | 67.189 | 36.163 | 14.8 | 7 | 8 | 7 | 0.965 | 0.963 | 0.97 | 0.995 | 1.086 | 1.054 | 1.082 | 9.41E-02 |

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| cds.Camellia_sinensis.comp32982_c0_seq1_m.22597 | PREDICTED: tryptophan synthase beta chain 1 [Cucumis melo] | 52.249 | 66.155 | 27.4 | 12 | 16 | 12 | 0.997 | 1.003 | 0.961 | 1.006 | 1.046 | 0.993 | 1.028 | 2.46E-01 |
| cds.Camellia_sinensis.comp32990_c0_seq1_m.16756 | PREDICTED: beta-hexosaminidase 3 [Juglans regia] | 63.604 | 144.08 | 31.3 | 17 | 44 | 16 | 1.013 | 1.011 | 1.014 | 0.993 | 1.012 | 0.968 | 0.979 | 2.33E-01 |
| cds.Camellia_sinensis.comp32992_c0_seq3_m.44235 | PREDICTED: 7-hydroxymethyl chlorophyll a reductase, chloroplastic [Daucus carota subsp. sativus] | 21.122 | 3.9041 | 9.7 | 2 | 3 | 2 | 1.033 | 1.027 | 0.997 | 1.034 | 0.94 | 0.972 | 0.964 | 2.78E-01 |
| cds.Camellia_sinensis.comp32994_c0_seq5_m.31489 | PREDICTED: beta-glucosidase 11-like [Vitis vinifera] | 15.516 | 4.7417 | 9.2 | 1 | 1 | 1 | 0.96 | 1.008 | 1.005 | 1.136 | 1.064 | 0.854 | 1.027 | 8.32E-01 |

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| cds.Camellia_sinensis.comp33001_c0_seq1_m.24338 | PREDICTED: probable envelope ADP,ATP carrier protein, chloroplastic [Sesamum indicum] | 46.369 | 1.7697 | 2.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33002_c0_seq2_m.11764 | PREDICTED: cleavage and polyadenylation specificity factor subunit 2 isoform X1 [Vitis vinifera] | 55.953 | 1.9264 | 2 | 1 | 2 | 1 | 1.014 | 0.927 | 0.992 | 0.975 | 1.068 | 1.036 | 1.05 | 2.70E-01 |
| cds.Camellia_sinensis.comp33002_c1_seq1_m.14584 | PREDICTED: TBCC domain-containing protein 1 [Vitis vinifera] | 62.496 | 25.606 | 9.9 | 5 | 9 | 5 | 0.983 | 1.014 | 0.915 | 1.035 | 1.079 | 1.057 | 1.089 | 5.83E-02 |

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| cds.Camellia_sinensis.comp33003_c0_seq1_m.29734 | PREDICTED: mitochondrial dicarboxylate/tricarboxylate transporter DTC [Sesamum indicum] | 31.998 | 72.629 | 28.2 | 7 | 16 | 6 | 1.008 | 0.982 | 0.987 | 1.007 | 1.001 | 1.026 | 1.019 | 1.57E-01 |
| cds.Camellia_sinensis.comp33003_c0_seq2_m.47039 | PREDICTED: mitochondrial dicarboxylate/tricarboxylate transporter DTC [Pyrus x bretschneideri] | 12.97 | -2 | 12.6 | 2 | 4 | 1 | 0.981 | 1.095 | 1.069 | 0.989 | 0.891 | 0.976 | 0.908 | 1.09E-01 |
| cds.Camellia_sinensis.comp33006_c0_seq1_m.2880 | PREDICTED: protein CROWDED NUCLEI 1 [Vitis | 125.75 | 8.027 | 4 | 5 | 6 | 4 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33007_c0_seq1_m.17728 | PREDICTED: sorting and assembly machinery component 50 homolog B-like [Solanum tuberosum | 18.616 | 4.8031 | 9.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33008_c0_seq1_m.20904 | PREDICTED: AT-hook motif nuclear-localized protein 1-like [Ipomoea nil] | 34.445 | 13.888 | 11.1 | 3 | 3 | 3 | 0.96 | 0.877 | 0.987 | 1.013 | 1.086 | 1.087 | 1.128 | 4.66E-02 |
| cds.Camellia_sinensis.comp33009_c0_seq1_m.13504 | PREDICTED: transmembrane 9 superfamily member 3 [Ipomoea nil] | 67.928 | 6.5648 | 7.8 | 5 | 6 | 4 | 0.968 | 0.989 | 1.114 | 1.033 | 0.954 | 0.954 | 0.958 | 4.57E-01 |
| cds.Camellia_sinensis.comp33009_c0_seq2_m.44801 | PREDICTED: transmembrane 9 superfamily member 3 [Nelumbo nucifera] | 24.91 | 3.5015 | 17.4 | 4 | 5 | 3 | 0.992 | 1.024 | 1.056 | 0.997 | 0.959 | 0.978 | 0.955 | 9.76E-02 |

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| cds.Camellia_sinensis.comp33013_c0_seq1_m.25050 | PREDICTED: protein TRIGALACTOSYLDIACYLGLYCEROL 4, chloroplastic [Vitis vinifera] | 52.738 | 5.8688 | 5.7 | 3 | 4 | 3 | 1.004 | 0.953 | 0.984 | 0.997 | 1.005 | 0.996 | 1.019 | 2.77E-01 |
| cds.Camellia_sinensis.comp33013_c0_seq2_m.25698 | PREDICTED: protein TRIGALACTOSYLDIACYLGLYCEROL 4, chloroplastic [Prunus mume] | 52.588 | 5.4637 | 6.5 | 3 | 5 | 3 | 0.96 | 1.018 | 1.1 | 1.062 | 0.918 | 0.956 | 0.954 | 4.63E-01 |
| cds.Camellia_sinensis.comp33014_c0_seq5_m.19830 | PREDICTED: zinc finger CCCH domain-containing protein 49 [Vitis vinifera] | 55.008 | 9.6304 | 13.8 | 6 | 6 | 6 | 1.018 | 1.006 | 1.07 | 0.958 | 0.948 | 1 | 0.939 | 6.63E-02 |
| cds.Camellia_sinensis.comp33017_c1_seq47_m.330 | NADH dehydrogenase subunit 7 (chloroplast) [Camellia sinensis] | 45.653 | 55.381 | 23.2 | 8 | 13 | 8 | 0.997 | 0.984 | 0.974 | 1.013 | 1.014 | 0.997 | 1.023 | 5.66E-02 |

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| cds.Camellia_sinensis.comp33017_c1_seq64_m.1059 | photosystem II p680 chlorophyll A apoprotein (chloroplast) [Camellia crapnelliana] | 39.493 | 212.71 | 27.2 | 9 | 64 | 9 | 0.965 | 1.013 | 0.978 | 1.034 | 1.007 | 1.018 | 1.035 | 1.04E-01 |
| cds.Camellia_sinensis.comp33017_c1_seq64_m.1060 | ATP-dependent Clp protease proteolytic subunit (chloroplast) [Diplopanax stachyanthus] | 21.995 | 46.072 | 18.4 | 4 | 11 | 4 | 0.992 | 1.014 | 1.016 | 0.998 | 1.009 | 0.985 | 0.99 | 3.90E-01 |
| cds.Camellia_sinensis.comp33017_c1_seq66_m.1341 | NADH dehydrogenase subunit 2 (chloroplast) [Ardisia polysticta] | 58.583 | 3.0367 | 3.1 | 2 | 2 | 2 | 1.036 | 1.034 | 1.023 | 0.97 | 0.902 | 1.03 | 0.938 | 2.33E-01 |
| cds.Camellia_sinensis.comp33017_c1_seq67_m.1798 | photosystem II protein D1 (chloroplast) [Scopolia parviflora] | 38.95 | 127.22 | 22.9 | 8 | 59 | 8 | 0.966 | 0.987 | 0.987 | 1.021 | 1.022 | 1.027 | 1.044 | 4.24E-03 |

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| cds.Camellia_sinensis.comp33017_c1_seq9_m.116 | Ycf2 (chloroplast) [Camellia sinensis] | 56.595 | 2.2689 | 2.7 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp33017_c1_seq9_m.118 | DNA-directed RNA polymerase alpha chain (chloroplast) [Camellia crapnelliana] | 39.538 | 19.373 | 18.7 | 6 | 8 | 6 | 0.951 | 0.919 | 0.982 | 1.032 | 0.995 | 1.071 | 1.086 | 4.46E-02 |
| cds.Camellia_sinensis.comp33017_c1_seq9_m.123 | ribosomal protein L2 (chloroplast) [Nicotiana otophora] | 15.145 | 9.8927 | 28.9 | 3 | 8 | 3 | 1.132 | 1.08 | 1.058 | 0.874 | 0.858 | 0.899 | 0.805 | 8.45E-04 |
| cds.Camellia_sinensis.comp33017_c1_seq9_m.125 | ribosomal protein S11 (plastid) [Lysimachia coreana] | 15.028 | 46.804 | 26.8 | 3 | 7 | 3 | 1.011 | 1.069 | 1.093 | 0.899 | 0.932 | 0.955 | 0.878 | 1.11E-02 |
| cds.Camellia_sinensis.comp33017_c1_seq9_m.131 | 50S ribosomal protein L14 (chloroplast) [Camellia crapnelliana] | 13.535 | 23.786 | 51.6 | 6 | 12 | 6 | 0.971 | 0.971 | 1.029 | 1.01 | 1.016 | 0.992 | 1.016 | 4.81E-01 |

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| cds.Camellia_sinensis.comp33017_c1_seq9_m.134 | 30S ribosomal protein S7 (chloroplast) [Camellia crapnelliana] | 12.03 | 7.9022 | 26.6 | 3 | 4 | 3 | 1.105 | 1.034 | 1.135 | 0.882 | 0.931 | 0.924 | 0.836 | 5.30E-03 |
| cds.Camellia_sinensis.comp33018_c1_seq1_m.33727 | PREDICTED: glutathione S-transferase T1 [Ziziphus jujuba] | 28.014 | 32.788 | 37.2 | 9 | 26 | 4 | 0.914 | 0.944 | 0.973 | 1.088 | 1.045 | 1.081 | 1.135 | 4.44E-03 |
| cds.Camellia_sinensis.comp33018_c1_seq2_m.49711 | PREDICTED: glutathione S-transferase T1 [Ricinus communis] | 21.296 | 100.49 | 58.8 | 11 | 27 | 6 | 0.867 | 0.869 | 0.879 | 1.174 | 1.091 | 1.129 | 1.298 | 2.76E-04 |
| cds.Camellia_sinensis.comp33019_c0_seq5_m.5844 | PREDICTED: ABC transporter A family member 7 [Vitis vinifera] | 106 | 5.1401 | 2.4 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33028_c0_seq1_m.3160 | PREDICTED: protein transport protein Sec24-like At3g07100 [Vitis vinifera] | 115.42 | 5.728 | 4.7 | 5 | 5 | 5 | 1.027 | 0.988 | 0.999 | 1 | 1.058 | 1.005 | 1.016 | 4.98E-01 |

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| cds.Camellia_sinensis.comp33032_c0_seq1_m.4992 | PREDICTED: chaperone protein ClpB3, chloroplastic isoform X2 [Sesamum indicum] | 110.2 | 296.03 | 42.7 | 39 | 73 | 36 | 1.02 | 1.023 | 1.026 | 0.984 | 0.981 | 0.976 | 0.958 | 1.24E-04 |
| cds.Camellia_sinensis.comp33033_c0_seq4_m.6390 | RNA ligase, putative [Medicago truncatula] | 29.422 | 6.8522 | 6.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33043_c1_seq1_m.8511 | PREDICTED: isoamylase 3, chloroplastic-like [Malus domestica] | 93.557 | 76.25 | 17.3 | 13 | 15 | 13 | 1.051 | 1.081 | 1.018 | 0.93 | 0.95 | 0.936 | 0.894 | 3.74E-03 |
| cds.Camellia_sinensis.comp33050_c1_seq1_m.7876 | PREDICTED: sucrose synthase 2 [Ziziphus jujuba] | 101.16 | 323.31 | 36.2 | 32 | 76 | 29 | 0.905 | 0.925 | 0.905 | 1.103 | 1.109 | 1.095 | 1.209 | 2.01E-05 |
| cds.Camellia_sinensis.comp33050_c2_seq5_m.26955 | PREDICTED: epimerase family protein SDR39U1 homolog, chloroplastic [Juglans regia] | 41.043 | 69.33 | 32.8 | 11 | 24 | 11 | 0.958 | 0.96 | 0.98 | 1.009 | 1.078 | 1.014 | 1.07 | 4.02E-02 |

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| cds.Camellia_sinensis.comp33055_c0_seq1_m.12922 | PREDICTED: ubiquitin domain-containing protein DSK2a-like [Nelumbo nucifera] | 59.193 | 46.334 | 16.5 | 6 | 11 | 5 | 1.034 | 1.039 | 1.024 | 1.035 | 0.97 | 0.969 | 0.96 | 1.39E-01 |
| cds.Camellia_sinensis.comp33067_c0_seq2_m.36662 | PREDICTED: 60S ribosomal protein L23a [Cucumis melo] | 17.502 | 31.985 | 26.5 | 4 | 9 | 4 | 1.15 | 1.116 | 1.084 | 0.831 | 0.917 | 0.881 | 0.785 | 1.88E-03 |
| cds.Camellia_sinensis.comp33067_c1_seq1_m.17116 | PREDICTED: calcium-dependent protein kinase 26-like [Gossypium hirsutum] | 60.422 | 17.947 | 16.4 | 7 | 8 | 7 | 0.989 | 1.028 | 1.02 | 1.028 | 0.966 | 0.964 | 0.974 | 3.32E-01 |
| cds.Camellia_sinensis.comp33070_c0_seq1_m.2815 | PREDICTED: fructokinase-like 2, chloroplastic isoform X2 [Vitis vinifera] | 64.81 | 1.8299 | 2.3 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp33070_c0_seq30_m.5410 | PREDICTED: folate synthesis bifunctional protein, mitochondrial [Vitis vinifera] | 55.462 | 8.9523 | 7.7 | 4 | 6 | 4 | 0.946 | 1.095 | 1.055 | 0.914 | 0.973 | 1.02 | 0.939 | 3.16E-01 |
| cds.Camellia_sinensis.comp33070_c1_seq1_m.4292 | PREDICTED: AP-4 complex subunit epsilon [Jatropha curcas] | 112.72 | 27.531 | 9.4 | 9 | 14 | 9 | 0.991 | 0.979 | 1 | 1.011 | 0.97 | 0.982 | 0.998 | 8.66E-01 |
| cds.Camellia_sinensis.comp33072_c0_seq1_m.25537 | PREDICTED: protein TIC 40, chloroplastic isoform X1 [Vitis vinifera] | 49.159 | 65.856 | 33 | 13 | 29 | 13 | 0.967 | 1.023 | 1.02 | 0.997 | 1.024 | 0.983 | 0.998 | 9.38E-01 |
| cds.Camellia_sinensis.comp33078_c0_seq1_m.10577 | PREDICTED: ABC transporter B family member 28 [Prunus mume] | 78.06 | 37.098 | 18.2 | 11 | 12 | 10 | 1.003 | 0.961 | 0.944 | 1.03 | 1.013 | 1.023 | 1.054 | 4.61E-02 |

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| cds.Camellia_sinensis.comp33084_c4_seq1_m.45006 | PREDICTED: nascent polypeptide-associated complex subunit alpha-like protein 1 [Elaeis guineensis | 21.74 | 25.533 | 22.1 | 3 | 9 | 3 | 1.01 | 1.026 | 1.023 | 0.978 | 1.004 | 0.922 | 0.949 | 1.10E-01 |
| cds.Camellia_sinensis.comp33084_c5_seq1_m.15203 | PREDICTED: ATP synthase subunit beta, mitochondrial-like [Solanum pennellii] | 59.463 | 323.31 | 53.2 | 22 | 91 | 19 | 1.034 | 1.003 | 1.02 | 0.991 | 0.971 | 0.981 | 0.963 | 2.31E-02 |
| cds.Camellia_sinensis.comp33084_c5_seq2_m.50711 | PREDICTED: ATP synthase subunit beta, mitochondrial-like [Nicotiana attenuata] | 17.821 | 6.558 | 22.5 | 3 | 14 | 1 | 0.98 | 0.985 | 0.959 | 1.022 | 1.016 | 1.055 | 1.058 | 1.71E-02 |
| cds.Camellia_sinensis.comp33087_c0_seq1_m.7166 | PREDICTED: phospholipase D delta isoform X3 [Vitis vinifera] | 97.908 | 13.033 | 10.2 | 8 | 9 | 8 | 0.907 | 0.899 | 0.961 | 1.077 | 1.069 | 1.012 | 1.141 | 9.94E-03 |

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| cds.Camellia_sinensis.comp33092_c0_seq1_m.9775 | PREDICTED: BEL1-like homeodomain protein 1 [Sesamum indicum] | 72.048 | 11.451 | 4.8 | 3 | 4 | 2 | 0.962 | 0.952 | 0.93 | 1.091 | 1.047 | 1.042 | 1.118 | 3.22E-03 |
| cds.Camellia_sinensis.comp33094_c1_seq3_m.7239 | | 18.899 | -2 | 4.1 | 1 | 2 | 1 | 0.986 | 0.93 | 1.021 | 0.972 | 1.037 | 1.068 | 1.048 | 2.98E-01 |
| cds.Camellia_sinensis.comp33096_c0_seq1_m.17329 | PREDICTED: dnaJ protein P58IPK homolog [Prunus mume] | 53.241 | 8.4665 | 13.6 | 6 | 6 | 6 | 0.954 | 0.982 | 0.999 | 1.089 | 0.98 | 1.02 | 1.052 | 2.08E-01 |
| cds.Camellia_sinensis.comp33098_c0_seq1_m.2140 | PREDICTED: ABC transporter C family member 14 [Juglans | 164.88 | 28.019 | 6.4 | 8 | 9 | 7 | 1.115 | 1.088 | 1.181 | 0.829 | 0.87 | 0.89 | 0.765 | 1.12E-03 |
| cds.Camellia_sinensis.comp33104_c0_seq1_m.8567 | PREDICTED: protein CHUP1, chloroplastic isoform X1 [Gossypium raimondii] | 33.717 | 12.278 | 24.8 | 7 | 9 | 7 | 1.083 | 1.064 | 1.072 | 0.913 | 0.911 | 0.943 | 0.86 | 2.44E-04 |

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| cds.Camellia_sinensis.comp33104_c0_seq1_m.8568 | P-loop nucleoside triphosphate hydrolase superfamily protein [Medicago truncatula] | 32.664 | 3.7664 | 11.2 | 3 | 3 | 3 | 0.973 | 0.994 | 0.954 | 1.123 | 0.971 | 1.007 | 1.062 | 2.69E-01 |
| cds.Camellia_sinensis.comp33104_c1_seq1_m.10864 | PREDICTED: protein CHUP1, chloroplastic [Vitis vinifera] | 76.402 | 28.278 | 14.6 | 10 | 10 | 10 | 1.098 | 1.072 | 1.096 | 0.899 | 0.883 | 0.924 | 0.829 | 2.45E-04 |
| cds.Camellia_sinensis.comp33106_c0_seq2_m.24466 | PREDICTED: proline iminopeptidase [Juglans regia] | 44.324 | 109.41 | 41.3 | 15 | 30 | 15 | 0.957 | 0.968 | 0.953 | 1.047 | 1.039 | 1.028 | 1.082 | 3.64E-04 |
| cds.Camellia_sinensis.comp33108_c0_seq2_m.12576 | PREDICTED: zinc finger CCCH domain-containing protein 64 isoform X2 [Vitis vinifera] | 40.297 | 4.0797 | 7.1 | 2 | 2 | 2 | 1.157 | 0.971 | 0.635 | 1.186 | 0.995 | 1.067 | 1.176 | 3.65E-01 |

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| cds.Camellia_sinensis.comp33109_c0_seq13_m.29073 | PREDICTED: CBS domain-containing protein CBSX2, chloroplastic [Eucalyptus grandis] | 27.432 | 61.034 | 26.6 | 8 | 12 | 7 | 1.04 | 1.022 | 1.044 | 0.973 | 0.959 | 0.987 | 0.94 | 4.20E-03 |
| cds.Camellia_sinensis.comp33115_c0_seq1_m.14614 | PREDICTED: monodehydroascorbate reductase 5, mitochondrial [Nelumbo nucifera] | 53.595 | 268.25 | 49.6 | 21 | 54 | 20 | 0.956 | 0.938 | 0.943 | 1.052 | 1.066 | 1.04 | 1.113 | 2.99E-04 |
| cds.Camellia_sinensis.comp33120_c0_seq2_m.23566 | PREDICTED: FKBP12-interacting protein of 37 kDa [Theobroma cacao] | 38.799 | 5.7355 | 10.1 | 4 | 4 | 4 | 0.889 | 1.027 | 1.055 | 1.1 | 1.015 | 0.945 | 1.03 | 6.82E-01 |
| cds.Camellia_sinensis.comp33121_c0_seq1_m.12663 | PREDICTED: acyl-CoA-binding domain-containing protein 4 [Vitis vinifera] | 55.599 | 46.401 | 15 | 7 | 10 | 7 | 1.071 | 1.086 | 1.042 | 0.971 | 0.896 | 0.928 | 0.874 | 6.70E-03 |

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| cds.Camellia_sinensis.comp33126_c0_seq1_m.36777 | PREDICTED: monothiol glutaredoxin-S15, mitochondrial [Juglans regia] | 20.607 | 3.227 | 11.3 | 2 | 2 | 2 | 1.035 | 0.97 | 0.994 | 0.982 | 1.007 | 1.018 | 1.003 | 9.00E-01 |
| cds.Camellia_sinensis.comp33128_c0_seq5_m.17158 | PREDICTED: probable sphingolipid transporter spinster homolog 2 isoform X2 [Theobroma cacao] | 54.879 | 2.9318 | 3.3 | 2 | 2 | 2 | 1.019 | 1.135 | 0.965 | 0.91 | 0.98 | 0.984 | 0.921 | 2.12E-01 |
| cds.Camellia_sinensis.comp33133_c0_seq1_m.7963 | PREDICTED: probable ADP-ribosylation factor GTPase-activating protein AGD8 [Ricinus communis] | 43.269 | 28.301 | 18.6 | 6 | 9 | 6 | 1.079 | 1.07 | 1.05 | 1.01 | 0.902 | 0.928 | 0.888 | 2.63E-02 |

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| cds.Camellia_sinensis.comp33133_c0_seq1_m.7964 | PREDICTED: 50S ribosomal protein L17, chloroplastic-like [Nicotiana tabacum] | 32.902 | 3.3185 | 7.1 | 2 | 2 | 2 | 1.034 | 1.208 | 1.094 | 0.858 | 0.932 | 0.853 | 0.792 | 1.25E-02 |
| cds.Camellia_sinensis.comp33134_c0_seq1_m.9785 | PREDICTED: YTH domain-containing family protein 3-like isoform X1 [Juglans regia] | 76.212 | 16.126 | 8.4 | 5 | 5 | 3 | 0.993 | 1.063 | 1.045 | 0.973 | 0.983 | 0.946 | 0.936 | 4.81E-02 |
| cds.Camellia_sinensis.comp33135_c1_seq15_m.24170 | Hop-interacting protein THI002 [Medicago truncatula] | 41.36 | 1.4159 | 2.2 | 1 | 1 | 1 | 1.1 | 1.003 | 1.039 | 0.938 | 0.946 | 0.961 | 0.905 | 2.39E-02 |
| cds.Camellia_sinensis.comp33135_c1_seq6_m.3926 | PREDICTED: DNA damage-binding protein 1-like [Ipomoea nil] | 47.553 | 29.162 | 19.4 | 8 | 11 | 8 | 0.976 | 1.029 | 0.953 | 1.016 | 0.99 | 1.039 | 1.029 | 3.33E-01 |

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| cds.Camellia_sinensis.comp33135_c1_seq8_m.4460 | PREDICTED: vacuolar-sorting receptor 1-like isoform X1 [Nelumbo nucifera] | 56.842 | 1.5406 | 2.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33135_c1_seq9_m.5256 | PREDICTED: DNA damage-binding protein 1 isoform X1 [Vitis vinifera] | 70.415 | 18.987 | 11.1 | 7 | 8 | 7 | 0.93 | 0.95 | 0.962 | 1.09 | 1.049 | 1.022 | 1.112 | 7.40E-03 |
| cds.Camellia_sinensis.comp33135_c1_seq9_m.5257 | PREDICTED: ankyrin repeat and KH domain-containing protein R11A8.7 [Jatropha curcas] | 41.956 | 6.5535 | 5.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33136_c0_seq1_m.635 | PREDICTED: E3 ubiquitin-protein ligase PRT6 [Vitis vinifera] | 231.72 | 2.1827 | 0.6 | 1 | 1 | 1 | 1.061 | 1.085 | 1.05 | 1.031 | 0.81 | 0.953 | 0.874 | 1.91E-01 |

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| cds.Camellia_sinensis.comp33139_c0_seq1_m.9505 | PREDICTED: calcium sensing receptor, chloroplastic isoform X1 [Citrus sinensis] | 38.973 | 59.77 | 20.1 | 7 | 17 | 7 | 1.022 | 1.006 | 1.016 | 0.997 | 0.98 | 0.997 | 0.977 | 3.40E-02 |
| cds.Camellia_sinensis.comp33139_c0_seq1_m.9506 | PREDICTED: calcium sensing receptor, chloroplastic isoform X2 [Citrus sinensis] | 34.998 | 73.64 | 33.1 | 12 | 24 | 12 | 1.049 | 0.977 | 1.021 | 0.985 | 0.987 | 0.998 | 0.975 | 2.99E-01 |
| cds.Camellia_sinensis.comp33147_c0_seq4_m.18745 | PREDICTED: mediator of RNA polymerase II transcription subunit 25 [Vitis vinifera] | 30.668 | 3.4694 | 6.7 | 2 | 2 | 2 | 0.981 | 0.959 | 1 | 1.032 | 0.987 | 1.057 | 1.046 | 1.28E-01 |
| cds.Camellia_sinensis.comp33149_c0_seq1_m.7064 | PREDICTED: calmodulin-binding receptor-like cytoplasmic kinase 3 isoform X1 [Vitis vinifera] | 51.687 | 2.0378 | 3.1 | 2 | 2 | 2 | 1.034 | 0.993 | 0.95 | 1.079 | 0.962 | 0.992 | 1.019 | 6.90E-01 |

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| cds.Camellia_sinensis.comp33150_c0_seq1_m.1236 | PREDICTED: UTP--glucose-1-phosphate uridylyltransferase 3, chloroplastic isoform X4 [Vitis vinifera] | 91.036 | 3.0028 | 2.6 | 1 | 1 | 1 | 0.867 | 0.984 | 0.983 | 0.912 | 1.14 | 1.142 | 1.127 | 2.48E-01 |
| cds.Camellia_sinensis.comp33153_c0_seq1_m.22690 | PREDICTED: phosphoribosylformylglycinamidine cyclo-ligase, chloroplastic/mitochondrial [Theobrom | 49.847 | 73.465 | 12.3 | 6 | 9 | 6 | 1.019 | 0.993 | 1.014 | 1.003 | 0.997 | 1.005 | 0.993 | 4.51E-01 |
| cds.Camellia_sinensis.comp33156_c0_seq2_m.19418 | PREDICTED: probable ATP-dependent RNA helicase ddx5 [Vitis | 48.589 | -2 | 2.3 | 1 | 1 | 1 | 1.045 | 0.968 | 0.966 | 1.012 | 1.011 | 1.005 | 1.016 | 5.80E-01 |
| cds.Camellia_sinensis.comp33158_c0_seq1_m.20871 | PREDICTED: selenium-binding protein 2 [Pyrus x bretschneideri] | 54.503 | 185.29 | 30.7 | 13 | 40 | 13 | 0.878 | 0.871 | 0.844 | 1.131 | 1.16 | 1.124 | 1.317 | 5.90E-05 |

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| cds.Camellia_sinensis.comp33158_c0_seq3_m.30038 | PREDICTED: probable acyl-activating enzyme 16, chloroplastic [Vitis | 51.082 | 14.194 | 14.8 | 6 | 6 | 5 | 0.971 | 0.968 | 1.028 | 1.129 | 0.991 | 1.038 | 1.064 | 2.26E-01 |
| cds.Camellia_sinensis.comp33158_c0_seq4_m.30027 | PREDICTED: probable acyl-activating enzyme 16, chloroplastic isoform X2 | 38.012 | 25.331 | 15.4 | 5 | 6 | 5 | 0.956 | 1.002 | 0.916 | 1.05 | 1.082 | 1.045 | 1.105 | 2.31E-02 |
| cds.Camellia_sinensis.comp33160_c0_seq1_m.1554 | PREDICTED: symplekin isoform X1 [Nicotiana attenuata] | 147.23 | 1.4087 | 1 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp33160_c1_seq1_m.11786 | PREDICTED: plant UBX domain-containing protein 8 [Vitis vinifera] | 66.641 | 3.9894 | 15.8 | 9 | 12 | 2 | 0.986 | 1.08 | 1.096 | 0.897 | 0.964 | 0.973 | 0.896 | 5.98E-02 |

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| cds.Camellia_sinensis.comp33160_c1_seq2_m.16209 | PREDICTED: plant UBX domain-containing protein 8 [Vitis vinifera] | 68.037 | 95.282 | 33.1 | 18 | 22 | 11 | 1.015 | 1.037 | 1.047 | 0.965 | 0.935 | 1.012 | 0.94 | 6.46E-02 |
| cds.Camellia_sinensis.comp33163_c0_seq1_m.21007 | PREDICTED: geraniol 8-hydroxylase-like [Nicotiana attenuata] | 58.702 | 1.5689 | 2.1 | 1 | 1 | 1 | 0.862 | 0.991 | 0.88 | 1.171 | 1.199 | 0.95 | 1.215 | 8.98E-02 |
| cds.Camellia_sinensis.comp33165_c0_seq3_m.11874 | PREDICTED: protease Do-like 2, chloroplastic [Theobroma cacao] | 69.038 | 38.773 | 19.5 | 10 | 12 | 10 | 1.063 | 1.067 | 1.041 | 0.963 | 0.953 | 0.938 | 0.9 | 6.23E-04 |
| cds.Camellia_sinensis.comp33167_c0_seq2_m.12525 | PREDICTED: malonate--CoA ligase isoform X2 [Vitis vinifera] | 54.797 | 28.27 | 19.8 | 8 | 11 | 8 | 1.002 | 1.008 | 1.009 | 0.98 | 0.97 | 0.992 | 0.974 | 1.94E-02 |
| cds.Camellia_sinensis.comp33170_c0_seq11_m.16683 | PREDICTED: GDHB glutamate dehydrogenase isoform X1 [Vitis vinifera] | 43.292 | 154.4 | 50.6 | 17 | 34 | 13 | 0.978 | 0.959 | 0.993 | 1.033 | 1.029 | 1.043 | 1.06 | 5.88E-03 |

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| cds.Camellia_sinensis.comp33170_c0_seq5_m.11453 | PREDICTED: TOM1-like protein 2 [Ricinus communis] | 71.744 | 2.8349 | 2.6 | 2 | 2 | 2 | 1.059 | 0.913 | 1.053 | 1.006 | 0.997 | 0.977 | 0.985 | 8.09E-01 |
| cds.Camellia_sinensis.comp33170_c0_seq60_m.11481 | PREDICTED: protein XRI1 isoform X1 [Ziziphus jujuba] | 26.516 | -2 | 4.2 | 1 | 1 | 1 | 1.054 | 0.964 | 1.113 | 0.932 | 0.969 | 0.963 | 0.915 | 1.15E-01 |
| cds.Camellia_sinensis.comp33174_c2_seq17_m.44746 | PREDICTED: protein phosphatase inhibitor 2 isoform X2 [Juglans regia] | 20.138 | 2.397 | 8.7 | 1 | 1 | 1 | 1.051 | 1.109 | 0.949 | 1.001 | 0.912 | 0.972 | 0.928 | 2.40E-01 |
| cds.Camellia_sinensis.comp33176_c0_seq1_m.23980 | PREDICTED: probable mitochondrial import inner membrane translocase subunit TIM21 [Vitis vinifera] | 34.672 | 7.7594 | 10.3 | 3 | 3 | 3 | 0.862 | 1.062 | 1.05 | 0.993 | 1.01 | 1.011 | 1.013 | 8.18E-01 |

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| cds.Camellia_sinensis.comp33177_c0_seq1_m.33010 | isoflavone reductase-like protein [Cajanus cajan] | 37.403 | 158.3 | 40.5 | 11 | 31 | 10 | 1.187 | 1.168 | 1.174 | 0.79 | 0.824 | 0.804 | 0.685 | 4.30E-06 |
| cds.Camellia_sinensis.comp33181_c0_seq1_m.4653 | PREDICTED: long chain acyl-CoA synthetase 6, peroxisomal-like isoform X1 [Nelumbo nucifera] | 19.538 | 1.4836 | 5.2 | 1 | 1 | 1 | 0.969 | 0.964 | 0.921 | 1.127 | 1.078 | 0.971 | 1.113 | 8.88E-02 |
| cds.Camellia_sinensis.comp33184_c0_seq4_m.35050 | PREDICTED: GTP-binding protein SAR1A-like [Juglans regia] | 13.203 | 52.141 | 60 | 5 | 11 | 2 | 0.924 | 0.987 | 1.009 | 1.033 | 1.022 | 1.024 | 1.054 | 1.81E-01 |
| cds.Camellia_sinensis.comp33187_c0_seq2_m.48458 | PREDICTED: vicianin hydrolase-like [Populus euphratica] | 18.361 | 3.7707 | 14 | 2 | 2 | 2 | 1.122 | 1.085 | 0.995 | 0.972 | 0.883 | 0.923 | 0.868 | 3.53E-02 |

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| cds.Camellia_sinensis.comp33194_c0_seq5_m.22855 | PREDICTED: mannose-1-phosphate guanyltransferase alpha [Capsicum annuum] | 45.754 | 12.245 | 10.1 | 4 | 4 | 3 | 1.039 | 1.066 | 0.956 | 1.016 | 0.863 | 1.057 | 0.959 | 5.62E-01 |
| cds.Camellia_sinensis.comp33196_c0_seq2_m.28361 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 14 homolog [Juglans regia] | 36.592 | 34.887 | 24.4 | 8 | 12 | 8 | 0.978 | 1.024 | 0.975 | 1.046 | 1.023 | 1.029 | 1.041 | 8.04E-02 |
| cds.Camellia_sinensis.comp33200_c0_seq1_m.32195 | PREDICTED: protein FLX-like 3 [Vitis vinifera] | 30.858 | 1.5811 | 16.8 | 4 | 5 | 2 | 0.891 | 0.983 | 1.099 | 0.981 | 1.084 | 0.987 | 1.027 | 6.96E-01 |
| cds.Camellia_sinensis.comp33200_c0_seq2_m.34220 | PREDICTED: protein FLX-like 3 isoform X1 [Nicotiana tabacum] | 31.569 | 26.988 | 33.3 | 7 | 12 | 6 | 1.009 | 0.997 | 1.013 | 0.981 | 1.018 | 0.988 | 0.989 | 4.31E-01 |

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| cds.Camellia_sinensis.comp33210_c0_seq10_m.934 | PREDICTED: protein argonaute 1-like [Solanum tuberosum | 111.95 | 108.01 | 20.5 | 19 | 25 | 19 | 1.05 | 1.065 | 1.048 | 0.947 | 0.929 | 0.95 | 0.893 | 1.99E-04 |
| cds.Camellia_sinensis.comp33211_c0_seq4_m.6750 | NADH dehydrogenase subunit 5 (mitochondrion) [Nelumbo nucifera] | 65.746 | 2.6632 | 1.7 | 1 | 1 | 1 | 0.986 | 0.979 | 1.041 | 1.067 | 0.906 | 1.034 | 1 | 9.75E-01 |
| cds.Camellia_sinensis.comp33215_c0_seq1_m.532 | PREDICTED: serine-rich adhesin for platelets isoform X2 [Prunus | 232.61 | 4.0934 | 1.5 | 3 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33215_c0_seq4_m.3227 | PREDICTED: serine-rich adhesin for platelets isoform X2 [Theobroma cacao] | 123.77 | 14.409 | 3.2 | 3 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33217_c0_seq2_m.9233 | PREDICTED: U-box domain-containing protein 44 [Jatropha curcas] | 71.843 | 13.476 | 5.9 | 4 | 4 | 4 | 1.039 | 0.989 | 1.005 | 0.979 | 1.016 | 0.975 | 0.979 | 3.44E-01 |

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| cds.Camellia_sinensis.comp33218_c0_seq22_m.55156 | PREDICTED: yrdC domain-containing protein, mitochondrial [Jatropha curcas] | 13.465 | 1.5347 | 9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33218_c0_seq8_m.28613 | PREDICTED: phospholipase D beta 1-like [Juglans regia] | 30.457 | 3.0651 | 3 | 1 | 2 | 1 | 0.858 | 1.031 | 0.904 | 1.065 | 1.064 | 1.114 | 1.161 | 5.50E-02 |
| cds.Camellia_sinensis.comp33218_c1_seq13_m.38803 | PREDICTED: alpha-galactosidase 3 [Malus domestica] | 24.141 | 2.5046 | 4.2 | 1 | 1 | 1 | 0.897 | 0.913 | 0.886 | 1.139 | 1.099 | 1.111 | 1.242 | 9.66E-05 |
| cds.Camellia_sinensis.comp33218_c1_seq6_m.23129 | PREDICTED: alpha-galactosidase 3 isoform X1 [Juglans regia] | 46.578 | 69.842 | 33.6 | 12 | 27 | 6 | 0.981 | 0.967 | 0.981 | 1.063 | 1.021 | 1.064 | 1.075 | 7.54E-03 |
| cds.Camellia_sinensis.comp33220_c1_seq3_m.37071 | transmembrane protein, putative [Medicago truncatula] | 32.171 | 3.3328 | 4.2 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp33221_c2_seq1_m.12402 | PREDICTED: protein IQ-DOMAIN 14 [Daucus carota subsp. sativus] | 61.594 | 4.0248 | 1.8 | 1 | 1 | 1 | 1.202 | 1.077 | 0.998 | 0.853 | 0.849 | 0.98 | 0.818 | 4.94E-02 |
| cds.Camellia_sinensis.comp33223_c0_seq10_m.48390 | PREDICTED: glycerol kinase [Juglans regia] | 21.665 | 23.946 | 14.9 | 3 | 5 | 3 | 0.899 | 0.974 | 0.952 | 1.094 | 1.061 | 1.098 | 1.152 | 5.68E-03 |
| cds.Camellia_sinensis.comp33224_c0_seq1_m.18045 | catalase isozyme 3 [Nicotiana tabacum] | 62.315 | 236.63 | 42 | 21 | 77 | 14 | 0.994 | 0.976 | 1.006 | 0.997 | 1.032 | 0.999 | 1.017 | 2.92E-01 |
| cds.Camellia_sinensis.comp33224_c0_seq3_m.44552 | catalase family protein [Populus trichocarpa] | 22.173 | 4.6852 | 25.5 | 4 | 15 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33227_c0_seq34_m.36211 | PREDICTED: peptidyl-tRNA hydrolase ICT1, mitochondrial isoform X1 [Nelumbo | 26.743 | 3.3688 | 4.6 | 1 | 1 | 1 | 1.139 | 1.068 | 1.172 | 0.845 | 0.851 | 0.89 | 0.765 | 1.12E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33228_c2_seq1_m.6837 | PREDICTED: mechanosensitive ion channel protein 1, mitochondrial [Vitis vinifera] | 59.262 | 2.6231 | 3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33229_c0_seq3_m.31359 | PREDICTED: trithorax group protein osa [Ziziphus jujuba] | 41.817 | 22.751 | 13.6 | 4 | 4 | 4 | 0.951 | 0.976 | 1.036 | 1.105 | 0.899 | 1.053 | 1.032 | 6.98E-01 |
| cds.Camellia_sinensis.comp33229_c0_seq4_m.43060 | PREDICTED: exocyst complex component SEC15B [Nelumbo nucifera] | 26.615 | 5.6746 | 10.1 | 2 | 2 | 2 | 0.97 | 0.956 | 1.003 | 1.027 | 1.101 | 0.964 | 1.056 | 2.66E-01 |
| cds.Camellia_sinensis.comp33232_c0_seq6_m.52447 | PREDICTED: 5'-nucleotidase domain-containing protein 4 isoform X4 [Vitis vinifera] | 13.525 | 1.8736 | 6.2 | 1 | 1 | 1 | 0.904 | 1.249 | 0.895 | 0.952 | 0.962 | 1.044 | 0.97 | 8.79E-01 |

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| cds.Camellia_sinensis.comp33237_c0_seq3_m.6037 | PREDICTED: endoplasmic reticulum metallopeptidase 1 [Vitis vinifera] | 101.09 | 17.359 | 7.6 | 7 | 9 | 7 | 0.969 | 0.966 | 0.955 | 1.053 | 1.056 | 0.991 | 1.073 | 3.02E-02 |
| cds.Camellia_sinensis.comp33238_c0_seq1_m.13409 | PREDICTED: glucose-6-phosphate 1-dehydrogenase, chloroplastic isoform X1 [Vitis vinifera] | 67.627 | 7.1256 | 14.9 | 9 | 15 | 4 | 0.952 | 0.979 | 1.004 | 1.031 | 1.015 | 1.038 | 1.051 | 4.11E-02 |
| cds.Camellia_sinensis.comp33239_c0_seq2_m.22246 | PREDICTED: mitochondrial fission protein ELM1 [Sesamum indicum] | 47.382 | 1.8547 | 3.5 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33240_c0_seq1_m.6214 | PREDICTED: transcriptional corepressor LEUNIG_HOMOLOG-like [Nicotiana tabacum] | 84.145 | 6.6767 | 3.4 | 2 | 2 | 2 | 0.911 | 1.051 | 1.024 | 1.052 | 0.994 | 0.991 | 1.017 | 7.20E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33243_c0_seq5_m.32025 | PREDICTED: lactoylglutathione lyase-like [Glycine max] | 27.943 | 49.157 | 40.4 | 10 | 22 | 10 | 0.961 | 0.972 | 0.968 | 1.053 | 1.035 | 1.055 | 1.083 | 3.21E-04 |
| cds.Camellia_sinensis.comp33245_c0_seq1_m.13680 | PREDICTED: laccase-14 [Vitis vinifera] | 63.033 | 27.115 | 6.2 | 3 | 5 | 3 | 1.089 | 1.004 | 1.079 | 0.894 | 0.932 | 0.935 | 0.87 | 9.36E-03 |
| cds.Camellia_sinensis.comp33247_c0_seq3_m.214 | DNA-directed RNA polymerase beta chain (chloroplast) [Camellia crapnelliana] | 121.03 | 24.446 | 7.6 | 6 | 6 | 6 | 0.959 | 0.979 | 0.989 | 1.04 | 1.042 | 1.013 | 1.057 | 1.22E-02 |
| cds.Camellia_sinensis.comp33247_c0_seq3_m.215 | DNA-directed RNA polymerase beta" subunit (chloroplast) [Camellia impressinervis] | 103.93 | 6.7058 | 4.4 | 4 | 4 | 4 | 1.047 | 1.01 | 1.048 | 0.942 | 0.96 | 0.979 | 0.928 | 1.05E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33247_c0_seq3_m.216 | RNA polymerase beta' subunit (chloroplast) [Camellia sinensis] | 79.614 | 10.2 | 8.1 | 5 | 5 | 5 | 1.003 | 1.115 | 1.049 | 0.918 | 0.926 | 0.981 | 0.892 | 3.74E-02 |
| cds.Camellia_sinensis.comp33247_c0_seq3_m.217 | RNA polymerase beta' subunit (chloroplast) [Camellia leptophylla] | 54.904 | 1.6292 | 1.4 | 1 | 1 | 1 | 1.041 | 0.988 | 0.938 | 0.968 | 1.109 | 0.964 | 1.025 | 6.92E-01 |
| cds.Camellia_sinensis.comp33247_c0_seq3_m.219 | ribosomal protein S2 (chloroplast) [Camellia pubicosta] | 26.894 | 25.399 | 22.9 | 5 | 8 | 5 | 1.027 | 1.086 | 1.153 | 0.913 | 0.913 | 0.908 | 0.837 | 3.40E-02 |
| cds.Camellia_sinensis.comp33248_c0_seq1_m.4358 | PREDICTED: glycine dehydrogenase (decarboxylating), mitochondrial [Nelumbo nucifera] | 114.39 | 323.31 | 40.3 | 36 | 108 | 36 | 1.046 | 1.034 | 1.037 | 0.96 | 0.978 | 0.964 | 0.931 | 4.17E-04 |

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| cds.Camellia_sinensis.comp33249_c0_seq1_m.20076 | PREDICTED: LON peptidase N-terminal domain and RING finger protein 1 isoform X1 [Sesamum indicum] | 61.012 | -2 | 1.5 | 1 | 1 | 1 | 1.168 | 1.091 | 1.121 | 0.815 | 0.843 | 0.92 | 0.763 | 2.74E-03 |
| cds.Camellia_sinensis.comp33251_c0_seq1_m.12241 | PREDICTED: inorganic pyrophosphatase 3-like isoform X1 [Nicotiana attenuata] | 28.55 | 6.0627 | 12.4 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp33251_c0_seq9_m.52859 | long chain base biosynthesis protein 1 [Cajanus cajan] | 12.25 | 2.9165 | 17.7 | 2 | 2 | 2 | 1.001 | 0.879 | 0.986 | 1.016 | 1.012 | 1.122 | 1.099 | 1.48E-01 |
| cds.Camellia_sinensis.comp33252_c0_seq1_m.35074 | PREDICTED: (+)-neomenthol dehydrogenase-like, partial [Juglans regia] | 29.037 | 31.462 | 24 | 6 | 7 | 6 | 0.963 | 0.937 | 0.952 | 1.049 | 1.038 | 1.071 | 1.107 | 1.10E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33254_c0_seq4_m.22604 | PREDICTED: putative clathrin assembly protein At5g35200 [Ziziphus | 48.43 | 2.0754 | 4.2 | 2 | 2 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp33258_c0_seq1_m.11478 | probable starch synthase 4, chloroplastic/amyloplastic [Vitis vinifera] | 77.21 | 9.532 | 6.1 | 4 | 4 | 4 | 0.94 | 0.918 | 0.941 | 1.052 | 1.045 | 1.132 | 1.154 | 6.10E-03 |
| cds.Camellia_sinensis.comp33258_c0_seq5_m.27121 | PREDICTED: small nuclear ribonucleoprotein-associated protein B' [Jatropha curcas] | 28.564 | 17.233 | 14.4 | 3 | 3 | 3 | 0.854 | 0.964 | 0.956 | 1.075 | 1.027 | 1.162 | 1.177 | 3.75E-02 |
| cds.Camellia_sinensis.comp33260_c0_seq1_m.19690 | PREDICTED: protein RNA-directed DNA methylation 3 [Vitis vinifera] | 54.421 | 4.3133 | 3.3 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |

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| cds.Camellia_sinensis.comp33260_c0_seq3_m.36353 | PREDICTED: protein RNA-directed DNA methylation 3 [Vitis vinifera] | 36.461 | 3.0432 | 3.4 | 1 | 2 | 1 | 1.109 | 1.035 | 0.889 | 1.112 | 0.957 | 0.901 | 0.979 | 8.30E-01 |
| cds.Camellia_sinensis.comp33261_c2_seq1_m.16769 | PREDICTED: metal transporter Nramp3-like [Nicotiana tomentosiformis] | 56.252 | 1.4928 | 3.1 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp33262_c0_seq1_m.1290 | PREDICTED: ABC transporter C family member 10-like [Nicotiana attenuata] | 164.51 | 18.033 | 6.3 | 8 | 10 | 6 | 1.063 | 1.064 | 1.105 | 0.907 | 0.936 | 0.896 | 0.847 | 8.18E-04 |
| cds.Camellia_sinensis.comp33263_c0_seq1_m.1372 | PREDICTED: AT-hook motif nuclear-localized protein 10-like [Nelumbo nucifera] | 34.272 | 31.241 | 10.4 | 3 | 4 | 3 | 0.964 | 1.018 | 0.951 | 1.019 | 0.987 | 1.073 | 1.05 | 2.05E-01 |

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| cds.Camellia_sinensis.comp33267_c1_seq4_m.44623 | PREDICTED: ribosome biogenesis protein erb1 isoform X2 [Citrus sinensis] | 12.982 | 4.0755 | 27.4 | 2 | 2 | 2 | 1.24 | 1.164 | 1.115 | 0.763 | 0.827 | 0.831 | 0.688 | 8.39E-04 |
| cds.Camellia_sinensis.comp33269_c0_seq1_m.34486 | PREDICTED: caffeoylshikimate esterase [Vitis vinifera] | 36.689 | 6.186 | 6.6 | 2 | 3 | 2 | 1.085 | 1.01 | 1.148 | 0.887 | 0.899 | 0.952 | 0.844 | 1.72E-02 |
| cds.Camellia_sinensis.comp33272_c0_seq1_m.18645 | PREDICTED: V-type proton ATPase subunit B 2 | 57.87 | 155.76 | 38.1 | 17 | 30 | 16 | 0.99 | 0.973 | 0.97 | 1.018 | 1.021 | 1.021 | 1.043 | 2.22E-02 |
| cds.Camellia_sinensis.comp33275_c0_seq1_m.14084 | PREDICTED: serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B beta isoform-like isoform X2 [Cicer arietinum] | 60.795 | 13.436 | 9.2 | 5 | 6 | 5 | 0.974 | 1.03 | 1.003 | 0.946 | 1.017 | 0.977 | 0.978 | 4.39E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33278_c0_seq3_m.39726 | PREDICTED: coatomer subunit delta [Vitis vinifera] | 12.178 | 3.5319 | 20.2 | 2 | 4 | 1 | 0.865 | 0.906 | 1.357 | 1.144 | 0.812 | 0.946 | 0.928 | 7.33E-01 |
| cds.Camellia_sinensis.comp33280_c0_seq1_m.9895 | PREDICTED: nucleobase-ascorbate transporter 6 [Sesamum indicum] | 57.668 | 3.98 | 2.5 | 1 | 4 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33280_c0_seq2_m.11931 | PREDICTED: nucleobase-ascorbate transporter 6 [Sesamum indicum] | 57.58 | 18.925 | 7.7 | 4 | 5 | 4 | 0.988 | 0.969 | 0.967 | 1.004 | 1.045 | 1 | 1.043 | 5.59E-02 |
| cds.Camellia_sinensis.comp33289_c0_seq3_m.41555 | thioredoxin protein [Medicago truncatula] | 27.874 | 6.0223 | 16 | 5 | 8 | 5 | 0.955 | 0.978 | 0.963 | 0.995 | 1.076 | 1.046 | 1.076 | 3.79E-02 |
| cds.Camellia_sinensis.comp33294_c0_seq29_m.26235 | PREDICTED: dynamin-like protein ARC5 [Daucus carota subsp. sativus] | 49.426 | 3.0027 | 6.9 | 3 | 3 | 3 | 0.987 | 1.04 | 1.124 | 0.899 | 0.938 | 0.998 | 0.9 | 9.57E-02 |

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| cds.Camellia_sinensis.comp33294_c0_seq38_m.31539 | PREDICTED: SNF1-related protein kinase regulatory subunit gamma-1-like [Nicotiana tabacum] | 32.685 | 10.479 | 15.2 | 4 | 5 | 4 | 0.824 | 0.853 | 0.962 | 1.111 | 1.141 | 1.11 | 1.274 | 6.92E-03 |
| cds.Camellia_sinensis.comp33295_c0_seq2_m.24156 | PREDICTED: pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic [Juglans regia] | 44.743 | 20.217 | 5.2 | 2 | 3 | 2 | 1.053 | 1.098 | 0.971 | 0.878 | 0.983 | 1.034 | 0.927 | 2.73E-01 |
| cds.Camellia_sinensis.comp33297_c0_seq1_m.7766 | PREDICTED: topless-related protein 4-like isoform X2 [Daucus carota subsp. sativus] | 99.254 | 6.082 | 9.1 | 8 | 9 | 3 | | | | | | | | |

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| cds.Camellia_sinensis.comp33298_c0_seq14_m.32209 | PREDICTED: ubiquitin carboxyl-terminal hydrolase isozyme L3 [Jatropha curcas] | 25.461 | 2.0136 | 7.4 | 2 | 2 | 2 | 0.963 | 0.968 | 1.004 | 1.03 | 0.988 | 1.064 | 1.05 | 1.25E-01 |
| cds.Camellia_sinensis.comp33299_c0_seq19_c0_seq1_m.7996 | PREDICTED: pentatricopeptide repeat-containing protein At2g37230 [Vitis vinifera] | 53.217 | 3.6998 | 5.8 | 3 | 3 | 3 | 1.007 | 0.998 | 0.96 | 0.963 | 1.075 | 1.007 | 1.027 | 5.03E-01 |
| cds.Camellia_sinensis.comp33300_c0_seq1_m.24462 | PREDICTED: UDP-glycosyltransferase 89A2-like isoform X2 [Juglans regia] | 53.695 | 11.497 | 9.6 | 4 | 4 | 4 | 0.985 | 0.99 | 0.998 | 0.965 | 0.988 | 1.007 | 0.996 | 7.44E-01 |
| cds.Camellia_sinensis.comp33300_c0_seq3_m.39256 | PREDICTED: DNA-binding protein DDB_G0278111 [Vitis vinifera] | 14.856 | 37.721 | 18.8 | 2 | 3 | 2 | 0.929 | 0.91 | 1.008 | 1.037 | 1.079 | 1.066 | 1.118 | 2.83E-02 |

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| cds.Camellia_sinensis.comp33302_c1_seq1_m.8446 | PREDICTED: protein transport protein Sec24-like At3g07100 [Vitis vinifera] | 83.814 | 6.0344 | 4 | 2 | 2 | 2 | 0.975 | 0.976 | 1.031 | 1.077 | 0.967 | 0.992 | 1.018 | 6.69E-01 |
| cds.Camellia_sinensis.comp33304_c0_seq2_m.12419 | PREDICTED: synaptotagmin-2 [Vitis vinifera] | 34.703 | 34.572 | 38.6 | 11 | 17 | 8 | 0.902 | 1.004 | 1.016 | 1.063 | 1.016 | 1.042 | 1.068 | 1.69E-01 |
| cds.Camellia_sinensis.comp33304_c0_seq2_m.12420 | PREDICTED: synaptotagmin-2 [Vitis vinifera] | 22.693 | 13.069 | 21.2 | 5 | 12 | 3 | 0.938 | 0.959 | 0.996 | 1.05 | 1.044 | 0.99 | 1.066 | 6.74E-02 |
| cds.Camellia_sinensis.comp33306_c0_seq15_m.34501 | transmembrane protein [Arabidopsis thaliana] | 36.872 | 1.8118 | 3.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33310_c0_seq1_m.2699 | PREDICTED: protein CROWDED NUCLEI 4-like [Nicotiana | 109.18 | 19.228 | 5.2 | 5 | 7 | 5 | 1.002 | 0.998 | 1.014 | 0.955 | 1 | 1.011 | 0.984 | 4.18E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33310_c0_seq4_m.30096 | PREDICTED: protein CROWDED NUCLEI 4-like [Daucus carota subsp. | 39.101 | 4.0506 | 8.9 | 2 | 2 | 2 | 1.055 | 1.03 | 0.95 | 0.946 | 1.019 | 0.996 | 0.976 | 5.65E-01 |
| cds.Camellia_sinensis.comp33312_c0_seq23_m.20101 | PREDICTED: ATP-dependent 6-phosphofructokinase 3-like isoform X1 [Juglans regia] | 54.198 | 49.435 | 30.7 | 15 | 21 | 10 | 1.032 | 1.055 | 1.019 | 0.979 | 0.999 | 0.951 | 0.943 | 2.85E-02 |
| cds.Camellia_sinensis.comp33312_c0_seq3_m.6920 | PREDICTED: putative ion channel POLLUX-like 2 isoform X2 [Sesamum indicum] | 56.638 | 3.8582 | 4 | 2 | 2 | 2 | 1.027 | 0.935 | 1.158 | 0.891 | 1.05 | 0.937 | 0.922 | 3.71E-01 |

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| cds.Camellia_sinensis.comp33312_c0_seq3_m.6921 | PREDICTED: putative ion channel POLLUX-like 2 [Ziziphus jujuba] | 38.942 | 25.843 | 28.8 | 10 | 10 | 10 | 1.084 | 1.035 | 1.058 | 0.94 | 0.953 | 0.964 | 0.899 | 2.22E-03 |
| cds.Camellia_sinensis.comp33313_c0_seq9_m.5082 | PREDICTED: conserved oligomeric Golgi complex subunit 6 [Vitis vinifera] | 56.639 | 6.6096 | 6.5 | 3 | 3 | 3 | 1.123 | 0.951 | 1.034 | 1.006 | 0.915 | 0.962 | 0.928 | 2.54E-01 |
| cds.Camellia_sinensis.comp33315_c0_seq1_m.7168 | PREDICTED: probable ADP-ribosylation factor GTPase-activating protein AGD14 isoform X1 [Juglans regia] | 81.628 | 9.284 | 5.2 | 4 | 4 | 4 | 1.161 | 1.14 | 1.079 | 0.85 | 0.867 | 0.933 | 0.784 | 2.46E-03 |

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| cds.Camellia_sinensis.comp33318_c0_seq1_m.2110 | PREDICTED: calcium-transporting ATPase 10, plasma membrane-type isoform X1 [Sesamum indicum] | 118.25 | 4.4966 | 5.6 | 4 | 4 | 4 | | | | | | | | |
| cds.Camellia_sinensis.comp33320_c1_seq1_m.27826 | PREDICTED: methionine adenosyltransferase 2 subunit beta isoform X1 [Solanum pennellii] | 35.571 | 9.3727 | 7.4 | 2 | 2 | 2 | 0.872 | 1.085 | 1.041 | 1.067 | 1.008 | 0.955 | 1.011 | 8.60E-01 |
| cds.Camellia_sinensis.comp33325_c0_seq1_m.21011 | PREDICTED: phospholipase A(1) LCAT3 isoform X2 [Theobroma cacao] | 50.15 | 14.466 | 6.1 | 3 | 3 | 3 | 0.981 | 0.993 | 1.031 | 0.991 | 1.003 | 1.012 | 1 | 9.76E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33327_c0_seq1_m.19277 | protein FAR1-RELATED SEQUENCE 4-like isoform X2 [Cajanus cajan] | 57.422 | 1.2308 | 3.5 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33332_c0_seq1_m.3881 | PREDICTED: protein STABILIZED1 [Nelumbo nucifera] | 73.663 | 5.7523 | 6.1 | 4 | 4 | 4 | 1.039 | 1.06 | 1.029 | 0.952 | 0.974 | 0.928 | 0.912 | 5.10E-03 |
| cds.Camellia_sinensis.comp33337_c0_seq1_m.13812 | PREDICTED: 4-hydroxy-tetrahydrodipicolinate reductase 1, chloroplastic-like isoform X1 [Nelumbo nucifera] | 36.246 | 13.711 | 14.4 | 5 | 6 | 5 | 0.999 | 0.963 | 0.966 | 1.074 | 1.03 | 1.015 | 1.065 | 3.77E-02 |
| cds.Camellia_sinensis.comp33340_c0_seq1_m.3039 | PREDICTED: beta-galactosidase-like [Sesamum indicum] | 24.029 | 1.3916 | 7.5 | 2 | 2 | 1 | 0.752 | 0.801 | 0.884 | 1.236 | 1.23 | 1.179 | 1.496 | 1.20E-03 |

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| cds.Camellia_sinensis.comp33340_c0_seq2_m.5151 | PREDICTED: beta-galactosidase-like [Sesamum indicum] | 93.865 | 9.1505 | 5.9 | 5 | 6 | 3 | 0.827 | 0.932 | 0.833 | 1.135 | 1.213 | 1.17 | 1.357 | 2.08E-03 |
| cds.Camellia_sinensis.comp33345_c1_seq2_m.46861 | PREDICTED: hydroxymethylglutaryl-CoA lyase, mitochondrial isoform X3 [Vitis | 20.699 | 1.5141 | 11.3 | 2 | 2 | 2 | 1.027 | 1.042 | 1.073 | 1 | 0.934 | 0.924 | 0.91 | 2.70E-02 |
| cds.Camellia_sinensis.comp33346_c0_seq2_m.36031 | PREDICTED: 60 kDa jasmonate-induced protein [Elaeis guineensis | 30.07 | 24.115 | 25 | 6 | 7 | 6 | 0.962 | 0.983 | 1.011 | 1.036 | 0.992 | 1.018 | 1.03 | 1.91E-01 |
| cds.Camellia_sinensis.comp33348_c2_seq1_m.10350 | PREDICTED: calmodulin-binding protein 60 B isoform X1 [Nicotiana attenuata] | 72.24 | 24.092 | 13.1 | 9 | 11 | 7 | 0.99 | 1.051 | 1.114 | 0.992 | 0.862 | 0.968 | 0.894 | 1.11E-01 |

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| cds.Camellia_sinensis.comp33352_c0_seq1_m.32981 | PREDICTED: probable CDP-diacylglycerol--inositol 3-phosphatidyltransferase 2 [Ricinus communis] | 30.807 | 1.3491 | 3 | 1 | 1 | 1 | 1.035 | 0.997 | 1.035 | 1.007 | 0.947 | 0.981 | 0.957 | 1.12E-01 |
| cds.Camellia_sinensis.comp33354_c0_seq1_m.13563 | PREDICTED: LOW QUALITY PROTEIN: alkaline/neutral invertase CINV2 [Sesamum indicum] | 63.531 | 41.672 | 15.5 | 9 | 11 | 8 | 0.937 | 0.991 | 0.988 | 1.095 | 1.002 | 1.06 | 1.083 | 6.70E-02 |
| cds.Camellia_sinensis.comp33354_c0_seq2_m.25461 | PREDICTED: PTI1-like tyrosine-protein kinase At3g15890 [Prunus mume] | 41.299 | 11.588 | 14.4 | 5 | 5 | 5 | 1.018 | 0.988 | 1.095 | 0.979 | 1.02 | 0.904 | 0.936 | 2.29E-01 |
| cds.Camellia_sinensis.comp33358_c0_seq1_m.2298 | PREDICTED: K(+) efflux antiporter 3, chloroplastic [Vitis vinifera] | 54.334 | 21.849 | 14.8 | 6 | 6 | 6 | 1.013 | 1.05 | 1.025 | 0.999 | 1.008 | 0.91 | 0.945 | 1.67E-01 |

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| cds.Camellia_sinensis.comp33360_c0_seq1_m.13258 | PREDICTED: glucose-1-phosphate adenylyltransferase large subunit 1-like isoform X1 [Juglans regia] | 58.663 | 33.295 | 13.7 | 6 | 9 | 5 | 1.193 | 1.167 | 1.164 | 0.899 | 0.868 | 0.796 | 0.727 | 9.83E-04 |
| cds.Camellia_sinensis.comp33365_c2_seq3_m.23252 | PREDICTED: 4-hydroxy-tetrahydrodipicolinate synthase, chloroplastic isoform X2 [Theobroma cacao] | 40.84 | 93.394 | 19.1 | 9 | 15 | 9 | 0.996 | 0.98 | 0.982 | 1.01 | 0.981 | 1.027 | 1.02 | 2.37E-01 |
| cds.Camellia_sinensis.comp33365_c2_seq6_m.29298 | PREDICTED: pectinesterase [Vitis vinifera] | 50.684 | 17.205 | 9.4 | 4 | 8 | 4 | 1.017 | 1.04 | 1.043 | 0.959 | 0.992 | 0.949 | 0.935 | 1.27E-02 |
| cds.Camellia_sinensis.comp33370_c0_seq1_m.9312 | PREDICTED: protein TolB [Oryza sativa Japonica Group] | 79.118 | 41.568 | 9.2 | 5 | 5 | 5 | 0.986 | 0.971 | 0.988 | 1.051 | 1.039 | 0.941 | 1.029 | 5.19E-01 |

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| cds.Camellia_sinensis.comp33371_c0_seq5_m.12685 | PREDICTED: chaperonin 60 subunit beta 4, chloroplastic [Vitis vinifera] | 55.331 | 18.182 | 14.1 | 7 | 8 | 7 | 1.06 | 1.054 | 1.027 | 0.943 | 0.949 | 0.987 | 0.917 | 7.22E-03 |
| cds.Camellia_sinensis.comp33373_c0_seq1_m.2756 | PREDICTED: guanylate-binding protein 2 [Vitis vinifera] | 120.52 | 101.33 | 16.7 | 18 | 23 | 14 | 0.975 | 1.009 | 0.985 | 1.001 | 0.985 | 1.024 | 1.014 | 4.18E-01 |
| cds.Camellia_sinensis.comp33379_c1_seq5_m.17768 | PREDICTED: zinc finger CCCH domain-containing protein ZFN-like [Vitis vinifera] | 47.127 | 7.1706 | 6.2 | 3 | 4 | 3 | 0.993 | 1.039 | 0.977 | 1.018 | 0.978 | 1.004 | 0.997 | 9.04E-01 |
| cds.Camellia_sinensis.comp33379_c1_seq6_m.18136 | PREDICTED: argininosuccinate synthase, chloroplastic [Ricinus communis] | 28.882 | 1.8687 | 33.2 | 9 | 12 | 1 | 0.861 | 1.005 | 1.061 | 1.073 | 0.997 | 1.036 | 1.061 | 3.96E-01 |

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| cds.Camellia_sinensis.comp33379_c1_seq7_m.18340 | PREDICTED: argininosuccinate synthase, chloroplastic isoform X1 [Theobroma cacao] | 57.7 | 162.29 | 37.3 | 21 | 35 | 6 | 0.969 | 1.002 | 0.958 | 1.046 | 0.989 | 0.987 | 1.032 | 2.53E-01 |
| cds.Camellia_sinensis.comp33379_c1_seq9_m.20280 | PREDICTED: argininosuccinate synthase, chloroplastic [Nelumbo nucifera] | 22.693 | -2 | 31.2 | 8 | 12 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33379_c3_seq1_m.20752 | PREDICTED: 4-coumarate--CoA ligase-like 9 isoform X1 [Lupinus angustifolius] | 60.818 | 11.402 | 6.2 | 3 | 3 | 3 | 1.056 | 1.025 | 1.01 | 1.032 | 0.965 | 0.915 | 0.942 | 1.78E-01 |
| cds.Camellia_sinensis.comp33380_c0_seq5_m.5253 | PREDICTED: eukaryotic translation initiation factor 4B1 [Solanum lycopersicum] | 24.027 | 7.8008 | 3.9 | 1 | 1 | 1 | 1.257 | 1.248 | 1.287 | 0.725 | 0.714 | 0.692 | 0.562 | 2.03E-06 |

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| cds.Camellia_sinensis.comp33383_c1_seq1_m.7617 | PREDICTED: receptor-like protein kinase HERK 1 [Fragaria vesca subsp. vesca] | 72.257 | 1.4273 | 2.3 | 2 | 5 | 1 | 0.999 | 0.949 | 1.031 | 0.996 | 1.053 | 0.982 | 1.017 | 6.17E-01 |
| cds.Camellia_sinensis.comp33383_c2_seq1_m.43851 | NAD(P)-binding Rossmann-fold superfamily protein [Arabidopsis thaliana] | 26.339 | 4.4534 | 11.8 | 3 | 4 | 3 | 0.971 | 1.05 | 1.029 | 1.033 | 0.952 | 0.975 | 0.97 | 4.24E-01 |
| cds.Camellia_sinensis.comp33384_c0_seq1_m.27191 | PREDICTED: probable uridine nucleosidase 2 [Prunus mume] | 34.706 | 7.0946 | 7.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33389_c0_seq1_m.11693 | PREDICTED: RNA-binding protein 39-like [Daucus carota subsp. sativus] | 67.271 | 1.5299 | 2.6 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp33396_c0_seq2_m.31354 | PREDICTED: conserved oligomeric Golgi complex subunit 5 [Nelumbo nucifera] | 32.801 | 1.923 | 7 | 2 | 2 | 2 | 0.98 | 1.034 | 1.115 | 0.915 | 0.929 | 1.025 | 0.917 | 1.69E-01 |
| cds.Camellia_sinensis.comp33399_c0_seq6_m.16738 | PREDICTED: CTP synthase [Prunus mume] | 53.507 | 1.7602 | 3.1 | 2 | 2 | 2 | 0.937 | 0.958 | 0.907 | 1.112 | 1.129 | 0.992 | 1.154 | 3.19E-02 |
| cds.Camellia_sinensis.comp33403_c4_seq3_m.15130 | kinase family protein [Populus trichocarpa] | 56.939 | 31.333 | 15.3 | 6 | 8 | 4 | 0.945 | 0.996 | 0.954 | 1.049 | 1.051 | 0.998 | 1.07 | 4.44E-02 |
| cds.Camellia_sinensis.comp33403_c4_seq5_m.18825 | PREDICTED: probable serine/threonine-protein kinase At4g35230 [Ziziphus | 56.334 | 10.209 | 14.6 | 6 | 7 | 3 | 0.918 | 0.941 | 0.895 | 1.144 | 1.08 | 1.062 | 1.193 | 2.76E-03 |

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| cds.Camellia_sinensis.comp33403_c4_seq7_m.38162 | PREDICTED: probable serine/threonine-protein kinase At5g41260, partial [Sesamum indicum] | 20.055 | 1.2302 | 9.4 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33404_c0_seq8_m.8014 | PREDICTED: protein TIC 62, chloroplastic isoform X1 [Vitis vinifera] | 50.288 | 134.51 | 33.5 | 15 | 34 | 15 | 1.028 | 1.008 | 0.982 | 0.966 | 0.989 | 1.008 | 0.982 | 3.67E-01 |
| cds.Camellia_sinensis.comp33409_c0_seq4_m.12014 | PREDICTED: far upstream element-binding protein 1 [Theobroma cacao] | 70.69 | 59.644 | 23.7 | 12 | 24 | 6 | 0.986 | 0.991 | 0.982 | 1 | 1.036 | 1.051 | 1.043 | 4.85E-02 |
| cds.Camellia_sinensis.comp33409_c0_seq7_m.12810 | PREDICTED: far upstream element-binding protein 1 [Theobroma cacao] | 71.501 | 171.76 | 22.8 | 12 | 23 | 6 | 1.079 | 0.959 | 0.942 | 0.982 | 1.02 | 0.994 | 1.005 | 8.80E-01 |

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| cds.Camellia_sinensis.comp33410_c0_seq3_m.12744 | PREDICTED: prohibitin-3, mitochondrial [Vitis vinifera] | 30.749 | 53.744 | 21.7 | 6 | 18 | 6 | 0.946 | 0.933 | 0.947 | 1.036 | 1.055 | 1.065 | 1.117 | 3.01E-04 |
| cds.Camellia_sinensis.comp33412_c0_seq2_m.15285 | PREDICTED: pyruvate kinase 1, cytosolic isoform X2 [Juglans regia] | 57.48 | 121.28 | 36.2 | 18 | 35 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33412_c0_seq3_m.16128 | PREDICTED: pyruvate kinase 1, cytosolic isoform X1 [Ipomoea nil] | 57.338 | 33.495 | 32.3 | 15 | 28 | 2 | 0.852 | 0.987 | 1.06 | 1.214 | 0.948 | 0.983 | 1.085 | 4.73E-01 |
| cds.Camellia_sinensis.comp33412_c0_seq6_m.16895 | PREDICTED: pyruvate kinase 1, cytosolic-like [Daucus carota subsp. sativus] | 57.701 | -2 | 38 | 17 | 34 | 0 | | | | | | | | |

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| cds.Camellia_sinensis.comp33412_c0_seq7_m.17502 | PREDICTED: pyruvate kinase 1, cytosolic isoform X2 [Juglans regia] | 57.52 | 4.4895 | 34.7 | 17 | 33 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp33412_c0_seq9_m.18397 | PREDICTED: pyruvate kinase 1, cytosolic-like [Daucus carota subsp. sativus] | 57.716 | 70.266 | 36.4 | 17 | 35 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp33424_c0_seq1_m.14287 | PREDICTED: beta-amylase 1, chloroplastic [Sesamum indicum] | 64.58 | 39.285 | 12.7 | 6 | 6 | 6 | 0.968 | 0.96 | 1.014 | 1.039 | 1.039 | 1.01 | 1.05 | 6.69E-02 |
| cds.Camellia_sinensis.comp33437_c0_seq17_c0_seq1_m.14754 | PREDICTED: imidazole glycerol phosphate synthase hisHF, chloroplastic [Sesamum indicum] | 63.537 | 88.875 | 27.1 | 13 | 15 | 13 | 0.988 | 1.014 | 0.973 | 1.01 | 0.981 | 1.014 | 1.01 | 5.62E-01 |

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| cds.Camellia_sinensis.comp33441_c0_seq4_m.29150 | PREDICTED: photosynthetic NDH subunit of subcomplex B 1, chloroplastic [Juglans regia] | 44.901 | 49.762 | 26.5 | 9 | 12 | 9 | 1.077 | 0.982 | 1.019 | 1.023 | 0.975 | 0.924 | 0.949 | 2.60E-01 |
| cds.Camellia_sinensis.comp33447_c0_seq1_m.22646 | PREDICTED: protein TRIGALACTOSYLDIACYLGLYCEROL 4, chloroplastic [Vitis vinifera] | 51.929 | 5.0868 | 3.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33448_c0_seq1_m.9535 | PREDICTED: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial [Jatropha curcas] | 53.334 | 113.48 | 38.9 | 15 | 27 | 15 | 1.021 | 1.047 | 0.988 | 0.964 | 0.96 | 0.981 | 0.951 | 4.91E-02 |

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| cds.Camellia_sinensis.comp33448_c0_seq2_m.21505 | PREDICTED: phosphoglycerate kinase, cytosolic [Vitis vinifera] | 42.607 | 114.92 | 58.7 | 24 | 94 | 17 | 0.975 | 0.94 | 0.946 | 1.055 | 1.063 | 1.054 | 1.109 | 8.78E-04 |
| cds.Camellia_sinensis.comp33451_c0_seq21_m.27864 | PREDICTED: tryptophan--tRNA ligase, cytoplasmic [Ipomoea | 50.612 | 60.487 | 21.5 | 8 | 12 | 8 | 0.971 | 0.937 | 0.972 | 1.04 | 1.041 | 1.007 | 1.072 | 1.27E-02 |
| cds.Camellia_sinensis.comp33453_c0_seq1_m.2831 | PREDICTED: importin-5-like [Juglans regia] | 123.52 | 106.96 | 12.4 | 12 | 17 | 9 | 1.066 | 1.021 | 1.024 | 0.962 | 0.969 | 0.965 | 0.931 | 3.67E-02 |
| cds.Camellia_sinensis.comp33453_c0_seq2_m.2999 | PREDICTED: importin-5 [Beta vulgaris subsp. vulgaris] | 123.51 | 29.723 | 6.3 | 7 | 9 | 4 | 1.03 | 0.865 | 1.154 | 0.823 | 0.996 | 1.126 | 0.966 | 7.86E-01 |
| cds.Camellia_sinensis.comp33459_c0_seq2_m.19681 | PREDICTED: uncharacterized membrane protein At1g75140 [Vitis vinifera] | 63.594 | 1.2739 | 1.2 | 1 | 1 | 1 | 1.069 | 1.019 | 0.905 | 0.974 | 0.938 | 1.091 | 1.003 | 9.59E-01 |

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| cds.Camellia_sinensis.comp33460_c0_seq1_m.36440 | PREDICTED: nicotinamidase 1-like [Juglans regia] | 27.077 | 24.661 | 18.4 | 4 | 7 | 4 | 0.956 | 1.043 | 1.025 | 0.968 | 1.011 | 1.044 | 1 | 9.98E-01 |
| cds.Camellia_sinensis.comp33465_c0_seq1_m.11018 | PREDICTED: serine/threonine-protein kinase STY46-like [Nicotiana tabacum] | 17.096 | 2.4822 | 16.9 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33465_c0_seq3_m.12575 | PREDICTED: serine/threonine-protein kinase STY46 isoform X1 [Vitis vinifera] | 62.76 | 1.7899 | 3.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33467_c1_seq1_m.38838 | PREDICTED: isoflavone reductase homolog [Arachis ipaensis] | 23.598 | 5.9644 | 9 | 2 | 3 | 1 | 0.947 | 0.993 | 1.052 | 0.967 | 1.068 | 0.989 | 1.011 | 8.16E-01 |
| cds.Camellia_sinensis.comp33469_c0_seq1_m.8798 | PREDICTED: nudix hydrolase 3 [Vitis vinifera] | 94.186 | 85.31 | 23.6 | 20 | 37 | 20 | 0.966 | 0.955 | 0.95 | 1.04 | 1.061 | 1.047 | 1.096 | 2.78E-04 |

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| cds.Camellia_sinensis.comp33469_c0_seq3_m.35195 | PREDICTED: NECAP-like protein CG9132 [Nicotiana tabacum] | 33.611 | 2.7696 | 8.7 | 3 | 4 | 3 | 0.904 | 0.991 | 0.989 | 1.05 | 1.067 | 1.06 | 1.102 | 8.60E-02 |
| cds.Camellia_sinensis.comp33472_c0_seq1_m.4299 | PREDICTED: ubiquitin fusion degradation protein 1 homolog isoform X2 [Juglans regia] | 35.518 | 1.618 | 5.3 | 2 | 3 | 1 | 1.107 | 1.086 | 1.038 | 0.922 | 0.896 | 0.93 | 0.851 | 1.88E-03 |
| cds.Camellia_sinensis.comp33473_c0_seq1_m.28691 | PREDICTED: probable cinnamyl alcohol dehydrogenase 1 [Arachis duranensis] | 39.779 | 4.3057 | 39.9 | 12 | 33 | 1 | 0.972 | 0.938 | 0.92 | 1.019 | 1.05 | 1.121 | 1.127 | 2.13E-02 |
| cds.Camellia_sinensis.comp33473_c0_seq2_m.31095 | PREDICTED: probable cinnamyl alcohol dehydrogenase 1 [Arachis duranensis] | 39.763 | 125.72 | 39.9 | 12 | 32 | 1 | 0.847 | 0.803 | 0.831 | 1.175 | 1.22 | 1.19 | 1.445 | 4.14E-05 |

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| cds.Camellia_sinensis.comp33473_c0_seq3_m.41971 | PREDICTED: probable cinnamyl alcohol dehydrogenase 1 [Arachis duranensis] | 29.866 | 22.196 | 17.7 | 5 | 12 | 5 | 0.929 | 0.856 | 0.919 | 1.096 | 1.104 | 1.072 | 1.21 | 2.14E-03 |
| cds.Camellia_sinensis.comp33473_c1_seq1_m.11925 | PREDICTED: actin-interacting protein 1-2-like [Nicotiana attenuata] | 66.021 | 51.651 | 23.8 | 13 | 17 | 13 | 0.977 | 0.949 | 0.964 | 1.051 | 1.036 | 1.017 | 1.074 | 4.92E-03 |
| cds.Camellia_sinensis.comp33475_c0_seq1_m.5850 | PREDICTED: proteinaceous RNase P 1, chloroplastic/mitochondrial [Vitis vinifera] | 98.504 | -2 | 1 | 1 | 1 | 1 | 0.921 | 0.871 | 0.929 | 1.094 | 1.13 | 1.096 | 1.22 | 9.40E-04 |
| cds.Camellia_sinensis.comp33476_c0_seq3_m.1571 | Kinesin-like protein KIF15 [Morus notabilis] | 134.78 | 1.4591 | 0.9 | 1 | 1 | 1 | 1.093 | 1.009 | 1.145 | 0.906 | 0.947 | 0.884 | 0.843 | 1.56E-02 |
| cds.Camellia_sinensis.comp33477_c1_seq1_m.14299 | RasGAP-activating-like protein 1 [Morus notabilis] | 71.92 | 1.4804 | 2.3 | 2 | 2 | 2 | 1.007 | 1.097 | 0.998 | 0.964 | 1.031 | 0.905 | 0.935 | 2.32E-01 |

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| cds.Camellia_sinensis.comp33484_c0_seq1_m.22585 | PREDICTED: golgin subfamily A member 6-like protein 6 isoform X2 [Citrus sinensis] | 43.579 | 17.026 | 15.9 | 5 | 6 | 3 | 0.972 | 1.245 | 0.96 | 0.907 | 1.04 | 0.873 | 0.888 | 3.15E-01 |
| cds.Camellia_sinensis.comp33490_c0_seq2_m.13230 | PREDICTED: ubiquitin domain-containing protein DSK2a-like [Ziziphus jujuba] | 58.553 | 72.574 | 20.4 | 8 | 15 | 7 | 0.959 | 0.926 | 0.993 | 1.071 | 1.004 | 1.071 | 1.093 | 3.93E-02 |
| cds.Camellia_sinensis.comp33490_c0_seq6_m.32432 | PREDICTED: ubiquitin domain-containing protein DSK2a-like [Juglans regia] | 27.796 | 9.8541 | 10.2 | 2 | 3 | 2 | 0.96 | 1.029 | 0.916 | 1.118 | 0.979 | 1.022 | 1.074 | 2.43E-01 |
| cds.Camellia_sinensis.comp33491_c0_seq1_m.10369 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 2, chloroplastic [Vitis vinifera] | 74.429 | 323.31 | 39.3 | 26 | 100 | 25 | 1.01 | 0.984 | 1.015 | 1.012 | 1 | 0.997 | 1 | 9.95E-01 |

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| cds.Camellia_sinensis.comp33495_c0_seq1_m.32618 | PREDICTED: riboflavin biosynthesis protein PYRD, chloroplastic [Vitis vinifera] | 27.785 | 2.3948 | 4 | 1 | 1 | 1 | 1.006 | 0.992 | 1.043 | 0.963 | 0.893 | 1.103 | 0.973 | 6.52E-01 |
| cds.Camellia_sinensis.comp33495_c0_seq1_m.32619 | PREDICTED: riboflavin biosynthesis protein PYRD, chloroplastic [Juglans regia] | 13.994 | 2.8471 | 16.2 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33498_c0_seq10_m.49841 | PREDICTED: pleiotropic drug resistance protein 2-like [Gossypium hirsutum] | 21.25 | 2.4554 | 21.2 | 4 | 4 | 2 | 1.085 | 0.984 | 0.989 | 0.946 | 1.034 | 0.958 | 0.961 | 3.99E-01 |
| cds.Camellia_sinensis.comp33502_c0_seq10_m.7346 | PREDICTED: protein ROOT HAIR DEFECTIVE 3 homolog 2 [Jatropha curcas] | 92.627 | 28.688 | 12.3 | 10 | 11 | 9 | 0.987 | 1 | 1.058 | 0.999 | 0.93 | 0.987 | 0.958 | 2.31E-01 |

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| cds.Camellia_sinensis.comp33502_c0_seq18_m.39296 | PREDICTED: sugar carrier protein C-like [Ipomoea nil] | 29.706 | 1.1983 | 5.3 | 2 | 3 | 1 | 0.964 | 0.961 | 0.975 | 1.074 | 0.983 | 1.065 | 1.077 | 1.25E-01 |
| cds.Camellia_sinensis.comp33502_c0_seq4_m.3342 | PREDICTED: sugar carrier protein C-like [Ipomoea nil] | 57.517 | 9.2049 | 7.7 | 4 | 5 | 3 | 1.039 | 0.992 | 1.006 | 0.91 | 1.005 | 1.046 | 0.975 | 5.71E-01 |
| cds.Camellia_sinensis.comp33502_c0_seq4_m.3343 | PREDICTED: fructokinase-like 1, chloroplastic [Gossypium raimondii] | 56.656 | 4.6011 | 9.7 | 4 | 4 | 4 | | | | | | | | |
| cds.Camellia_sinensis.comp33502_c0_seq8_m.7124 | protein ROOT HAIR DEFECTIVE 3-like [Cajanus cajan] | 57.917 | 2.7256 | 3.6 | 2 | 3 | 1 | 0.992 | 1.005 | 1.009 | 1.044 | 0.937 | 1.024 | 1 | 9.71E-01 |
| cds.Camellia_sinensis.comp33505_c0_seq15_m.522 | PREDICTED: trafficking protein particle complex subunit 13 isoform X1 [Vitis vinifera] | 49.836 | 1.814 | 3.8 | 2 | 2 | 2 | 1.018 | 1.017 | 1.083 | 0.94 | 0.911 | 1.026 | 0.923 | 1.20E-01 |

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| cds.Camellia_sinensis.comp33506_c1_seq1_m.16384 | PREDICTED: dihydrolipoyl dehydrogenase 2, chloroplastic-like isoform X2 [Nicotiana tabacum] | 59.902 | 10.661 | 10.4 | 6 | 7 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33506_c1_seq2_m.23251 | PREDICTED: 3-isopropylmalate dehydrogenase, chloroplastic isoform X2 [Sesamum indicum] | 41.541 | 100.08 | 27.2 | 9 | 20 | 5 | 1.001 | 0.976 | 0.97 | 1.043 | 0.981 | 1.049 | 1.043 | 1.52E-01 |
| cds.Camellia_sinensis.comp33506_c1_seq5_m.38168 | PREDICTED: isocitrate dehydrogenase [NAD] catalytic subunit 5, mitochondrial [Jatropha curcas] | 16.264 | 41.319 | 19.1 | 3 | 5 | 2 | 0.962 | 0.937 | 0.943 | 1.038 | 1.049 | 1.077 | 1.113 | 1.38E-03 |

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| cds.Camellia_sinensis.comp33506_c1_seq8_m.53720 | PREDICTED: 3-isopropylmalate dehydrogenase, chloroplastic-like [Erythranthe guttata] | 16.733 | 13.354 | 40.7 | 4 | 9 | 1 | 0.937 | 0.834 | 0.931 | 1.038 | 1.055 | 1.237 | 1.232 | 3.73E-02 |
| cds.Camellia_sinensis.comp33515_c0_seq15_m.9639 | PREDICTED: protein QUIRKY-like [Nicotiana tabacum] | 88.969 | 22.857 | 6.2 | 5 | 6 | 5 | 0.958 | 1.026 | 1.043 | 1.072 | 0.931 | 0.986 | 0.987 | 7.93E-01 |
| cds.Camellia_sinensis.comp33515_c1_seq13_m.30685 | PREDICTED: cytochrome P450 CYP72A219-like isoform X2 [Juglans regia] | 45.166 | 7.1653 | 2.8 | 1 | 1 | 1 | 0.858 | 0.865 | 0.967 | 1.145 | 1.058 | 1.157 | 1.249 | 9.54E-03 |
| cds.Camellia_sinensis.comp33516_c0_seq1_m.500 | vacuolar protein sorting protein [Medicago truncatula] | 277.54 | 37.559 | 5.6 | 12 | 12 | 12 | 0.9 | 0.996 | 0.951 | 1.011 | 1.068 | 1.032 | 1.093 | 5.55E-02 |
| cds.Camellia_sinensis.comp33516_c0_seq2_m.904 | vacuolar protein sorting protein [Medicago truncatula] | 209.64 | 4.0715 | 2.2 | 4 | 6 | 4 | 0.977 | 1.004 | 1.046 | 1.041 | 0.995 | 1.011 | 1.007 | 7.90E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33518_c0_seq1_m.16947 | PREDICTED: ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic isoform X1 [Vitis vinifera] | 52.007 | 323.31 | 64.6 | 28 | 229 | 5 | 1.055 | 1.015 | 1.014 | 0.99 | 1.008 | 0.951 | 0.956 | 1.06E-01 |
| cds.Camellia_sinensis.comp33518_c0_seq2_m.16961 | PREDICTED: ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic isoform X1 [Vitis vinifera] | 52.182 | 104.4 | 62.7 | 27 | 222 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp33518_c0_seq3_m.18225 | PREDICTED: ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic [Vitis vinifera] | 52.204 | 193.73 | 56.1 | 25 | 170 | 11 | 1.039 | 1.012 | 1.023 | 0.967 | 0.99 | 0.973 | 0.953 | 9.90E-03 |

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| cds.Camellia_sinensis.comp33518_c0_seq4_m.18496 | PREDICTED: ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic isoform X2 [Vitis vinifera] | 48.053 | 80.308 | 62.3 | 25 | 220 | 1 | 1.028 | 1.079 | 1.041 | 0.949 | 0.98 | 0.928 | 0.908 | 1.07E-02 |
| cds.Camellia_sinensis.comp33519_c0_seq1_m.26361 | L-ascorbate peroxidase 3, peroxisomal [Jatropha curcas] | 31.925 | 68.585 | 38.5 | 11 | 27 | 9 | 0.991 | 0.988 | 0.986 | 0.984 | 1.066 | 1 | 1.029 | 3.76E-01 |
| cds.Camellia_sinensis.comp33519_c0_seq2_m.53802 | PREDICTED: L-ascorbate peroxidase 3, peroxisomal [Citrus sinensis] | 13.35 | 1.651 | 19.8 | 2 | 7 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp33521_c0_seq2_m.6031 | PREDICTED: U-box domain-containing protein 4 [Theobroma cacao] | 73.804 | 1.263 | 2 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |

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| cds.Camellia_sinensis.comp33522_c1_seq1_m.3043 | PREDICTED: beta-fructofuranosidase, soluble isoenzyme I-like isoform X1 [Nelumbo nucifera] | 21.882 | 4.3444 | 14.1 | 2 | 2 | 2 | 0.896 | 0.956 | 0.981 | 1.094 | 1.02 | 1.088 | 1.13 | 2.50E-02 |
| cds.Camellia_sinensis.comp33524_c0_seq8_m.15295 | PREDICTED: DNA ligase 1-like [Sesamum indicum] | 71.98 | 1.815 | 1.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33531_c0_seq1_m.1329 | PREDICTED: methionine S-methyltransferase isoform X1 [Vitis vinifera] | 121.24 | 4.4648 | 2.2 | 3 | 4 | 3 | 1.012 | 1.028 | 1.064 | 0.959 | 0.99 | 0.949 | 0.934 | 2.45E-02 |
| cds.Camellia_sinensis.comp33545_c2_seq7_m.24297 | PREDICTED: long chain acyl-CoA synthetase 4-like [Juglans regia] | 15.039 | 1.2136 | 9.9 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp33546_c0_seq21_m.10170 | NADH dehydrogenase subunit 7 (mitochondrion) [Citrullus lanatus] | 33.092 | 124.95 | 32.1 | 8 | 17 | 8 | 0.98 | 0.982 | 0.975 | 1.051 | 1.018 | 0.99 | 1.042 | 1.46E-01 |
| cds.Camellia_sinensis.comp33546_c0_seq33_m.34860 | cytochrome c oxidase subunit 2 (mitochondrion) [Beta macrocarp | 29.284 | 11.783 | 14.8 | 4 | 6 | 4 | 1.006 | 0.957 | 1.013 | 1.018 | 1.035 | 1.002 | 1.027 | 2.61E-01 |
| cds.Camellia_sinensis.comp33546_c0_seq8_m.3383 | NADH dehydrogenase subunit 2 (mitochondrion) [Nelumbo nucifera] | 16.559 | 13.47 | 7.4 | 1 | 1 | 1 | 0.944 | 0.952 | 0.977 | 1.061 | 1.056 | 1.036 | 1.097 | 1.82E-03 |
| cds.Camellia_sinensis.comp33549_c0_seq17_m.17070 | PREDICTED: splicing factor U2af large subunit B isoform X4 [Daucus carota subsp. sativus] | 33.167 | 2.2872 | 3.3 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |

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| cds.Camellia_sinensis.comp33553_c0_seq10_m.22919 | PREDICTED: gluconokinase isoform X2 [Citrus sinensis] | 42.295 | 33.831 | 19.1 | 6 | 7 | 6 | 0.92 | 1.018 | 0.94 | 1.085 | 1.043 | 1.037 | 1.1 | 4.76E-02 |
| cds.Camellia_sinensis.comp33554_c0_seq2_m.16296 | PREDICTED: FGGY carbohydrate kinase domain-containing protein [Vitis vinifera] | 66.651 | 30.546 | 13.6 | 8 | 13 | 8 | 0.935 | 0.978 | 0.967 | 1.033 | 1.025 | 0.996 | 1.06 | 2.83E-02 |
| cds.Camellia_sinensis.comp33556_c0_seq1_m.6069 | PREDICTED: lon protease homolog 2, peroxisomal [Vitis | 98.253 | 3.0766 | 2.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33558_c0_seq5_m.35964 | PREDICTED: syntaxin-51-like [Sesamum indicum] | 25.715 | 30.448 | 29.2 | 8 | 14 | 8 | 0.961 | 1.005 | 0.974 | 1.027 | 1.027 | 1.003 | 1.04 | 6.42E-02 |
| cds.Camellia_sinensis.comp33558_c3_seq1_m.40063 | PREDICTED: thioredoxin O2, mitochondrial [Sesamum indicum] | 16.298 | 15.794 | 22.6 | 3 | 6 | 3 | 1.037 | 1.037 | 1.118 | 0.927 | 0.887 | 0.984 | 0.877 | 2.80E-02 |

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| cds.Camellia_sinensis.comp33561_c1_seq1_m.5928 | PREDICTED: nuclear pore complex protein NUP1 [Vitis vinifera] | 70.092 | 1.4038 | 2.6 | 2 | 2 | 2 | 1.106 | 1.026 | 1.008 | 0.998 | 0.895 | 0.956 | 0.907 | 8.40E-02 |
| cds.Camellia_sinensis.comp33562_c0_seq8_m.5046 | PREDICTED: riboflavin synthase [Vitis vinifera] | 30.636 | 63.606 | 39.1 | 8 | 13 | 8 | 1.056 | 0.971 | 0.984 | 0.938 | 0.998 | 0.997 | 0.974 | 4.77E-01 |
| cds.Camellia_sinensis.comp33567_c0_seq4_m.25188 | transmembrane protein, putative [Medicago truncatula] | 35.594 | 10.409 | 6.9 | 2 | 2 | 2 | 1.019 | 1.188 | 1.001 | 0.867 | 0.953 | 0.957 | 0.866 | 8.75E-02 |
| cds.Camellia_sinensis.comp33568_c0_seq10_m.48518 | PREDICTED: cysteine synthase isoform X1 [Glycine max] | 15.483 | 6.5529 | 13 | 2 | 4 | 1 | 1.075 | 1.277 | 1.072 | 0.881 | 0.816 | 0.846 | 0.743 | 8.94E-03 |
| cds.Camellia_sinensis.comp33568_c0_seq4_m.28856 | PREDICTED: cysteine synthase isoform X1 [Glycine max] | 40.437 | 74.078 | 38.2 | 12 | 28 | 10 | 1.009 | 1.007 | 1 | 0.983 | 1.025 | 0.997 | 0.996 | 7.78E-01 |

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| cds.Camellia_sinensis.comp33570_c0_seq13_m.43530 | PREDICTED: adenylosuccinate lyase [Theobroma cacao] | 14.693 | 15.167 | 31.3 | 4 | 6 | 2 | 1.002 | 1.008 | 1.049 | 0.932 | 1 | 1.012 | 0.962 | 2.58E-01 |
| cds.Camellia_sinensis.comp33570_c0_seq3_m.15855 | PREDICTED: adenylosuccinate lyase [Theobroma cacao] | 61.638 | 43.604 | 22.3 | 12 | 17 | 10 | 0.992 | 0.964 | 1.022 | 1.034 | 1.003 | 1.032 | 1.031 | 1.96E-01 |
| cds.Camellia_sinensis.comp33576_c0_seq4_m.32648 | PREDICTED: chlorophyll(ide) b reductase NOL, chloroplastic isoform X1 [Populus euphratica] | 36.34 | 10.424 | 19.5 | 6 | 7 | 6 | 0.98 | 0.983 | 0.97 | 0.999 | 1.052 | 1.031 | 1.051 | 3.39E-02 |
| cds.Camellia_sinensis.comp33577_c0_seq17_m.10507 | PREDICTED: serine/threonine protein phosphatase 2A regulatory subunit B"beta-like [Sesamum indicum] | 61.941 | 46.756 | 14.9 | 6 | 8 | 6 | 1.03 | 0.977 | 0.93 | 1.024 | 1.031 | 1.018 | 1.046 | 2.61E-01 |

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| cds.Camellia_sinensis.comp33579_c0_seq9_m.18067 | PREDICTED: phosphoinositide phospholipase C 2 [Vitis vinifera] | 68.055 | 54.331 | 26.3 | 16 | 29 | 16 | 0.953 | 0.97 | 0.959 | 1.033 | 1.04 | 1.022 | 1.074 | 6.00E-04 |
| cds.Camellia_sinensis.comp33579_c1_seq1_m.50294 | PREDICTED: 14-3-3-like protein GF14 kappa [Nelumbo nucifera] | 21.135 | 90.547 | 54.8 | 11 | 31 | 8 | 0.964 | 0.974 | 0.908 | 1.056 | 1.07 | 1.087 | 1.129 | 6.54E-03 |
| cds.Camellia_sinensis.comp33582_c0_seq6_m.35475 | PREDICTED: putative 4-hydroxy-tetrahydrodipicolinate reductase 3, chloroplastic [Populus euphratica] | 17.41 | 12.795 | 36.2 | 4 | 4 | 4 | 0.94 | 1.024 | 1.031 | 1.016 | 0.954 | 1.05 | 1.008 | 8.47E-01 |
| cds.Camellia_sinensis.comp33583_c0_seq17_m.28135 | PREDICTED: splicing factor 3A subunit 2-like [Nicotiana sylvestris] | 38.298 | 47.905 | 16 | 5 | 8 | 5 | 1.004 | 1.023 | 0.994 | 0.982 | 0.998 | 1.01 | 0.99 | 4.29E-01 |

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| cds.Camellia_sinensis.comp33583_c0_seq1_m.1570 | PREDICTED: ABC transporter D family member 1 isoform X2 [Daucus carota subsp. sativus] | 151.04 | 16.629 | 5.3 | 8 | 9 | 8 | 1.025 | 1.068 | 1.08 | 0.952 | 0.935 | 0.935 | 0.889 | 2.32E-03 |
| cds.Camellia_sinensis.comp33588_c0_seq1_m.8929 | PREDICTED: gamma-glutamyltranspeptidase 3-like [Juglans regia] | 68.035 | 6.4163 | 4.3 | 3 | 4 | 3 | 1.072 | 1.096 | 1.088 | 0.894 | 0.99 | 0.944 | 0.869 | 9.32E-03 |
| cds.Camellia_sinensis.comp33592_c0_seq1_m.12654 | PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2-like [Juglans regia] | 83.854 | 125.68 | 29.2 | 17 | 31 | 17 | 0.994 | 0.988 | 0.99 | 1.041 | 1.042 | 1.001 | 1.038 | 1.10E-01 |

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| cds.Camellia_sinensis.comp33596_c1_seq16_m.36604 | PREDICTED: epidermal growth factor receptor substrate 15-like isoform X2 [Nicotiana tomentosiformis] | 27.017 | 5.7515 | 12.2 | 2 | 2 | 2 | 1.068 | 1.119 | 0.983 | 0.874 | 1.017 | 0.924 | 0.888 | 1.10E-01 |
| cds.Camellia_sinensis.comp33596_c1_seq1_m.3182 | PREDICTED: epidermal growth factor receptor substrate 15-like 1 [Solanum tuberosum | 113.82 | 6.2309 | 8.2 | 8 | 8 | 6 | 1.038 | 1.119 | 1.092 | 0.939 | 0.936 | 0.864 | 0.843 | 8.20E-03 |
| cds.Camellia_sinensis.comp33596_c1_seq2_m.6425 | PREDICTED: epidermal growth factor receptor substrate 15-like [Nelumbo nucifera] | 90.117 | 12.65 | 9.7 | 10 | 10 | 8 | 1.069 | 1.08 | 1.092 | 0.864 | 0.969 | 0.912 | 0.847 | 7.70E-03 |

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| cds.Camellia_sinensis.comp33599_c0_seq1_m.28484 | PREDICTED: mitochondrial import receptor subunit TOM40-1-like [Nicotiana tabacum] | 40.638 | 5.4752 | 12 | 4 | 4 | 4 | 1.134 | 0.879 | 0.979 | 1.153 | 1.002 | 0.863 | 1.009 | 9.52E-01 |
| cds.Camellia_sinensis.comp33599_c1_seq11_m.43029 | PREDICTED: histone H2AX [Citrus sinensis] | 14.658 | 6.2367 | 25 | 5 | 15 | 2 | 1.193 | 1.245 | 1.316 | 0.749 | 0.739 | 0.704 | 0.584 | 9.72E-05 |
| cds.Camellia_sinensis.comp33604_c0_seq4_m.28246 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 6 [Vitis vinifera] | 45.026 | 26.945 | 13.6 | 5 | 6 | 5 | 0.969 | 1.075 | 1.013 | 1.044 | 0.85 | 1.056 | 0.965 | 6.33E-01 |
| cds.Camellia_sinensis.comp33605_c0_seq11_m.35919 | PREDICTED: glutathione S-transferase L3-like isoform X1 [Nicotiana tabacum] | 31.234 | 56.243 | 33.8 | 8 | 20 | 5 | 0.934 | 0.895 | 0.869 | 1.095 | 1.117 | 1.122 | 1.236 | 6.78E-04 |

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| cds.Camellia_sinensis.comp33605_c0_seq4_m.13858 | PREDICTED: eukaryotic translation initiation factor 3 subunit H [Vitis vinifera] | 38.617 | 60.538 | 21.1 | 6 | 6 | 6 | 0.974 | 0.962 | 0.986 | 1.045 | 1.036 | 1.018 | 1.061 | 4.96E-03 |
| cds.Camellia_sinensis.comp33605_c0_seq6_m.24251 | PREDICTED: glutathione S-transferase L3 [Vitis vinifera] | 27.424 | 182.85 | 56.1 | 14 | 46 | 12 | 0.902 | 0.887 | 0.904 | 1.117 | 1.145 | 1.125 | 1.258 | 1.87E-05 |
| cds.Camellia_sinensis.comp33606_c0_seq1_m.24840 | PREDICTED: probable indole-3-acetic acid-amido synthetase GH3.6 [Juglans regia] | 58.518 | 6.0999 | 7.1 | 3 | 3 | 3 | 0.841 | 0.973 | 0.996 | 1.005 | 1.129 | 1.093 | 1.148 | 9.14E-02 |
| cds.Camellia_sinensis.comp33611_c0_seq1_m.11426 | PREDICTED: glycerol-3-phosphate dehydrogenase SDP6, mitochondrial-like [Sesamum indicum] | 71.729 | 96.499 | 20.3 | 12 | 16 | 12 | 0.987 | 0.986 | 0.986 | 1.047 | 1.006 | 1.008 | 1.034 | 1.22E-01 |

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| cds.Camellia_sinensis.comp33613_c0_seq1_m.2133 | PREDICTED: protein TSS [Vitis vinifera] | 160.29 | 3.4852 | 2.6 | 4 | 4 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp33613_c0_seq3_m.4842 | PREDICTED: protein TSS [Vitis vinifera] | 101.64 | 20.313 | 6.1 | 6 | 7 | 4 | 1.187 | 1.114 | 1.098 | 0.867 | 0.789 | 0.876 | 0.745 | 1.98E-03 |
| cds.Camellia_sinensis.comp33613_c0_seq8_m.14007 | PREDICTED: protein TSS [Vitis vinifera] | 11.895 | 1.7316 | 10.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33614_c1_seq1_m.4575 | PREDICTED: dynamin-2A-like [Nicotiana tabacum] | 63.783 | 77 | 18.1 | 10 | 11 | 10 | 1.142 | 1.167 | 1.152 | 0.833 | 0.78 | 0.849 | 0.711 | 2.04E-04 |
| cds.Camellia_sinensis.comp33614_c1_seq4_m.11953 | PREDICTED: LOW QUALITY PROTEIN: dynamin-2A-like [Ziziphus jujuba] | 25.277 | 3.5301 | 15 | 3 | 3 | 3 | 1.22 | 1.199 | 1.178 | 0.78 | 0.797 | 0.766 | 0.651 | 4.81E-06 |
| cds.Camellia_sinensis.comp33616_c0_seq9_m.1487 | PREDICTED: ABC transporter C family member 14 [Juglans | 38.954 | 11.198 | 7.2 | 2 | 2 | 2 | 1.047 | 1.09 | 0.998 | 0.99 | 0.901 | 0.967 | 0.912 | 7.18E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33617_c0_seq3_m.36051 | PREDICTED: hippocampus abundant transcript-like protein 1 isoform X3 [Nicotiana tabacum] | 17.546 | 5.5301 | 10.2 | 1 | 1 | 1 | | | | | | | | | |
| cds.Camellia_sinensis.comp33622_c1_seq1_m.39647 | esterase/lipase/thioesterase family protein [Populus trichocarpa] | 24.368 | 16.259 | 32.4 | 7 | 10 | 7 | 0.973 | 1.004 | 1.003 | 1.029 | 1.025 | 0.956 | 1.01 | 7.32E-01 |
| cds.Camellia_sinensis.comp33623_c0_seq1_m.17480 | PREDICTED: RNA-binding protein 1 isoform X1 [Vitis vinifera] | 24.198 | 43.399 | 21.6 | 4 | 9 | 4 | 1.001 | 1.031 | 1.027 | 0.938 | 0.94 | 0.944 | 0.923 | 1.04E-03 |
| cds.Camellia_sinensis.comp33624_c0_seq11_m.49384 | PREDICTED: NAD-dependent malic enzyme 62 kDa isoform, mitochondrial [Jatropha curcas] | 15.224 | 1.5362 | 49.6 | 6 | 17 | 1 | 0.957 | 0.958 | 0.995 | 1.037 | 1.069 | 1.007 | 1.07 | 3.51E-02 |

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| cds.Camellia_sinensis.comp33624_c0_seq1_m.8477 | PREDICTED: ubiquitin receptor RAD23c [Vitis vinifera] | 40.93 | 14.004 | 24.6 | 7 | 15 | 3 | 1 | 1.031 | 0.987 | 1.029 | 0.987 | 0.957 | 0.985 | 5.69E-01 |
| cds.Camellia_sinensis.comp33624_c0_seq2_m.10448 | PREDICTED: NAD-dependent malic enzyme 62 kDa isoform, mitochondrial [Jatropha curcas] | 69.135 | 63.189 | 26.8 | 15 | 28 | 10 | 1.002 | 0.973 | 1.035 | 1.001 | 0.963 | 0.989 | 0.981 | 4.22E-01 |
| cds.Camellia_sinensis.comp33625_c1_seq15_m.31691 | PREDICTED: NADH-cytochrome b5 reductase-like protein [Nelumbo nucifera] | 36.397 | 38.217 | 23.4 | 9 | 17 | 9 | 1.033 | 1.002 | 0.979 | 0.998 | 1.001 | 0.996 | 0.994 | 7.34E-01 |
| cds.Camellia_sinensis.comp33625_c2_seq45_m.19700 | PREDICTED: protein LST8 homolog isoform X1 [Sesamum indicum] | 19.682 | 3.066 | 10.9 | 2 | 2 | 2 | 0.98 | 0.992 | 0.937 | 1.127 | 0.968 | 1.018 | 1.07 | 2.41E-01 |

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| cds.Camellia_sinensis.comp33629_c0_seq1_m.23642 | probable E3 ubiquitin-protein ligase HERC1-like [Vitis vinifera] | 31.952 | 82.445 | 50.3 | 11 | 16 | 11 | 0.892 | 0.94 | 0.985 | 1.044 | 1.081 | 1.078 | 1.137 | 1.37E-02 |
| cds.Camellia_sinensis.comp33629_c1_seq1_m.6279 | PREDICTED: alpha-glucan phosphorylase, H isozyme [Ricinus communis] | 73.512 | 122.77 | 24.8 | 13 | 32 | 12 | 0.957 | 0.975 | 0.99 | 1.017 | 1.067 | 1.023 | 1.063 | 2.73E-02 |
| cds.Camellia_sinensis.comp33629_c1_seq1_m.6280 | PREDICTED: alpha-glucan phosphorylase, H isozyme [Gossypium arboreum] | 25.645 | 73.265 | 48.9 | 8 | 10 | 8 | 1.007 | 0.956 | 0.95 | 0.991 | 1.064 | 1.017 | 1.055 | 1.29E-01 |
| cds.Camellia_sinensis.comp33638_c0_seq2_m.512 | PREDICTED: CCR4-NOT transcription complex subunit 1 [Nicotiana attenuata] | 262.71 | 22.537 | 2.9 | 7 | 8 | 7 | 0.886 | 0.937 | 0.994 | 1.091 | 1.049 | 1.051 | 1.133 | 2.42E-02 |

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| cds.Camellia_sinensis.comp33644_c0_seq1_m.1783 | PREDICTED: ethylene-insensitive protein 2 [Vitis vinifera] | 141.7 | 2.5473 | 1.5 | 2 | 2 | 2 | 1.005 | 1.157 | 0.98 | 0.94 | 0.986 | 0.928 | 0.908 | 1.63E-01 |
| cds.Camellia_sinensis.comp33650_c1_seq2_m.10063 | PREDICTED: protein LYK5 [Vitis vinifera] | 75.823 | 3.4138 | 3 | 2 | 2 | 2 | 1.046 | 1.084 | 0.978 | 0.892 | 0.988 | 1.001 | 0.927 | 1.82E-01 |
| cds.Camellia_sinensis.comp33650_c1_seq7_m.35695 | PREDICTED: ferritin-3, chloroplastic [Theobroma cacao] | 30.802 | 78.547 | 34.3 | 9 | 24 | 8 | 0.851 | 0.853 | 0.872 | 1.126 | 1.196 | 1.144 | 1.345 | 1.16E-04 |
| cds.Camellia_sinensis.comp33653_c0_seq15_m.32110 | PREDICTED: probable protein phosphatase 2C 11 isoform X2 [Nicotiana tabacum] | 31.382 | 51.334 | 29.1 | 7 | 8 | 5 | 0.961 | 1.051 | 0.955 | 1.07 | 0.937 | 1.068 | 1.036 | 5.52E-01 |
| cds.Camellia_sinensis.comp33654_c0_seq3_m.37515 | PREDICTED: glycylpeptide N-tetradecanoyltransferase 1-like [Jatropha curcas] | 33.858 | 14.953 | 10.1 | 3 | 5 | 3 | 0.934 | 1.002 | 0.941 | 1.038 | 1.072 | 1.056 | 1.1 | 1.64E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33656_c0_seq1_m.9924 | PREDICTED: hydroquinone glucosyltransferase [Jatropha curcas] | 55.279 | 10.737 | 6.8 | 4 | 6 | 1 | 1.097 | 1.011 | 1.011 | 0.951 | 0.962 | 0.958 | 0.92 | 9.58E-02 |
| cds.Camellia_sinensis.comp33656_c0_seq6_m.24112 | PREDICTED: hydroquinone glucosyltransferase [Jatropha curcas] | 55.305 | 7.9968 | 10.3 | 6 | 8 | 2 | 0.948 | 0.961 | 0.979 | 1.016 | 0.992 | 1.123 | 1.084 | 1.12E-01 |
| cds.Camellia_sinensis.comp33659_c0_seq2_m.20927 | glutamine synthetase cytosolic isozyme 1 [Gossypium hirsutum] | 41.319 | 156.74 | 53 | 16 | 76 | 8 | 1.061 | 1.015 | 0.977 | 0.983 | 0.954 | 0.986 | 0.957 | 1.74E-01 |
| cds.Camellia_sinensis.comp33659_c1_seq3_m.35435 | PREDICTED: acylpyruvase FAHD1, mitochondrial [Ricinus communis] | 29.712 | 11.224 | 15.8 | 5 | 10 | 5 | 0.996 | 0.985 | 0.979 | 1.003 | 1.004 | 1.042 | 1.03 | 9.47E-02 |
| cds.Camellia_sinensis.comp33665_c2_seq27_m.12080 | PREDICTED: monosaccharide-sensing protein 2 [Ricinus communis] | 80.555 | 6.5353 | 3.5 | 2 | 2 | 2 | 0.969 | 1.148 | 1.149 | 0.857 | 0.868 | 0.995 | 0.833 | 6.99E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33666_c0_seq1_m.13386 | PREDICTED: serine/threonine-protein phosphatase BSL1 [Vitis vinifera] | 71.364 | 13.607 | 11.1 | 7 | 7 | 1 | 0.961 | 1.007 | 1.021 | 1.035 | 0.988 | 1.004 | 1.013 | 6.06E-01 |
| cds.Camellia_sinensis.comp33666_c0_seq2_m.13614 | PREDICTED: serine/threonine-protein phosphatase BSL1 [Vitis vinifera] | 71.134 | 33.019 | 12.8 | 8 | 8 | 2 | 1.024 | 0.979 | 0.963 | 1.002 | 1.026 | 1.015 | 1.026 | 2.56E-01 |
| cds.Camellia_sinensis.comp33668_c0_seq2_m.14633 | PREDICTED: T-complex protein 1 subunit gamma [Nelumbo nucifera] | 60.595 | 85.649 | 41.7 | 23 | 36 | 23 | 0.917 | 0.935 | 0.95 | 1.042 | 1.083 | 1.053 | 1.134 | 1.22E-03 |
| cds.Camellia_sinensis.comp33672_c0_seq1_m.4477 | PREDICTED: puromycin-sensitive aminopeptidase isoform X1 [Vitis vinifera] | 111.03 | 323.31 | 42.5 | 38 | 71 | 33 | 0.996 | 0.999 | 1.014 | 1.006 | 1.017 | 1.005 | 1.006 | 4.01E-01 |

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| cds.Camellia_sinensis.comp33672_c0_seq2_m.32085 | PREDICTED: puromycin-sensitive aminopeptidase [Theobroma cacao] | 35.749 | 107.86 | 48.9 | 13 | 28 | 9 | 0.943 | 1.002 | 0.947 | 1.077 | 1.004 | 1.014 | 1.07 | 8.25E-02 |
| cds.Camellia_sinensis.comp33673_c0_seq2_m.27338 | PREDICTED: probable inactive purple acid phosphatase 29 [Jatropha curcas] | 42.338 | 11.937 | 14.7 | 6 | 14 | 6 | 1.039 | 1.034 | 0.993 | 0.978 | 0.982 | 1.006 | 0.967 | 1.21E-01 |
| cds.Camellia_sinensis.comp33674_c0_seq1_m.21430 | PREDICTED: serine hydroxymethyltransferase 4 [Sesamum indicum] | 53.634 | 287.31 | 48.1 | 23 | 56 | 23 | 1.063 | 1.042 | 1.029 | 0.96 | 0.963 | 0.946 | 0.915 | 1.28E-03 |
| cds.Camellia_sinensis.comp33674_c1_seq1_m.33814 | PREDICTED: annexin D5-like isoform X1 [Gossypium raimondii] | 36.828 | 8.9928 | 13.6 | 5 | 6 | 5 | 0.911 | 0.933 | 0.926 | 1.089 | 1.13 | 1.091 | 1.195 | 2.18E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33677_c0_seq1_m.35450 | PREDICTED: probable glutathione S-transferase [Gossypium raimondii] | 24.87 | 48.903 | 36.5 | 10 | 21 | 5 | 0.984 | 0.948 | 0.942 | 1.047 | 1.071 | 1.049 | 1.102 | 3.24E-03 |
| cds.Camellia_sinensis.comp33677_c0_seq37_m.39927 | PREDICTED: probable glutathione S-transferase [Gossypium raimondii] | 24.968 | 2.0858 | 7.2 | 2 | 3 | 1 | 0.95 | 0.865 | 0.984 | 1.095 | 1.21 | 0.936 | 1.158 | 1.65E-01 |
| cds.Camellia_sinensis.comp33679_c0_seq1_m.30047 | PREDICTED: protein transport protein SEC13 homolog B [Vitis vinifera] | 32.584 | 48.755 | 25.6 | 6 | 10 | 4 | 0.906 | 1.013 | 0.99 | 1.023 | 1.055 | 1.025 | 1.067 | 1.38E-01 |
| cds.Camellia_sinensis.comp33680_c1_seq10_c1_seq1_m.21491 | PREDICTED: DEAD-box ATP-dependent RNA helicase 8 [Vitis vinifera] | 51.714 | 22.726 | 19.5 | 8 | 11 | 3 | 0.984 | 0.985 | 0.97 | 1 | 1.014 | 1.031 | 1.036 | 2.50E-02 |

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| cds.Camellia_sinensis.comp33680_c2_seq30_m.23462 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 4 homolog [Vitis vinifera] | 44.876 | 70.859 | 27.2 | 8 | 15 | 8 | 1.022 | 1.022 | 0.992 | 1.007 | 0.947 | 1.035 | 0.985 | 5.95E-01 |
| cds.Camellia_sinensis.comp33685_c0_seq1_m.434 | PREDICTED: MAG2-interacting protein 2 isoform X1 [Vitis vinifera] | 274.48 | 1.1904 | 0.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33690_c0_seq1_m.25763 | PREDICTED: 40S ribosomal protein S4-like [Ziziphus jujuba] | 29.877 | 119.54 | 53 | 14 | 30 | 10 | 1.147 | 1.13 | 1.143 | 0.84 | 0.875 | 0.846 | 0.749 | 2.35E-05 |
| cds.Camellia_sinensis.comp33691_c0_seq1_m.1922 | PREDICTED: cullin-associated NEDD8-dissociated protein 1 [Vitis vinifera] | 134.6 | 7.3362 | 4.4 | 5 | 5 | 5 | 0.976 | 1.015 | 1.053 | 0.968 | 0.939 | 1.055 | 0.973 | 5.33E-01 |

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| cds.Camellia_sinensis.comp33691_c1_seq3_m.8486 | PREDICTED: leucine-rich repeat extensin-like protein 2 [Theobroma cacao] | 78.473 | 1.1971 | 1.9 | 1 | 1 | 1 | 0.837 | 1.024 | 0.881 | 1.156 | 1.063 | 1.088 | 1.206 | 4.37E-02 |
| cds.Camellia_sinensis.comp33693_c0_seq1_m.8033 | PREDICTED: sucrose synthase 7 isoform X3 [Vitis vinifera] | 69.517 | 7.497 | 8.3 | 5 | 8 | 4 | 0.844 | 0.917 | 0.887 | 1.189 | 1.072 | 1.099 | 1.269 | 3.82E-03 |
| cds.Camellia_sinensis.comp33693_c0_seq1_m.8034 | PREDICTED: sucrose synthase 7-like [Jatropha curcas] | 35.542 | 2.9563 | 10.9 | 4 | 4 | 3 | 0.965 | 0.9 | 0.976 | 1.003 | 1.088 | 1.083 | 1.117 | 3.88E-02 |
| cds.Camellia_sinensis.comp33694_c0_seq1_m.21873 | plant/F20D21-34 protein [Medicago truncatula] | 42.817 | 26.193 | 13.7 | 6 | 9 | 6 | 0.925 | 0.904 | 0.952 | 1.084 | 1.062 | 1.109 | 1.17 | 1.28E-03 |
| cds.Camellia_sinensis.comp33697_c0_seq2_m.4997 | PREDICTED: mannose-1-phosphate guanyltransferase alpha-like [Juglans regia] | 45.559 | 7.0289 | 8 | 3 | 4 | 2 | 0.884 | 0.854 | 0.966 | 1.068 | 1.074 | 1.072 | 1.189 | 4.17E-02 |

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| cds.Camellia_sinensis.comp33702_c0_seq2_m.7924 | PREDICTED: uncharacterized TPR repeat-containing protein At1g05150-like [Ipomoea nil] | 90.324 | 22.367 | 9.3 | 7 | 9 | 7 | 0.988 | 1.029 | 1.051 | 0.953 | 0.963 | 0.975 | 0.942 | 3.75E-02 |
| cds.Camellia_sinensis.comp33702_c0_seq3_m.51726 | PREDICTED: cyprosin-like [Nicotiana attenuata] | 12.418 | 1.8133 | 8 | 1 | 2 | 1 | 1.071 | 1.147 | 1.079 | 0.926 | 0.882 | 0.875 | 0.814 | 1.82E-03 |
| cds.Camellia_sinensis.comp33705_c2_seq1_m.6268 | PREDICTED: L-arabinokinase-like [Gossypium arboreum] | 110.46 | 68.209 | 11.8 | 11 | 11 | 11 | 0.921 | 0.961 | 0.914 | 1.093 | 1.077 | 1.015 | 1.139 | 9.10E-03 |
| cds.Camellia_sinensis.comp33707_c0_seq1_m.23833 | DNA-directed RNA polymerase subunit alpha [Arabidopsis thaliana] | 46.089 | 55.689 | 20.5 | 7 | 8 | 7 | 0.991 | 1.031 | 1.008 | 1.002 | 0.988 | 0.993 | 0.984 | 2.72E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33711_c1_seq11_m.40423 | PREDICTED: DNA-directed RNA polymerase V subunit 7 [Vitis | 20.286 | 3.8428 | 14 | 2 | 2 | 2 | 0.941 | 0.966 | 0.98 | 1.052 | 1.054 | 1.033 | 1.087 | 3.44E-03 |
| cds.Camellia_sinensis.comp33711_c1_seq2_m.23785 | PREDICTED: methionine aminopeptidase 2B isoform X2 [Vitis vinifera] | 32.046 | 1.9604 | 6.2 | 2 | 2 | 2 | 1.076 | 1.059 | 1.101 | 0.919 | 0.938 | 0.893 | 0.85 | 8.61E-04 |
| cds.Camellia_sinensis.comp33714_c0_seq4_m.5479 | PREDICTED: probable NOT transcription complex subunit VIP2 isoform X1 [Theobroma cacao] | 70.871 | 3.2544 | 3.3 | 2 | 2 | 2 | 0.947 | 0.966 | 0.963 | 1.059 | 1.02 | 1.069 | 1.095 | 4.44E-03 |
| cds.Camellia_sinensis.comp33717_c0_seq1_m.15910 | PREDICTED: 3-ketoacyl-CoA thiolase 2, peroxisomal isoform X1 [Erythranthe guttata] | 54.836 | 135.52 | 32.2 | 14 | 29 | 12 | 1.011 | 0.972 | 1.003 | 1.017 | 1.006 | 1.032 | 1.023 | 1.79E-01 |

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| cds.Camellia_sinensis.comp33718_c0_seq2_m.8004 | PREDICTED: protein transport protein SEC23 [Vitis vinifera] | 84.491 | 43.856 | 12.6 | 8 | 16 | 7 | 0.969 | 0.951 | 0.981 | 1.013 | 1.031 | 1.042 | 1.064 | 7.18E-03 |
| cds.Camellia_sinensis.comp33727_c0_seq39_m.19053 | aminopeptidase (DUF3754) [Arabidopsis thaliana] | 41.023 | 8.1704 | 7.3 | 3 | 3 | 3 | 1.03 | 1.007 | 1.078 | 0.993 | 0.972 | 0.922 | 0.927 | 6.30E-02 |
| cds.Camellia_sinensis.comp33729_c0_seq2_m.7772 | PREDICTED: uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic isoform X2[Gossypium raimondii] | 64.802 | 1.2861 | 1.7 | 1 | 1 | 1 | 1.045 | 1.042 | 0.965 | 1.074 | 0.945 | 0.936 | 0.968 | 5.49E-01 |
| cds.Camellia_sinensis.comp33730_c0_seq16_m.33689 | PREDICTED: acetyl-CoA acetyltransferase, cytosolic 1-like [Nicotiana attenuata] | 30.582 | 23.631 | 23.4 | 5 | 8 | 5 | 0.984 | 0.983 | 1.072 | 0.986 | 1.006 | 1.074 | 1.009 | 8.27E-01 |

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| cds.Camellia_sinensis.comp33730_c0_seq3_m.22338 | PREDICTED: uroporphyrinogen decarboxylase 1, chloroplastic [Vitis vinifera] | 46.487 | 8.6837 | 9.5 | 4 | 8 | 4 | 0.998 | 0.98 | 1.023 | 1.041 | 0.968 | 0.959 | 0.989 | 7.08E-01 |
| cds.Camellia_sinensis.comp33730_c0_seq7_m.25290 | PREDICTED: acetyl-CoA acetyltransferase, cytosolic 1-like isoform X2 [Nelumbo nucifera] | 23.859 | 24.556 | 30.5 | 5 | 9 | 5 | 0.987 | 0.934 | 0.978 | 0.993 | 1.056 | 1.032 | 1.063 | 6.99E-02 |
| cds.Camellia_sinensis.comp33730_c1_seq1_m.45250 | PREDICTED: acetyl-CoA acetyltransferase, cytosolic 1 isoform X1 [Pyrus x bretschneideri] | 18.638 | 52.128 | 32.4 | 5 | 7 | 1 | 0.99 | 1.047 | 1.031 | 0.962 | 1.007 | 0.968 | 0.957 | 1.19E-01 |

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| cds.Camellia_sinensis.comp33730_c1_seq2_m.46525 | PREDICTED: acetyl-CoA acetyltransferase, cytosolic 1 [Sesamum indicum] | 16.163 | 2.0639 | 15.3 | 3 | 3 | 2 | 0.968 | 1.068 | 0.982 | 1.041 | 0.968 | 0.986 | 0.992 | 8.58E-01 |
| cds.Camellia_sinensis.comp33730_c1_seq3_m.47110 | PREDICTED: acetyl-CoA acetyltransferase, cytosolic 1 isoform X1 [Pyrus x bretschneideri] | 18.589 | 6.5008 | 32.4 | 5 | 7 | 1 | 0.95 | 1.057 | 0.993 | 0.984 | 1.044 | 0.986 | 1.005 | 8.93E-01 |
| cds.Camellia_sinensis.comp33735_c0_seq6_m.39680 | PREDICTED: short-chain dehydrogenase TIC 32, chloroplastic isoform X2 [Vitis vinifera] | 29.874 | 2.9154 | 4.8 | 1 | 1 | 1 | 0.954 | 0.943 | 1.07 | 1.132 | 0.986 | 0.942 | 1.031 | 6.89E-01 |

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| cds.Camellia_sinensis.comp33736_c0_seq1_m.12198 | PREDICTED: ATP-citrate synthase beta chain protein 2-like [Gossypium hirsutum] | 65.798 | 162.57 | 41.3 | 21 | 39 | 21 | 1.071 | 1.085 | 1.08 | 0.948 | 0.937 | 0.919 | 0.867 | 1.24E-04 |
| cds.Camellia_sinensis.comp33739_c0_seq1_m.15479 | PREDICTED: protein PHOSPHATE STARVATION RESPONSE 1 isoform X2 [Nelumbo nucifera] | 54.187 | 3.5745 | 6.5 | 3 | 3 | 3 | 1.038 | 1.024 | 0.838 | 0.965 | 1.071 | 1.071 | 1.071 | 4.03E-01 |
| cds.Camellia_sinensis.comp33740_c0_seq1_m.40906 | PREDICTED: putative quinone-oxidoreductase homolog, chloroplastic [Prunus mume] | 25.49 | 12.034 | 21.7 | 5 | 10 | 5 | 0.922 | 0.895 | 0.9 | 1.147 | 1.088 | 1.11 | 1.231 | 3.17E-04 |

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| cds.Camellia_sinensis.comp33740_c0_seq4_m.44344 | PREDICTED: putative quinone-oxidoreductase homolog, chloroplastic [Vitis vinifera] | 26.873 | 48.773 | 37.5 | 8 | 16 | 8 | 0.76 | 0.787 | 0.842 | 1.169 | 1.224 | 1.244 | 1.522 | 2.83E-04 |
| cds.Camellia_sinensis.comp33751_c0_seq1_m.26198 | PREDICTED: protein AUXIN RESPONSE 4-like [Nicotiana tabacum] | 49.845 | 10.701 | 11.4 | 4 | 6 | 4 | 0.984 | 0.998 | 1.024 | 1.015 | 0.897 | 0.987 | 0.964 | 3.93E-01 |
| cds.Camellia_sinensis.comp33753_c0_seq3_m.13069 | PREDICTED: transmembrane 9 superfamily member 1 [Daucus carota subsp. sativus] | 73.379 | 28.64 | 8.7 | 5 | 8 | 5 | 1.023 | 1.014 | 1.108 | 0.931 | 0.961 | 0.935 | 0.899 | 2.40E-02 |
| cds.Camellia_sinensis.comp33754_c0_seq1_m.2989 | Calcium-transporting ATPase 2, plasma membrane-type [Morus notabilis] | 110.65 | 21.117 | 7.9 | 9 | 11 | 7 | 0.972 | 0.969 | 1.014 | 1.019 | 1.061 | 0.989 | 1.039 | 2.08E-01 |

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| cds.Camellia_sinensis.comp33758_c0_seq3_m.2481 | PREDICTED: protein lava lamp isoform X5 [Vitis vinifera] | 67.343 | 23.233 | 7.1 | 4 | 5 | 4 | 1.002 | 1.079 | 0.98 | 0.94 | 1.023 | 1.008 | 0.971 | 4.90E-01 |
| cds.Camellia_sinensis.comp33758_c0_seq6_m.11488 | PREDICTED: golgin subfamily B member 1 isoform X3 [Vitis vinifera] | 90.128 | 1.2589 | 1.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33758_c0_seq7_m.35167 | PREDICTED: protein lava lamp isoform X5 [Vitis vinifera] | 40.89 | 2.5239 | 3.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33759_c0_seq1_m.17652 | PREDICTED: glycerophosphodiester phosphodiesterase GDPD6 [Prunus mume] | 46.132 | 48.826 | 22.7 | 7 | 13 | 7 | 1.023 | 0.985 | 1.047 | 1.006 | 0.977 | 0.97 | 0.967 | 1.83E-01 |
| cds.Camellia_sinensis.comp33763_c1_seq1_m.2508 | PREDICTED: abscisic-aldehyde oxidase isoform X1 [Vitis vinifera] | 149.07 | 3.1233 | 2.3 | 3 | 3 | 3 | | | | | | | | |

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| cds.Camellia_sinensis.comp33765_c1_seq1_m.22427 | PREDICTED: metal tolerance protein 4-like [Daucus carota subsp. sativus] | 46.275 | 9.8506 | 9.2 | 3 | 3 | 3 | 1.007 | 0.957 | 0.989 | 1.022 | 0.991 | 1.047 | 1.036 | 1.78E-01 |
| cds.Camellia_sinensis.comp33768_c0_seq1_m.12313 | PREDICTED: probable methylenetetrahydrofolate reductase [Sesamum indicum] | 67.159 | 77.244 | 29.8 | 14 | 24 | 14 | 1.058 | 1.062 | 1.063 | 0.906 | 0.939 | 0.922 | 0.869 | 5.50E-03 |
| cds.Camellia_sinensis.comp33771_c0_seq10_m.21552 | PREDICTED: developmentally-regulated G-protein 2 [Jatropha curcas] | 44.539 | 8.8989 | 16.8 | 6 | 6 | 6 | 1.013 | 0.967 | 1.106 | 0.97 | 0.916 | 0.89 | 0.9 | 8.84E-02 |
| cds.Camellia_sinensis.comp33771_c0_seq4_m.2898 | PREDICTED: protein MLP1 [Prunus mume] | 89.027 | 37.497 | 13.4 | 10 | 13 | 10 | 1.077 | 1.111 | 1.101 | 0.902 | 0.865 | 0.905 | 0.812 | 2.75E-04 |

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| cds.Camellia_sinensis.comp33774_c0_seq1_m.647 | PREDICTED: DExH-box ATP-dependent RNA helicase DExH14 [Juglans regia] | 236.14 | 3.3879 | 0.8 | 2 | 2 | 2 | 1.028 | 1.059 | 1.045 | 0.916 | 0.942 | 1.003 | 0.913 | 3.18E-02 |
| cds.Camellia_sinensis.comp33775_c0_seq12_m.43731 | PREDICTED: phenazine biosynthesis-like domain-containing protein 1 [Sesamum indicum] | 28.619 | 9.3833 | 16.7 | 3 | 4 | 3 | 1.021 | 0.996 | 0.866 | 1.029 | 1.084 | 1.018 | 1.086 | 1.97E-01 |
| cds.Camellia_sinensis.comp33776_c0_seq1_m.19252 | PREDICTED: (-)-alpha-terpineol synthase [Vitis vinifera] | 70.02 | 47.141 | 12.2 | 7 | 10 | 7 | 1.351 | 1.265 | 1.304 | 0.639 | 0.691 | 0.651 | 0.505 | 2.15E-05 |
| cds.Camellia_sinensis.comp33777_c0_seq27_m.11553 | PREDICTED: NADP-dependent malic enzyme [Jatropha curcas] | 63.849 | 124.66 | 33.2 | 18 | 49 | 11 | 0.902 | 0.908 | 0.899 | 1.109 | 1.12 | 1.11 | 1.233 | 5.36E-07 |

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| cds.Camellia_sinensis.comp33777_c0_seq5_m.13395 | PREDICTED: NADP-dependent malic enzyme isoform X1 [Elaeis guineensis | 63.776 | -2 | 15.9 | 8 | 21 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp33779_c0_seq1_m.5726 | AMP deaminase [Morus notabilis] | 97.692 | 5.8963 | 2.9 | 2 | 2 | 2 | 1.123 | 1.099 | 0.996 | 0.916 | 0.915 | 0.929 | 0.858 | 5.50E-02 |
| cds.Camellia_sinensis.comp33780_c0_seq6_m.35358 | NF-kappa-B inhibitor-like protein [Arabidopsis thaliana] | 20.06 | 8.9984 | 11.8 | 2 | 3 | 2 | 0.957 | 1.037 | 0.984 | 1.002 | 0.966 | 1.066 | 1.019 | 6.47E-01 |
| cds.Camellia_sinensis.comp33784_c0_seq4_m.22630 | Bifunctional aspartokinase/homoserine dehydrogenase [Morus notabilis] | 53.058 | 1.4244 | 32.2 | 11 | 21 | 1 | 0.984 | 0.999 | 1.068 | 0.94 | 1.017 | 0.998 | 0.969 | 4.09E-01 |
| cds.Camellia_sinensis.comp33785_c0_seq2_m.24838 | PREDICTED: caffeine synthase 1 [Theobroma cacao] | 41.41 | 21.465 | 5.1 | 2 | 6 | 2 | 1.076 | 1.107 | 1.075 | 0.914 | 0.928 | 0.879 | 0.835 | 6.61E-04 |

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| cds.Camellia_sinensis.comp33788_c0_seq2_m.6647 | PREDICTED: linoleate 13S-lipoxygenase 2-1, chloroplastic-like [Ziziphus jujuba] | 103 | 252.63 | 42.9 | 41 | 115 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp33788_c0_seq3_m.6645 | PREDICTED: linoleate 13S-lipoxygenase 2-1, chloroplastic [Citrus sinensis] | 103.18 | 323.31 | 56.1 | 52 | 187 | 37 | 0.999 | 0.978 | 0.983 | 1.012 | 1.028 | 1.012 | 1.031 | 2.08E-02 |
| cds.Camellia_sinensis.comp33790_c0_seq27_m.37002 | PREDICTED: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase [Vitis | 30.61 | 1.3112 | 12.4 | 3 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33792_c0_seq12_m.25225 | PREDICTED: centromere protein O isoform X2 [Gossypium raimondii] | 15.471 | 1.2867 | 5.2 | 1 | 1 | 1 | 0.889 | 0.931 | 1.019 | 0.919 | 1.153 | 1.116 | 1.123 | 2.38E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33793_c0_seq9_m.50887 | PREDICTED: ATPase 11, plasma membrane-type-like, partial [Ziziphus jujuba] | 19.483 | -2 | 26.1 | 4 | 7 | 1 | 1.16 | 1.111 | 1.11 | 0.872 | 0.906 | 0.806 | 0.764 | 1.96E-03 |
| cds.Camellia_sinensis.comp33794_c0_seq1_m.11067 | PREDICTED: GDP-L-galactose phosphorylase 2-like [Juglans regia] | 50.598 | 1.471 | 2 | 1 | 1 | 1 | 1.016 | 0.987 | 1.034 | 0.955 | 1.017 | 0.996 | 0.977 | 3.70E-01 |
| cds.Camellia_sinensis.comp33805_c0_seq1_m.3088 | PREDICTED: peptidyl-prolyl cis-trans isomerase CYP26-2, chloroplastic [Daucus carota subsp. sativus] | 42.714 | 30.237 | 17.9 | 7 | 14 | 7 | 0.957 | 0.963 | 0.986 | 1.032 | 1.006 | 1.007 | 1.048 | 1.93E-02 |

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| cds.Camellia_sinensis.comp33810_c0_seq12_m.16459 | PREDICTED: peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase-like isoform X3 [Nicotiana tabacum] | 47.329 | 34.231 | 12 | 5 | 8 | 5 | 0.982 | 0.967 | 1.035 | 0.961 | 1.046 | 0.992 | 1.005 | 8.88E-01 |
| cds.Camellia_sinensis.comp33810_c0_seq16_m.21013 | PREDICTED: elongation factor Tu, mitochondrial [Ziziphus jujuba] | 49.151 | 4.0318 | 26 | 10 | 34 | 1 | | 0.969 | | | | | | |
| cds.Camellia_sinensis.comp33810_c0_seq17_m.21163 | PREDICTED: elongation factor Tu, mitochondrial [Ziziphus jujuba] | 49.41 | 183.58 | 58.3 | 23 | 59 | 13 | 1.002 | 0.997 | 0.971 | 1.008 | 0.98 | 1.036 | 1.018 | 3.95E-01 |
| cds.Camellia_sinensis.comp33816_c0_seq1_m.11403 | PREDICTED: probable methyltransferase PMT3 [Sesamum indicum] | 70.795 | 11.198 | 10.5 | 7 | 7 | 7 | 1.136 | 1.095 | 1.13 | 0.916 | 0.917 | 0.858 | 0.801 | 8.56E-04 |

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| cds.Camellia_sinensis.comp33821_c0_seq1_m.3784 | PREDICTED: calmodulin-binding transcription activator 4 isoform X4 [Vitis vinifera] | 102.32 | 1.9756 | 0.9 | 1 | 1 | 1 | 1.144 | 0.939 | 1.252 | 0.854 | 0.78 | 0.998 | 0.789 | 1.03E-01 |
| cds.Camellia_sinensis.comp33824_c0_seq2_m.36478 | PREDICTED: uncharacterized mitochondrial protein AtMg00820-like [Solanum pennellii] | 13.265 | 1.1996 | 7.8 | 1 | 1 | 1 | 0.38 | 1.355 | 1.338 | 1.39 | 0.9 | 0.736 | 0.985 | 8.44E-01 |
| cds.Camellia_sinensis.comp33827_c0_seq17_m.7425 | triacylglycerol lipase, putative [Medicago truncatula] | 97.312 | 35.235 | 11.9 | 10 | 18 | 10 | 0.997 | 0.99 | 0.975 | 1.011 | 0.989 | 0.993 | 1.01 | 3.32E-01 |
| cds.Camellia_sinensis.comp33830_c0_seq40_m.37216 | PREDICTED: soluble inorganic pyrophosphatase 2 isoform X1 [Ziziphus jujuba] | 24.22 | 36.447 | 27.8 | 6 | 14 | 4 | 1.052 | 1.013 | 0.966 | 0.931 | 1.033 | 0.987 | 0.974 | 5.25E-01 |

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| cds.Camellia_sinensis.comp33832_c0_seq3_m.4772 | PREDICTED: vacuolar protein sorting-associated protein 18 homolog [Citrus sinensis] | 40.004 | 4.7417 | 6.9 | 3 | 4 | 3 | 0.958 | 0.988 | 0.999 | 1.018 | 1.001 | 1.032 | 1.036 | 8.19E-02 |
| cds.Camellia_sinensis.comp33832_c0_seq7_m.15327 | PREDICTED: vacuolar protein sorting-associated protein 18 homolog [Vitis vinifera] | 24.52 | 1.9945 | 4 | 1 | 1 | 1 | 1.06 | 1.028 | 0.926 | 1.028 | 1.009 | 0.952 | 0.992 | 8.86E-01 |
| cds.Camellia_sinensis.comp33833_c0_seq1_m.1745 | PREDICTED: phytochrome B [Nicotiana attenuata] | 92.778 | 2.3612 | 2 | 1 | 1 | 1 | 0.828 | 1.039 | 1.07 | 1.005 | 1.032 | 1.057 | 1.053 | 5.18E-01 |
| cds.Camellia_sinensis.comp33835_c0_seq1_m.2917 | PREDICTED: calmodulin-binding transcription activator 3 isoform X2 [Vitis vinifera] | 101.35 | 3.8512 | 3.1 | 2 | 3 | 2 | 1.042 | 1.343 | 1.269 | 0.742 | 0.729 | 0.825 | 0.628 | 5.88E-03 |

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| cds.Camellia_sinensis.comp33837_c0_seq1_m.1657 | PREDICTED: ABC transporter C family member 3 [Juglans regia] | 162.49 | 2.4264 | 1.7 | 2 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33844_c0_seq1_m.7097 | PREDICTED: urease isoform X1 [Vitis vinifera] | 89.823 | 12.235 | 6.2 | 6 | 6 | 6 | 0.925 | 0.972 | 1.021 | 1.076 | 1.008 | 1.043 | 1.072 | 1.11E-01 |
| cds.Camellia_sinensis.comp33848_c0_seq22_m.32635 | PREDICTED: serine carboxypeptidase-like 34 [Nicotiana attenuata] | 43.487 | 9.0222 | 6.8 | 2 | 4 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33848_c0_seq32_m.51761 | PREDICTED: serine carboxypeptidase-like 34 [Gossypium hirsutum] | 11.371 | 6.7125 | 18 | 2 | 3 | 2 | 0.999 | 0.996 | 1.035 | 0.983 | 1.026 | 0.971 | 0.983 | 4.65E-01 |
| cds.Camellia_sinensis.comp33852_c0_seq1_m.4083 | PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g06840 [Sesamum | 10.719 | 5.4683 | 26.3 | 2 | 2 | 2 | 0.968 | 1.019 | 1.148 | 1.084 | 0.875 | 0.917 | 0.917 | 3.46E-01 |

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| cds.Camellia_sinensis.comp33856_c0_seq1_m.4923 | PREDICTED: U4/U6 small nuclear ribonucleoprotein PRP4-like protein [Capsicum | 65.943 | 2.96 | 3.2 | 2 | 3 | 2 | 0.968 | 1.05 | 1.07 | 0.994 | 0.93 | 0.987 | 0.943 | 1.92E-01 |
| cds.Camellia_sinensis.comp33856_c0_seq2_m.19953 | PREDICTED: L-idonate 5-dehydrogenase isoform X1 [Vitis vinifera] | 40.424 | 1.3814 | 4.8 | 2 | 2 | 1 | 0.891 | 0.879 | 0.896 | 1.144 | 1.103 | 1.134 | 1.268 | 4.18E-05 |
| cds.Camellia_sinensis.comp33862_c0_seq1_m.24624 | PREDICTED: aspartate carbamoyltransferase, chloroplastic [Vitis vinifera] | 20.835 | 2.2978 | 16.8 | 3 | 4 | 1 | 1.121 | 1.094 | 0.895 | 0.985 | 0.935 | 0.957 | 0.925 | 3.73E-01 |
| cds.Camellia_sinensis.comp33862_c0_seq2_m.25605 | PREDICTED: aspartate carbamoyltransferase, chloroplastic [Vitis vinifera] | 48.528 | 80.381 | 20.4 | 9 | 12 | 7 | 0.965 | 0.985 | 1.001 | 1.095 | 1.028 | 1.028 | 1.068 | 5.04E-02 |

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| cds.Camellia_sinensis.comp33864_c0_seq1_m.18334 | PREDICTED: phosphoacetylglucosamine mutase [Sesamum indicum] | 21.564 | 20.752 | 19.5 | 3 | 3 | 3 | 0.985 | 1.027 | 0.968 | 1.006 | 0.989 | 1.069 | 1.028 | 4.02E-01 |
| cds.Camellia_sinensis.comp33864_c0_seq4_m.31714 | phosphoacetylglucosamine mutase family protein [Populus trichocarpa] | 25.32 | 3.0009 | 6.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33865_c0_seq1_m.12153 | PREDICTED: alpha-L-arabinofuranosidase 1 [Theobroma cacao] | 73.682 | 145.76 | 26.5 | 14 | 29 | 14 | 1.068 | 1.001 | 1.028 | 0.965 | 0.956 | 0.949 | 0.927 | 1.75E-02 |
| cds.Camellia_sinensis.comp33869_c0_seq9_m.15654 | PREDICTED: dihydroorotate dehydrogenase (quinone), mitochondrial [Nicotiana tomentosiformis] | 48.933 | 21.725 | 16.2 | 5 | 8 | 5 | 0.973 | 1.001 | 0.991 | 1.041 | 1.021 | 0.987 | 1.028 | 1.91E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33870_c0_seq1_m.320 | PREDICTED: BEACH domain-containing protein C2 isoform X1 [Vitis vinifera] | 239.69 | 1.1736 | 0.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33870_c0_seq1_m.321 | PREDICTED: BEACH domain-containing protein C2 isoform X1 [Vitis vinifera] | 81.947 | 7.2691 | 4.9 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp33871_c0_seq3_m.5629 | PREDICTED: signal recognition particle subunit SRP72 [Solanum lycopersicum] | 73.239 | 3.9676 | 2.9 | 2 | 2 | 2 | 1.1 | 1.084 | 1.017 | 0.91 | 0.937 | 0.934 | 0.869 | 5.58E-03 |
| cds.Camellia_sinensis.comp33871_c0_seq50_m.42386 | PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 3 isoform X5 [Juglans regia] | 28.024 | 50.901 | 36.8 | 8 | 13 | 8 | 0.996 | 0.99 | 0.974 | 1.002 | 1.01 | 1.021 | 1.025 | 4.73E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33886_c0_seq1_m.19146 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 12 homolog A [Juglans regia] | 50.601 | 34.445 | 30.1 | 13 | 19 | 5 | 0.972 | 0.995 | 0.985 | 1.031 | 1.012 | 1.011 | 1.035 | 2.17E-02 |
| cds.Camellia_sinensis.comp33886_c0_seq4_m.36703 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 12 homolog A-like [Malus domestica] | 37.632 | 1.3554 | 27.4 | 9 | 15 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp33887_c0_seq1_m.271 | PREDICTED: auxin transport protein BIG [Vitis vinifera] | 333.18 | 32.131 | 4.4 | 13 | 13 | 13 | 1.116 | 1.114 | 1.142 | 0.861 | 0.89 | 0.953 | 0.802 | 2.02E-03 |
| cds.Camellia_sinensis.comp33887_c0_seq4_m.373 | PREDICTED: auxin transport protein BIG [Fragaria vesca subsp. vesca] | 19.515 | 3.717 | 5.7 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp33888_c0_seq1_m.2131 | PREDICTED: myosin-1 [Vitis vinifera] | 132.59 | 3.8075 | 1.6 | 2 | 2 | 2 | 0.999 | 1.095 | 1.014 | 1.057 | 0.888 | 0.952 | 0.932 | 2.82E-01 |
| cds.Camellia_sinensis.comp33889_c0_seq28_m.25885 | PREDICTED: structural maintenance of chromosomes domain-containing protein isoform X1 [Citrus sinensis] | 34.54 | 4.4585 | 13.8 | 5 | 6 | 2 | 0.958 | 1.016 | 1.01 | 0.986 | 1.063 | 0.982 | 1.016 | 6.56E-01 |
| cds.Camellia_sinensis.comp33889_c0_seq30_m.29004 | PREDICTED: structural maintenance of chromosomes domain-containing protein isoform X1 [Citrus sinensis] | 34.724 | 27.86 | 28.8 | 8 | 11 | 5 | 0.984 | 1.008 | 0.931 | 1.011 | 1.046 | 1.097 | 1.079 | 8.49E-02 |
| cds.Camellia_sinensis.comp33896_c0_seq1_m.3923 | PREDICTED: phospholipase D beta 2-like [Juglans regia] | 123.44 | 5.5244 | 1.1 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33898_c0_seq3_m.18677 | PREDICTED: chaperone protein ClpD, chloroplastic-like isoform X1 [Nicotiana tabacum] | 64.975 | 1.4974 | 2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33900_c0_seq8_m.36305 | PREDICTED: structural maintenance of chromosomes protein 2-1-like [Jatropha curcas] | 35.458 | 1.7112 | 2.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33901_c0_seq1_m.12359 | PREDICTED: ruBisCO large subunit-binding protein subunit beta, chloroplastic [Prunus mume] | 64.509 | 323.31 | 68.3 | 39 | 143 | 39 | 1.026 | 0.983 | 1 | 0.982 | 1.014 | 0.994 | 0.994 | 7.08E-01 |

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| cds.Camellia_sinensis.comp33906_c0_seq2_m.25830 | PREDICTED: cinnamoyl-CoA reductase 1-like [Juglans regia] | 35.449 | 48.443 | 29 | 8 | 16 | 8 | 0.964 | 0.981 | 0.994 | 1.039 | 1.006 | 1.017 | 1.042 | 3.43E-02 |
| cds.Camellia_sinensis.comp33906_c0_seq3_m.27977 | PREDICTED: cinnamoyl-CoA reductase 1-like [Populus euphratica] | 37.368 | 25.105 | 23.7 | 8 | 18 | 8 | 1.004 | 1.022 | 1.038 | 0.98 | 1.025 | 0.987 | 0.977 | 2.31E-01 |
| cds.Camellia_sinensis.comp33908_c0_seq1_m.29164 | PREDICTED: probable 2-oxoglutarate-dependent dioxygenase At3g49630 isoform X2 [Gossypium hirsutum] | 38.545 | 60.667 | 32.3 | 9 | 20 | 9 | 0.972 | 0.947 | 0.971 | 1.047 | 1.045 | 1.049 | 1.087 | 1.05E-02 |
| cds.Camellia_sinensis.comp33909_c1_seq24_m.41178 | PREDICTED: prefoldin subunit 6 [Eucalyptus grandis] | 14.698 | 86.539 | 46.9 | 8 | 14 | 8 | 0.984 | 0.961 | 0.941 | 1.024 | 1.058 | 1.033 | 1.079 | 9.16E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33910_c0_seq2_m.15403 | PREDICTED: polypyrimidine tract-binding protein homolog 3 isoform X1 [Vitis vinifera] | 49.338 | 13.329 | 4.7 | 2 | 5 | 2 | 0.959 | 1.005 | 0.952 | 1.074 | 1.059 | 1.015 | 1.08 | 3.33E-02 |
| cds.Camellia_sinensis.comp33911_c0_seq1_m.15177 | PREDICTED: eukaryotic peptide chain release factor subunit 1-3 [Vitis vinifera] | 49.119 | 23.01 | 12.6 | 5 | 7 | 5 | 1.045 | 1.09 | 1.115 | 0.96 | 0.874 | 0.9 | 0.841 | 6.72E-03 |
| cds.Camellia_sinensis.comp33912_c0_seq1_m.4257 | PREDICTED: ribonuclease TUDOR 1 [Vitis vinifera] | 108.05 | 173.05 | 39.1 | 34 | 55 | 32 | 1.073 | 1.059 | 1.055 | 0.941 | 0.944 | 0.929 | 0.883 | 6.09E-05 |
| cds.Camellia_sinensis.comp33912_c0_seq3_m.52756 | PREDICTED: ribonuclease TUDOR 1 [Vitis vinifera] | 17.419 | 40.241 | 26.9 | 3 | 7 | 1 | 1.058 | 0.937 | 1.126 | 0.873 | 0.989 | 1.007 | 0.919 | 3.01E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33913_c0_seq3_m.10650 | PREDICTED: chitin elicitor receptor kinase 1 isoform X2 [Ricinus communis] | 30.026 | 1.2562 | 7.8 | 2 | 2 | 2 | 0.965 | 0.983 | 1.021 | 0.94 | 1.014 | 1.087 | 1.024 | 6.45E-01 |
| cds.Camellia_sinensis.comp33915_c0_seq13_m.14647 | PREDICTED: SWI/SNF complex component SNF12 homolog [Prunus mume] | 60.533 | 3.1169 | 4.6 | 2 | 2 | 2 | 0.899 | 0.922 | 1.031 | 0.997 | 1.102 | 1.08 | 1.115 | 1.03E-01 |
| cds.Camellia_sinensis.comp33917_c0_seq5_m.17790 | CBL-interacting protein kinase 12 [Vitis vinifera] | 23.858 | 1.2942 | 5.2 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp33918_c4_seq1_m.22509 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 11 homolog [Juglans regia] | 49.861 | 85.341 | 31.5 | 15 | 25 | 15 | 0.96 | 0.972 | 0.98 | 1.053 | 1.033 | 1.019 | 1.066 | 4.68E-03 |
| cds.Camellia_sinensis.comp33922_c0_seq2_m.15111 | transmembrane protein [Arabidopsis thaliana] | 54.251 | 11.879 | 12.6 | 7 | 9 | 7 | 1.074 | 1.065 | 1.071 | 0.884 | 0.976 | 0.936 | 0.871 | 4.04E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33925_c0_seq16_m.56713 | PREDICTED: 2-oxoglutarate-Fe(II) type oxidoreductase [Nicotiana tomentosiformis] | 12.585 | 1.5248 | 8.1 | 1 | 1 | 1 | 0.864 | 1.012 | 0.958 | 1.086 | 1.085 | 1.033 | 1.131 | 6.46E-02 |
| cds.Camellia_sinensis.comp33925_c0_seq2_m.3411 | PREDICTED: eukaryotic translation initiation factor 3 subunit A [Vitis vinifera] | 55.415 | 41.034 | 19.5 | 10 | 16 | 10 | 1.054 | 1.054 | 1.027 | 0.935 | 0.944 | 0.961 | 0.906 | 1.12E-03 |
| cds.Camellia_sinensis.comp33925_c0_seq2_m.3412 | PREDICTED: eukaryotic translation initiation factor 3 subunit A [Vitis vinifera] | 47.53 | 16.462 | 19 | 8 | 13 | 8 | 1.03 | 1.053 | 1.055 | 0.975 | 0.917 | 0.944 | 0.904 | 6.28E-03 |
| cds.Camellia_sinensis.comp33930_c0_seq10_m.8955 | PREDICTED: methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial isoform X2 [Vitis | 70.867 | 56.37 | 20.7 | 10 | 17 | 10 | 0.978 | 1.04 | 0.97 | 1.013 | 0.983 | 0.958 | 0.989 | 7.02E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33932_c0_seq1_m.28186 | PREDICTED: cytosolic sulfotransferase 15-like [Pyrus x bretschneideri] | 43.31 | 43.773 | 17.6 | 6 | 16 | 5 | 0.958 | 0.999 | 0.998 | 1.017 | 0.978 | 1.037 | 1.026 | 3.10E-01 |
| cds.Camellia_sinensis.comp33933_c0_seq1_m.2733 | PREDICTED: protein transport protein SEC31 homolog B isoform X2 [Vitis vinifera] | 100.81 | 93.229 | 23.7 | 17 | 23 | 13 | 0.959 | 1.004 | 1.011 | 1.031 | 1.008 | 1.006 | 1.024 | 2.64E-01 |
| cds.Camellia_sinensis.comp33933_c0_seq3_m.14914 | PREDICTED: protein transport protein SEC31 homolog B isoform X2 [Vitis vinifera] | 66.449 | 31.616 | 17.9 | 11 | 13 | 7 | 0.957 | 0.96 | 0.978 | 1.025 | 1.043 | 1.048 | 1.076 | 1.54E-03 |

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| cds.Camellia_sinensis.comp33935_c0_seq3_m.47980 | PREDICTED: probable sodium/metabolite cotransporter BASS2, chloroplastic isoform X1 [Nelumbo nucifera] | 20.286 | 6.6018 | 6.9 | 1 | 1 | 1 | 1.089 | 1.057 | 1.128 | 0.848 | 0.923 | 0.932 | 0.826 | 5.58E-03 |
| cds.Camellia_sinensis.comp33941_c0_seq17_m.22888 | PREDICTED: putative transferase At4g12130, mitochondrial [Juglans regia] | 45.722 | 2.5172 | 2.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33941_c0_seq30_m.30670 | PREDICTED: carbon catabolite repressor protein 4 homolog 5 isoform X2 [Vitis vinifera] | 19.971 | -2 | 4.1 | 1 | 1 | 1 | 0.932 | 0.975 | 0.979 | 1.078 | 1.029 | 1.033 | 1.088 | 1.77E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33943_c0_seq1_m.12954 | PREDICTED: probable inactive purple acid phosphatase 1 isoform X1 [Citrus sinensis] | 68.668 | 203.44 | 36.1 | 16 | 26 | 10 | 0.942 | 0.918 | 0.935 | 1.105 | 1.1 | 1.049 | 1.164 | 1.16E-03 |
| cds.Camellia_sinensis.comp33943_c0_seq4_m.15739 | PREDICTED: probable inactive purple acid phosphatase 1 [Malus domestica] | 40.079 | 7.7103 | 23.3 | 7 | 9 | 3 | 1.027 | 1.011 | 0.935 | 1.088 | 0.915 | 1.034 | 1.022 | 7.57E-01 |
| cds.Camellia_sinensis.comp33944_c1_seq11_m.40983 | PREDICTED: acyl-CoA-binding domain-containing protein 4 [Juglans regia] | 21.779 | 13.464 | 20.1 | 4 | 6 | 3 | 1.042 | 1.054 | 1.094 | 0.932 | 0.944 | 0.965 | 0.891 | 2.92E-03 |
| cds.Camellia_sinensis.comp33944_c1_seq4_m.13093 | PREDICTED: probable calcium-binding protein CML43 [Theobroma cacao] | 28.13 | 7.8116 | 22.5 | 7 | 8 | 7 | 1.036 | 1.038 | 1.036 | 0.999 | 0.971 | 0.965 | 0.944 | 3.22E-02 |

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| cds.Camellia_sinensis.comp33944_c2_seq1_m.32174 | PREDICTED: clathrin light chain 1-like [Nicotiana attenuata] | 36.048 | 8.4553 | 5.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp33947_c1_seq37_c1_seq3_m.2586 | PREDICTED: UPF0603 protein At1g54780, chloroplastic [Cucumis melo] | 32.325 | 97.449 | 23.4 | 6 | 27 | 6 | 1.01 | 0.985 | 1.006 | 0.967 | 1.027 | 1.031 | 1.008 | 7.49E-01 |
| cds.Camellia_sinensis.comp33947_c1_seq9_m.13318 | PREDICTED: acetolactate synthase 1, chloroplastic [Sesamum indicum] | 73.223 | 41.869 | 17.1 | 9 | 13 | 9 | 0.944 | 0.999 | 1.014 | 1.027 | 1.01 | 1.009 | 1.03 | 2.53E-01 |
| cds.Camellia_sinensis.comp33955_c0_seq1_m.3353 | PREDICTED: villin-4 [Vitis vinifera] | 83.45 | 126.54 | 24.1 | 15 | 21 | 15 | 1.028 | 1.069 | 1.077 | 0.95 | 0.941 | 0.924 | 0.887 | 1.94E-03 |
| cds.Camellia_sinensis.comp33955_c0_seq1_m.3354 | PREDICTED: villin-4-like [Juglans regia] | 20.984 | 12.487 | 28.3 | 4 | 5 | 4 | 0.987 | 0.976 | 1.113 | 1 | 1.016 | 0.918 | 0.954 | 4.26E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33956_c0_seq1_m.27445 | PREDICTED: zeaxanthin epoxidase, chloroplastic isoform X1 [Nelumbo nucifera] | 24.213 | 49.34 | 23.1 | 5 | 14 | 5 | 0.984 | 1.026 | 1.001 | 0.987 | 0.997 | 0.997 | 0.99 | 4.77E-01 |
| cds.Camellia_sinensis.comp33959_c1_seq2_m.24595 | PREDICTED: eukaryotic translation initiation factor 5B-like isoform X2 [Capsicum annuum] | 29.222 | 1.3872 | 3.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33965_c0_seq1_m.33803 | PREDICTED: probable glutathione S-transferase parC [Arachis ipaensis] | 25.816 | 46.468 | 34.5 | 10 | 27 | 8 | 1.04 | 0.973 | 1.015 | 1.006 | 0.984 | 0.985 | 0.982 | 4.50E-01 |
| cds.Camellia_sinensis.comp33966_c0_seq2_m.7726 | PREDICTED: VHS domain-containing protein At3g16270 [Vitis vinifera] | 77.822 | 3.2652 | 2.8 | 2 | 2 | 2 | 1.022 | 1.052 | 1.042 | 0.912 | 0.95 | 1.016 | 0.924 | 6.93E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33972_c1_seq3_m.2695 | PREDICTED: probable isoleucine--tRNA ligase, cytoplasmic [Sesamum indicum] | 132.26 | 55.389 | 15.1 | 18 | 20 | 18 | 1.008 | 1.012 | 0.992 | 1.015 | 0.991 | 1.012 | 1.002 | 8.49E-01 |
| cds.Camellia_sinensis.comp33978_c1_seq3_m.5793 | PREDICTED: dynamin-related protein 3A-like [Nicotiana tabacum] | 72.769 | 31.305 | 17.9 | 12 | 16 | 10 | 0.994 | 1.011 | 0.987 | 1.022 | 1.006 | 1.01 | 1.015 | 1.49E-01 |
| cds.Camellia_sinensis.comp33978_c1_seq3_m.5794 | PREDICTED: dynamin-related protein 3A-like, partial [Nicotiana tabacum] | 18.096 | 1.9426 | 14.8 | 2 | 2 | 1 | 0.985 | 1.037 | 1.091 | 1.012 | 1.011 | 0.874 | 0.931 | 2.67E-01 |
| cds.Camellia_sinensis.comp33978_c1_seq5_m.27523 | PREDICTED: dynamin-related protein 3A [Sesamum indicum] | 36.661 | 8.9523 | 14.4 | 4 | 7 | 2 | 0.942 | 1.045 | 0.969 | 0.969 | 1.055 | 1.035 | 1.035 | 4.39E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33980_c1_seq1_m.8778 | PREDICTED: vacuolar protein sorting-associated protein 52 A [Jatropha curcas] | 80.486 | 3.0987 | 1.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33981_c0_seq2_m.6161 | PREDICTED: dentin sialophosphoprotein [Pyrus x bretschneideri] | 105.54 | 9.7128 | 3.8 | 3 | 3 | 3 | 1.008 | 1.038 | 1.069 | 0.985 | 0.947 | 1.005 | 0.943 | 7.29E-02 |
| cds.Camellia_sinensis.comp33982_c1_seq3_m.7198 | cyclopropane-fatty-acyl-phospholipid synthase family protein [Populus trichocarpa] | 66.255 | 1.6065 | 1.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp33983_c0_seq2_m.40866 | Glucan endo-1,3-beta-glucosidase, basic isoform [Morus notabilis] | 30.21 | 58.25 | 33.8 | 6 | 10 | 6 | 0.981 | 1.01 | 1.1 | 0.988 | 0.973 | 0.957 | 0.944 | 1.87E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33986_c1_seq3_m.35934 | PREDICTED: chlorophyll a-b binding protein of LHCII type 1 [Vitis | 30.915 | 102.14 | 41.2 | 7 | 61 | 3 | 0.928 | 0.906 | 1.014 | 1.074 | 1.042 | 1.019 | 1.101 | 6.09E-02 |
| cds.Camellia_sinensis.comp33988_c1_seq2_m.15117 | PREDICTED: signal recognition particle subunit SRP68 [Ipomoea nil] | 59.751 | 3.9188 | 3.4 | 2 | 2 | 2 | 0.916 | 1.171 | 1.112 | 1.004 | 0.873 | 0.929 | 0.877 | 2.09E-01 |
| cds.Camellia_sinensis.comp33988_c1_seq6_m.31549 | PREDICTED: nudix hydrolase 14, chloroplastic isoform X2 [Citrus sinensis] | 17.716 | 10.655 | 22.9 | 3 | 5 | 3 | 0.982 | 0.899 | 0.934 | 1.12 | 1.083 | 1.046 | 1.154 | 1.13E-02 |
| cds.Camellia_sinensis.comp33988_c1_seq6_m.31550 | PREDICTED: nudix hydrolase 14, chloroplastic isoform X2 [Daucus carota subsp. sativus] | 11.266 | 1.9009 | 8.7 | 1 | 2 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp33989_c0_seq4_m.26489 | PREDICTED: src substrate protein p85 [Sesamum indicum] | 38.921 | 19.452 | 22.4 | 7 | 8 | 7 | 0.979 | 0.981 | 0.977 | 0.987 | 0.956 | 1.065 | 1.024 | 5.50E-01 |
| cds.Camellia_sinensis.comp33994_c0_seq2_m.42269 | PREDICTED: protein FLUORESCENT IN BLUE LIGHT, chloroplastic isoform X2 [Juglans regia] | 23.548 | 16.725 | 28.9 | 6 | 10 | 6 | 0.996 | 1.053 | 1.153 | 0.918 | 0.939 | 0.945 | 0.875 | 3.90E-02 |
| cds.Camellia_sinensis.comp33995_c0_seq2_m.2476 | PREDICTED: trafficking protein particle complex subunit 8 [Vitis vinifera] | 125.51 | 3.7889 | 2 | 3 | 4 | 3 | 1.007 | 1.032 | 0.998 | 1.008 | 1.024 | 0.941 | 0.979 | 4.76E-01 |
| cds.Camellia_sinensis.comp33998_c0_seq1_m.9870 | PREDICTED: vesicle-fusing ATPase-like [Nicotiana tabacum] | 81.052 | 70.707 | 32.8 | 22 | 24 | 22 | 0.954 | 0.999 | 0.994 | 1.009 | 0.995 | 1.03 | 1.03 | 1.75E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp34003_c0_seq9_m.5917 | PREDICTED: probable transmembrane GTPase FZO-like, chloroplastic isoform X2 [Vitis vinifera] | 55.531 | 31.512 | 15.1 | 6 | 11 | 6 | 0.973 | 1.058 | 0.999 | 0.988 | 0.979 | 0.95 | 0.963 | 2.43E-01 |
| cds.Camellia_sinensis.comp34003_c0_seq9_m.5918 | PREDICTED: probable transmembrane GTPase FZO-like, chloroplastic isoform X1 [Vitis vinifera] | 36.545 | 13.777 | 19.8 | 6 | 6 | 6 | 1.017 | 1.022 | 1.039 | 0.957 | 0.945 | 0.986 | 0.938 | 1.08E-02 |
| cds.Camellia_sinensis.comp34005_c2_seq9_m.33257 | PREDICTED: UPF0047 protein C4A8.02c [Sesamum indicum] | 21.143 | 4.8625 | 9.3 | 2 | 3 | 2 | 0.995 | 1.001 | 1.033 | 1.012 | 0.99 | 0.98 | 0.984 | 3.57E-01 |
| cds.Camellia_sinensis.comp34008_c0_seq3_m.6454 | PREDICTED: protein SMG7 [Ipomoea nil] | 103.43 | -2 | 1.5 | 1 | 1 | 1 | 1.025 | 1.051 | 0.994 | 1.009 | 0.963 | 0.96 | 0.955 | 1.14E-01 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp34012_c0_seq12_m.9574 | PREDICTED: histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1 [Vitis vinifera] | 62.024 | 18.599 | 12 | 6 | 6 | 6 | 1.133 | 1.139 | 1.052 | 0.858 | 0.918 | 0.868 | 0.795 | 2.30E-03 |
| cds.Camellia_sinensis.comp34012_c0_seq9_m.30706 | PREDICTED: carboxymethylenebutenolidase homolog [Citrus sinensis] | 34.366 | 141.17 | 30.8 | 7 | 20 | 7 | 0.948 | 0.982 | 0.934 | 1.014 | 1.028 | 1.045 | 1.078 | 1.20E-02 |
| cds.Camellia_sinensis.comp34014_c0_seq3_m.37894 | PREDICTED: triacylglycerol lipase SDP1 [Vitis vinifera] | 37.195 | -2 | 3 | 1 | 2 | 1 | 1.032 | 0.985 | 1.076 | 0.977 | 0.961 | 0.97 | 0.94 | 7.84E-02 |
| cds.Camellia_sinensis.comp34017_c0_seq1_m.26436 | PREDICTED: DEAD-box ATP-dependent RNA helicase 50 isoform X2 [Nelumbo nucifera] | 51.415 | 3.1721 | 2.8 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp34018_c0_seq2_m.20619 | PREDICTED: protein KINESIN LIGHT CHAIN-RELATED 2 [Vitis vinifera] | 58.212 | 4.9927 | 7.3 | 3 | 3 | 3 | 0.932 | 0.909 | 0.868 | 1.065 | 1.116 | 1.145 | 1.228 | 2.32E-03 |
| cds.Camellia_sinensis.comp34025_c0_seq20_m.22499 | PREDICTED: protein disulfide isomerase-like 5-4 [Sesamum indicum] | 53.83 | 3.7179 | 2.1 | 1 | 2 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp34025_c0_seq9_m.18171 | PREDICTED: YTH domain-containing family protein 2-like isoform X5 [Gossypium raimondii] | 24.909 | 2.5779 | 4.1 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp34027_c0_seq1_m.4704 | PREDICTED: valine--tRNA ligase, mitochondrial isoform X1 [Sesamum | 62.244 | 22.744 | 14.3 | 8 | 12 | 7 | 1.016 | 1.021 | 1.018 | 0.975 | 0.985 | 0.978 | 0.962 | 3.03E-04 |

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| cds.Camellia_sinensis.comp34027_c0_seq1_m.4705 | PREDICTED: valine--tRNA ligase, chloroplastic/mitochondrial 2 isoform X2 [Vitis vinifera] | 47.632 | 11.537 | 16.3 | 7 | 7 | 7 | 1.01 | 0.993 | 1.035 | 1.045 | 0.977 | 0.969 | 0.985 | 5.82E-01 |
| cds.Camellia_sinensis.comp34029_c0_seq1_m.14296 | PREDICTED: protein GDAP2 homolog isoform X1 [Sesamum indicum] | 62.986 | 3.4381 | 2.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34030_c0_seq1_m.10720 | PREDICTED: dynamin-related protein 3A isoform X2 [Ricinus communis] | 90.887 | 25.712 | 2.8 | 2 | 3 | 1 | 0.931 | 0.984 | 1.065 | 1.098 | 0.989 | 0.958 | 1.022 | 7.25E-01 |
| cds.Camellia_sinensis.comp34031_c0_seq2_m.14854 | PREDICTED: carboxyl-terminal-processing peptidase 2, chloroplastic isoform X1 [Vitis vinifera] | 27.679 | 2.6932 | 10.5 | 3 | 3 | 2 | 0.961 | 1.026 | 1.063 | 1.021 | 0.961 | 0.979 | 0.971 | 4.48E-01 |

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| cds.Camellia_sinensis.comp34037_c0_seq1_m.20889 | PREDICTED: sorting nexin 1 [Nicotiana sylvestris] | 45.871 | 13.756 | 18.3 | 8 | 9 | 8 | 0.965 | 0.968 | 0.982 | 1.002 | 0.998 | 1.042 | 1.044 | 4.52E-02 |
| cds.Camellia_sinensis.comp34040_c0_seq1_m.20513 | PREDICTED: 3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic-like [Solanum pennellii] | 54.079 | 49.836 | 13.1 | 8 | 15 | 8 | 0.973 | 1.064 | 1.05 | 0.996 | 0.972 | 0.954 | 0.947 | 1.50E-01 |
| cds.Camellia_sinensis.comp34044_c2_seq11_m.28589 | PREDICTED: syntaxin-22-like [Ipomoea nil] | 29.996 | 4.0373 | 8.4 | 3 | 3 | 2 | 0.983 | 0.988 | 0.998 | 0.996 | 1.027 | 1.021 | 1.025 | 7.49E-02 |
| cds.Camellia_sinensis.comp34044_c2_seq21_m.42698 | PREDICTED: probable receptor-like protein kinase At5g47070 [Ricinus communis] | 30.79 | 1.4183 | 6.5 | 2 | 2 | 1 | 0.908 | 0.884 | 0.89 | 1.226 | 1.154 | 0.992 | 1.257 | 7.12E-02 |
| cds.Camellia_sinensis.comp34044_c2_seq74_c2_seq7_m.27172 | PREDICTED: syntaxin-22 [Vitis vinifera] | 30.388 | 2.2144 | 7.3 | 2 | 2 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34048_c0_seq1_m.4458 | PREDICTED: ATPase 11, plasma membrane-type [Theobroma cacao] | 105.09 | 85.251 | 33.6 | 29 | 61 | 10 | 0.973 | 0.972 | 0.945 | 1.027 | 1.044 | 1.059 | 1.083 | 3.62E-03 |
| cds.Camellia_sinensis.comp34051_c2_seq2_m.45356 | ureidoglycolate hydrolase, putative [Medicago truncatula] | 21.358 | 10.422 | 26.6 | 5 | 5 | 5 | 0.867 | 0.908 | 0.955 | 1.231 | 1.029 | 1.064 | 1.218 | 3.44E-02 |
| cds.Camellia_sinensis.comp34052_c0_seq1_m.14055 | PREDICTED: ERAD-associated E3 ubiquitin-protein ligase HRD1B [Theobroma cacao] | 62.437 | 13.215 | 3.1 | 1 | 1 | 1 | 0.914 | 0.927 | 1.12 | 1.075 | 0.938 | 1.051 | 1.035 | 6.61E-01 |
| cds.Camellia_sinensis.comp34053_c0_seq1_m.3953 | PREDICTED: alpha-mannosidase isoform X2 [Populus euphratica] | 22.514 | 15.463 | 24.8 | 4 | 4 | 4 | 0.994 | 1.08 | 1.082 | 1.014 | 0.88 | 0.981 | 0.911 | 1.39E-01 |

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| cds.Camellia_sinensis.comp34054_c0_seq1_m.7832 | PREDICTED: cell division cycle protein 48 homolog [Gossypium hirsutum] | 89.762 | 8.7774 | 40.7 | 28 | 67 | 1 | 0.996 | 1.166 | 0.961 | 0.988 | 0.98 | 0.91 | 0.922 | 2.92E-01 |
| cds.Camellia_sinensis.comp34055_c0_seq1_m.3127 | plant/MOJ9-14 protein [Medicago truncatula] | 88.701 | 2.7142 | 1.2 | 1 | 1 | 1 | 1.091 | 1.096 | 0.959 | 0.913 | 0.906 | 1.016 | 0.901 | 1.45E-01 |
| cds.Camellia_sinensis.comp34056_c1_seq2_m.9658 | PREDICTED: cullin-3A-like [Nicotiana tabacum] | 85.255 | 4.0169 | 3.3 | 2 | 2 | 2 | 0.993 | 0.995 | 0.999 | 1.088 | 0.965 | 0.977 | 1.014 | 7.69E-01 |
| cds.Camellia_sinensis.comp34065_c3_seq1_m.1918 | Elongation factor Ts [Morus notabilis] | 135.44 | 261.06 | 34.4 | 40 | 91 | 40 | 1.095 | 1.081 | 1.08 | 0.902 | 0.9 | 0.907 | 0.832 | 1.65E-06 |
| cds.Camellia_sinensis.comp34068_c2_seq1_m.15283 | PREDICTED: eukaryotic translation initiation factor 2A isoform X1 [Nelumbo nucifera] | 56.865 | 21.105 | 12.6 | 6 | 7 | 6 | 0.987 | 1.036 | 1.009 | 0.982 | 1.011 | 0.986 | 0.983 | 3.53E-01 |

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| cds.Camellia_sinensis.comp34072_c0_seq2_m.25478 | PREDICTED: probable L-type lectin-domain containing receptor kinase II.1 [Juglans regia] | 57.269 | 5.7128 | 2.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp340748_c0_seq1_m.58494 | PREDICTED: stachyose synthase [Jatropha curcas] | 11.651 | 33.483 | 19.6 | 1 | 2 | 1 | 1.086 | 1.04 | 0.928 | 1.038 | 0.985 | 0.923 | 0.965 | 5.78E-01 |
| cds.Camellia_sinensis.comp34075_c0_seq3_m.11466 | PREDICTED: AP-2 complex subunit alpha-1-like isoform X2 [Nicotiana tomentosiformis] | 69.07 | 16.721 | 10.1 | 6 | 6 | 6 | 0.929 | 1.004 | 1.003 | 0.981 | 1.086 | 1.019 | 1.051 | 2.75E-01 |
| cds.Camellia_sinensis.comp34075_c0_seq3_m.11467 | PREDICTED: AP-2 complex subunit alpha-1 [Vitis vinifera] | 12.898 | 1.4788 | 9.2 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34075_c0_seq7_m.34932 | PREDICTED: AP-2 complex subunit alpha-1 [Vitis vinifera] | 31.815 | 4.9637 | 7.9 | 2 | 2 | 2 | 1.045 | 0.952 | 0.983 | 1.033 | 1.033 | 0.965 | 1.017 | 6.54E-01 |
| cds.Camellia_sinensis.comp34083_c0_seq2_m.8412 | PREDICTED: tyrosine--tRNA ligase, cytoplasmic-like [Jatropha curcas] | 43.794 | 8.7453 | 8.6 | 2 | 2 | 2 | 0.949 | 0.92 | 1.089 | 0.977 | 1.11 | 0.976 | 1.035 | 6.23E-01 |
| cds.Camellia_sinensis.comp34083_c0_seq2_m.8413 | | 35.482 | 1.7408 | 3.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34084_c0_seq10_m.46247 | PREDICTED: histidinol dehydrogenase, chloroplastic isoform X7 [Vitis vinifera] | 24.454 | 25.154 | 17.7 | 3 | 4 | 3 | 0.938 | 0.978 | 0.957 | 1.051 | 1.083 | 1.02 | 1.098 | 1.15E-02 |
| cds.Camellia_sinensis.comp34085_c1_seq1_m.20728 | glycine-rich family protein [Populus trichocarpa] | 49.596 | 35.995 | 14.8 | 6 | 8 | 6 | 1.114 | 1.101 | 1.093 | 0.889 | 0.905 | 0.881 | 0.809 | 2.26E-05 |

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| cds.Camellia_sinensis.comp34086_c0_seq36_m.34160 | PREDICTED: chaperonin CPN60-like 2, mitochondrial isoform X2 [Vitis | 30.119 | 2.5101 | 3.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34086_c1_seq1_m.19789 | PREDICTED: probable ADP-ribosylation factor GTPase-activating protein AGD6 [Nelumbo nucifera] | 50.492 | 2.1232 | 4 | 2 | 2 | 2 | 1.107 | 1.06 | 1.121 | 0.888 | 0.832 | 0.965 | 0.817 | 1.15E-02 |
| cds.Camellia_sinensis.comp34089_c0_seq1_m.14562 | PREDICTED: nicalin-1 [Vitis vinifera] | 62.37 | 22.888 | 10.5 | 5 | 5 | 5 | 0.992 | 1.004 | 1.027 | 1.028 | 0.981 | 0.991 | 0.992 | 6.81E-01 |
| cds.Camellia_sinensis.comp34092_c0_seq1_m.28868 | PREDICTED: 3-hydroxyisobutyryl-CoA hydrolase-like protein 1, mitochondrial [Prunus | 46.256 | 3.8994 | 3.6 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34094_c1_seq22_m.42788 | PREDICTED: proline-, glutamic acid- and leucine-rich protein 1 [Theobroma cacao] | 18.942 | 2.4182 | 5.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34095_c2_seq5_m.9186 | PREDICTED: probable serine/threonine-protein kinase DDB_G0276461 [Solanum tuberosum | 50.746 | 6.7516 | 6 | 2 | 2 | 2 | 1.031 | 1.142 | 1.047 | 0.963 | 0.901 | 0.906 | 0.86 | 1.73E-02 |
| cds.Camellia_sinensis.comp34096_c0_seq1_m.9195 | PREDICTED: CAAX prenyl protease 1 homolog [Ipomoea nil] | 48.48 | 12.5 | 12.7 | 5 | 8 | 5 | 0.927 | 0.936 | 0.982 | 0.996 | 1.138 | 1.049 | 1.119 | 5.99E-02 |
| cds.Camellia_sinensis.comp34099_c1_seq1_m.12104 | PREDICTED: cytosolic endo-beta-N-acetylglucosaminidase 1 isoform X3 [Vitis vinifera] | 81.311 | 64.775 | 15.7 | 9 | 14 | 9 | 0.937 | 0.986 | 0.986 | 1.041 | 1.027 | 1.045 | 1.07 | 1.87E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp34100_c0_seq1_m.24455 | putative pyruvate, phosphate dikinase regulatory protein [Morus notabilis] | 44.46 | 15.26 | 16.8 | 6 | 6 | 6 | 0.871 | 0.959 | 0.882 | 1.062 | 1.027 | 1.199 | 1.212 | 2.67E-02 |
| cds.Camellia_sinensis.comp34105_c0_seq4_m.5315 | PREDICTED: large proline-rich protein BAG6-like isoform X1 [Juglans regia] | 97.531 | 28.617 | 14.2 | 10 | 13 | 10 | 0.986 | 1.021 | 1.022 | 1.013 | 0.982 | 0.995 | 0.987 | 4.34E-01 |
| cds.Camellia_sinensis.comp34105_c0_seq5_m.6640 | PREDICTED: large proline-rich protein bag6-A isoform X3 [Vitis vinifera] | 94.314 | 7.3546 | 2.4 | 2 | 3 | 2 | 1.143 | 0.924 | 1.138 | 0.902 | 0.826 | 1.043 | 0.865 | 2.11E-01 |
| cds.Camellia_sinensis.comp34108_c0_seq3_m.10334 | PREDICTED: pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 [Vitis vinifera] | 65.568 | 1.3772 | 2.3 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34111_c0_seq1_m.15589 | PREDICTED: carotene epsilon-monooxygenase, chloroplastic isoform X1 [Vitis vinifera] | 62.123 | 71.213 | 16.2 | 8 | 12 | 8 | 1.056 | 1.026 | 1.007 | 0.951 | 0.976 | 0.979 | 0.941 | 2.14E-02 |
| cds.Camellia_sinensis.comp34112_c0_seq12_m.1183 | PREDICTED: UDP-glucose:glycoprotein glucosyltransferase isoform X2 [Vitis vinifera] | 126.55 | 47.391 | 9.3 | 9 | 10 | 9 | 1.088 | 1.063 | 1.082 | 0.951 | 0.916 | 0.902 | 0.856 | 8.39E-04 |
| cds.Camellia_sinensis.comp34112_c0_seq12_m.1184 | PREDICTED: UDP-glucose:glycoprotein glucosyltransferase isoform X1 [Solanum tuberosum | 61.979 | 20.19 | 10.9 | 6 | 6 | 6 | 1.086 | 1.095 | 1.135 | 0.946 | 0.858 | 0.9 | 0.815 | 2.82E-03 |
| cds.Camellia_sinensis.comp34114_c0_seq13_m.35078 | PREDICTED: polyol transporter 5 [Theobroma cacao] | 37.876 | 4.2453 | 9 | 3 | 4 | 3 | 0.973 | 1.039 | 1.075 | 0.927 | 1.012 | 0.978 | 0.945 | 2.20E-01 |

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| cds.Camellia_sinensis.comp34116_c0_seq2_m.4556 | PREDICTED: coatomer subunit beta'-2 isoform X1 [Ricinus communis] | 104.45 | 20.525 | 8.1 | 6 | 6 | 6 | 1.066 | 1.107 | 1.038 | 0.965 | 0.874 | 0.99 | 0.881 | 3.93E-02 |
| cds.Camellia_sinensis.comp34117_c0_seq17_m.2876 | PREDICTED: extensin isoform X1 [Vitis vinifera] | 21.63 | 2.8677 | 7.1 | 1 | 1 | 1 | 1.11 | 1.095 | 1.006 | 0.89 | 0.901 | 0.975 | 0.861 | 2.38E-02 |
| cds.Camellia_sinensis.comp34120_c0_seq1_m.4606 | PREDICTED: glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic [Nicotiana sylvestris] | 56.727 | 230.67 | 53.6 | 21 | 67 | 21 | 1.083 | 1.044 | 1.046 | 0.926 | 0.938 | 0.944 | 0.885 | 7.59E-04 |
| cds.Camellia_sinensis.comp34120_c1_seq10_m.21354 | PREDICTED: serine carboxypeptidase-like 17 [Juglans regia] | 59.467 | 70.042 | 18.7 | 9 | 17 | 7 | 1.066 | 0.997 | 1.088 | 0.957 | 0.923 | 0.972 | 0.905 | 3.13E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp34121_c0_seq1_m.11319 | cystathionine gamma synthase [Solanum lycopersicum] | 61.571 | 42.812 | 13.6 | 7 | 9 | 4 | 0.962 | 0.854 | 0.97 | 1.105 | 1.071 | 1.095 | 1.174 | 1.84E-02 |
| cds.Camellia_sinensis.comp34121_c0_seq2_m.17596 | cystathionine gamma synthase [Solanum lycopersicum] | 61.6 | 33.408 | 12 | 7 | 8 | 4 | 0.948 | 0.963 | 0.908 | 1.045 | 1.089 | 1.059 | 1.133 | 4.30E-03 |
| cds.Camellia_sinensis.comp34123_c0_seq1_m.23759 | PREDICTED: bifunctional nitrilase/nitrile hydratase NIT4A [Citrus sinensis] | 41.769 | 40.315 | 18.1 | 6 | 7 | 6 | 1.017 | 1.02 | 0.951 | 1.033 | 0.953 | 0.987 | 0.995 | 8.84E-01 |
| cds.Camellia_sinensis.comp34123_c1_seq1_m.6016 | PREDICTED: heat shock protein 83 [Populus euphratica] | 81.075 | 57.041 | 22 | 17 | 33 | 9 | 1.011 | 1.064 | 1.039 | 0.998 | 0.926 | 0.956 | 0.925 | 4.05E-02 |
| cds.Camellia_sinensis.comp34123_c1_seq4_m.18635 | PREDICTED: eukaryotic initiation factor 4A-14 [Sesamum indicum] | 22.008 | 49.11 | 33.5 | 7 | 25 | 2 | 0.94 | 0.873 | 0.9 | 1.063 | 1.098 | 1.119 | 1.209 | 1.92E-03 |

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| cds.Camellia_sinensis.comp34123_c1_seq6_m.19320 | PREDICTED: eukaryotic initiation factor 4A-6-like [Nicotiana tabacum] | 25.518 | 8.2718 | 41 | 10 | 26 | 3 | 0.928 | 0.985 | 0.958 | 1.082 | 0.959 | 1.079 | 1.087 | 1.32E-01 |
| cds.Camellia_sinensis.comp34128_c0_seq3_m.18780 | PREDICTED: prolycopene isomerase, chloroplastic isoform X1 [Juglans regia] | 33.855 | 16.813 | 13.2 | 3 | 5 | 3 | 1.011 | 1.031 | 1.112 | 1.009 | 0.92 | 0.918 | 0.903 | 7.37E-02 |
| cds.Camellia_sinensis.comp34128_c0_seq3_m.18781 | PREDICTED: prolycopene isomerase, chloroplastic isoform X1 [Jatropha curcas] | 32.556 | 8.6008 | 9.1 | 3 | 3 | 3 | 0.979 | 1.059 | 1.157 | 0.918 | 1.041 | 0.848 | 0.879 | 1.64E-01 |
| cds.Camellia_sinensis.comp34132_c1_seq12_m.26547 | PREDICTED: ruvB-like protein 1 [Glycine max] | 50.618 | 55.934 | 29.3 | 11 | 15 | 11 | 0.978 | 1.023 | 0.971 | 1.01 | 0.995 | 1.028 | 1.021 | 3.38E-01 |

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| cds.Camellia_sinensis.comp34132_c2_seq2_m.479 | PREDICTED: acetyl-CoA carboxylase 1 [Theobroma cacao] | 252.94 | 89.799 | 14.8 | 30 | 35 | 30 | 1.296 | 1.316 | 1.3 | 0.677 | 0.649 | 0.673 | 0.511 | 5.66E-07 |
| cds.Camellia_sinensis.comp34135_c0_seq1_m.8698 | PREDICTED: isoamylase 1, chloroplastic [Vitis vinifera] | 73.898 | 8.0902 | 3.8 | 2 | 2 | 2 | 1.041 | 1.056 | 1.09 | 0.912 | 0.987 | 0.904 | 0.88 | 1.42E-02 |
| cds.Camellia_sinensis.comp34135_c0_seq2_m.9029 | PREDICTED: inter alpha-trypsin inhibitor, heavy chain 4 [Vitis vinifera] | 83.599 | 3.5325 | 2.2 | 1 | 1 | 1 | 0.918 | 0.791 | 0.81 | 1.242 | 1.18 | 1.121 | 1.407 | 3.36E-03 |
| cds.Camellia_sinensis.comp34137_c0_seq1_m.31036 | PREDICTED: enoyl-CoA hydratase 2, peroxisomal-like [Nicotiana tabacum] | 34.204 | 13.839 | 19.1 | 5 | 8 | 5 | 0.974 | 0.961 | 0.981 | 1.021 | 1.028 | 1.029 | 1.056 | 1.16E-03 |

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| cds.Camellia_sinensis.comp34138_c0_seq1_m.417 | PREDICTED: eIF-2-alpha kinase activator GCN1 isoform X2 [Vitis vinifera] | 178.54 | 10.868 | 4.1 | 6 | 6 | 6 | 1.023 | 1.151 | 1.013 | 1.04 | 0.906 | 0.866 | 0.882 | 1.39E-01 |
| cds.Camellia_sinensis.comp34138_c0_seq1_m.418 | PREDICTED: eIF-2-alpha kinase activator GCN1 isoform X1 [Vitis vinifera] | 105.96 | 9.1554 | 5.7 | 5 | 5 | 5 | 1.028 | 1.1 | 1.058 | 0.992 | 0.91 | 0.907 | 0.882 | 2.31E-02 |
| cds.Camellia_sinensis.comp34146_c1_seq2_m.12594 | PREDICTED: cysteine-rich receptor-like protein kinase 10 isoform X1 [Vitis vinifera] | 74.868 | 33.5 | 15.3 | 9 | 11 | 9 | 0.968 | 0.958 | 0.984 | 1.102 | 0.971 | 1.067 | 1.079 | 1.26E-01 |
| cds.Camellia_sinensis.comp34154_c0_seq1_m.1213 | PREDICTED: nuclear pore complex protein NUP155 isoform X1 [Vitis vinifera] | 162.98 | 97.943 | 13.8 | 17 | 18 | 17 | 0.938 | 1.009 | 1 | 1.028 | 1.002 | 1.006 | 1.03 | 2.82E-01 |

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| cds.Camellia_sinensis.comp34158_c0_seq1_m.6372 | colon cancer-associated Mic1-like protein [Medicago truncatula] | 83.17 | 63.592 | 17.7 | 12 | 17 | 12 | 0.93 | 0.947 | 0.939 | 1.051 | 1.026 | 1.095 | 1.126 | 3.82E-03 |
| cds.Camellia_sinensis.comp34159_c0_seq1_m.20017 | PREDICTED: probable protein phosphatase 2C BIPP2C1 isoform X1 [Vitis vinifera] | 51.124 | 15.429 | 7.7 | 3 | 4 | 3 | 0.95 | 0.983 | 0.99 | 0.978 | 1.11 | 1.009 | 1.06 | 2.32E-01 |
| cds.Camellia_sinensis.comp34162_c0_seq2_m.20178 | PREDICTED: glycerol-3-phosphate acyltransferase, chloroplastic [Vitis vinifera] | 50.505 | 2.8519 | 5 | 3 | 3 | 3 | 0.973 | 0.98 | 0.998 | 1.035 | 0.989 | 1.04 | 1.038 | 1.02E-01 |
| cds.Camellia_sinensis.comp34164_c0_seq1_m.29465 | PREDICTED: probable aldo-keto reductase 2 [Arachis ipaensis] | 37.729 | 161.63 | 47.8 | 18 | 48 | 17 | 0.955 | 0.948 | 0.968 | 1.05 | 1.076 | 1.044 | 1.104 | 8.76E-04 |

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| cds.Camellia_sinensis.comp34165_c0_seq4_m.51327 | PREDICTED: solanesyl diphosphate synthase 3, chloroplastic/mitochondrial-like, partial [Ziziphus jujuba] | 13.092 | 2.3417 | 6.7 | 1 | 1 | 1 | 0.925 | 0.887 | 1.083 | 1.085 | 0.986 | 1.062 | 1.082 | 2.91E-01 |
| cds.Camellia_sinensis.comp34165_c1_seq1_m.2418 | PREDICTED: malate dehydrogenase [NADP], chloroplastic-like [Juglans regia] | 39.089 | 115.22 | 36.9 | 13 | 41 | 13 | 1.011 | 0.978 | 1.014 | 0.977 | 1.006 | 0.991 | 0.99 | 5.38E-01 |
| cds.Camellia_sinensis.comp34166_c1_seq1_m.6035 | PREDICTED: 1,4-alpha-glucan-branching enzyme 2-2, chloroplastic/amyloplastic [Jatropha curcas] | 77.526 | 27.744 | 11.6 | 9 | 13 | 9 | 1.026 | 1.061 | 1.058 | 0.945 | 0.952 | 0.948 | 0.905 | 7.97E-04 |

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| cds.Camellia_sinensis.comp34166_c1_seq5_m.48364 | PREDICTED: 1,4-alpha-glucan-branching enzyme 2-2, chloroplastic/amyloplastic isoform X2 [Ipomoea nil] | 21.48 | 5.4569 | 18.2 | 3 | 5 | 3 | 0.941 | 1.049 | 1.071 | 0.893 | 1.004 | 1.047 | 0.962 | 5.59E-01 |
| cds.Camellia_sinensis.comp34167_c0_seq10_m.30539 | PREDICTED: probable inactive shikimate kinase like 2, chloroplastic isoform X1 [Gossypium raimondii] | 38.936 | 18.861 | 13.6 | 3 | 3 | 3 | 0.993 | 1.002 | 0.951 | 0.986 | 0.98 | 1.098 | 1.04 | 3.97E-01 |
| cds.Camellia_sinensis.comp34171_c0_seq3_m.31358 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 10, mitochondrial [Theobroma cacao] | 19.986 | 1.8133 | 5 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34177_c0_seq1_m.15509 | PREDICTED: chaperonin CPN60-2, mitochondrial-like [Nelumbo nucifera] | 63.01 | 299.88 | 56 | 32 | 89 | 23 | 1 | 0.973 | 0.986 | 1.033 | 1.007 | 1.022 | 1.035 | 3.41E-02 |
| cds.Camellia_sinensis.comp34179_c0_seq13_m.38394 | PREDICTED: transmembrane protein 120 homolog [Solanum lycopersicum] | 29.474 | 1.7629 | 7.4 | 2 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34181_c0_seq1_m.5894 | PREDICTED: beta-galactosidase 8 [Vitis vinifera] | 91.583 | 88.547 | 14.2 | 11 | 20 | 8 | 1.05 | 1.063 | 1.074 | 0.934 | 0.929 | 0.925 | 0.875 | 4.35E-05 |
| cds.Camellia_sinensis.comp34189_c0_seq1_m.9539 | PREDICTED: protein NUCLEAR FUSION DEFECTIVE 5, mitochondrial [Vitis vinifera] | 87.668 | 6.402 | 5.8 | 5 | 5 | 5 | 1.012 | 1 | 0.999 | 0.915 | 1.017 | 1.057 | 0.993 | 8.52E-01 |

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| cds.Camellia_sinensis.comp34190_c0_seq1_m.8571 | PREDICTED: nuclear pore complex protein NUP93A [Vitis vinifera] | 78.532 | 12.872 | 10.1 | 7 | 8 | 7 | 0.997 | 1.008 | 0.948 | 1.041 | 0.959 | 1.06 | 1.036 | 3.88E-01 |
| cds.Camellia_sinensis.comp34190_c0_seq6_m.52408 | PREDICTED: nuclear pore complex protein NUP93A-like [Camelina sativa] | 18.523 | 12.529 | 13.4 | 2 | 3 | 2 | 0.963 | 0.988 | 0.998 | 1.046 | 0.996 | 1.058 | 1.051 | 8.05E-02 |
| cds.Camellia_sinensis.comp34192_c0_seq1_m.6581 | PREDICTED: protein pleiotropic regulatory locus 1 [Vitis vinifera] | 50.665 | 3.2312 | 2.9 | 1 | 1 | 1 | 0.886 | 1.052 | 0.957 | 1.077 | 0.984 | 1.072 | 1.082 | 2.35E-01 |
| cds.Camellia_sinensis.comp34195_c1_seq1_m.37697 | PREDICTED: nucleosome assembly protein 1;4 isoform X3 [Nelumbo nucifera] | 34.725 | 6.474 | 3.6 | 1 | 1 | 1 | 0.872 | 1.109 | 0.915 | 0.93 | 1.145 | 1.052 | 1.08 | 4.55E-01 |

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| cds.Camellia_sinensis.comp34197_c0_seq1_m.11738 | PREDICTED: serine hydroxymethyltransferase 3, chloroplastic-like [Juglans regia] | 56.738 | 171.64 | 40 | 20 | 43 | 20 | 1.007 | 1.004 | 0.999 | 0.983 | 0.983 | 1.012 | 0.989 | 3.40E-01 |
| cds.Camellia_sinensis.comp34199_c1_seq1_m.13823 | PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform [Jatropha curcas] | 65.686 | 30.549 | 16.2 | 9 | 14 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34199_c1_seq2_m.14936 | PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform [Cucumis melo] | 65.673 | 7.1609 | 13.5 | 8 | 13 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34203_c0_seq1_m.10841 | PREDICTED: protein SIEVE ELEMENT OCCLUSION B-like [Juglans regia] | 86.102 | 169.64 | 29.8 | 23 | 107 | 22 | 0.94 | 0.94 | 0.93 | 1.069 | 1.084 | 1.083 | 1.152 | 1.81E-05 |
| cds.Camellia_sinensis.comp34203_c0_seq2_m.52934 | PREDICTED: protein SIEVE ELEMENT OCCLUSION B [Vitis vinifera] | 18.907 | 3.1796 | 13.2 | 2 | 5 | 1 | 0.879 | 0.995 | 0.922 | 1.085 | 1.156 | 1.002 | 1.16 | 5.44E-02 |
| cds.Camellia_sinensis.comp34205_c0_seq7_m.3600 | PREDICTED: protein translocase subunit SECA2, chloroplastic isoform X2 [Cucumis sativus] | 30.71 | 2.5828 | 3.7 | 1 | 1 | 1 | 0.974 | 0.944 | 1.077 | 1.065 | 0.974 | 0.985 | 1.01 | 8.41E-01 |
| cds.Camellia_sinensis.comp34215_c0_seq4_m.366 | PREDICTED: proteasome activator subunit 4 [Vitis vinifera] | 189.89 | 42.092 | 7.2 | 11 | 11 | 11 | 0.975 | 1.012 | 1.017 | 0.99 | 1.018 | 0.992 | 0.999 | 9.42E-01 |

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| cds.Camellia_sinensis.comp34215_c0_seq58_m.42722 | PREDICTED: proteasome activator subunit 4 [Solanum tuberosum | 13.701 | 3.7334 | 13.6 | 2 | 2 | 2 | 0.925 | 1.074 | 1.057 | 0.887 | 1.031 | 1.033 | 0.966 | 6.37E-01 |
| cds.Camellia_sinensis.comp34219_c0_seq6_m.53809 | PREDICTED: D-aminoacyl-tRNA deacylase-like isoform X1 [Sesamum indicum] | 12.778 | 1.4169 | 12.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34220_c1_seq1_m.11670 | PREDICTED: GTP-binding protein TypA/BipA homolog [Citrus | 76.152 | 87.425 | 14.1 | 8 | 11 | 8 | 0.994 | 0.99 | 0.97 | 1.028 | 1.025 | 0.997 | 1.032 | 6.08E-02 |
| cds.Camellia_sinensis.comp34223_c0_seq1_m.7172 | PREDICTED: WD repeat-containing protein 48 isoform X2 [Vitis vinifera] | 83.43 | 3.5801 | 3.1 | 3 | 3 | 3 | 0.996 | 1.033 | 0.94 | 0.945 | 1.053 | 1.039 | 1.023 | 6.38E-01 |

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| cds.Camellia_sinensis.comp34227_c0_seq1_m.5314 | PREDICTED: vacuolar protein sorting-associated protein 53 A isoform X1 [Vitis vinifera] | 91.929 | 9.1242 | 4.4 | 3 | 3 | 3 | 1.076 | 1.012 | 1.009 | 0.898 | 0.919 | 1.073 | 0.933 | 2.95E-01 |
| cds.Camellia_sinensis.comp34230_c0_seq14_m.26616 | PREDICTED: ubiquitin-like modifier-activating enzyme 5 isoform X1 [Theobroma cacao] | 49.031 | 10.752 | 10.1 | 4 | 7 | 4 | 0.958 | 0.987 | 1.007 | 1.055 | 1.011 | 1.034 | 1.05 | 6.16E-02 |
| cds.Camellia_sinensis.comp34231_c0_seq1_m.1045 | Inactive ubiquitin carboxyl-terminal hydrolase 54 [Morus notabilis] | 147.88 | 2.0751 | 0.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34232_c0_seq1_m.11671 | PREDICTED: D-lactate dehydrogenase [cytochrome], mitochondrial [Sesamum indicum] | 62.078 | 27.377 | 17.7 | 10 | 12 | 10 | 1.016 | 0.985 | 0.999 | 0.939 | 1.025 | 1.012 | 0.992 | 7.78E-01 |

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| cds.Camellia_sinensis.comp34233_c0_seq8_m.18519 | PREDICTED: insulin-degrading enzyme-like 1, peroxisomal [Vitis vinifera] | 63.407 | 14.863 | 9.4 | 6 | 8 | 6 | 0.934 | 0.961 | 0.981 | 1.064 | 1.042 | 1.045 | 1.096 | 4.28E-03 |
| cds.Camellia_sinensis.comp34234_c0_seq1_m.9086 | PREDICTED: long chain acyl-CoA synthetase 6, peroxisomal [Vitis vinifera] | 76.776 | 52.236 | 17.5 | 10 | 12 | 8 | 0.927 | 0.937 | 0.912 | 1.092 | 1.058 | 1.052 | 1.153 | 5.22E-04 |
| cds.Camellia_sinensis.comp34234_c0_seq2_m.11139 | PREDICTED: long chain acyl-CoA synthetase 4 [Sesamum indicum] | 47.856 | 17.676 | 16 | 8 | 11 | 8 | 0.957 | 0.945 | 1.024 | 1.028 | 1.02 | 1.066 | 1.064 | 9.17E-02 |
| cds.Camellia_sinensis.comp34234_c0_seq4_m.33542 | PREDICTED: long chain acyl-CoA synthetase 6, peroxisomal [Ipomoea nil] | 42.515 | 3.6646 | 9.1 | 3 | 4 | 1 | 1.017 | 1 | 0.951 | 1.061 | 0.946 | 1.036 | 1.025 | 5.82E-01 |

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| cds.Camellia_sinensis.comp34234_c0_seq5_m.34016 | PREDICTED: long chain acyl-CoA synthetase 4 [Camelina sativa] | 18.244 | 19.357 | 28.2 | 5 | 8 | 5 | 0.978 | 0.991 | 0.955 | 1.047 | 1.025 | 1.017 | 1.056 | 1.67E-02 |
| cds.Camellia_sinensis.comp34234_c1_seq1_m.26920 | PREDICTED: protein DJ-1 homolog B-like [Gossypium raimondii] | 28.292 | 38.337 | 46 | 9 | 21 | 9 | 0.989 | 0.981 | 0.942 | 1.048 | 1.048 | 1.04 | 1.077 | 8.24E-03 |
| cds.Camellia_sinensis.comp34234_c1_seq1_m.26921 | PREDICTED: protein DJ-1 homolog B-like [Gossypium hirsutum] | 20.874 | 20.78 | 10.7 | 3 | 6 | 3 | 1.007 | 0.969 | 1.005 | 1.006 | 0.972 | 1.044 | 1.014 | 6.08E-01 |
| cds.Camellia_sinensis.comp34235_c0_seq12_m.36539 | PREDICTED: nuclear transcription factor Y subunit C-9-like [Juglans regia] | 27.116 | 4.6883 | 12 | 3 | 4 | 2 | 0.824 | 0.979 | 0.938 | 1.111 | 1.066 | 1.13 | 1.206 | 2.54E-02 |

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| cds.Camellia_sinensis.comp34237_c2_seq1_m.4193 | PREDICTED: beta-galactosidase [Theobroma cacao] | 124.74 | 97.904 | 19.1 | 20 | 28 | 20 | 0.953 | 0.915 | 0.943 | 1.064 | 1.08 | 1.07 | 1.143 | 4.95E-04 |
| cds.Camellia_sinensis.comp34240_c0_seq7_m.27449 | PREDICTED: ATPase 5, plasma membrane-type-like [Pyrus x bretschneideri] | 40.722 | 5.5014 | 21.9 | 8 | 13 | 3 | 0.926 | 0.881 | 1.028 | 1.083 | 1.031 | 1.084 | 1.128 | 6.49E-02 |
| cds.Camellia_sinensis.comp34240_c1_seq10_m.17883 | PREDICTED: plasma membrane ATPase 4-like [Pyrus x bretschneideri] | 64.498 | 69.466 | 38.7 | 21 | 40 | 8 | 0.963 | 0.943 | 0.994 | 1.074 | 1.026 | 1.039 | 1.082 | 1.81E-02 |
| cds.Camellia_sinensis.comp34240_c1_seq2_m.39347 | PREDICTED: ATPase 11, plasma membrane-type [Theobroma cacao] | 25.215 | 6.8186 | 25.3 | 5 | 12 | 2 | 0.995 | 0.983 | 1.126 | 1.042 | 0.908 | 0.955 | 0.936 | 3.27E-01 |
| cds.Camellia_sinensis.comp34248_c0_seq7_m.20367 | PREDICTED: polyadenylate-binding protein RBP47B' [Vitis | 50.238 | 6.7628 | 6.9 | 3 | 4 | 3 | 0.964 | 0.954 | 0.961 | 1.035 | 1.044 | 1.064 | 1.092 | 5.56E-04 |

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| cds.Camellia_sinensis.comp34249_c0_seq1_m.1198 | PREDICTED: ALG-2 interacting protein X [Vitis vinifera] | 77.238 | 32.773 | 14.7 | 10 | 13 | 8 | 0.988 | 1.023 | 0.988 | 1.062 | 1.074 | 0.957 | 1.031 | 4.84E-01 |
| cds.Camellia_sinensis.comp34249_c0_seq6_m.27601 | PREDICTED: ALG-2 interacting protein X [Vitis vinifera] | 33.68 | 2.3031 | 8.4 | 3 | 4 | 1 | 1.06 | 0.98 | 0.898 | 1.08 | 1.047 | 0.947 | 1.046 | 5.01E-01 |
| cds.Camellia_sinensis.comp34252_c0_seq1_m.14690 | serine carboxypeptidase S10 family protein [Populus trichocarpa] | 54.234 | 12.881 | 5.8 | 2 | 3 | 2 | 1.024 | 1.075 | 1.024 | 0.969 | 0.961 | 0.945 | 0.921 | 9.76E-03 |
| cds.Camellia_sinensis.comp34253_c0_seq1_m.1260 | transducin family protein [Populus trichocarpa] | 164.82 | 36.503 | 7.7 | 11 | 13 | 11 | 0.973 | 1.05 | 0.962 | 1.028 | 1.012 | 1.006 | 1.02 | 4.99E-01 |
| cds.Camellia_sinensis.comp34253_c1_seq2_m.45510 | PREDICTED: actin-depolymerizing factor 2 [Nelumbo nucifera] | 15.575 | 7.7002 | 17.3 | 2 | 3 | 1 | 1.202 | 1.063 | 0.878 | 0.889 | 0.922 | 1.015 | 0.899 | 3.74E-01 |

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| cds.Camellia_sinensis.comp34256_c0_seq2_m.4266 | PREDICTED: DExH-box ATP-dependent RNA helicase DExH1 isoform X3 [Nelumbo nucifera] | 52.217 | 3.0576 | 3.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34256_c0_seq6_m.34640 | PREDICTED: proteasome assembly chaperone 2 [Juglans regia] | 31.034 | 4.0489 | 7.1 | 2 | 3 | 2 | 0.957 | 0.94 | 1.033 | 1.006 | 1.006 | 1.076 | 1.054 | 2.22E-01 |
| cds.Camellia_sinensis.comp34263_c0_seq2_m.23362 | PREDICTED: heterogeneous nuclear ribonucleoprotein 1-like [Ziziphus jujuba] | 36.715 | 150.85 | 33 | 11 | 27 | 10 | 1.006 | 0.977 | 0.94 | 1.012 | 1.038 | 1.053 | 1.062 | 5.82E-02 |
| cds.Camellia_sinensis.comp34268_c0_seq11_m.13029 | PREDICTED: calcium-dependent protein kinase 13 isoform X1 [Vitis vinifera] | 38.172 | 2.3621 | 3.5 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34268_c0_seq14_m.18047 | PREDICTED: cleft lip and palate transmembrane protein 1 homolog [Populus euphratica] | 70.701 | 4.2399 | 3.9 | 2 | 3 | 2 | 1.011 | 1.212 | 1.057 | 1.226 | 0.716 | 0.782 | 0.83 | 2.94E-01 |
| cds.Camellia_sinensis.comp34274_c0_seq5_m.7141 | PREDICTED: far upstream element-binding protein 1 isoform X2 [Vitis vinifera] | 43.512 | 50.677 | 29.9 | 8 | 13 | 2 | 0.984 | 1.067 | 0.943 | 0.896 | 1.004 | 1.107 | 1.004 | 9.80E-01 |
| cds.Camellia_sinensis.comp34274_c0_seq6_m.7377 | PREDICTED: far upstream element-binding protein 1 isoform X2 [Vitis vinifera] | 43.918 | 11.689 | 30.2 | 7 | 12 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34275_c0_seq5_m.32368 | PREDICTED: N-carbamoyl putrescine amidase-like [Juglans regia] | 33.158 | 35.213 | 21.5 | 5 | 9 | 5 | 0.962 | 0.924 | 0.948 | 1.081 | 1.057 | 1.069 | 1.132 | 7.77E-04 |

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| cds.Camellia_sinensis.comp34277_c0_seq1_m.15838 | PREDICTED: chitinase-like protein PB1E7.04c [Nelumbo nucifera] | 64.873 | 1.8879 | 1.5 | 1 | 1 | 1 | 1.033 | 1.074 | 1.015 | 0.974 | 0.926 | 0.973 | 0.92 | 2.44E-02 |
| cds.Camellia_sinensis.comp34279_c0_seq20_m.34635 | PREDICTED: HVA22-like protein a isoform X1 [Sesamum indicum] | 13.946 | 3.6905 | 23.3 | 2 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34283_c0_seq1_m.6318 | PREDICTED: nuclear cap-binding protein subunit 1 isoform X2 [Vitis vinifera] | 98.126 | 40.113 | 11 | 7 | 9 | 7 | 0.947 | 1.003 | 1.005 | 1.024 | 0.998 | 1.053 | 1.041 | 1.84E-01 |
| cds.Camellia_sinensis.comp34284_c0_seq1_m.5548 | PREDICTED: DEAD-box ATP-dependent RNA helicase 46 [Ziziphus jujuba] | 30.838 | 1.3184 | 7.9 | 2 | 3 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34285_c0_seq1_m.3525 | PREDICTED: cullin-4-like [Solanum pennellii] | 86.326 | 11.251 | 7.2 | 6 | 7 | 6 | 1.006 | 1.007 | 0.998 | 0.991 | 1.028 | 1.01 | 1.006 | 6.21E-01 |
| cds.Camellia_sinensis.comp34287_c0_seq1_m.12262 | DPP6 N-terminal domain-like protein [Arabidopsis thaliana] | 77.632 | 137.24 | 30 | 17 | 31 | 17 | 1.057 | 1.018 | 0.998 | 0.973 | 0.979 | 0.974 | 0.952 | 1.03E-01 |
| cds.Camellia_sinensis.comp34292_c0_seq9_m.10938 | PREDICTED: 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 1 [Vitis vinifera] | 24.088 | 9.6973 | 20.9 | 5 | 5 | 5 | 1.064 | 1.179 | 1.016 | 0.847 | 0.908 | 0.961 | 0.833 | 3.36E-02 |
| cds.Camellia_sinensis.comp34294_c1_seq1_m.16054 | PREDICTED: protein SUPPRESSOR OF GENE SILENCING 3 homolog [Vigna angularis] | 52.393 | 16.872 | 12.8 | 6 | 6 | 6 | 1.189 | 1.137 | 1.201 | 0.812 | 0.834 | 0.805 | 0.695 | 5.64E-05 |

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| cds.Camellia_sinensis.comp34294_c4_seq1_m.1774 | PREDICTED: alpha-glucan water dikinase, chloroplastic isoform X1 [Vitis vinifera] | 158.71 | 135.59 | 21.4 | 28 | 36 | 28 | 1.047 | 1.032 | 1.064 | 0.955 | 0.964 | 0.928 | 0.906 | 2.38E-03 |
| cds.Camellia_sinensis.comp34294_c4_seq7_m.53283 | PREDICTED: plant UBX domain-containing protein 8-like isoform X1 [Nicotiana attenuata] | 13.459 | 5.8208 | 27.4 | 3 | 3 | 3 | 1.015 | 1.083 | 1.084 | 0.911 | 0.937 | 0.961 | 0.883 | 9.56E-03 |
| cds.Camellia_sinensis.comp34295_c0_seq1_m.18899 | PREDICTED: serine carboxypeptidase-like 40 [Citrus sinensis] | 56.083 | 11.229 | 10.8 | 4 | 4 | 4 | 0.963 | 0.99 | 1.103 | 1.011 | 0.957 | 0.989 | 0.968 | 5.18E-01 |
| cds.Camellia_sinensis.comp34297_c0_seq1_m.1942 | PREDICTED: Niemann-Pick C1 protein [Vitis vinifera] | 142.73 | 7.8943 | 3.2 | 4 | 4 | 4 | 1.02 | 1.006 | 1.083 | 1.033 | 0.955 | 0.908 | 0.931 | 1.76E-01 |

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| cds.Camellia_sinensis.comp34297_c0_seq7_m.2291 | PREDICTED: Niemann-Pick C1 protein isoform X2 [Vitis vinifera] | 86.649 | 5.5979 | 1.4 | 1 | 1 | 1 | 1.062 | 1.111 | 0.997 | 0.933 | 0.965 | 0.921 | 0.889 | 2.74E-02 |
| cds.Camellia_sinensis.comp34297_c0_seq7_m.2292 | PREDICTED: Niemann-Pick C1 protein isoform X2 [Vitis vinifera] | 35.217 | 2.4454 | 6.2 | 1 | 1 | 1 | 1.107 | 0.924 | 0.922 | 0.96 | 1.044 | 1.042 | 1.031 | 6.37E-01 |
| cds.Camellia_sinensis.comp34298_c0_seq3_m.11240 | PREDICTED: exocyst complex component SEC6 [Vitis vinifera] | 88.748 | 9.3636 | 5.2 | 4 | 5 | 4 | 0.984 | 1.044 | 1.047 | 0.989 | 0.97 | 0.971 | 0.953 | 8.64E-02 |
| cds.Camellia_sinensis.comp34299_c2_seq4_m.53960 | PREDICTED: photosynthetic NDH subunit of lumenal location 5, chloroplastic [Ziziphus jujuba] | 15.568 | 5.7357 | 19.7 | 2 | 5 | 1 | 1.055 | 1.139 | 1.009 | 0.944 | 0.892 | 0.947 | 0.869 | 2.58E-02 |

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| cds.Camellia_sinensis.comp34299_c3_seq1_m.27800 | PREDICTED: mitochondrial outer membrane protein porin of 34 kDa [Nicotiana attenuata] | 29.486 | 89.402 | 33 | 10 | 25 | 6 | 1.023 | 0.979 | 0.96 | 0.978 | 1.022 | 1.018 | 1.019 | 4.66E-01 |
| cds.Camellia_sinensis.comp34299_c3_seq2_m.31009 | PREDICTED: mitochondrial outer membrane protein porin of 34 kDa [Nicotiana attenuata] | 31.604 | 127.01 | 43.4 | 12 | 28 | 8 | 1.003 | 0.963 | 0.988 | 0.994 | 1.019 | 1.011 | 1.024 | 1.67E-01 |
| cds.Camellia_sinensis.comp34303_c0_seq13_m.1171 | Serine/threonine-protein kinase [Morus notabilis] | 128.74 | 11.375 | 4.8 | 6 | 6 | 4 | 0.943 | 1.094 | 0.977 | 1.01 | 0.952 | 1 | 0.983 | 7.62E-01 |
| cds.Camellia_sinensis.comp34303_c0_seq13_m.1172 | PREDICTED: MLP-like protein 423 isoform X2 [Ziziphus jujuba] | 17.014 | 106.91 | 51.7 | 9 | 20 | 9 | 1.255 | 1.332 | 1.276 | 0.671 | 0.675 | 0.674 | 0.523 | 7.58E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp34303_c0_seq2_m.1564 | Serine/threonine-protein kinase [Morus notabilis] | 150.83 | 1.8473 | 2.2 | 3 | 3 | 2 | 0.969 | 0.997 | 1.002 | 0.975 | 1.064 | 1.007 | 1.026 | 4.09E-01 |
| cds.Camellia_sinensis.comp34308_c0_seq1_m.15055 | PREDICTED: T-complex protein 1 subunit theta [Ziziphus jujuba] | 66.985 | 174.46 | 40.7 | 21 | 37 | 21 | 0.956 | 0.951 | 0.945 | 1.079 | 1.064 | 1.057 | 1.122 | 7.86E-05 |
| cds.Camellia_sinensis.comp34318_c0_seq2_m.34825 | PREDICTED: probable zinc metalloprotease EGY1, chloroplastic [Cucumis sativus] | 33.297 | 5.5672 | 7 | 2 | 3 | 2 | 1.057 | 1.012 | 0.998 | 1.004 | 0.944 | 0.984 | 0.956 | 1.47E-01 |
| cds.Camellia_sinensis.comp34320_c0_seq5_m.4979 | PREDICTED: putative GTP diphosphokinase RSH1, chloroplastic isoform X2 [Citrus sinensis] | 61.549 | 2.0247 | 1.5 | 1 | 1 | 1 | 1.12 | 1.116 | 1.086 | 0.869 | 0.896 | 0.884 | 0.797 | 6.35E-05 |

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| cds.Camellia_sinensis.comp34323_c2_seq1_m.31968 | PREDICTED: poly(rC)-binding protein 4-like [Nicotiana tomentosiformis] | 29.299 | 1.2756 | 3.6 | 1 | 1 | 1 | 0.933 | 1.062 | 1.03 | 1.061 | 0.957 | 0.975 | 0.989 | 8.50E-01 |
| cds.Camellia_sinensis.comp34328_c0_seq20_m.15224 | PREDICTED: DNA polymerase delta catalytic subunit [Sesamum indicum] | 70.096 | 1.3498 | 1.3 | 1 | 1 | 1 | 1.015 | 0.983 | 0.985 | 0.987 | 1.023 | 1.014 | 1.014 | 4.13E-01 |
| cds.Camellia_sinensis.comp34331_c1_seq1_m.11534 | PREDICTED: transmembrane 9 superfamily member 7 [Glycine max] | 57.195 | 8.8688 | 4.8 | 2 | 2 | 1 | 1.071 | 1.092 | 0.972 | 1.058 | 0.895 | 0.909 | 0.913 | 2.23E-01 |
| cds.Camellia_sinensis.comp34331_c1_seq2_m.12395 | PREDICTED: transmembrane 9 superfamily member 7 [Gossypium hirsutum] | 13.744 | 27.575 | 18.2 | 2 | 3 | 1 | 0.987 | 1.023 | 1.033 | 1.055 | 1.003 | 0.912 | 0.976 | 5.95E-01 |

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| cds.Camellia_sinensis.comp34335_c1_seq1_m.24901 | PREDICTED: beta-hexosaminidase 2 [Vitis vinifera] | 55.016 | 3.6431 | 4.2 | 2 | 2 | 2 | 1.039 | 1.144 | 1.103 | 1.021 | 0.787 | 0.893 | 0.822 | 6.65E-02 |
| cds.Camellia_sinensis.comp34337_c0_seq1_m.6146 | PREDICTED: helicase-like transcription factor CHR28 isoform X1 [Vitis vinifera] | 98.952 | 11.483 | 1.6 | 1 | 1 | 1 | 0.951 | 0.914 | 0.922 | 1.12 | 1.117 | 1.013 | 1.166 | 1.22E-02 |
| cds.Camellia_sinensis.comp34341_c0_seq3_m.4779 | PREDICTED: importin beta-like SAD2 [Ziziphus jujuba] | 52.991 | 5.4683 | 5 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34342_c0_seq1_m.3848 | PREDICTED: probable starch synthase 4, chloroplastic/amyloplastic [Vitis vinifera] | 114.51 | 24.798 | 9.2 | 7 | 9 | 7 | 0.995 | 1.166 | 1.047 | 0.95 | 0.916 | 0.948 | 0.877 | 5.55E-02 |
| cds.Camellia_sinensis.comp34343_c0_seq1_m.1828 | dentin sialophosphoprotein [Populus trichocarpa] | 164.05 | 35.27 | 8.7 | 12 | 13 | 12 | 1.025 | 1.062 | 1.039 | 1.022 | 0.962 | 0.952 | 0.939 | 6.10E-02 |

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| cds.Camellia_sinensis.comp34350_c0_seq10_m.46921 | PREDICTED: probable alpha-mannosidase At5g13980 [Vitis vinifera] | 24.634 | 9.9395 | 21.7 | 4 | 12 | 2 | 0.986 | 1.021 | 0.891 | 1.012 | 1.003 | 1.1 | 1.075 | 2.21E-01 |
| cds.Camellia_sinensis.comp34350_c0_seq6_m.4895 | PREDICTED: alpha-mannosidase isoform X2 [Gossypium raimondii] | 115.64 | 36.673 | 12 | 13 | 19 | 13 | 0.998 | 1.022 | 1.033 | 0.962 | 0.986 | 0.988 | 0.962 | 4.27E-02 |
| cds.Camellia_sinensis.comp34352_c0_seq2_m.1656 | PREDICTED: MAP3K epsilon protein kinase 1 isoform X1 [Vitis vinifera] | 152.21 | 1.8503 | 0.7 | 1 | 1 | 1 | 1.027 | 1.107 | 0.934 | 0.918 | 0.979 | 1.029 | 0.954 | 4.80E-01 |
| cds.Camellia_sinensis.comp34354_c0_seq1_m.18787 | PREDICTED: 7-deoxyloganetin glucosyltransferase-like isoform X4 [Prunus | 55.626 | 2.6867 | 2.8 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34360_c0_seq26_m.5184 | K(+) efflux antiporter 2 [Morus notabilis] | 12.95 | 4.0614 | 14.6 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp34364_c0_seq4_m.4091 | PREDICTED: villin-3-like [Citrus sinensis] | 104.08 | 185 | 32.7 | 26 | 38 | 26 | 0.975 | 0.96 | 0.958 | 1.03 | 1.023 | 1.057 | 1.075 | 3.18E-03 |
| cds.Camellia_sinensis.comp34368_c0_seq1_m.18665 | PREDICTED: farnesylcysteine lyase [Theobroma cacao] | 60.529 | 1.563 | 3.5 | 2 | 2 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp34371_c3_seq61_m.43394 | PREDICTED: expansin-A10 [Theobroma cacao] | 14.598 | 4.6309 | 7.5 | 1 | 2 | 1 | 0.996 | 1.028 | 0.931 | 1.034 | 0.999 | 1.025 | 1.035 | 3.22E-01 |
| cds.Camellia_sinensis.comp34374_c0_seq1_m.23217 | PREDICTED: cytochrome c1-2, heme protein, mitochondrial [Citrus sinensis] | 39.622 | 27.58 | 20.8 | 5 | 14 | 3 | 0.962 | 1.063 | 0.954 | 1.033 | 0.994 | 1.009 | 1.019 | 6.12E-01 |

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| cds.Camellia_sinensis.comp34374_c0_seq2_m.23931 | PREDICTED: cytochrome c1-2, heme protein, mitochondrial [Nicotiana attenuata] | 39.537 | 96.985 | 25.6 | 6 | 19 | 4 | 0.936 | 1.047 | 0.957 | 1.073 | 0.998 | 1.035 | 1.056 | 2.38E-01 |
| cds.Camellia_sinensis.comp34376_c0_seq16_c0_seq1_m.7966 | PREDICTED: beta-adaptin-like protein C [Solanum pennellii] | 87.647 | 78.468 | 17.5 | 12 | 24 | 12 | 0.966 | 0.984 | 1.019 | 1.052 | 1.027 | 0.995 | 1.035 | 1.97E-01 |
| cds.Camellia_sinensis.comp34376_c0_seq8_m.44486 | PREDICTED: DNA-directed RNA polymerase II subunit 4 [Jatropha | 13.233 | 2.8975 | 14.9 | 2 | 3 | 2 | 0.983 | 0.949 | 0.941 | 1.033 | 1.02 | 1.092 | 1.095 | 2.22E-02 |
| cds.Camellia_sinensis.comp34380_c0_seq3_m.15281 | PREDICTED: serine/threonine-protein phosphatase 6 regulatory subunit 3 isoform X4 [Vitis vinifera] | 74.971 | 2.2651 | 3.2 | 2 | 2 | 2 | 1.193 | 1.072 | 1.09 | 0.746 | 0.859 | 0.992 | 0.774 | 4.20E-02 |

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| cds.Camellia_sinensis.comp34384_c0_seq3_m.25787 | PREDICTED: glycine--tRNA ligase 1, mitochondrial-like [Nicotiana sylvestris] | 51.633 | 17.204 | 31.7 | 13 | 22 | 4 | 0.95 | 0.931 | 0.938 | 1.057 | 1.075 | 1.052 | 1.129 | 1.60E-04 |
| cds.Camellia_sinensis.comp34384_c1_seq7_m.22974 | PREDICTED: conserved oligomeric Golgi complex subunit 1 [Vitis vinifera] | 46.186 | 14.842 | 4.4 | 2 | 2 | 2 | 1.06 | 1.019 | 1.081 | 0.89 | 1 | 0.939 | 0.895 | 4.23E-02 |
| cds.Camellia_sinensis.comp34386_c0_seq1_m.3887 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 1 homolog A [Vitis vinifera] | 103.45 | 123.65 | 16.2 | 13 | 24 | 11 | 0.983 | 0.977 | 1.003 | 1.041 | 1.004 | 1.016 | 1.033 | 7.07E-02 |
| cds.Camellia_sinensis.comp34386_c0_seq2_m.36640 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 1 homolog A-like [Prunus mume] | 24.693 | 32.551 | 32.9 | 7 | 12 | 5 | 0.99 | 1.012 | 0.96 | 1.018 | 0.979 | 1.02 | 1.019 | 4.15E-01 |

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| cds.Camellia_sinensis.comp34387_c0_seq3_m.4957 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 9, chloroplastic isoform X2 [Ziziphus jujuba] | 90.027 | 3.2078 | 4.1 | 3 | 3 | 3 | 0.947 | 1.076 | 1.062 | 1.081 | 0.948 | 0.902 | 0.95 | 4.80E-01 |
| cds.Camellia_sinensis.comp34391_c0_seq31_m.16332 | PREDICTED: probable serine/threonine-protein phosphatase 2A regulatory subunit B" subunit TON2 [Phoenix dactylifera] | 54.772 | 3.6363 | 4.6 | 3 | 3 | 3 | 1.03 | 1.113 | 1.086 | 0.934 | 0.911 | 0.902 | 0.851 | 3.02E-03 |
| cds.Camellia_sinensis.comp34393_c0_seq93_m.28437 | PREDICTED: phosphatase IMPL1, chloroplastic [Daucus carota subsp. sativus] | 41.26 | 41.241 | 14 | 4 | 4 | 4 | 1.021 | 0.975 | 1.01 | 0.935 | 0.992 | 1.05 | 0.99 | 7.84E-01 |

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| cds.Camellia_sinensis.comp34394_c0_seq8_m.5071 | PREDICTED: protein MEI2-like 5 [Vitis vinifera] | 71.595 | 2.5959 | 3.3 | 2 | 2 | 2 | 1.061 | 1.128 | 1.014 | 0.991 | 0.859 | 0.935 | 0.869 | 5.31E-02 |
| cds.Camellia_sinensis.comp34396_c0_seq2_m.38667 | PREDICTED: polyadenylate-binding protein 2 isoform X1 | 24.789 | 24.247 | 19.9 | 4 | 5 | 3 | 1.019 | 1.052 | 0.981 | 1.018 | 0.993 | 0.943 | 0.968 | 3.40E-01 |
| cds.Camellia_sinensis.comp34396_c2_seq6_m.44576 | PREDICTED: subtilisin-like protease [Sesamum indicum] | 15.093 | 1.458 | 11.6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34398_c0_seq18_m.2676 | PREDICTED: carbamoyl-phosphate synthase large chain, chloroplastic-like [Ipomoea nil] | 104.3 | 124.56 | 19.2 | 17 | 30 | 17 | 0.982 | 0.984 | 0.969 | 1.022 | 1.033 | 1.018 | 1.047 | 2.12E-03 |

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| cds.Camellia_sinensis.comp34398_c0_seq1_m.2677 | PREDICTED: carbamoyl-phosphate synthase large chain, chloroplastic [Vitis vinifera] | 28.476 | 6.8659 | 13.3 | 4 | 7 | 4 | 0.992 | 0.989 | 0.993 | 0.989 | 1.04 | 1.038 | 1.031 | 2.05E-01 |
| cds.Camellia_sinensis.comp34399_c1_seq49_c1_seq4_m.6514 | PREDICTED: importin subunit alpha-2 [Vitis vinifera] | 58.401 | 13.971 | 20.2 | 10 | 12 | 2 | 1.066 | 1.004 | 1.018 | 0.929 | 1.02 | 0.956 | 0.941 | 1.36E-01 |
| cds.Camellia_sinensis.comp34399_c1_seq4_m.6515 | RAB GTPase-like protein A5B [Medicago truncatula] | 23.924 | 13.406 | 40.3 | 9 | 20 | 2 | 0.916 | 0.962 | 0.966 | 1.072 | 1.043 | 1.01 | 1.099 | 1.77E-02 |
| cds.Camellia_sinensis.comp34399_c1_seq9_m.15209 | PREDICTED: importin subunit alpha-2 [Jatropha curcas] | 58.693 | 46.464 | 24.1 | 11 | 13 | 3 | 1.001 | 1.057 | 0.963 | 0.987 | 0.931 | 1.065 | 0.987 | 7.91E-01 |
| cds.Camellia_sinensis.comp34400_c0_seq12_m.17770 | PREDICTED: cullin-1-like isoform X2 [Nicotiana tabacum] | 63.353 | 4.209 | 9.2 | 5 | 5 | 1 | 1.032 | 1.067 | 1.085 | 0.953 | 0.916 | 0.941 | 0.883 | 2.66E-03 |

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| cds.Camellia_sinensis.comp34400_c0_seq4_m.8026 | PREDICTED: cullin-1 isoform X1 [Vitis vinifera] | 86.372 | 16.424 | 7.8 | 6 | 6 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34400_c0_seq9_m.12194 | PREDICTED: granule-bound starch synthase 1, chloroplastic/amyloplastic isoform X2 [Theobroma cacao] | 67.174 | 39.882 | 21.9 | 12 | 21 | 11 | 1.242 | 1.24 | 1.25 | 0.718 | 0.734 | 0.744 | 0.588 | 4.87E-07 |
| cds.Camellia_sinensis.comp34400_c1_seq1_m.48780 | thionin-like protein [Arabidopsis thaliana] | 22.293 | 6.1601 | 14.3 | 2 | 2 | 2 | 0.947 | 1.095 | 1.066 | 0.911 | 0.891 | 1.088 | 0.93 | 3.88E-01 |
| cds.Camellia_sinensis.comp34401_c1_seq1_m.16024 | PREDICTED: NAD-dependent malic enzyme 59 kDa isoform, mitochondrial [Sesamum indicum] | 66.219 | 78.478 | 27.3 | 15 | 22 | 11 | 1.002 | 0.991 | 0.977 | 0.999 | 1.018 | 1.001 | 1.016 | 1.64E-01 |

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| cds.Camellia_sinensis.comp34401_c1_seq3_m.37084 | PREDICTED: NAD-dependent malic enzyme 59 kDa isoform, mitochondrial [Juglans regia] | 27.044 | 40.641 | 30.7 | 7 | 14 | 4 | 0.981 | 0.96 | 0.944 | 1.027 | 1.063 | 1.055 | 1.09 | 4.82E-03 |
| cds.Camellia_sinensis.comp34401_c2_seq1_m.38626 | PREDICTED: chorismate mutase 2 [Nelumbo nucifera] | 29.023 | 15.511 | 33.2 | 7 | 9 | 7 | 0.988 | 0.991 | 1.008 | 1.041 | 0.99 | 1.031 | 1.025 | 2.13E-01 |
| cds.Camellia_sinensis.comp34403_c0_seq2_m.16300 | PREDICTED: protein decapping 5 isoform X1 [Vitis vinifera] | 63.679 | 15.289 | 11.4 | 6 | 6 | 6 | 1.022 | 0.988 | 1.061 | 0.978 | 0.982 | 0.962 | 0.951 | 8.36E-02 |
| cds.Camellia_sinensis.comp34406_c0_seq1_m.24451 | PREDICTED: UDP-glucose flavonoid 3-O-glucosyltransferase 6-like [Fragaria vesca subsp. vesca] | 41.357 | 6.3523 | 2.9 | 1 | 2 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34406_c0_seq6_m.55028 | PREDICTED: anthocyanidin 3-O-glucosyltransferase 2-like [Daucus carota subsp. sativus] | 13.482 | 1.8133 | 7.4 | 1 | 1 | 1 | 1.036 | 0.972 | 1.003 | 1.003 | 1.029 | 0.963 | 0.995 | 8.51E-01 |
| cds.Camellia_sinensis.comp34407_c0_seq1_m.15211 | PREDICTED: diaminopimelate decarboxylase 2, chloroplastic [Vitis vinifera] | 52.851 | 117.76 | 30.4 | 13 | 25 | 13 | 1.016 | 1.021 | 0.998 | 0.985 | 1.002 | 0.986 | 0.98 | 8.07E-02 |
| cds.Camellia_sinensis.comp34409_c0_seq2_m.1102 | sulfate adenylyltransferase subunit [Arabidopsis thaliana] | 23.254 | 48.53 | 12.9 | 2 | 3 | 2 | 0.914 | 0.928 | 1.01 | 1.007 | 1.048 | 1.12 | 1.113 | 7.09E-02 |
| cds.Camellia_sinensis.comp34413_c0_seq2_m.26389 | PREDICTED: ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic [Cicer arietinum] | 49.902 | 28.752 | 13.8 | 6 | 8 | 6 | 1.024 | 1.058 | 1.047 | 0.894 | 0.979 | 0.951 | 0.903 | 2.23E-02 |

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| cds.Camellia_sinensis.comp34414_c0_seq2_m.24049 | PREDICTED: probable inactive shikimate kinase like 1, chloroplastic isoform X4 [Vitis vinifera] | 33.47 | 22.122 | 14.6 | 4 | 6 | 4 | 1.052 | 0.962 | 0.951 | 1.003 | 0.984 | 1.009 | 1.01 | 7.46E-01 |
| cds.Camellia_sinensis.comp34415_c1_seq1_m.31227 | chaperonin-like RbcX protein 2, chloroplastic [Cajanus cajan] | 25.662 | 2.7286 | 4.9 | 1 | 1 | 1 | 1.024 | 1.053 | 1.062 | 1.01 | 0.956 | 0.898 | 0.912 | 6.02E-02 |
| cds.Camellia_sinensis.comp34415_c2_seq1_m.57003 | PREDICTED: cysteine proteinase inhibitor [Juglans regia] | 13.541 | 2.0271 | 14.3 | 2 | 2 | 2 | 0.874 | 0.95 | 0.968 | 1.089 | 1.061 | 1.097 | 1.163 | 1.00E-02 |
| cds.Camellia_sinensis.comp34416_c0_seq1_m.6374 | putative cytoskeletal protein mRNA [Populus trichocarpa] | 85.626 | 10.155 | 7.9 | 7 | 8 | 7 | 1.168 | 1.074 | 1.135 | 0.845 | 0.812 | 0.882 | 0.752 | 1.14E-03 |

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| cds.Camellia_sinensis.comp34418_c1_seq1_m.3485 | PREDICTED: valine--tRNA ligase, mitochondrial 1 isoform X2 [Vitis vinifera] | 121.15 | 58.702 | 11.3 | 12 | 13 | 11 | 1.054 | 1.113 | 1.106 | 0.947 | 0.883 | 0.902 | 0.835 | 2.56E-03 |
| cds.Camellia_sinensis.comp34418_c2_seq1_m.25656 | PREDICTED: alpha-galactosidase 1-like [Nelumbo nucifera] | 45.832 | 155.78 | 40.1 | 15 | 33 | 13 | 0.923 | 0.92 | 0.912 | 1.1 | 1.068 | 1.088 | 1.182 | 5.86E-05 |
| cds.Camellia_sinensis.comp34423_c0_seq1_m.1154 | PREDICTED: phosphatidylinositol 4-kinase alpha 1 isoform X1 [Theobroma cacao] | 196.84 | 3.1816 | 1.7 | 3 | 3 | 3 | 1.075 | 1.075 | 0.999 | 0.948 | 0.945 | 0.947 | 0.902 | 5.23E-02 |
| cds.Camellia_sinensis.comp34432_c0_seq6_m.4366 | PREDICTED: homeobox-leucine zipper protein ATHB-15 [Vitis vinifera] | 93.697 | 1.3829 | 1.1 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34434_c1_seq2_m.33206 | mitochondrial glycoprotein [Populus trichocarpa] | 27.672 | 11.641 | 15.2 | 3 | 3 | 3 | 0.898 | 1.071 | 0.951 | 1.118 | 1.024 | 0.969 | 1.065 | 3.88E-01 |
| cds.Camellia_sinensis.comp34436_c0_seq1_m.23561 | PREDICTED: putative GPI-anchor transamidase [Vitis vinifera] | 47.14 | 4.5401 | 4.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34438_c1_seq5_m.21556 | PREDICTED: peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic [Jatropha curcas] | 34.068 | 61.016 | 27.7 | 8 | 18 | 8 | 1.013 | 0.954 | 0.96 | 1.041 | 1.044 | 1.033 | 1.065 | 3.01E-02 |
| cds.Camellia_sinensis.comp34438_c1_seq5_m.21557 | PREDICTED: peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic [Vigna angularis] | 12.34 | 3.6704 | 18.8 | 3 | 5 | 3 | 0.986 | 0.939 | 1.018 | 1.065 | 1.033 | 1.032 | 1.064 | 7.29E-02 |

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| cds.Camellia_sinensis.comp34439_c0_seq1_m.36377 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 11, chloroplastic/mitochondrial-like [Vigna angularis] | 29.058 | 12.512 | 16.1 | 5 | 5 | 5 | 0.981 | 0.972 | 1 | 1.036 | 0.938 | 1.011 | 1.011 | 7.64E-01 |
| cds.Camellia_sinensis.comp34443_c0_seq1_m.11218 | PREDICTED: V-type proton ATPase catalytic subunit A [Nelumbo | 68.663 | 323.31 | 53.9 | 34 | 78 | 34 | 0.97 | 0.976 | 0.972 | 1.025 | 1.042 | 1.035 | 1.063 | 2.80E-04 |
| cds.Camellia_sinensis.comp34444_c0_seq6_m.37666 | K(+) efflux antiporter 2, chloroplastic-like [Cajanus | 28.159 | 36.533 | 25 | 5 | 9 | 5 | 1.037 | 1.062 | 1.086 | 0.976 | 0.917 | 0.964 | 0.897 | 9.44E-03 |
| cds.Camellia_sinensis.comp34446_c0_seq1_m.10981 | PREDICTED: proton pump-interactor 1 [Vitis vinifera] | 72.596 | 30.611 | 14.3 | 8 | 9 | 8 | 1.081 | 1.137 | 1.164 | 0.882 | 0.896 | 0.85 | 0.777 | 7.18E-04 |

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| cds.Camellia_sinensis.comp34446_c2_seq1_m.19110 | PREDICTED: monogalactosyldiacylglycerol synthase, chloroplastic [Theobroma cacao] | 35.826 | 2.8526 | 5.2 | 2 | 2 | 2 | 0.927 | 0.969 | 1.023 | 1.054 | 1.036 | 1.017 | 1.064 | 1.06E-01 |
| cds.Camellia_sinensis.comp34447_c0_seq1_m.1754 | Transducin/WD40 repeat-like superfamily protein [Arabidopsis thaliana] | 143.41 | 32.448 | 5.3 | 6 | 8 | 6 | 0.942 | 0.987 | 0.987 | 0.977 | 1.009 | 1.058 | 1.044 | 2.01E-01 |
| cds.Camellia_sinensis.comp34451_c0_seq1_m.3457 | PREDICTED: 110 kDa U5 small nuclear ribonucleoprotein component CLO [Vitis | 110.5 | 7.4798 | 4.4 | 3 | 3 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp34451_c1_seq1_m.17892 | sodium/calcium exchanger family protein [Populus trichocarpa] | 64.451 | 5.3938 | 6.4 | 3 | 4 | 3 | 1.099 | 1.137 | 1.083 | 0.846 | 0.914 | 0.892 | 0.799 | 1.14E-03 |

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| cds.Camellia_sinensis.comp34451_c2_seq2_m.41716 | PREDICTED: 40S ribosomal protein S13-like [Erythranthe guttata] | 17.136 | 12.895 | 24.5 | 4 | 8 | 4 | 1.107 | 1.092 | 1.073 | 0.894 | 0.925 | 0.87 | 0.822 | 5.95E-04 |
| cds.Camellia_sinensis.comp34452_c0_seq1_m.3869 | PREDICTED: probable phosphoinositide phosphatase SAC9 [Vitis vinifera] | 120.62 | 3.2276 | 1.6 | 2 | 2 | 2 | 1.031 | 1.003 | 1.01 | 0.956 | 0.972 | 1.028 | 0.971 | 2.74E-01 |
| cds.Camellia_sinensis.comp34455_c0_seq3_m.6116 | PREDICTED: protein FAR1-RELATED SEQUENCE 3 [Vitis | 44.559 | 3.4653 | 9.3 | 3 | 4 | 1 | 0.897 | 1.023 | 0.906 | 1.04 | 1.154 | 1.014 | 1.135 | 9.33E-02 |
| cds.Camellia_sinensis.comp34457_c0_seq1_m.13702 | PREDICTED: probable acyl-activating enzyme 17, peroxisomal isoform X2 [Ziziphus | 80.7 | 26.051 | 10.5 | 7 | 12 | 7 | 0.962 | 1.018 | 1.009 | 1 | 1.015 | 1.046 | 1.024 | 3.38E-01 |

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| cds.Camellia_sinensis.comp34458_c0_seq1_m.4994 | PREDICTED: pentatricopeptide repeat-containing protein At5g46580, chloroplastic [Nicotiana tomentosiformis] | 78.976 | 3.1051 | 6.2 | 5 | 5 | 2 | 0.911 | 1.005 | 1.019 | 1.099 | 0.963 | 1.031 | 1.054 | 3.72E-01 |
| cds.Camellia_sinensis.comp34458_c0_seq5_m.26948 | PREDICTED: pentatricopeptide repeat-containing protein At5g46580, chloroplastic [Sesamum indicum] | 51.333 | 11.137 | 15.9 | 7 | 8 | 4 | 0.951 | 0.997 | 0.93 | 1.079 | 1.08 | 0.993 | 1.095 | 5.88E-02 |
| cds.Camellia_sinensis.comp34460_c2_seq11_m.10323 | PREDICTED: neutral alpha-glucosidase C [Nicotiana sylvestris] | 51.942 | 105.06 | 27.8 | 12 | 18 | 12 | 0.988 | 0.998 | 1.033 | 0.975 | 0.978 | 0.993 | 0.976 | 1.72E-01 |

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| cds.Camellia_sinensis.comp34460_c2_seq19_m.31055 | PREDICTED: alpha-glucosidase 2-like [Citrus sinensis] | 30.786 | 9.0573 | 13.8 | 4 | 8 | 4 | 0.952 | 1.029 | 1.031 | 0.99 | 1.037 | 1.051 | 1.022 | 5.28E-01 |
| cds.Camellia_sinensis.comp34460_c2_seq26_m.42758 | transmembrane protein, putative [Medicago truncatula] | 25.22 | 5.4741 | 7.7 | 2 | 2 | 2 | 0.873 | 0.873 | 0.917 | 1.172 | 1.113 | 1.106 | 1.273 | 6.02E-04 |
| cds.Camellia_sinensis.comp34466_c0_seq1_m.25934 | PREDICTED: DNA-directed RNA polymerases II, IV and V subunit 3 [Theobroma cacao] | 35.758 | 79.419 | 20.7 | 5 | 5 | 5 | 0.957 | 0.922 | 1.028 | 1.021 | 1.039 | 1.033 | 1.064 | 1.23E-01 |
| cds.Camellia_sinensis.comp34468_c1_seq28_m.18467 | PREDICTED: ornithine aminotransferase, mitochondrial-like [Juglans regia] | 52.303 | 72.236 | 33.2 | 12 | 26 | 12 | 0.943 | 0.959 | 0.979 | 1.04 | 1.067 | 1.031 | 1.089 | 4.64E-03 |
| cds.Camellia_sinensis.comp34468_c1_seq3_m.20334 | PREDICTED: KH domain-containing protein At4g18375-like [Malus domestica] | 41.231 | 1.5079 | 2.4 | 1 | 1 | 1 | 1.211 | 1.186 | 1.27 | 0.841 | 0.722 | 0.713 | 0.621 | 1.08E-03 |

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| cds.Camellia_sinensis.comp34468_c1_seq6_m.20890 | PREDICTED: KH domain-containing protein At4g18375-like [Prunus mume] | 26.268 | 12.034 | 12.8 | 3 | 4 | 3 | 1.156 | 1.142 | 1.255 | 0.789 | 0.797 | 0.811 | 0.675 | 2.18E-04 |
| cds.Camellia_sinensis.comp34470_c0_seq10_m.5228 | PREDICTED: golgin candidate 5 [Jatropha curcas] | 109.71 | 4.4135 | 2.8 | 3 | 3 | 3 | 0.948 | 1.008 | 1.039 | 1.034 | 0.975 | 1.013 | 1.009 | 7.83E-01 |
| cds.Camellia_sinensis.comp34474_c0_seq1_m.4870 | PREDICTED: heat shock 70 kDa protein 17 [Nelumbo nucifera] | 51.457 | 7.1507 | 7.3 | 3 | 4 | 3 | 0.941 | 1.099 | 1.035 | 1.088 | 0.954 | 0.999 | 0.989 | 8.67E-01 |
| cds.Camellia_sinensis.comp34474_c0_seq1_m.4871 | PREDICTED: heat shock 70 kDa protein 17-like [Populus euphratica] | 33.998 | 4.8345 | 12.8 | 3 | 3 | 3 | 0.94 | 1.058 | 0.943 | 1.004 | 1.068 | 1.006 | 1.047 | 3.48E-01 |
| cds.Camellia_sinensis.comp34480_c0_seq10_m.23118 | PREDICTED: glucan endo-1,3-beta-glucosidase 8 [Vitis | 52.902 | 14.094 | 12.4 | 5 | 5 | 5 | 0.909 | 0.95 | 1.017 | 1.051 | 0.938 | 1.034 | 1.051 | 3.61E-01 |

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| cds.Camellia_sinensis.comp34481_c0_seq1_m.8834 | PREDICTED: protein TOC75-3, chloroplastic-like [Sesamum indicum] | 89.873 | 123.2 | 27.1 | 19 | 32 | 19 | 0.98 | 0.985 | 0.986 | 0.998 | 1.007 | 1.01 | 1.022 | 6.16E-03 |
| cds.Camellia_sinensis.comp34481_c0_seq3_m.20244 | PREDICTED: leucine-rich repeat extensin-like protein 4 [Citrus sinensis] | 52.66 | 23.249 | 7.8 | 3 | 5 | 3 | 0.918 | 0.989 | 1.017 | 1.006 | 1.002 | 1.017 | 1.035 | 3.76E-01 |
| cds.Camellia_sinensis.comp34487_c0_seq1_m.16775 | PREDICTED: eukaryotic translation initiation factor 2 subunit gamma-like [Jatropha curcas] | 50.748 | 88.553 | 24.6 | 10 | 14 | 10 | 0.961 | 0.95 | 0.95 | 1.031 | 1.058 | 1.046 | 1.096 | 4.03E-04 |
| cds.Camellia_sinensis.comp34487_c0_seq7_m.35493 | PREDICTED: MICOS complex subunit mic25a-like isoform X2 [Nelumbo nucifera] | 21.575 | 2.2728 | 20.5 | 4 | 4 | 4 | 1.141 | 1.133 | 1.106 | 0.827 | 0.832 | 0.92 | 0.763 | 1.62E-03 |

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| cds.Camellia_sinensis.comp34488_c1_seq1_m.29564 | PREDICTED: AB hydrolase superfamily protein YfhM-like [Prunus mume] | 43.349 | 10.761 | 12.9 | 6 | 8 | 4 | 0.988 | 1.005 | 0.97 | 1.065 | 0.987 | 0.989 | 1.026 | 4.00E-01 |
| cds.Camellia_sinensis.comp34488_c1_seq2_m.29851 | PREDICTED: bifunctional epoxide hydrolase 2 [Citrus sinensis] | 35.255 | 4.0585 | 17.7 | 6 | 10 | 4 | 0.991 | 0.955 | 1.033 | 1.019 | 1.037 | 0.983 | 1.02 | 5.05E-01 |
| cds.Camellia_sinensis.comp34490_c0_seq1_m.3865 | PREDICTED: isoleucine--tRNA ligase, chloroplastic/mitochondrial isoform X2 [Vitis vinifera] | 110.79 | 38.967 | 13.2 | 13 | 14 | 13 | 0.993 | 1.025 | 1.039 | 0.982 | 0.986 | 0.967 | 0.96 | 5.05E-02 |
| cds.Camellia_sinensis.comp34490_c1_seq2_m.18307 | At2g47010/F14M4.16 [Arabidopsis lyrata subsp. | 56.641 | 68.133 | 19.4 | 9 | 19 | 9 | 0.958 | 0.978 | 0.955 | 1.042 | 1.035 | 1.053 | 1.083 | 9.03E-04 |
| cds.Camellia_sinensis.comp34493_c0_seq21_m.38449 | PREDICTED: probable cytosolic oligopeptidase A [Sesamum indicum] | 28.832 | 1.2475 | 6.6 | 2 | 4 | 2 | 0.904 | 1.018 | 1.097 | 0.981 | 0.996 | 1.022 | 0.993 | 9.53E-01 |

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| cds.Camellia_sinensis.comp34493_c0_seq83_m.11683 | PREDICTED: probable cytosolic oligopeptidase A [Theobroma cacao] | 18.812 | 2.1577 | 9.2 | 1 | 1 | 1 | 0.802 | 0.915 | 1.052 | 1.089 | 1.149 | 1.047 | 1.186 | 1.00E-01 |
| cds.Camellia_sinensis.comp34499_c1_seq29_m.5013 | PREDICTED: pantothenate kinase 2 [Prunus mume] | 101.98 | 32.834 | 10.3 | 9 | 12 | 9 | 0.943 | 0.944 | 0.944 | 0.977 | 1.032 | 1.022 | 1.071 | 5.64E-02 |
| cds.Camellia_sinensis.comp34500_c0_seq10_m.1120 | PREDICTED: prolyl endopeptidase-like [Sesamum indicum] | 80.844 | 52.152 | 20.2 | 12 | 15 | 12 | 0.978 | 0.956 | 0.97 | 1.04 | 1.06 | 1.041 | 1.082 | 9.95E-04 |
| cds.Camellia_sinensis.comp34502_c0_seq22_m.29373 | PREDICTED: alcohol dehydrogenase-like 7 [Eucalyptus grandis] | 39.085 | 6.3619 | 9.2 | 3 | 4 | 3 | 0.983 | 0.959 | 0.859 | 1.038 | 1.115 | 1.07 | 1.151 | 3.78E-02 |
| cds.Camellia_sinensis.comp34502_c1_seq5_m.34199 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic-like [Camelina sativa] | 13.437 | 11.072 | 22.2 | 4 | 12 | 4 | 0.975 | 0.975 | 0.988 | 1.04 | 1.026 | 1.02 | 1.05 | 2.48E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp34506_c0_seq19_m.24942 | PREDICTED: agmatine deiminase [Ziziphus jujuba] | 42.533 | 16.916 | 18.4 | 8 | 9 | 8 | 0.993 | 1.007 | 1.024 | 1.024 | 0.982 | 1.023 | 1.002 | 9.30E-01 |
| cds.Camellia_sinensis.comp34507_c0_seq23_m.34462 | PREDICTED: ribonuclease J-like isoform X2 [Arachis duranensis] | 30.201 | 1.8403 | 6.2 | 2 | 2 | 1 | 1.031 | 1.105 | 1.105 | 0.953 | 0.839 | 0.955 | 0.848 | 2.67E-02 |
| cds.Camellia_sinensis.comp34508_c2_seq1_m.27588 | PREDICTED: protein STRICTOSIDINE SYNTHASE-LIKE 5-like [Fragaria vesca subsp. vesca] | 46.318 | 26.613 | 16.3 | 7 | 14 | 7 | 0.961 | 0.971 | 0.975 | 1.035 | 1.072 | 1.029 | 1.079 | 4.96E-03 |
| cds.Camellia_sinensis.comp34513_c0_seq1_m.8059 | PREDICTED: conserved oligomeric Golgi complex subunit 3 isoform X1 [Nelumbo nucifera] | 66.093 | 4.7409 | 6.5 | 4 | 4 | 4 | 1.034 | 1.014 | 1.005 | 0.983 | 1.007 | 1.018 | 0.985 | 3.26E-01 |

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| cds.Camellia_sinensis.comp34513_c1_seq1_m.16451 | PREDICTED: beta-(1,2)-xylosyltransferase [Nicotiana attenuata] | 57.07 | 23.518 | 8.1 | 3 | 3 | 3 | 0.919 | 0.999 | 1.046 | 1.007 | 1.014 | 0.975 | 1.011 | 7.78E-01 |
| cds.Camellia_sinensis.comp34514_c0_seq9_m.24763 | PREDICTED: dihydroorotase, mitochondrial isoform X2 [Vitis | 26.318 | 2.1729 | 7.6 | 2 | 2 | 2 | 1.11 | 0.966 | 0.916 | 1.079 | 0.883 | 1.045 | 1.005 | 9.60E-01 |
| cds.Camellia_sinensis.comp34516_c0_seq2_m.44947 | PREDICTED: glutamate synthase 1 [NADH], chloroplastic isoform X2 [Nicotiana attenuata] | 27.441 | 10.571 | 8.4 | 2 | 5 | 2 | 0.973 | 0.941 | 0.963 | 1.086 | 1.112 | 1.034 | 1.123 | 7.94E-03 |
| cds.Camellia_sinensis.comp34516_c1_seq1_m.14271 | PREDICTED: glutamate synthase 1 [NADH], chloroplastic isoform X1 [Vitis vinifera] | 66.623 | 21.001 | 11.4 | 6 | 7 | 4 | 1.034 | 1.033 | 1.016 | 0.992 | 0.99 | 0.91 | 0.938 | 8.94E-02 |

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| cds.Camellia_sinensis.comp34516_c1_seq2_m.46745 | PREDICTED: glutamate synthase [NADH], amyloplastic-like, partial [Nicotiana tabacum] | 25.891 | 24.9 | 26.8 | 5 | 6 | 3 | 0.993 | 0.929 | 1.024 | 0.98 | 1.016 | 1.071 | 1.041 | 3.54E-01 |
| cds.Camellia_sinensis.comp34518_c1_seq1_m.25912 | PREDICTED: novel plant SNARE 13 [Theobrom | 29.468 | 4.8579 | 14.2 | 4 | 4 | 4 | 0.921 | 1.01 | 0.993 | 0.912 | 1.011 | 0.97 | 0.989 | 8.07E-01 |
| cds.Camellia_sinensis.comp34525_c2_seq1_m.3453 | PREDICTED: protein EXPORTIN 1A [Vitis vinifera] | 92.645 | 17.826 | 13.7 | 10 | 14 | 10 | 0.983 | 0.918 | 0.938 | 1.038 | 1.065 | 1.075 | 1.119 | 7.64E-03 |
| cds.Camellia_sinensis.comp34525_c2_seq1_m.3454 | PREDICTED: exportin-1-like isoform X3 [Nicotiana sylvestris] | 29.726 | 36.271 | 21.2 | 6 | 9 | 6 | 0.968 | 0.937 | 0.974 | 1.074 | 1.066 | 1.061 | 1.112 | 1.06E-03 |
| cds.Camellia_sinensis.comp34526_c0_seq2_m.10529 | PREDICTED: luminal-binding protein 5 [Theobroma cacao] | 73.573 | 240.54 | 44 | 30 | 69 | 23 | 1.135 | 1.17 | 1.147 | 0.844 | 0.839 | 0.841 | 0.731 | 2.10E-06 |

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| cds.Camellia_sinensis.comp34526_c1_seq1_m.8583 | PREDICTED: glycerophosphodiester phosphodiesterase GDPDL3-like [Juglans regia] | 86.642 | 67.282 | 10.1 | 6 | 7 | 6 | 0.946 | 0.921 | 0.922 | 1.066 | 1.094 | 1.056 | 1.153 | 4.83E-04 |
| cds.Camellia_sinensis.comp34526_c2_seq2_m.42838 | PREDICTED: RNA-binding protein 8A-B [Nelumbo nucifera] | 22.988 | 11.346 | 22.1 | 4 | 4 | 4 | 0.977 | 1.087 | 1.041 | 0.928 | 0.912 | 0.958 | 0.901 | 3.90E-02 |
| cds.Camellia_sinensis.comp34532_c1_seq1_m.1859 | Mitogen-activated protein kinase kinase kinase 13-A [Morus notabilis] | 59.684 | 6.4866 | 3.1 | 2 | 2 | 1 | 0.962 | 0.972 | 1.055 | 1.006 | 1.015 | 1.005 | 1.012 | 6.98E-01 |
| cds.Camellia_sinensis.comp34532_c1_seq3_m.3564 | Mitogen-activated protein kinase kinase kinase 13-A [Morus notabilis] | 123.02 | 10.571 | 3.2 | 4 | 4 | 2 | 0.911 | 1.011 | 1.094 | 0.876 | 1.157 | 0.967 | 0.995 | 9.29E-01 |

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| cds.Camellia_sinensis.comp34533_c0_seq11_m.1139 | PREDICTED: glutamate synthase 1 [NADH], chloroplastic isoform X1 [Gossypium raimondii] | 135.57 | 2.3808 | 11.2 | 12 | 34 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp34533_c0_seq12_m.1258 | PREDICTED: ferredoxin-dependent glutamate synthase, chloroplastic [Vitis vinifera] | 172.94 | 323.31 | 38.5 | 52 | 154 | 43 | 0.997 | 0.986 | 0.994 | 1.019 | 1.02 | 1.006 | 1.023 | 1.52E-02 |
| cds.Camellia_sinensis.comp34538_c0_seq17_m.16360 | PREDICTED: uncharacterized hydrolase YNR064C-like isoform X2 [Vigna angularis] | 12.823 | 5.5762 | 25.4 | 2 | 2 | 2 | 0.962 | 1.064 | 1.054 | 1.022 | 0.935 | 0.973 | 0.951 | 2.95E-01 |

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| cds.Camellia_sinensis.comp34541_c0_seq1_m.9840 | PREDICTED: ATP-dependent zinc metalloprotease FTSH, chloroplastic [Jatropha curcas] | 76.797 | 323.31 | 51.9 | 30 | 101 | 24 | 0.974 | 0.984 | 0.985 | 1.006 | 1.032 | 1.023 | 1.04 | 9.10E-03 |
| cds.Camellia_sinensis.comp34544_c0_seq2_m.18151 | PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X1 [Vitis vinifera] | 38.735 | 7.7274 | 12.7 | 4 | 4 | 4 | | | | | | | | |
| cds.Camellia_sinensis.comp34545_c0_seq1_m.1794 | PREDICTED: probable inactive ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic [Vitis vinifera] | 152.43 | 1.2732 | 0.5 | 1 | 1 | 1 | 1.164 | 1.155 | 1.165 | 0.796 | 0.886 | 0.79 | 0.71 | 1.14E-02 |

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| cds.Camellia_sinensis.comp34548_c0_seq1_m.8240 | PREDICTED: programmed cell death protein 4 [Vitis vinifera] | 79.412 | 37.641 | 18.4 | 11 | 18 | 8 | 0.971 | 1.012 | 1.007 | 0.998 | 1.006 | 1.002 | 1.005 | 6.99E-01 |
| cds.Camellia_sinensis.comp34548_c0_seq2_m.34446 | PREDICTED: programmed cell death protein 4 [Vitis vinifera] | 28.431 | 9.0893 | 16.9 | 4 | 5 | 1 | 0.979 | 1.042 | 0.975 | 1.035 | 0.929 | 1.052 | 1.007 | 9.06E-01 |
| cds.Camellia_sinensis.comp34549_c1_seq1_m.3197 | PREDICTED: protein CLP1 homolog [Sesamum indicum] | 46.684 | 8.7579 | 8.2 | 3 | 3 | 3 | 0.932 | 1.044 | 0.976 | 1.049 | 0.909 | 1.105 | 1.038 | 6.33E-01 |
| cds.Camellia_sinensis.comp34553_c0_seq10_m.35414 | PREDICTED: glutathionyl-hydroquinone reductase YqjG-like [Nicotiana tabacum] | 31.986 | 7.0224 | 7.4 | 2 | 2 | 2 | 1.017 | 0.977 | 0.979 | 1.08 | 0.973 | 0.988 | 1.023 | 5.69E-01 |
| cds.Camellia_sinensis.comp34553_c0_seq11_m.37196 | PREDICTED: protein VAC14 homolog [Sesamum indicum] | 25.829 | 1.9708 | 4.3 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34553_c0_seq19_m.46997 | PREDICTED: protein VAC14 homolog [Ricinus communis] | 24.907 | 1.2425 | 4.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34553_c0_seq4_m.21377 | PREDICTED: protein VAC14 homolog [Jatropha curcas] | 57.909 | 10.571 | 8.8 | 4 | 5 | 4 | 0.948 | 0.931 | 0.96 | 1.075 | 1.05 | 1.065 | 1.124 | 4.83E-04 |
| cds.Camellia_sinensis.comp34553_c0_seq5_m.24176 | PREDICTED: dynamin-related protein 1C [Juglans regia] | 51.436 | 12.331 | 13.5 | 5 | 7 | 2 | 0.974 | 0.945 | 0.991 | 1.009 | 1.041 | 1.005 | 1.05 | 5.21E-02 |
| cds.Camellia_sinensis.comp34557_c0_seq17_m.14225 | PREDICTED: ABC transporter C family member 2 [Vitis vinifera] | 81.457 | 96.453 | 22.1 | 18 | 26 | 18 | 0.995 | 1.001 | 1.02 | 0.998 | 0.982 | 0.971 | 0.978 | 1.17E-01 |
| cds.Camellia_sinensis.comp34560_c1_seq1_m.10301 | PREDICTED: wall-associated receptor kinase-like 1 [Vitis vinifera] | 81.16 | 8.2556 | 4.4 | 3 | 3 | 3 | 1.09 | 0.948 | 1.142 | 0.848 | 0.936 | 1.018 | 0.881 | 1.76E-01 |

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| cds.Camellia_sinensis.comp34561_c0_seq5_m.12030 | PREDICTED: LOW QUALITY PROTEIN: protein furry homolog-like [Sesamum indicum] | 89.56 | 1.1866 | 1.3 | 1 | 1 | 1 | 0.869 | 0.976 | 1.037 | 0.975 | 1.091 | 1.081 | 1.092 | 2.30E-01 |
| cds.Camellia_sinensis.comp34564_c0_seq5_m.14216 | PREDICTED: dynamin-related protein 4C-like [Erythranthe guttata] | 77.371 | 20.686 | 11.9 | 8 | 10 | 8 | 1.022 | 1.053 | 1.018 | 0.981 | 0.975 | 0.965 | 0.944 | 8.16E-03 |
| cds.Camellia_sinensis.comp34568_c0_seq4_m.3640 | PREDICTED: ubiquitin-activating enzyme E1 1 [Vitis vinifera] | 121.65 | 154.31 | 28.3 | 26 | 38 | 20 | 0.975 | 0.982 | 1 | 1.013 | 1.006 | 0.998 | 1.02 | 8.13E-02 |
| cds.Camellia_sinensis.comp34568_c0_seq7_m.14820 | PREDICTED: glucose-6-phosphate isomerase, cytosolic [Sesamum indicum] | 62.775 | 99.277 | 25.2 | 15 | 35 | 15 | 1.001 | 0.964 | 0.958 | 1.024 | 1.038 | 1.034 | 1.059 | 1.57E-02 |
| cds.Camellia_sinensis.comp34570_c0_seq2_m.2150 | PREDICTED: transportin-1 isoform X1 [Vitis vinifera] | 100.93 | 52.604 | 12.9 | 10 | 11 | 10 | 0.934 | 0.971 | 1.012 | 1.032 | 1.001 | 1.074 | 1.065 | 1.10E-01 |

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| cds.Camellia_sinensis.comp34575_c0_seq1_m.23342 | PREDICTED: bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase isoform X2 [Vitis | 52.631 | 69.467 | 23.8 | 9 | 11 | 9 | 1.061 | 1.113 | 1.066 | 0.881 | 0.876 | 0.956 | 0.837 | 5.14E-03 |
| cds.Camellia_sinensis.comp34575_c1_seq35_m.27645 | PREDICTED: ranBP2-type zinc finger protein At1g67325 isoform X1 [Vitis vinifera] | 30.904 | 3.5299 | 6.4 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34576_c0_seq2_m.20834 | PREDICTED: ATP-dependent 6-phosphofructokinase 2 [Theobrom | 56.344 | 4.6632 | 8.2 | 4 | 5 | 3 | 1.021 | 1.055 | 0.99 | 0.971 | 0.993 | 0.971 | 0.957 | 9.38E-02 |
| cds.Camellia_sinensis.comp34580_c0_seq5_m.8252 | PREDICTED: protein fluG [Vitis vinifera] | 94.155 | 101.14 | 18.5 | 12 | 16 | 12 | 0.928 | 0.955 | 0.98 | 1.026 | 1.041 | 1.056 | 1.091 | 8.10E-03 |

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| cds.Camellia_sinensis.comp34583_c0_seq1_m.9794 | PREDICTED: glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2 [Vitis vinifera] | 74.672 | 17.668 | 7.9 | 5 | 5 | 5 | 0.936 | 0.931 | 0.864 | 1.076 | 1.086 | 1.113 | 1.199 | 2.78E-03 |
| cds.Camellia_sinensis.comp34585_c0_seq8_m.15571 | PREDICTED: CBL-interacting protein kinase 04 isoform X1 [Vitis vinifera] | 41.985 | 2.53 | 3.2 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34586_c0_seq4_m.32396 | PREDICTED: endochitinase PR4-like [Nelumbo nucifera] | 24.711 | 10.503 | 11.5 | 2 | 2 | 2 | 0.855 | 0.774 | 0.763 | 1.226 | 1.205 | 1.246 | 1.537 | 3.16E-04 |
| cds.Camellia_sinensis.comp34588_c0_seq1_m.16583 | PREDICTED: adenylosuccinate synthetase 2, chloroplastic-like [Nelumbo nucifera] | 54.314 | 118.54 | 27.5 | 13 | 26 | 13 | 0.984 | 1.004 | 1.003 | 1.021 | 1.013 | 1.008 | 1.017 | 8.79E-02 |

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| cds.Camellia_sinensis.comp34590_c1_seq4_m.24841 | PREDICTED: L-2-hydroxyglutarate dehydrogenase, mitochondrial isoform X1 [Vitis | 46.031 | 2.037 | 4.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34593_c0_seq13_m.30739 | PREDICTED: arginine--tRNA ligase, cytoplasmic-like isoform X2 [Sesamum indicum] | 38.734 | 49.981 | 47.5 | 15 | 21 | 15 | 0.976 | 0.963 | 0.964 | 1.034 | 1.056 | 1 | 1.064 | 1.94E-02 |
| cds.Camellia_sinensis.comp34593_c1_seq8_m.38584 | PREDICTED: arginine--tRNA ligase, cytoplasmic-like isoform X2 [Sesamum indicum] | 28.805 | 73.985 | 40.5 | 9 | 12 | 9 | 0.974 | 0.99 | 1.004 | 1.039 | 1.035 | 0.991 | 1.033 | 1.42E-01 |
| cds.Camellia_sinensis.comp34595_c0_seq15_m.9001 | UDP-glycosyltransferase 73C2 [Morus notabilis] | 56.321 | 83.053 | 20.5 | 11 | 26 | 11 | 0.993 | 0.998 | 1.001 | 0.998 | 1.036 | 0.992 | 1.011 | 4.65E-01 |

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| cds.Camellia_sinensis.comp34599_c0_seq1_m.633 | PREDICTED: protein lingerer isoform X1 [Vitis vinifera] | 93.084 | 4.1394 | 1.7 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34604_c1_seq6_m.34115 | PREDICTED: 50S ribosomal protein L1, chloroplastic [Sesamum indicum] | 34.331 | 83.202 | 40.3 | 14 | 28 | 14 | 1.075 | 1.035 | 1.033 | 0.953 | 0.947 | 0.946 | 0.906 | 1.68E-03 |
| cds.Camellia_sinensis.comp34606_c0_seq6_m.25994 | PREDICTED: 2-alkenal reductase (NADP(+)-dependent)-like [Sesamum indicum] | 38.633 | 64.812 | 37.3 | 13 | 34 | 12 | 0.948 | 0.936 | 0.933 | 1.06 | 1.072 | 1.053 | 1.131 | 6.35E-05 |
| cds.Camellia_sinensis.comp34608_c0_seq8_m.29269 | PREDICTED: replication factor C subunit 5 [Theobroma cacao] | 39.34 | 8.6074 | 13.7 | 5 | 5 | 5 | 0.886 | 0.961 | 0.905 | 1.062 | 1.082 | 1.139 | 1.193 | 5.32E-03 |

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| cds.Camellia_sinensis.comp34614_c0_seq18_m.43313 | putative ADP-ribosylation factor GTPase-activating protein AGD5 [Morus notabilis] | 29.563 | 1.8704 | 5.2 | 2 | 2 | 2 | 1.079 | 1.029 | 0.957 | 0.95 | 0.953 | 1.024 | 0.955 | 3.46E-01 |
| cds.Camellia_sinensis.comp34614_c0_seq20_m.44756 | PREDICTED: probable ADP-ribosylation factor GTPase-activating protein AGD5 [Capsicum annuum] | 21.264 | 1.9202 | 4.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34619_c0_seq3_m.17747 | PREDICTED: phosphomevalonate kinase isoform X1 [Vitis vinifera] | 54.117 | 1.4173 | 2.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34627_c0_seq4_m.31090 | PREDICTED: clavaminate synthase-like protein At3g21360 [Vitis vinifera] | 36.8 | 12.654 | 16.1 | 5 | 5 | 5 | 0.951 | 0.93 | 0.989 | 1.059 | 1.03 | 1.066 | 1.099 | 1.04E-02 |

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| cds.Camellia_sinensis.comp34633_c0_seq5_m.39298 | PREDICTED: NADH--cytochrome b5 reductase 1 isoform X2 [Ricinus communis] | 30.415 | 1.4866 | 5.9 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34641_c0_seq5_m.25316 | PREDICTED: leucine--tRNA ligase, cytoplasmic-like [Nelumbo nucifera] | 50.012 | 20.908 | 31.8 | 12 | 15 | 7 | 0.965 | 1.02 | 0.93 | 1.051 | 1.029 | 1.032 | 1.068 | 7.52E-02 |
| cds.Camellia_sinensis.comp34641_c0_seq9_m.35789 | PREDICTED: leucine--tRNA ligase, cytoplasmic-like [Nelumbo nucifera] | 41.856 | 20.258 | 23.3 | 7 | 14 | 7 | 0.968 | 0.964 | 0.969 | 1.062 | 1.016 | 1.037 | 1.074 | 3.14E-02 |
| cds.Camellia_sinensis.comp34643_c0_seq2_m.5535 | PREDICTED: formin-like protein 3 isoform X1 [Fragaria vesca subsp. | 57.687 | 3.8452 | 2.8 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp34643_c0_seq3_m.10744 | PREDICTED: beta-galactosidase 9 isoform X1 [Citrus sinensis] | 81.319 | 23.389 | 12.3 | 9 | 17 | 9 | 0.994 | 0.98 | 0.99 | 1.007 | 1 | 0.981 | 1.008 | 4.18E-01 |
| cds.Camellia_sinensis.comp34643_c0_seq7_m.44936 | PREDICTED: beta-galactosidase 9 [Ziziphus jujuba] | 18.296 | 12.838 | 25.2 | 4 | 8 | 4 | 0.938 | 0.988 | 1.023 | 1.048 | 1.041 | 1.01 | 1.051 | 1.44E-01 |
| cds.Camellia_sinensis.comp34645_c2_seq10_m.12522 | PREDICTED: TBC1 domain family member 17 isoform X3 [Vitis vinifera] | 80.592 | 18.723 | 12.3 | 7 | 8 | 7 | 0.951 | 0.963 | 0.999 | 1.057 | 0.994 | 1.008 | 1.05 | 1.09E-01 |
| cds.Camellia_sinensis.comp34645_c2_seq6_m.4156 | PREDICTED: probable sucrose-phosphate synthase isoform X3 [Nicotiana tabacum] | 118.13 | 15.906 | 9.5 | 11 | 13 | 7 | 1.089 | 1.163 | 1.099 | 0.87 | 0.874 | 0.877 | 0.782 | 7.04E-03 |
| cds.Camellia_sinensis.comp34645_c2_seq7_m.4543 | PREDICTED: probable sucrose-phosphate synthase 3 [Prunus mume] | 119.66 | 40.225 | 12.3 | 15 | 18 | 11 | 1.092 | 1.022 | 1.092 | 0.883 | 0.926 | 0.937 | 0.857 | 5.64E-03 |

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| cds.Camellia_sinensis.comp34650_c0_seq1_m.31180 | PREDICTED: probable S-adenosylmethionine-dependent methyltransferase At5g37990 [Vitis vinifera] | 40.715 | 11.405 | 15.5 | 6 | 8 | 6 | 0.977 | 0.942 | 1.042 | 0.987 | 1.03 | 1.021 | 1.026 | 4.59E-01 |
| cds.Camellia_sinensis.comp34652_c0_seq1_m.14108 | PREDICTED: patatin-like phospholipase domain-containing protein 2 isoform X1 [Nicotiana tomentosiformis] | 47.37 | 1.883 | 2.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34662_c1_seq5_m.34836 | PREDICTED: nucleoid-associated protein At2g24020, chloroplastic-like [Nelumbo nucifera] | 21.74 | 75.859 | 55.2 | 9 | 23 | 9 | 0.972 | 0.991 | 0.983 | 1.041 | 1.01 | 1.031 | 1.046 | 1.29E-02 |

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| cds.Camellia_sinensis.comp34663_c0_seq10_m.34729 | PREDICTED: 50S ribosomal protein L15, chloroplastic [Vitis vinifera] | 29.408 | 47.897 | 29.7 | 7 | 10 | 7 | 1.179 | 1.227 | 1.204 | 0.766 | 0.789 | 0.787 | 0.649 | 4.20E-06 |
| cds.Camellia_sinensis.comp34663_c0_seq4_m.5288 | ATP-NAD kinase family protein [Populus trichocarpa] | 104.87 | 7.2113 | 4.9 | 4 | 5 | 4 | 0.957 | 0.889 | 0.861 | 1.09 | 1.075 | 1.159 | 1.228 | 6.14E-03 |
| cds.Camellia_sinensis.comp34664_c1_seq3_m.34598 | PREDICTED: peroxisomal (S)-2-hydroxy-acid oxidase GLO4 [Solanum lycopersicum] | 37.428 | 27.271 | 19.2 | 6 | 9 | 6 | 0.956 | 1.015 | 1.013 | 1.004 | 1.002 | 1.045 | 1.022 | 4.02E-01 |
| cds.Camellia_sinensis.comp34665_c2_seq9_m.7129 | PREDICTED: ABC transporter C family member 2 [Theobroma cacao] | 102.12 | 78.415 | 10.2 | 9 | 15 | 9 | 1.01 | 0.996 | 1.041 | 0.964 | 0.962 | 0.995 | 0.959 | 6.82E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp34674_c0_seq1_m.19224 | PREDICTED: phosphoribosylamine--glycine ligase [Daucus carota subsp. sativus] | 55.786 | 100.69 | 34.3 | 13 | 13 | 13 | 1.012 | 0.947 | 1.055 | 1.035 | 0.961 | 1.039 | 1.007 | 8.66E-01 |
| cds.Camellia_sinensis.comp34674_c1_seq1_m.45225 | PREDICTED: protein CutA, chloroplastic [Citrus sinensis] | 20.119 | 31.688 | 24.1 | 5 | 9 | 5 | 0.989 | 0.88 | 0.912 | 1.09 | 1.118 | 1.046 | 1.17 | 1.63E-02 |
| cds.Camellia_sinensis.comp34685_c0_seq1_m.17248 | group 1 family glycosyltransferase [Medicago truncatula] | 56.927 | 23.804 | 9.8 | 5 | 9 | 5 | 0.985 | 1.028 | 1.023 | 0.992 | 0.991 | 0.957 | 0.968 | 1.48E-01 |
| cds.Camellia_sinensis.comp34691_c0_seq2_m.30056 | PREDICTED: stromal 70 kDa heat shock-related protein, chloroplastic-like [Lupinus angustifolius] | 37.758 | 124.04 | 44.3 | 16 | 45 | 9 | 0.94 | 0.925 | 0.905 | 1.084 | 1.093 | 1.082 | 1.177 | 1.41E-04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp34695_c0_seq5_m.19447 | PREDICTED: DEAD-box ATP-dependent RNA helicase 35 [Gossypium raimondii] | 60.629 | 1.3572 | 1.3 | 1 | 1 | 1 | 1.025 | 1.054 | 0.976 | 1.003 | 0.962 | 0.981 | 0.964 | 2.31E-01 |
| cds.Camellia_sinensis.comp34697_c1_seq1_m.2737 | PREDICTED: 5'-3' exoribonuclease 3 [Vitis vinifera] | 126.6 | 2.0083 | 1.4 | 2 | 2 | 2 | 1.027 | 1.058 | 1.03 | 0.949 | 0.977 | 0.955 | 0.925 | 3.80E-03 |
| cds.Camellia_sinensis.comp34698_c0_seq1_m.3023 | PREDICTED: DNA-directed RNA polymerases IV and V subunit 2 [Solanum lycopersic | 137.92 | 3.0848 | 1.6 | 2 | 2 | 2 | 1.063 | 1.027 | 1.069 | 0.946 | 0.919 | 0.966 | 0.896 | 4.58E-03 |
| cds.Camellia_sinensis.comp34700_c0_seq1_m.18868 | UDP-glycosyltransferase 71C3 [Morus notabilis] | 56.597 | 37.281 | 12.1 | 6 | 15 | 6 | 1.086 | 1.021 | 1.053 | 0.909 | 0.923 | 0.983 | 0.891 | 1.78E-02 |

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| cds.Camellia_sinensis.comp34706_c0_seq9_m.31711 | PREDICTED: glutamyl-tRNA reductase-binding protein, chloroplastic isoform X1 [Nelumbo nucifera] | 37.928 | 15.911 | 15.3 | 5 | 6 | 5 | 1.034 | 1.126 | 1.07 | 0.932 | 0.936 | 0.858 | 0.844 | 1.07E-02 |
| cds.Camellia_sinensis.comp34712_c0_seq4_m.22172 | PREDICTED: importin subunit beta-1 [Vitis vinifera] | 57.069 | 8.9628 | 16.7 | 6 | 9 | 3 | 1.038 | 1.042 | 0.984 | 0.94 | 0.929 | 0.952 | 0.921 | 1.41E-02 |
| cds.Camellia_sinensis.comp34717_c0_seq1_m.15886 | PREDICTED: probable splicing factor 3A subunit 1 [Beta vulgaris subsp. vulgaris] | 44.567 | 23.655 | 6.4 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34717_c0_seq1_m.15888 | PREDICTED: probable splicing factor 3A subunit 1 [Vitis vinifera] | 23.346 | 46.449 | 47.6 | 8 | 11 | 8 | 1.018 | 0.975 | 1.021 | 1.01 | 0.972 | 1.031 | 1 | 9.87E-01 |

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| cds.Camellia_sinensis.comp34717_c1_seq3_m.37342 | PREDICTED: probable splicing factor 3A subunit 1 [Vitis vinifera] | 25.445 | 14.626 | 10.5 | 2 | 2 | 2 | 0.962 | 0.923 | 0.99 | 1.059 | 0.996 | 1.094 | 1.095 | 5.69E-02 |
| cds.Camellia_sinensis.comp34722_c0_seq1_m.7470 | PREDICTED: alpha-L-fucosidase 2-like isoform X1 [Populus euphratica] | 45.366 | 9.3131 | 6.2 | 2 | 2 | 2 | 0.986 | 0.979 | 0.935 | 0.921 | 1.072 | 1.116 | 1.072 | 3.35E-01 |
| cds.Camellia_sinensis.comp34722_c0_seq2_m.21225 | PREDICTED: alpha-L-fucosidase 2-like isoform X2 [Juglans regia] | 46.676 | 14.981 | 6.4 | 2 | 3 | 2 | 0.983 | 1.002 | 0.917 | 1.039 | 1.07 | 1.008 | 1.074 | 8.78E-02 |
| cds.Camellia_sinensis.comp34728_c0_seq1_m.3101 | PREDICTED: serine/threonine-protein phosphatase BSL3 [Gossypium arboreum] | 106.39 | 26.306 | 8.7 | 8 | 9 | 8 | 0.97 | 0.99 | 0.989 | 0.999 | 0.987 | 1.032 | 1.023 | 1.97E-01 |

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| cds.Camellia_sinensis.comp34735_c0_seq10_m.10269 | PREDICTED: DNA gyrase subunit B, chloroplastic/mitochondrial [Vitis vinifera] | 84.962 | 2.7479 | 7.1 | 4 | 5 | 2 | 0.968 | 1.069 | 1.054 | 0.957 | 0.954 | 0.996 | 0.94 | 1.49E-01 |
| cds.Camellia_sinensis.comp34735_c0_seq6_m.9683 | PREDICTED: DNA gyrase subunit B, chloroplastic/mitochondrial [Nicotiana tabacum] | 69.374 | 15.312 | 9.7 | 5 | 5 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp34739_c0_seq2_m.24439 | PREDICTED: ribosome-binding ATPase YchF [Ricinus communis] | 46.296 | 48.637 | 31.3 | 11 | 17 | 11 | 1.033 | 1.07 | 1.037 | 0.953 | 0.969 | 0.945 | 0.913 | 2.44E-03 |
| cds.Camellia_sinensis.comp34739_c0_seq4_m.27322 | PREDICTED: transcription factor Pur-alpha 1 [Vitis vinifera] | 32.266 | 48.111 | 40.4 | 12 | 17 | 12 | 0.983 | 0.976 | 0.979 | 1.045 | 0.99 | 1.009 | 1.036 | 1.58E-01 |
| cds.Camellia_sinensis.comp34743_c1_seq4_m.16761 | PREDICTED: chaperone protein dnaJ 13 [Vitis vinifera] | 60.258 | 11.678 | 5.4 | 3 | 3 | 3 | 1.005 | 1.015 | 1.022 | 1.042 | 0.922 | 1.002 | 0.975 | 5.41E-01 |

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| cds.Camellia_sinensis.comp34744_c0_seq7_m.6769 | PREDICTED: probable alanine--tRNA ligase, chloroplastic isoform X2 [Sesamum indicum] | 43.522 | 70.825 | 31.2 | 10 | 14 | 8 | 1.051 | 0.983 | 1.028 | 0.968 | 0.953 | 0.987 | 0.95 | 8.13E-02 |
| cds.Camellia_sinensis.comp34745_c0_seq3_m.30675 | PREDICTED: 3-methyl-2-oxobutanoate hydroxymethyltransferase 1, mitochondrial [Juglans regia] | 38.47 | 12.005 | 7.9 | 3 | 4 | 3 | 1.094 | 1.034 | 1.153 | 1.014 | 0.862 | 0.831 | 0.825 | 4.70E-02 |
| cds.Camellia_sinensis.comp34747_c0_seq1_m.25473 | PREDICTED: protein ECERIFERUM 1 [Theobroma cacao] | 38.368 | 1.8741 | 4.7 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34748_c1_seq9_m.32783 | PREDICTED: tetratricopeptide repeat protein 1 [Theobroma cacao] | 31.663 | 10.31 | 13.1 | 3 | 3 | 3 | 1.073 | 1.045 | 0.987 | 1.052 | 0.892 | 0.948 | 0.931 | 2.50E-01 |

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| cds.Camellia_sinensis.comp34751_c1_seq2_m.18448 | PREDICTED: trafficking protein particle complex II-specific subunit 120 homolog isoform X1 [Vitis vinifera] | 49.679 | 3.8305 | 5 | 2 | 3 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34751_c2_seq1_m.4380 | PREDICTED: probable polyribonucleotide nucleotidyltransferase 1, chloroplastic [Vitis vinifera] | 69.87 | 29.843 | 12.9 | 7 | 8 | 7 | 1.138 | 1.204 | 1.142 | 0.772 | 0.88 | 0.9 | 0.732 | 3.62E-03 |
| cds.Camellia_sinensis.comp34751_c2_seq1_m.4381 | PREDICTED: polyribonucleotide nucleotidyltransferase 1, chloroplastic-like [Nicotiana tabacum] | 33.056 | 2.9873 | 9.3 | 3 | 3 | 3 | 1.075 | 1.083 | 1.152 | 0.889 | 0.875 | 0.904 | 0.806 | 8.39E-04 |

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| cds.Camellia_sinensis.comp34753_c0_seq2_m.17644 | PREDICTED: nuclear pore complex protein NUP98A [Vitis vinifera] | 69.604 | 7.6347 | 8.6 | 6 | 6 | 5 | 0.941 | 1.025 | 1.005 | 1.06 | 0.991 | 0.998 | 1.026 | 4.80E-01 |
| cds.Camellia_sinensis.comp34756_c1_seq2_m.1669 | PREDICTED: sister chromatid cohesion protein PDS5 homolog A isoform X2 [Vitis vinifera] | 95.499 | 1.421 | 1.2 | 1 | 1 | 1 | 0.977 | 0.948 | 0.938 | 1.141 | 1.014 | 1.009 | 1.105 | 7.89E-02 |
| cds.Camellia_sinensis.comp34763_c0_seq1_m.14738 | glutamate--cysteine ligase, chloroplastic [Nicotiana tabacum] | 59.457 | 98.571 | 26.4 | 13 | 26 | 13 | 0.996 | 1.004 | 0.973 | 0.986 | 1.005 | 0.995 | 1.004 | 7.06E-01 |
| cds.Camellia_sinensis.comp34765_c0_seq33_m.14153 | PREDICTED: thioredoxin reductase NTRC [Ipomoea | 36.436 | 52.225 | 30 | 8 | 16 | 8 | 0.98 | 0.978 | 1.026 | 1.019 | 0.983 | 1.014 | 1.011 | 6.06E-01 |

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| cds.Camellia_sinensis.comp34765_c0_seq72_m.31574 | PREDICTED: U2 small nuclear ribonucleoprotein A' [Ipomoea nil] | 33.296 | 56.787 | 29.8 | 7 | 9 | 7 | 1.143 | 1.172 | 1.146 | 0.895 | 0.872 | 0.816 | 0.746 | 5.16E-04 |
| cds.Camellia_sinensis.comp34765_c0_seq9_m.9901 | PREDICTED: thioredoxin reductase NTRC isoform X1 [Theobrom | 25.838 | 52.381 | 23.8 | 4 | 7 | 4 | 1.029 | 0.973 | 1.009 | 1.033 | 1.022 | 1 | 1.015 | 4.82E-01 |
| cds.Camellia_sinensis.comp34770_c0_seq1_m.4049 | PREDICTED: exocyst complex component SEC5A [Vitis vinifera] | 123.42 | 6.4798 | 1.5 | 1 | 1 | 1 | 1.005 | 1.129 | 1.021 | 1.008 | 0.919 | 0.918 | 0.902 | 9.75E-02 |
| cds.Camellia_sinensis.comp34770_c1_seq1_m.5193 | PREDICTED: L-ascorbate oxidase homolog [Juglans regia] | 59.889 | 18.432 | 7 | 4 | 4 | 3 | 1.009 | 1.057 | 1.038 | 0.942 | 0.943 | 1.009 | 0.932 | 5.63E-02 |

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| cds.Camellia_sinensis.comp34780_c0_seq2_m.3092 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 12 isoform X1 [Vitis vinifera] | 128.19 | 51.784 | 13.4 | 18 | 22 | 12 | 0.975 | 1.016 | 1.01 | 0.988 | 0.995 | 1.023 | 1.002 | 9.23E-01 |
| cds.Camellia_sinensis.comp34783_c0_seq6_m.39458 | PREDICTED: transmembrane emp24 domain-containing protein p24beta2-like [Prunus mume] | 24.746 | 17.025 | 14.5 | 3 | 5 | 3 | 0.933 | 0.997 | 1.006 | 1.006 | 1.037 | 1.065 | 1.059 | 1.19E-01 |
| cds.Camellia_sinensis.comp34786_c0_seq1_m.1054 | PREDICTED: brefeldin A-inhibited guanine nucleotide-exchange protein 2 [Vitis vinifera] | 135.25 | 7.9774 | 1.6 | 2 | 2 | 0 | | | | | | | | |

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| cds.Camellia_sinensis.comp34786_c0_seq1_m.1055 | PREDICTED: brefeldin A-inhibited guanine nucleotide-exchange protein 2 [Citrus sinensis] | 69.982 | 1.6028 | 3.8 | 3 | 3 | 1 | | | | | | | |
| cds.Camellia_sinensis.comp34786_c0_seq3_m.6334 | PREDICTED: brefeldin A-inhibited guanine nucleotide-exchange protein 2-like [Jatropha curcas] | 111.33 | 8.0893 | 5 | 5 | 5 | 2 | | | | | | | |
| cds.Camellia_sinensis.comp34788_c0_seq15_m.2755 | DUF1350 family protein [Medicago truncatula] | 42.48 | 14.013 | 9.2 | 3 | 4 | 1 | 0.93 | 0.888 | 0.965 | 1.082 | 1.086 | 1.084 | 1.169 | 2.29E-02 |

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| cds.Camellia_sinensis.comp34789_c1_seq1_m.8540 | PREDICTED: uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic [Sesamum indicum] | 59.937 | 7.2469 | 3.7 | 2 | 2 | 2 | 0.98 | 0.886 | 1.009 | 1.122 | 1.032 | 0.999 | 1.097 | 1.52E-01 |
| cds.Camellia_sinensis.comp34789_c1_seq2_m.9243 | PREDICTED: uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic isoform X1[Gossypium raimondii] | 21.324 | 2.93 | 6.6 | 1 | 1 | 1 | 0.658 | 1.549 | 0.858 | 0.961 | 1.044 | 0.96 | 0.967 | 9.11E-01 |
| cds.Camellia_sinensis.comp34793_c0_seq4_m.2146 | PREDICTED: tripeptidyl-peptidase 2 isoform X1 [Vitis vinifera] | 109.19 | 130.06 | 34.9 | 30 | 49 | 30 | 1.029 | 1.023 | 1.039 | 0.989 | 0.977 | 0.985 | 0.955 | 1.30E-03 |

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| cds.Camellia_sinensis.comp34793_c0_seq4_m.2147 | PREDICTED: tripeptidyl-peptidase 2 [Nelumbo nucifera] | 15.278 | 5.4707 | 17.3 | 2 | 3 | 2 | 1.121 | 0.917 | 1.036 | 0.97 | 1.041 | 0.911 | 0.951 | 5.24E-01 |
| cds.Camellia_sinensis.comp34798_c0_seq1_m.436 | PREDICTED: serine/threonine-protein kinase TOR [Theobroma cacao] | 277.53 | 14.952 | 3 | 7 | 7 | 7 | 0.804 | 1.867 | 0.819 | 0.714 | 0.785 | 0.977 | 0.709 | 4.09E-01 |
| cds.Camellia_sinensis.comp34802_c1_seq1_m.780 | PREDICTED: chromatin structure-remodeling complex protein SYD isoform X1 [Ziziphus jujuba] | 88.729 | 3.0965 | 3.4 | 3 | 3 | 3 | 1.074 | 1.42 | 1.076 | 0.746 | 0.925 | 0.711 | 0.667 | 3.08E-02 |

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| cds.Camellia_sinensis.comp34805_c0_seq5_m.5158 | PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X4 [Vitis vinifera] | 60.775 | 1.4735 | 2.1 | 1 | 1 | 1 | 0.896 | 1.019 | 1.125 | 1.032 | 0.935 | 1.014 | 0.981 | 8.34E-01 |
| cds.Camellia_sinensis.comp34807_c0_seq18_m.28811 | PREDICTED: adenylate cyclase, terminal-differentiation specific [Vitis vinifera] | 40.865 | 2.0589 | 3.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34809_c0_seq1_m.4649 | PREDICTED: exosome complex exonuclease RRP44 homolog A [Ziziphus | 98.005 | 4.6841 | 2.6 | 2 | 2 | 2 | 0.945 | 0.924 | 0.943 | 1.064 | 1.083 | 1.071 | 1.144 | 1.04E-04 |
| cds.Camellia_sinensis.comp34815_c1_seq34_m.13298 | PREDICTED: zinc finger protein ZPR1 [Vitis vinifera] | 55.299 | 8.5994 | 3.2 | 1 | 1 | 1 | 0.84 | 1.038 | 1.022 | 0.891 | 1.07 | 1.161 | 1.077 | 5.24E-01 |

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| cds.Camellia_sinensis.comp34815_c1_seq62_m.37747 | PREDICTED: bifunctional aspartokinase/homoserine dehydrogenase isoform X5 [Solanum tuberosum | 33.059 | 5.768 | 6.5 | 2 | 2 | 2 | 0.891 | 0.969 | 1.01 | 1.081 | 1.024 | 1.058 | 1.102 | 7.03E-02 |
| cds.Camellia_sinensis.comp34817_c0_seq1_m.16288 | PREDICTED: SEC1 family transport protein SLY1-like [Populus euphratica] | 61.494 | 19.022 | 10.6 | 5 | 5 | 5 | 0.968 | 1.046 | 1.018 | 1.004 | 0.93 | 1.034 | 0.979 | 6.05E-01 |
| cds.Camellia_sinensis.comp34819_c0_seq1_m.987 | PREDICTED: clathrin heavy chain 1 [Vigna radiata var. radiata] | 192.51 | 323.31 | 33.8 | 56 | 98 | 10 | 0.993 | 0.984 | 0.972 | 1.026 | 0.999 | 1.031 | 1.036 | 3.73E-02 |
| cds.Camellia_sinensis.comp34819_c0_seq4_m.1484 | PREDICTED: clathrin heavy chain 1-like [Nelumbo nucifera] | 183.31 | 15.903 | 33.9 | 52 | 93 | 6 | 1.009 | 1.028 | 0.981 | 0.976 | 0.998 | 1.057 | 1.004 | 8.93E-01 |

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| cds.Camellia_sinensis.comp34821_c0_seq1_m.3529 | PREDICTED: protease Do-like 7 isoform X1 [Vitis vinifera] | 122.44 | 79.554 | 17 | 18 | 20 | 12 | 1.004 | 1.018 | 1.014 | 1.006 | 0.981 | 0.968 | 0.973 | 8.67E-02 |
| cds.Camellia_sinensis.comp34821_c0_seq3_m.44578 | PREDICTED: protease Do-like 7 isoform X3 [Lupinus angustifolius] | 27.768 | 36.057 | 33.5 | 8 | 9 | 3 | 0.96 | 0.994 | 1.073 | 1.047 | 0.98 | 0.986 | 0.995 | 9.23E-01 |
| cds.Camellia_sinensis.comp34822_c0_seq70_m.49511 | PREDICTED: allantoinase isoform X2 [Daucus carota subsp. sativus] | 16.693 | 2.6798 | 21.6 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34824_c0_seq1_m.11780 | PREDICTED: cellulose synthase-like protein G3 isoform X2 [Ziziphus jujuba] | 48.382 | 1.5015 | 3.7 | 2 | 2 | 2 | 0.977 | 1.088 | 0.996 | 0.951 | 0.978 | 1.012 | 0.961 | 3.57E-01 |

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| cds.Camellia_sinensis.comp34826_c2_seq3_m.16973 | PREDICTED: eukaryotic translation initiation factor 3 subunit E [Arachis ipaensis] | 51.27 | 110.27 | 28.1 | 12 | 16 | 12 | 0.949 | 0.985 | 0.959 | 1.046 | 0.993 | 1.013 | 1.055 | 4.66E-02 |
| cds.Camellia_sinensis.comp34838_c1_seq1_m.2286 | PREDICTED: coatomer subunit alpha-1 [Ricinus communis] | 136.7 | 124.24 | 17.8 | 22 | 32 | 22 | 1.119 | 1.106 | 1.094 | 0.91 | 0.89 | 0.879 | 0.807 | 5.94E-05 |
| cds.Camellia_sinensis.comp34844_c0_seq1_m.2284 | PREDICTED: ABC transporter B family member 11 [Vitis vinifera] | 114.31 | 14.011 | 6.5 | 5 | 6 | 3 | 1.023 | 0.997 | 1.013 | 1.047 | 0.978 | 0.929 | 0.974 | 4.80E-01 |
| cds.Camellia_sinensis.comp34851_c2_seq1_m.3514 | PREDICTED: cell division cycle 5-like protein [Vitis vinifera] | 113.21 | 2.3616 | 1.9 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34851_c2_seq4_m.8374 | PREDICTED: pre-mRNA-processing protein 40A [Nelumbo nucifera] | 57.399 | 2.4999 | 4.5 | 2 | 2 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp34851_c2_seq4_m.8375 | PREDICTED: pre-mRNA-processing protein 40A isoform X2 [Vitis vinifera] | 44.437 | 4.0584 | 5.7 | 2 | 2 | 2 | 0.839 | 1.253 | 0.834 | 1.133 | 0.982 | 0.99 | 1.061 | 6.22E-01 |
| cds.Camellia_sinensis.comp34867_c0_seq1_m.407 | DUF2921 family protein [Medicago truncatula] | 85.938 | 1.3491 | 1.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp34869_c0_seq1_m.249 | PREDICTED: E3 ubiquitin-protein ligase UPL1 isoform X2 [Vitis vinifera] | 386.46 | 17.637 | 2.8 | 10 | 10 | 7 | 0.977 | 1.134 | 1.069 | 0.946 | 0.917 | 0.933 | 0.879 | 4.56E-02 |
| cds.Camellia_sinensis.comp34870_c0_seq1_m.6900 | PREDICTED: subtilisin-like protease SBT1.5 [Vitis vinifera] | 82.486 | 28.675 | 10 | 6 | 8 | 6 | 0.868 | 0.89 | 0.923 | 1.12 | 1.119 | 1.104 | 1.247 | 2.79E-04 |

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| cds.Camellia_sinensis.comp34876_c1_seq2_m.32424 | PREDICTED: geranylgeranyl transferase type-2 subunit alpha 1 [Vitis vinifera] | 32.118 | 8.5522 | 7.7 | 2 | 2 | 2 | 0.818 | 0.963 | 0.674 | 1.281 | 0.953 | 1.373 | 1.469 | 6.55E-02 |
| cds.Camellia_sinensis.comp34880_c1_seq5_m.13829 | PREDICTED: E3 ubiquitin-protein ligase UPL2 [Vitis vinifera] | 81.209 | 3.3157 | 6.6 | 4 | 5 | 3 | 0.93 | 1.076 | 1.02 | 0.981 | 1.078 | 0.931 | 0.988 | 8.52E-01 |
| cds.Camellia_sinensis.comp34896_c1_seq4_m.388 | PREDICTED: probable phosphoribosylformylglycinamidine synthase, chloroplastic/mitochondrial [Vitis vinifera] | 154.82 | 113.16 | 22.6 | 29 | 43 | 29 | 0.97 | 1.018 | 0.99 | 1.004 | 1.003 | 0.994 | 1.008 | 6.12E-01 |
| cds.Camellia_sinensis.comp34896_c1_seq4_m.390 | PREDICTED: topless-related protein 3-like [Sesamum indicum] | 30.977 | 13.056 | 25.2 | 7 | 10 | 4 | 0.892 | 0.96 | 0.847 | 0.924 | 1.016 | 1.098 | 1.126 | 1.30E-01 |

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| cds.Camellia_sinensis.comp34897_c0_seq1_m.551 | PREDICTED: DExH-box ATP-dependent RNA helicase DExH12-like [Nelumbo nucifera] | 204.09 | 4.9096 | 0.9 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp34899_c0_seq2_m.2747 | PREDICTED: beta-glucosidase 44-like [Citrus sinensis] | 14.95 | 1.4665 | 5.6 | 1 | 2 | 1 | 0.999 | 0.985 | 0.991 | 0.997 | 1.058 | 0.981 | 1.021 | 4.44E-01 |
| cds.Camellia_sinensis.comp34899_c1_seq1_m.31033 | PREDICTED: probable ATP synthase 24 kDa subunit, mitochondrial [Vitis vinifera] | 28.086 | 121.01 | 54.8 | 17 | 51 | 17 | 1.028 | 1.028 | 1.029 | 0.976 | 0.979 | 0.964 | 0.946 | 7.22E-03 |
| cds.Camellia_sinensis.comp34899_c2_seq1_m.7036 | PREDICTED: glutamine--tRNA ligase, cytoplasmic [Vitis vinifera] | 90.976 | 54.287 | 23 | 18 | 28 | 18 | 0.999 | 0.974 | 0.984 | 1.015 | 0.965 | 1.041 | 1.022 | 4.22E-01 |

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| cds.Camellia_sinensis.comp34914_c0_seq1_m.885 | PREDICTED: probable tRNA N6-adenosine threonylcarbamoyltransferase [Theobroma cacao] | 38.531 | 14.1 | 14.5 | 4 | 5 | 4 | 0.887 | 0.993 | 1.063 | 1.062 | 1.003 | 0.96 | 1.028 | 6.52E-01 |
| cds.Camellia_sinensis.comp34919_c0_seq1_m.38285 | PREDICTED: early light-induced protein, chloroplastic [Arachis ipaensis] | 24.048 | 31.945 | 19.2 | 4 | 6 | 4 | 0.91 | 0.941 | 0.964 | 1.001 | 1.06 | 1.114 | 1.128 | 2.71E-02 |
| cds.Camellia_sinensis.comp34921_c0_seq1_m.57219 | PREDICTED: chlorophyll a-b binding protein 151, chloroplastic [Ricinus communis] | 12.857 | 43.093 | 12 | 2 | 19 | 2 | 0.939 | 0.937 | 0.937 | 1.068 | 1.065 | 1.056 | 1.134 | 1.75E-06 |
| cds.Camellia_sinensis.comp34927_c0_seq1_m.40973 | PREDICTED: plastocyanin B'/B" [Ricinus communis] | 17.157 | 87.079 | 38.2 | 3 | 42 | 3 | 0.945 | 0.96 | 0.924 | 1.099 | 1.024 | 1.067 | 1.128 | 6.78E-03 |

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| cds.Camellia_sinensis.comp34929_c0_seq1_m.29202 | PREDICTED: chlorophyll a-b binding protein CP24 10A, chloroplastic [Gossypium hirsutum] | 27.483 | 50.377 | 23.6 | 5 | 20 | 5 | 0.921 | 0.888 | 0.888 | 1.052 | 1.163 | 1.122 | 1.237 | 2.60E-03 |
| cds.Camellia_sinensis.comp34935_c0_seq1_m.42009 | PREDICTED: ferredoxin [Ziziphus jujuba] | 15.691 | 2.9641 | 6.8 | 1 | 3 | 1 | 1.181 | 1.077 | 1.01 | 0.821 | 0.84 | 1.031 | 0.824 | 8.23E-02 |
| cds.Camellia_sinensis.comp34946_c0_seq1_m.36496 | PREDICTED: photosystem I reaction center subunit XI, chloroplastic [Theobroma cacao] | 22.982 | 84.35 | 17.5 | 5 | 13 | 5 | 0.869 | 0.963 | 0.929 | 1.103 | 1.088 | 1.113 | 1.197 | 4.24E-03 |
| cds.Camellia_sinensis.comp34950_c0_seq1_m.37352 | PREDICTED: glutathione S-transferase-like [Sesamum indicum] | 23.86 | 65.342 | 56.6 | 9 | 36 | 9 | 0.99 | 0.996 | 0.937 | 1.056 | 1.01 | 1.026 | 1.058 | 7.35E-02 |

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| cds.Camellia_sinensis.comp34958_c0_seq1_m.22394 | PREDICTED: carbonic anhydrase 2 isoform X1 [Vitis vinifera] | 35.791 | 244.11 | 66.1 | 18 | 90 | 16 | 1.094 | 1.066 | 1.096 | 0.93 | 0.936 | 0.901 | 0.85 | 3.84E-04 |
| cds.Camellia_sinensis.comp34971_c0_seq1_m.24340 | PREDICTED: 60S ribosomal protein L3 [Vitis vinifera] | 44.428 | 36.622 | 27.2 | 13 | 26 | 9 | 1.095 | 1.107 | 1.126 | 0.905 | 0.858 | 0.869 | 0.791 | 2.00E-04 |
| cds.Camellia_sinensis.comp34975_c0_seq1_m.47652 | thylakoid soluble phosphoprotein TSP9 protein [Medicago truncatula] | 11.379 | 18.233 | 44.8 | 6 | 28 | 6 | 1.06 | 1.051 | 1.045 | 0.943 | 0.941 | 0.951 | 0.898 | 3.70E-05 |
| cds.Camellia_sinensis.comp34977_c0_seq1_m.38399 | PREDICTED: 60S ribosomal protein L18-2 [Eucalyptus grandis] | 20.934 | 55.785 | 28.3 | 5 | 9 | 5 | 1.09 | 1.074 | 1.055 | 0.895 | 0.954 | 0.906 | 0.856 | 2.00E-03 |
| cds.Camellia_sinensis.comp34979_c0_seq1_m.37351 | plant/F25P12-18 protein [Medicago truncatula] | 18.363 | 77.213 | 47.3 | 6 | 14 | 6 | 1.332 | 1.28 | 1.31 | 0.71 | 0.626 | 0.669 | 0.511 | 6.05E-05 |

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| cds.Camellia_sinensis.comp34981_c0_seq1_m.15901 | PREDICTED: fructose-bisphosphate aldolase cytoplasmic isozyme [Sesamum | 39.634 | 313.78 | 58.1 | 17 | 55 | 17 | 0.978 | 0.976 | 0.97 | 1.022 | 1.027 | 1.042 | 1.057 | 9.24E-04 |
| cds.Camellia_sinensis.comp34991_c0_seq1_m.15071 | PREDICTED: phosphoglycerate kinase, chloroplastic [Nicotiana sylvestris] | 53.529 | 323.31 | 61.5 | 29 | 145 | 22 | 1.048 | 1.007 | 1.023 | 0.976 | 0.999 | 0.98 | 0.96 | 4.06E-02 |
| cds.Camellia_sinensis.comp34996_c0_seq1_m.19097 | flavonoid 3' hydroxylase [Vitis vinifera] | 57.059 | 17.251 | 19.1 | 9 | 14 | 9 | 1.248 | 1.29 | 1.269 | 0.668 | 0.678 | 0.703 | 0.538 | 2.09E-06 |
| cds.Camellia_sinensis.comp35001_c0_seq1_m.38543 | PREDICTED: glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic [Ziziphus jujuba] | 32.204 | 64.996 | 21.5 | 7 | 29 | 7 | 1.031 | 1.002 | 1.004 | 0.988 | 0.997 | 0.995 | 0.981 | 1.21E-01 |

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| cds.Camellia_sinensis.comp35002_c0_seq1_m.43995 | PREDICTED: 60S ribosomal protein L32-1-like [Cucumis melo] | 15.662 | 11.261 | 26.3 | 4 | 8 | 4 | 1.107 | 1.185 | 1.187 | 0.802 | 0.822 | 0.831 | 0.706 | 1.60E-04 |
| cds.Camellia_sinensis.comp35021_c0_seq1_m.26701 | PREDICTED: 14-3-3-like protein D isoform X1 [Ricinus communis] | 29.45 | 136.13 | 54.8 | 15 | 54 | 11 | 1.002 | 0.984 | 0.959 | 1.012 | 1.023 | 1.02 | 1.037 | 4.86E-02 |
| cds.Camellia_sinensis.comp35026_c0_seq1_m.46440 | photosystem II 5 kD family protein [Populus trichocarpa] | 11.685 | 12.832 | 11.7 | 2 | 14 | 2 | 0.987 | 0.988 | 0.929 | 1.045 | 1.066 | 1.042 | 1.086 | 1.86E-02 |
| cds.Camellia_sinensis.comp35031_c0_seq1_m.8910 | PREDICTED: 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase-like [Nicotiana tabacum] | 84.844 | 187.45 | 35.6 | 27 | 57 | 20 | 1.032 | 1.039 | 1.078 | 0.952 | 0.935 | 0.957 | 0.903 | 2.64E-03 |

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| cds.Camellia_sinensis.comp35037_c0_seq1_m.45235 | macrophage migration inhibition factor-like protein [Medicago | 13.043 | 15.924 | 50 | 4 | 9 | 4 | 1.005 | 0.975 | 0.973 | 1.024 | 1.002 | 1.016 | 1.03 | 7.18E-02 |
| cds.Camellia_sinensis.comp35043_c0_seq1_m.40382 | PREDICTED: 50S ribosomal protein L12, chloroplastic [Solanum lycopersicum] | 19.234 | 79.068 | 41.8 | 11 | 32 | 11 | 0.989 | 0.962 | 0.977 | 1.009 | 1.044 | 1.03 | 1.053 | 1.55E-02 |
| cds.Camellia_sinensis.comp35044_c0_seq1_m.44426 | PREDICTED: cytochrome b5 [Vitis vinifera] | 17.783 | 29.766 | 39.6 | 4 | 8 | 4 | 1.317 | 1.204 | 1.242 | 0.773 | 0.657 | 0.768 | 0.584 | 8.04E-04 |
| cds.Camellia_sinensis.comp35045_c0_seq1_m.29822 | CS domain protein [Medicago truncatula] | 23.006 | 46.815 | 32.7 | 8 | 19 | 8 | 1.184 | 1.134 | 1.152 | 0.794 | 0.808 | 0.858 | 0.709 | 2.03E-04 |
| cds.Camellia_sinensis.comp35046_c0_seq1_m.27092 | PREDICTED: glutamine synthetase nodule isozyme [Ziziphus jujuba] | 39.204 | 24.323 | 36.2 | 12 | 50 | 4 | 1.158 | 1.121 | 1.104 | 0.808 | 0.888 | 0.873 | 0.759 | 1.02E-03 |

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| cds.Camellia_sinensis.comp35051_c0_seq1_m.22526 | PREDICTED: geranylgeranyl diphosphate reductase, chloroplastic [Vitis vinifera] | 54.645 | 67.049 | 23 | 10 | 20 | 10 | 1.046 | 1.025 | 1.084 | 0.94 | 0.95 | 0.95 | 0.9 | 3.30E-03 |
| cds.Camellia_sinensis.comp35057_c0_seq1_m.37888 | PREDICTED: thioredoxin F1, chloroplastic-like [Sesamum indicum] | 19.7 | 17.969 | 19.3 | 4 | 12 | 4 | 1.037 | 1.019 | 1.05 | 0.983 | 0.981 | 0.932 | 0.932 | 2.26E-02 |
| cds.Camellia_sinensis.comp35063_c0_seq1_m.37893 | PREDICTED: peptidyl-prolyl cis-trans isomerase CYP19-4 [Malus domestica] | 22.45 | 48.611 | 36.5 | 7 | 23 | 5 | 1.107 | 1.116 | 1.074 | 0.896 | 0.882 | 0.901 | 0.813 | 9.94E-05 |
| cds.Camellia_sinensis.comp35073_c0_seq1_m.47663 | PREDICTED: 40S ribosomal protein S25-2 [Citrus sinensis] | 14.911 | 4.9295 | 19 | 3 | 3 | 3 | 1.013 | 1.142 | 1.126 | 0.9 | 0.923 | 0.883 | 0.825 | 8.70E-03 |

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| cds.Camellia_sinensis.comp35081_c0_seq1_m.58830 | PREDICTED: elongation factor 1-alpha-like, partial [Gossypium arboreum] | 11.563 | 3.3328 | 63.5 | 7 | 29 | 1 | 0.963 | 1.092 | 0.998 | 1.059 | 0.748 | 1.145 | 0.967 | 7.39E-01 |
| cds.Camellia_sinensis.comp35106_c0_seq1_m.6667 | PREDICTED: inositol-3-phosphate synthase [Nicotiana tomentosiformis] | 56.19 | 186.79 | 29 | 16 | 49 | 16 | 0.901 | 0.884 | 0.874 | 1.103 | 1.142 | 1.123 | 1.267 | 6.03E-05 |
| cds.Camellia_sinensis.comp35107_c0_seq1_m.44017 | PREDICTED: 60S ribosomal protein L30-like [Juglans regia] | 12.241 | 7.8302 | 16.1 | 2 | 5 | 2 | 1.018 | 1.038 | 1.011 | 0.963 | 0.994 | 0.931 | 0.942 | 4.20E-02 |
| cds.Camellia_sinensis.comp35113_c0_seq1_m.25625 | PREDICTED: porphobilinogen deaminase, chloroplastic [Vitis vinifera] | 41.897 | 22.951 | 17.7 | 7 | 11 | 7 | 1.047 | 1.068 | 1.072 | 0.916 | 0.94 | 0.946 | 0.879 | 4.63E-04 |

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| cds.Camellia_sinensis.comp35127_c0_seq1_m.49698 | PREDICTED: phosphoprotein ECPP44-like [Gossypium arboreum] | 13.331 | 96.74 | 73.1 | 7 | 12 | 7 | 0.943 | 0.957 | 0.98 | 1.02 | 1.065 | 1.068 | 1.095 | 8.30E-03 |
| cds.Camellia_sinensis.comp35145_c0_seq1_m.54819 | PREDICTED: stromal 70 kDa heat shock-related protein, chloroplastic-like [Nelumbo nucifera] | 15.126 | 6.7673 | 77 | 12 | 42 | 3 | 1.061 | 1.049 | 1.049 | 0.97 | 0.947 | 0.95 | 0.908 | 3.23E-04 |
| cds.Camellia_sinensis.comp35153_c0_seq1_m.36410 | PREDICTED: universal stress protein PHOS32-like isoform X2 [Juglans regia] | 17.419 | 67.543 | 42.1 | 5 | 10 | 5 | 1 | 0.983 | 0.966 | 1.007 | 1.065 | 1.012 | 1.046 | 9.55E-02 |

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| cds.Camellia_sinensis.comp35156_c0_seq1_m.46856 | PREDICTED: succinate dehydrogenase subunit 7B, mitochondrial-like isoform X1 [Jatropha | 11.324 | 4.8037 | 9.9 | 1 | 4 | 1 | 0.996 | 0.916 | 1.028 | 0.985 | 1.029 | 1.021 | 1.032 | 4.25E-01 |
| cds.Camellia_sinensis.comp35173_c0_seq1_m.9433 | Elongation factor G [Morus notabilis] | 90.514 | 323.31 | 43.5 | 29 | 78 | 29 | 1.01 | 1 | 0.981 | 1.003 | 1.027 | 0.997 | 1.012 | 3.91E-01 |
| cds.Camellia_sinensis.comp35183_c0_seq1_m.41778 | PREDICTED: nucleoside diphosphate kinase 1 [Daucus carota subsp. sativus] | 16.414 | 70.709 | 33.8 | 6 | 15 | 6 | 0.941 | 0.943 | 0.98 | 1.051 | 1.036 | 1.051 | 1.096 | 2.86E-03 |
| cds.Camellia_sinensis.comp35195_c0_seq1_m.31710 | PREDICTED: 30S ribosomal protein S5, chloroplastic-like [Gossypium raimondii] | 37.255 | 98.51 | 32.1 | 12 | 29 | 12 | 1.087 | 1.034 | 1.07 | 0.914 | 0.935 | 0.923 | 0.869 | 9.60E-04 |

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| cds.Camellia_sinensis.comp35198_c0_seq1_m.15306 | PREDICTED: pyruvate kinase, cytosolic isozyme [Jatropha curcas] | 55.114 | 177.63 | 40 | 18 | 34 | 18 | 0.99 | 0.994 | 0.988 | 0.981 | 0.999 | 1.013 | 1.007 | 5.03E-01 |
| cds.Camellia_sinensis.comp35200_c0_seq1_m.30284 | PREDICTED: GDSL esterase/lipase 1-like [Fragaria vesca subsp. vesca] | 40.596 | 1.9736 | 5.2 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp35217_c0_seq1_m.27870 | PREDICTED: leucoanthocyanidin dioxygenase [Theobroma cacao] | 40.057 | 51.661 | 24.5 | 7 | 9 | 7 | 1.343 | 1.36 | 1.416 | 0.567 | 0.584 | 0.561 | 0.416 | 8.03E-07 |
| cds.Camellia_sinensis.comp35229_c0_seq1_m.39687 | PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-B [Daucus carota subsp. sativus] | 21.891 | 23.45 | 38 | 7 | 15 | 7 | 1.016 | 0.995 | 0.988 | 0.993 | 1.004 | 1.002 | 1 | 9.95E-01 |

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| cds.Camellia_sinensis.comp35231_c0_seq1_m.48564 | PREDICTED: stress-response A/B barrel domain-containing protein HS1 [Eucalyptus grandis] | 13.499 | 40.212 | 35 | 3 | 11 | 3 | 0.922 | 0.881 | 0.914 | 1.119 | 1.072 | 1.101 | 1.212 | 5.15E-04 |
| cds.Camellia_sinensis.comp35236_c0_seq1_m.43555 | PREDICTED: small ubiquitin-related modifier 1 [Pyrus x bretschneideri] | 13.194 | 1.4869 | 30.4 | 4 | 8 | 0 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp35241_c0_seq1_m.57775 | PREDICTED: ATP synthase subunit d, mitochondrial-like [Gossypium hirsutum] | 12.944 | 55.631 | 68.8 | 9 | 24 | 7 | 0.998 | 0.996 | 1.018 | 1.005 | 1.028 | 0.971 | 0.997 | 8.80E-01 |
| cds.Camellia_sinensis.comp35255_c0_seq1_m.31469 | PREDICTED: alcohol dehydrogenase class-3 [Elaeis guineensis | 42.624 | 74.052 | 22.9 | 9 | 31 | 9 | 0.954 | 0.955 | 0.967 | 1.04 | 1.066 | 1.038 | 1.093 | 7.57E-04 |

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| cds.Camellia_sinensis.comp35258_c0_seq1_m.47005 | PREDICTED: SKP1-like protein 1A isoform X5 [Vitis vinifera] | 11.688 | 52.826 | 59 | 8 | 9 | 4 | 0.981 | 0.927 | 0.943 | 1.083 | 1.063 | 1.028 | 1.113 | 9.06E-03 |
| cds.Camellia_sinensis.comp35270_c0_seq1_m.24855 | PREDICTED: glycerate dehydrogenase [Malus domestica] | 43.829 | 144.18 | 59.2 | 21 | 64 | 21 | 0.984 | 0.974 | 0.978 | 1.02 | 1.018 | 1.005 | 1.036 | 2.90E-03 |
| cds.Camellia_sinensis.comp35272_c0_seq1_m.43385 | PREDICTED: small nuclear ribonucleoprotein SmD3b-like [Juglans regia] | 18.612 | 30.504 | 37.5 | 5 | 11 | 5 | 0.97 | 0.993 | 0.991 | 1.013 | 1.006 | 1.019 | 1.028 | 2.84E-02 |
| cds.Camellia_sinensis.comp35287_c0_seq1_m.32879 | PREDICTED: 50S ribosomal protein L3, chloroplastic [Beta vulgaris subsp. vulgaris] | 34.481 | 38.478 | 20 | 6 | 10 | 5 | 1.101 | 1.217 | 1.172 | 0.855 | 0.827 | 0.763 | 0.701 | 1.34E-03 |

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| cds.Camellia_sinensis.comp35291_c0_seq1_m.30274 | PREDICTED: 28 kDa ribonucleoprotein, chloroplastic-like [Nelumbo nucifera] | 35.919 | 168.49 | 30.1 | 10 | 38 | 8 | 0.997 | 1.033 | 1.023 | 0.987 | 0.98 | 0.992 | 0.969 | 4.91E-02 |
| cds.Camellia_sinensis.comp35293_c0_seq1_m.28986 | PREDICTED: 24-methylenesterol C-methyltransferase 2 [Prunus mume] | 40.392 | 30.98 | 17.6 | 5 | 5 | 5 | 0.918 | 0.998 | 0.973 | 1.064 | 1.053 | 1.031 | 1.09 | 3.08E-02 |
| cds.Camellia_sinensis.comp35310_c0_seq1_m.46730 | PREDICTED: endoplasmin homolog [Vitis | 22.179 | 7.0517 | 28 | 6 | 9 | 4 | 0.969 | 0.909 | 0.949 | 1.018 | 1.081 | 1.084 | 1.126 | 1.30E-02 |
| cds.Camellia_sinensis.comp35321_c0_seq1_m.34345 | PREDICTED: aquaporin SIP1-1-like [Ziziphus jujuba] | 28.011 | 1.9884 | 3.4 | 1 | 2 | 1 | 1.058 | 0.986 | 1.021 | 0.96 | 0.985 | 0.987 | 0.957 | 1.19E-01 |
| cds.Camellia_sinensis.comp35325_c0_seq1_m.38167 | PREDICTED: desiccation protectant protein Lea14 homolog [Juglans regia] | 16.566 | 24.062 | 43.8 | 6 | 13 | 6 | 0.929 | 0.933 | 0.963 | 1.017 | 1.072 | 1.139 | 1.143 | 1.87E-02 |

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| cds.Camellia_sinensis.comp35329_c0_seq1_m.34688 | PREDICTED: 50S ribosomal protein L5, chloroplastic [Sesamum indicum] | 28.944 | 43.108 | 34.1 | 8 | 14 | 8 | 1.076 | 1.195 | 1.139 | 0.834 | 0.879 | 0.83 | 0.746 | 1.18E-03 |
| cds.Camellia_sinensis.comp35338_c0_seq1_m.58333 | PREDICTED: heat shock protein 90-2, partial [Cucumis melo] | 12.776 | 2.1117 | 34.3 | 4 | 10 | 2 | 1.158 | 1.072 | 1.072 | 0.874 | 0.884 | 0.907 | 0.807 | 1.58E-03 |
| cds.Camellia_sinensis.comp35345_c0_seq1_m.29931 | Thioredoxin family protein [Arabidopsis thaliana] | 39.56 | 75.683 | 31.2 | 9 | 15 | 9 | 1.061 | 1.033 | 1.005 | 0.955 | 0.954 | 0.958 | 0.925 | 3.86E-02 |
| cds.Camellia_sinensis.comp35351_c0_seq1_m.16248 | PREDICTED: cytochrome P450 82C4-like [Nicotiana tabacum] | 60.067 | 1.2892 | 1.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp35353_c0_seq1_m.47317 | PREDICTED: calvin cycle protein CP12-3, chloroplastic [Theobroma cacao] | 21.807 | 16.26 | 6.5 | 1 | 2 | 1 | 0.908 | 0.956 | 1.072 | 0.955 | 0.996 | 1.131 | 1.05 | 5.31E-01 |

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| cds.Camellia_sinensis.comp35355_c0_seq1_m.52503 | PREDICTED: 60S ribosomal protein L14-2 [Ipomoea nil] | 12.528 | 24.42 | 44.4 | 5 | 15 | 2 | 1.067 | 1.115 | 1.136 | 0.923 | 0.863 | 0.872 | 0.801 | 1.36E-03 |
| cds.Camellia_sinensis.comp35362_c0_seq1_m.37823 | PREDICTED: ubiquitin-conjugating enzyme E2 2 isoform X1 [Gossypium hirsutum] | 17.348 | 6.6963 | 15.8 | 2 | 3 | 1 | 1.01 | 1.009 | 0.9 | 0.931 | 1.011 | 1.143 | 1.057 | 4.95E-01 |
| cds.Camellia_sinensis.comp35365_c0_seq1_m.39330 | PREDICTED: probable phospholipid hydroperoxide glutathione peroxidase isoform X1 [Sesamum indicum] | 28.822 | 45.75 | 28.7 | 8 | 18 | 5 | 1.025 | 1.014 | 0.993 | 0.995 | 0.998 | 0.997 | 0.986 | 2.76E-01 |
| cds.Camellia_sinensis.comp35367_c0_seq1_m.32300 | PREDICTED: iron-sulfur cluster assembly protein 1-like [Malus domestica] | 18.352 | 16.06 | 28.3 | 4 | 9 | 4 | 0.93 | 0.967 | 0.948 | 1.072 | 1.025 | 1.094 | 1.122 | 6.80E-03 |

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| cds.Camellia_sinensis.comp35368_c0_seq1_m.58448 | PREDICTED: ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic [Eucalyptus grandis] | 11.731 | 2.5004 | 43 | 4 | 33 | 1 | 1.041 | 1.002 | 1.078 | 0.93 | 1.007 | 0.938 | 0.921 | 6.66E-02 |
| cds.Camellia_sinensis.comp35369_c0_seq1_m.32992 | PREDICTED: ATP-dependent zinc metalloprotease FTSH, chloroplastic-like [Nicotiana tabacum] | 38.443 | 100.36 | 34.8 | 11 | 31 | 5 | 0.997 | 0.99 | 0.97 | 1.006 | 1.022 | 1.004 | 1.025 | 6.56E-02 |
| cds.Camellia_sinensis.comp35376_c0_seq1_m.33068 | PREDICTED: light-harvesting complex-like protein 3 isotype 1, chloroplastic [Vitis vinifera] | 28.668 | 74.731 | 24 | 7 | 13 | 7 | 1.023 | 1.022 | 1.051 | 0.943 | 1.002 | 0.929 | 0.928 | 3.96E-02 |

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| cds.Camellia_sinensis.comp35389_c0_seq1_m.56728 | PREDICTED: heat shock protein 90-1-like [Gossypium raimondii] | 14.198 | 5.8399 | 33.1 | 3 | 6 | 1 | 1.074 | 1.207 | 1.064 | 0.879 | 0.839 | 0.909 | 0.785 | 6.77E-03 |
| cds.Camellia_sinensis.comp35390_c0_seq1_m.27691 | PREDICTED: thylakoid lumenal 29 kDa protein, chloroplastic [Vitis vinifera] | 38.211 | 190.71 | 49.7 | 16 | 62 | 16 | 1.015 | 0.977 | 0.993 | 0.995 | 1.036 | 1.016 | 1.021 | 2.70E-01 |
| cds.Camellia_sinensis.comp35393_c0_seq1_m.41325 | PREDICTED: nascent polypeptide-associated complex subunit alpha-like protein 2 [Vitis vinifera] | 26.78 | 4.474 | 9.4 | 2 | 2 | 2 | 1.052 | 1.038 | 0.935 | 0.891 | 1.057 | 1.022 | 0.982 | 7.75E-01 |

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| cds.Camellia_sinensis.comp35402_c0_seq1_m.34998 | PREDICTED: ATP-dependent Clp protease proteolytic subunit 6, chloroplastic-like [Gossypium arboreum] | 29.068 | 12.287 | 21.9 | 5 | 10 | 5 | 1.011 | 0.987 | 0.95 | 1.026 | 1.027 | 1.021 | 1.043 | 1.47E-01 |
| cds.Camellia_sinensis.comp35415_c0_seq1_m.34796 | PREDICTED: proteasome subunit beta type-6 [Theobroma cacao] | 29.448 | 155.07 | 40.4 | 12 | 31 | 12 | 0.985 | 0.967 | 0.959 | 1.039 | 1.037 | 1.014 | 1.061 | 5.82E-03 |
| cds.Camellia_sinensis.comp35416_c0_seq1_m.4189 | PREDICTED: 2-oxoglutarate dehydrogenase, mitochondrial [Vitis vinifera] | 115.44 | 323.31 | 35.4 | 30 | 51 | 30 | 0.992 | 0.993 | 0.995 | 1.015 | 1.006 | 1.013 | 1.018 | 3.22E-03 |
| cds.Camellia_sinensis.comp35420_c0_seq1_m.48498 | PREDICTED: 40S ribosomal protein S2-2 [Theobroma cacao] | 13.297 | 30.235 | 41.3 | 6 | 10 | 2 | 1.135 | 1.167 | 1.142 | 0.862 | 0.793 | 0.863 | 0.731 | 4.24E-04 |
| cds.Camellia_sinensis.comp35423_c0_seq1_m.48297 | PREDICTED: actin-like [Ziziphus jujuba] | 23.241 | 21.478 | 35.7 | 8 | 22 | 0 | | | | | | | | |

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| cds.Camellia_sinensis.comp35424_c0_seq1_m.42554 | PREDICTED: calvin cycle protein CP12-1, chloroplastic [Vitis vinifera] | 19.146 | 97.515 | 30.9 | 6 | 15 | 6 | 1.074 | 1.055 | 1.074 | 0.909 | 0.904 | 0.926 | 0.855 | 7.80E-05 |
| cds.Camellia_sinensis.comp35447_c0_seq1_m.38935 | PREDICTED: late embryogenesis abundant protein-like [Capsicum annuum] | 24.057 | 49.586 | 31.7 | 7 | 18 | 7 | 1.134 | 1.079 | 1.144 | 0.881 | 0.852 | 0.87 | 0.775 | 2.56E-04 |
| cds.Camellia_sinensis.comp35455_c0_seq1_m.30880 | PREDICTED: probable cinnamyl alcohol dehydrogenase 6 isoform X1 [Jatropha curcas] | 42.005 | 19.105 | 9.4 | 4 | 8 | 4 | 1.051 | 0.997 | 1.009 | 1.01 | 0.964 | 0.974 | 0.964 | 1.64E-01 |
| cds.Camellia_sinensis.comp35459_c0_seq1_m.25644 | PREDICTED: chloroplast stem-loop binding protein of 41 kDa b, chloroplastic isoform X2 [Juglans regia] | 42.393 | 139.42 | 52.4 | 19 | 69 | 19 | 1.073 | 1.031 | 1.033 | 0.955 | 0.957 | 0.943 | 0.91 | 2.42E-03 |

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| cds.Camellia_sinensis.comp35466_c0_seq1_m.31835 | PREDICTED: aspartate-semialdehyde dehydrogenase [Arachis duranensis] | 42.612 | 126.71 | 37.2 | 11 | 22 | 11 | 0.98 | 1.007 | 1.016 | 0.968 | 1.009 | 0.951 | 0.975 | 2.84E-01 |
| cds.Camellia_sinensis.comp35493_c0_seq1_m.19331 | PREDICTED: aspartic proteinase-like isoform X1 [Nicotiana tabacum] | 56.98 | 17.012 | 14.3 | 6 | 7 | 6 | 1.003 | 1.06 | 1.002 | 0.979 | 0.937 | 0.993 | 0.949 | 1.10E-01 |
| cds.Camellia_sinensis.comp35503_c0_seq1_m.31945 | PREDICTED: probable pyridoxal 5'-phosphate synthase subunit PDX1 [Erythranthe guttata] | 33.22 | 77.227 | 41.6 | 13 | 31 | 3 | 0.988 | 0.906 | 0.915 | 0.995 | 1.043 | 1.171 | 1.142 | 7.72E-02 |
| cds.Camellia_sinensis.comp35522_c0_seq1_m.26786 | PREDICTED: fructose-1,6-bisphosphatase, cytosolic [Sesamum indicum] | 37.136 | 161.77 | 52.6 | 16 | 44 | 16 | 0.967 | 0.949 | 0.959 | 1.033 | 1.073 | 1.051 | 1.098 | 1.58E-03 |

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| cds.Camellia_sinensis.comp35528_c0_seq1_m.44861 | protein PHLOEM PROTEIN 2-LIKE A9-like [Malus domestica] | 17.764 | 5.8544 | 12.5 | 2 | 2 | 2 | 1.045 | 0.959 | 0.947 | 1.005 | 1.031 | 1.021 | 1.036 | 3.19E-01 |
| cds.Camellia_sinensis.comp35531_c0_seq1_m.42382 | PREDICTED: mitochondrial pyruvate carrier 1 [Eucalyptus grandis] | 14.775 | 3.76 | 7.6 | 1 | 3 | 1 | 0.921 | 0.933 | 0.926 | 1.057 | 1.146 | 1.053 | 1.171 | 3.00E-02 |
| cds.Camellia_sinensis.comp35556_c0_seq1_m.33839 | PREDICTED: adenine phosphoribosyltransferase 1-like [Ipomoea | 29.058 | 178.54 | 32.2 | 10 | 21 | 10 | 1.008 | 0.96 | 1.01 | 1.012 | 0.998 | 1.032 | 1.021 | 3.27E-01 |
| cds.Camellia_sinensis.comp35566_c0_seq1_m.52597 | dual specificity phosphatase Cdc25 [Cajanus cajan] | 14.406 | 3.3768 | 10.8 | 1 | 1 | 1 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp35567_c0_seq1_m.24399 | PREDICTED: basic leucine zipper and W2 domain-containing protein 2-like [Daucus carota subsp. sativus] | 47.198 | 65.478 | 20.9 | 7 | 8 | 7 | 1.123 | 1.1 | 1.141 | 0.866 | 0.849 | 0.869 | 0.768 | 3.66E-05 |
| cds.Camellia_sinensis.comp35568_c0_seq1_m.15312 | PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1A [Vitis vinifera] | 70.656 | 49.356 | 17.1 | 11 | 15 | 11 | 0.988 | 0.977 | 0.933 | 1.02 | 1.057 | 1.026 | 1.071 | 2.97E-02 |
| cds.Camellia_sinensis.comp35571_c0_seq1_m.42364 | PREDICTED: huntingtin-interacting protein K [Sesamum indicum] | 12.131 | 33.053 | 52.7 | 7 | 15 | 7 | 1.001 | 0.982 | 1.016 | 0.961 | 1.004 | 1.027 | 0.998 | 9.10E-01 |
| cds.Camellia_sinensis.comp35577_c0_seq1_m.48965 | PREDICTED: heat shock 70 kDa protein 15-like [Prunus mume] | 22.539 | 30.279 | 19.8 | 4 | 8 | 1 | 1.026 | 1.01 | 0.996 | 0.979 | 1.058 | 0.935 | 0.98 | 5.98E-01 |

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| cds.Camellia_sinensis.comp35581_c0_seq1_m.39136 | PREDICTED: probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 [Nicotiana attenuata] | 21.792 | 17.451 | 35.8 | 7 | 11 | 7 | 1.068 | 1.042 | 1.054 | 0.928 | 0.962 | 0.945 | 0.896 | 9.56E-04 |
| cds.Camellia_sinensis.comp35582_c0_seq1_m.29174 | PREDICTED: putative GDP-L-fucose synthase 2 [Eucalyptus grandis] | 35.115 | 11.916 | 15.7 | 6 | 10 | 6 | 1.026 | 1.01 | 1.01 | 0.982 | 0.992 | 0.982 | 0.97 | 8.60E-03 |
| cds.Camellia_sinensis.comp35584_c0_seq1_m.33004 | PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP17-2, chloroplastic [Vitis vinifera] | 27.691 | 35.255 | 21.6 | 4 | 7 | 4 | 1.001 | 1.009 | 0.959 | 1.004 | 1.003 | 1.035 | 1.025 | 2.65E-01 |

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| cds.Camellia_sinensis.comp35586_c0_seq1_m.34293 | PREDICTED: protein HHL1, chloroplastic isoform X1 [Juglans regia] | 26.68 | 24.876 | 22.9 | 5 | 7 | 5 | 1.191 | 1.171 | 1.167 | 0.808 | 0.816 | 0.803 | 0.688 | 5.76E-07 |
| cds.Camellia_sinensis.comp35589_c0_seq1_m.31522 | PREDICTED: clathrin light chain 2-like [Nelumbo nucifera] | 33.283 | 8.3437 | 14.4 | 4 | 6 | 4 | 1.076 | 1.024 | 1.112 | 0.96 | 0.963 | 0.856 | 0.865 | 3.30E-02 |
| cds.Camellia_sinensis.comp35593_c0_seq1_m.42827 | PREDICTED: FK506-binding protein 2 [Populus euphratica] | 19.619 | 78.26 | 29.4 | 5 | 12 | 5 | 1.156 | 1.099 | 1.086 | 0.898 | 0.842 | 0.893 | 0.788 | 1.06E-03 |
| cds.Camellia_sinensis.comp35597_c0_seq1_m.22562 | PREDICTED: protease Do-like 1, chloroplastic [Nelumbo nucifera] | 45.86 | 96.78 | 22.7 | 9 | 20 | 9 | 0.992 | 0.983 | 0.991 | 0.982 | 1.01 | 1.024 | 1.017 | 2.61E-01 |
| cds.Camellia_sinensis.comp35605_c0_seq1_m.40316 | PREDICTED: protein P21-like [Juglans regia] | 27.051 | 57.679 | 28.7 | 6 | 13 | 6 | 0.938 | 0.968 | 0.975 | 1.027 | 1.076 | 1.057 | 1.097 | 6.88E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp35614_c0_seq1_m.19095 | regulator of chromosome condensation family protein [Populus trichocarpa] | 57.099 | 14.624 | 9.2 | 5 | 5 | 5 | 0.984 | 1.055 | 0.976 | 1.048 | 0.978 | 0.943 | 0.985 | 7.12E-01 |
| cds.Camellia_sinensis.comp35619_c0_seq1_m.47230 | pectinesterase (Protein of unknown function, DUF538) [Arabidopsis thaliana] | 18.162 | 9.4808 | 11.4 | 2 | 6 | 2 | 1.034 | 1.059 | 1.033 | 0.894 | 0.926 | 0.961 | 0.89 | 6.34E-03 |
| cds.Camellia_sinensis.comp35623_c0_seq1_m.29238 | PREDICTED: rhodanese-like domain-containing protein 11, chloroplastic isoform X1 [Vitis vinifera] | 33.647 | 54 | 36 | 9 | 11 | 9 | 1.043 | 1.036 | 1.059 | 0.984 | 0.948 | 0.956 | 0.92 | 3.10E-03 |
| cds.Camellia_sinensis.comp35641_c0_seq1_m.17743 | PREDICTED: 3-isopropylmalate dehydratase large subunit-like [Nicotiana sylvestris] | 55.293 | 94.438 | 40.2 | 17 | 35 | 17 | 0.98 | 1.01 | 1.004 | 1.002 | 1.034 | 1.005 | 1.016 | 3.17E-01 |

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| cds.Camellia_sinensis.comp35658_c0_seq1_m.42642 | PREDICTED: cyanate hydratase 2 isoform X1 [Populus euphratica] | 21.41 | 135.07 | 48.2 | 8 | 23 | 8 | 0.921 | 0.945 | 0.917 | 1.086 | 1.084 | 1.073 | 1.165 | 1.15E-04 |
| cds.Camellia_sinensis.comp35664_c0_seq1_m.36076 | PREDICTED: heat shock 70 kDa protein 15-like [Gossypium hirsutum] | 21.054 | 11.653 | 26.6 | 6 | 10 | 4 | 1.05 | 1.048 | 1.015 | 0.899 | 0.954 | 1.041 | 0.93 | 1.65E-01 |
| cds.Camellia_sinensis.comp35666_c0_seq1_m.32810 | PREDICTED: bifunctional protein FolD 2 [Vitis vinifera] | 32.468 | 102.34 | 50.8 | 16 | 28 | 16 | 0.957 | 0.964 | 0.961 | 1.048 | 1.045 | 1.038 | 1.086 | 1.99E-05 |
| cds.Camellia_sinensis.comp35670_c0_seq1_m.50049 | PREDICTED: LOW QUALITY PROTEIN: glutamate--glyoxylate aminotransferase 2-like [Sesamum indicum] | 14.554 | 60.831 | 79.8 | 9 | 34 | 5 | 1.053 | 1.067 | 1.046 | 0.897 | 0.943 | 0.962 | 0.885 | 4.78E-03 |

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| cds.Camellia_sinensis.comp35671_c0_seq1_m.27606 | PREDICTED: protein-tyrosine-phosphatase PTP1 isoform X4 [Vitis vinifera] | 38.978 | 3.8124 | 5.5 | 2 | 3 | 2 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp35694_c0_seq1_m.52626 | PREDICTED: cytochrome b-c1 complex subunit Rieske-4, mitochondrial-like [Sesamum indicum] | 13.98 | 1.3086 | 7.8 | 1 | 2 | 1 | 1.021 | 0.902 | 1.005 | 1.018 | 0.966 | 1.098 | 1.053 | 3.94E-01 |
| cds.Camellia_sinensis.comp35697_c0_seq1_m.49233 | zinc finger/BTB domain protein [Arabidopsis thaliana] | 17.019 | 12.721 | 25.5 | 4 | 5 | 4 | 1.128 | 1.096 | 1.156 | 0.889 | 0.893 | 0.868 | 0.784 | 1.62E-04 |
| cds.Camellia_sinensis.comp35698_c0_seq1_m.53260 | PREDICTED: dnaJ protein homolog 2 isoform X2 [Solanum pennellii] | 16.8 | 1.2587 | 32.3 | 5 | 9 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp35708_c0_seq1_m.33676 | Cytochrome b5 isoform 1 [Morus notabilis] | 18.896 | 30.788 | 20.1 | 2 | 4 | 2 | 0.926 | 1.054 | 1.055 | 0.996 | 1 | 0.916 | 0.959 | 4.81E-01 |

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| cds.Camellia_sinensis.comp35725_c0_seq1_m.40948 | PREDICTED: protein SRC2 homolog [Ricinus communis] | 26.043 | 6.7499 | 5.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp35727_c0_seq1_m.58807 | PREDICTED: phosphoribulokinase, chloroplastic-like [Nelumbo | 10.544 | 11.602 | 26.2 | 2 | 9 | 1 | 0.946 | 0.99 | 0.976 | 0.99 | 1.086 | 1.032 | 1.067 | 9.72E-02 |
| cds.Camellia_sinensis.comp35729_c0_seq1_m.33389 | PREDICTED: coiled-coil domain-containing protein 124 [Vitis vinifera] | 26.485 | 1.7892 | 3.9 | 1 | 1 | 1 | 1.093 | 1.101 | 1.013 | 0.927 | 0.903 | 0.945 | 0.865 | 8.34E-03 |
| cds.Camellia_sinensis.comp35730_c0_seq1_m.24381 | PREDICTED: thiamine pyrophosphokinase 1 isoform X1 [Juglans regia] | 35.054 | 7.251 | 14.9 | 5 | 5 | 5 | 1.071 | 1.061 | 0.985 | 0.935 | 0.966 | 0.974 | 0.922 | 5.18E-02 |
| cds.Camellia_sinensis.comp35731_c0_seq1_m.25816 | PREDICTED: 5'-nucleotidase SurE [Prunus mume] | 33.19 | 10.332 | 7.1 | 2 | 2 | 2 | 1.056 | 1.043 | 1.035 | 0.944 | 0.912 | 1.001 | 0.912 | 2.85E-02 |

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| cds.Camellia_sinensis.comp35736_c0_seq1_m.15954 | PREDICTED: uncharacterized membrane protein At1g16860-like [Ipomoea nil] | 51.735 | 4.6506 | 4.3 | 2 | 2 | 2 | 0.83 | 1.179 | 1.029 | 1.032 | 1.028 | 0.93 | 0.984 | 9.53E-01 |
| cds.Camellia_sinensis.comp35757_c0_seq1_m.13862 | PREDICTED: 3-phosphoshikimate 1-carboxyvinyltransferase 2 [Juglans regia] | 55.63 | 53.83 | 20.8 | 9 | 18 | 9 | 1.124 | 1.158 | 1.158 | 0.814 | 0.822 | 0.808 | 0.71 | 3.33E-06 |
| cds.Camellia_sinensis.comp35765_c0_seq1_m.14995 | PREDICTED: nephrocystin-3 [Daucus carota subsp. sativus] | 66.62 | 9.7843 | 8.6 | 4 | 4 | 4 | 1.444 | 1.201 | 0.695 | 0.798 | 0.81 | 0.974 | 0.773 | 3.98E-01 |
| cds.Camellia_sinensis.comp35772_c0_seq1_m.9930 | PREDICTED: glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a [Jatropha curcas] | 79.026 | 73.568 | 31.3 | 23 | 46 | 23 | 0.973 | 0.977 | 1.004 | 1.019 | 1.023 | 1.012 | 1.034 | 3.20E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp35775_c0_seq1_m.39035 | PREDICTED: dnaJ protein homolog [Nicotiana tabacum] | 26.466 | 2.2782 | 4.7 | 1 | 1 | 1 | 1.215 | 1.207 | 1.163 | 0.726 | 0.827 | 0.8 | 0.656 | 5.20E-04 |
| cds.Camellia_sinensis.comp35776_c0_seq1_m.30569 | PREDICTED: ER membrane protein complex subunit 10 [Theobroma cacao] | 33.904 | 5.3731 | 14.9 | 5 | 5 | 5 | 0.953 | 0.979 | 1.037 | 0.994 | 1.002 | 1.084 | 1.037 | 3.82E-01 |
| cds.Camellia_sinensis.comp35781_c0_seq1_m.36035 | PREDICTED: putative UDP-rhamnose:rhamnosyltransferase 1 [Vitis vinifera] | 35.201 | 3.8539 | 6 | 2 | 3 | 2 | 1.048 | 1.179 | 1.209 | 0.864 | 0.842 | 0.83 | 0.738 | 2.70E-03 |
| cds.Camellia_sinensis.comp35782_c0_seq1_m.21655 | PREDICTED: calreticulin-3-like [Populus euphratica] | 53.159 | 24.522 | 16.7 | 8 | 8 | 6 | 1.088 | 1.068 | 1.125 | 0.905 | 0.942 | 0.868 | 0.827 | 2.50E-03 |

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| cds.Camellia_sinensis.comp35788_c0_seq1_m.35839 | PREDICTED: single-stranded DNA-binding protein WHY1, chloroplastic-like [Nicotiana tomentosiformis] | 30.892 | 78.031 | 32.7 | 7 | 8 | 7 | 0.987 | 1.008 | 0.987 | 0.961 | 0.993 | 1.023 | 0.998 | 9.24E-01 |
| cds.Camellia_sinensis.comp35803_c0_seq1_m.54656 | PREDICTED: GTP-binding protein SAR1A-like [Arachis ipaensis] | 12.06 | 8.8721 | 50.5 | 4 | 9 | 1 | 1.027 | 0.972 | 1.022 | 0.938 | 1.053 | 0.991 | 0.987 | 7.33E-01 |
| cds.Camellia_sinensis.comp35812_c0_seq1_m.44084 | PREDICTED: leiomodin-2 isoform X1 [Capsicum annuum] | 19.714 | 21.876 | 17.7 | 4 | 9 | 4 | 1.02 | 0.951 | 1.004 | 0.995 | 1.048 | 1.028 | 1.032 | 2.87E-01 |
| cds.Camellia_sinensis.comp35815_c0_seq1_m.45037 | PREDICTED: heat shock factor-binding protein 1 [Theobroma cacao] | 14.518 | 21.426 | 32.6 | 4 | 5 | 4 | 0.941 | 0.963 | 0.972 | 1.052 | 1.045 | 1.031 | 1.088 | 1.76E-03 |

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| cds.Camellia_sinensis.comp35826_c0_seq1_m.50055 | PREDICTED: aldehyde dehydrogenase family 2 member B4, mitochondrial-like, partial [Malus domestica] | 11.685 | 17.758 | 38.7 | 6 | 13 | 4 | 1.033 | 0.997 | 0.989 | 0.962 | 0.995 | 1.009 | 0.982 | 4.14E-01 |
| cds.Camellia_sinensis.comp35836_c0_seq1_m.16144 | PREDICTED: 4-coumarate--CoA ligase-like 7 [Nicotiana tabacum] | 59.481 | 116.84 | 36 | 18 | 29 | 18 | 0.996 | 0.981 | 0.989 | 1.007 | 1.003 | 1.028 | 1.024 | 5.29E-02 |
| cds.Camellia_sinensis.comp35854_c0_seq1_m.36569 | PREDICTED: apoptotic chromatin condensation inducer in the nucleus-like isoform X2 [Juglans regia] | 22.996 | 1.9246 | 7.1 | 2 | 3 | 2 | 1.021 | 1.101 | 1.113 | 0.922 | 0.885 | 0.946 | 0.851 | 8.48E-03 |

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| cds.Camellia_sinensis.comp35858_c0_seq1_m.34257 | PREDICTED: gamma carbonic anhydrase-like 2, mitochondrial [Jatropha curcas] | 27.529 | 18.788 | 17.1 | 5 | 9 | 5 | 1.019 | 1.04 | 1.046 | 0.949 | 0.917 | 1.058 | 0.942 | 2.31E-01 |
| cds.Camellia_sinensis.comp35860_c0_seq1_m.31307 | PREDICTED: beta-carotene isomerase D27, chloroplastic [Juglans regia] | 31.178 | 4.6969 | 8.6 | 2 | 4 | 2 | 1.036 | 1.125 | 1.098 | 0.855 | 0.918 | 0.957 | 0.838 | 1.23E-02 |
| cds.Camellia_sinensis.comp35861_c0_seq1_m.53807 | PREDICTED: reticulon-like protein B1 [Vitis vinifera] | 16.668 | 1.5626 | 7.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp35876_c0_seq1_m.40720 | quinone reductase family protein [Arabidopsis lyrata subsp. lyrata] | 21.74 | 132.29 | 53.7 | 9 | 16 | 5 | 0.973 | 1.041 | 1.053 | 1.039 | 1.008 | 0.929 | 0.97 | 5.02E-01 |

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| cds.Camellia_sinensis.comp35880_c0_seq1_m.17775 | PREDICTED: proline--tRNA ligase, cytoplasmic-like [Nelumbo nucifera] | 58.213 | 113.25 | 35.7 | 15 | 24 | 7 | 1.025 | 1.005 | 1.05 | 0.924 | 0.955 | 0.93 | 0.912 | 4.74E-03 |
| cds.Camellia_sinensis.comp35884_c0_seq1_m.33763 | PREDICTED: glutathione S-transferase DHAR3, chloroplastic-like [Juglans regia] | 30.256 | 73.884 | 44.3 | 12 | 35 | 11 | 0.958 | 0.965 | 0.979 | 1.046 | 1.061 | 1.044 | 1.086 | 5.41E-04 |
| cds.Camellia_sinensis.comp35887_c0_seq1_m.54467 | PREDICTED: glycine dehydrogenase (decarboxylating), mitochondrial [Nelumbo nucifera] | 15.759 | 17.381 | 14.8 | 2 | 7 | 2 | 1.006 | 0.99 | 1 | 0.988 | 0.985 | 0.998 | 0.992 | 2.44E-01 |
| cds.Camellia_sinensis.comp35890_c0_seq1_m.40314 | heterogeneous nuclear ribonucleoprotein A1-like 2 [Cajanus cajan] | 32.541 | 3.8679 | 9.5 | 3 | 11 | 2 | 1.005 | 1.014 | 0.997 | 0.971 | 1.071 | 0.991 | 1.006 | 8.83E-01 |

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| cds.Camellia_sinensis.comp35892_c0_seq1_m.47220 | PREDICTED: putative UDP-rhamnose:rhamnosyltransferase 1 [Populus euphratica] | 18.03 | 2.0242 | 11.8 | 2 | 2 | 2 | 1.127 | 1.079 | 1.064 | 0.948 | 0.871 | 0.89 | 0.828 | 3.58E-03 |
| cds.Camellia_sinensis.comp35902_c0_seq1_m.7329 | PREDICTED: V-type proton ATPase subunit a3 [Vitis | 92.954 | 91.381 | 21.3 | 14 | 22 | 14 | 1.007 | 1.016 | 0.958 | 1.018 | 1.031 | 0.999 | 1.022 | 3.34E-01 |
| cds.Camellia_sinensis.comp35952_c0_seq1_m.28377 | PREDICTED: calcyclin-binding protein [Vitis vinifera] | 25.139 | 7.4392 | 14.8 | 4 | 4 | 4 | 0.99 | 0.969 | 0.988 | 0.988 | 1.023 | 1.031 | 1.032 | 9.92E-02 |
| cds.Camellia_sinensis.comp35956_c0_seq1_m.38504 | PREDICTED: eukaryotic translation initiation factor 3 subunit K-like [Populus euphratica] | 26.977 | 4.5408 | 14 | 4 | 4 | 4 | 0.862 | 0.946 | 0.943 | 1.141 | 1.037 | 1.092 | 1.189 | 1.36E-02 |

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| cds.Camellia_sinensis.comp35959_c0_seq1_m.28749 | PREDICTED: phosphoenolpyruvate carboxylase [Capsicum annuum] | 37.521 | 78.93 | 49.2 | 15 | 27 | 10 | 1.027 | 1.035 | 1.021 | 0.941 | 0.974 | 0.954 | 0.931 | 2.60E-03 |
| cds.Camellia_sinensis.comp35960_c0_seq1_m.40073 | PREDICTED: probable xyloglucan endotransglucosylase/hydrolase protein 21 [Gossypium hirsutum] | 25.651 | 18.331 | 6.6 | 1 | 1 | 1 | 1.073 | 0.99 | 0.922 | 0.931 | 1.013 | 1.067 | 1.009 | 8.86E-01 |
| cds.Camellia_sinensis.comp35961_c0_seq1_m.31683 | calcium homeostasis regulator CHoR1 [Solanum tuberosum | 36.586 | 51.282 | 15.9 | 4 | 5 | 4 | 1.017 | 1.011 | 1.015 | 1.002 | 1.019 | 0.944 | 0.974 | 3.73E-01 |
| cds.Camellia_sinensis.comp35964_c0_seq1_m.25987 | PREDICTED: photosystem II stability/assembly factor HCF136, chloroplastic [Nelumbo nucifera] | 46.271 | 254.44 | 39 | 14 | 38 | 14 | 0.999 | 0.98 | 0.999 | 1.005 | 0.991 | 1.008 | 1.009 | 3.52E-01 |

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| cds.Camellia_sinensis.comp3598_c0_seq1_m.48410 | PREDICTED: trans-resveratrol di-O-methyltransferase [Vitis vinifera] | 21.142 | 23.263 | 28 | 4 | 6 | 4 | 0.892 | 0.868 | 0.888 | 1.126 | 1.156 | 1.145 | 1.294 | 2.14E-05 |
| cds.Camellia_sinensis.comp35991_c0_seq1_m.6464 | PREDICTED: beta-galactosidase 10 [Vitis vinifera] | 103.07 | 37.854 | 18.6 | 17 | 22 | 15 | 1.083 | 1.062 | 1.061 | 0.875 | 0.941 | 0.948 | 0.862 | 4.88E-03 |
| cds.Camellia_sinensis.comp36001_c0_seq1_m.34430 | PREDICTED: vesicle-associated protein 4-1-like isoform X2 [Ipomoea nil] | 28.964 | 7.0504 | 16.7 | 4 | 4 | 4 | 0.992 | 0.97 | 1.086 | 0.902 | 1.003 | 1.049 | 0.969 | 6.00E-01 |
| cds.Camellia_sinensis.comp36014_c0_seq1_m.41139 | PREDICTED: RNA polymerase II subunit A C-terminal domain phosphatase SSU72 [Ricinus communis] | 22.681 | 7.3112 | 6.2 | 1 | 1 | 1 | 0.956 | 0.971 | 0.96 | 1.146 | 1.058 | 0.94 | 1.089 | 2.91E-01 |

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| cds.Camellia_sinensis.comp36040_c0_seq1_m.13820 | PREDICTED: cell division protein FtsZ homolog 2-1, chloroplastic isoform X1 [Citrus sinensis] | 51.412 | 39.442 | 18.1 | 7 | 12 | 6 | 0.964 | 1.063 | 1.078 | 0.893 | 0.969 | 1 | 0.922 | 1.70E-01 |
| cds.Camellia_sinensis.comp36045_c0_seq1_m.37397 | PREDICTED: nectarin-1 [Eucalyptus grandis] | 23.629 | 6.1942 | 11.1 | 3 | 6 | 3 | 1.015 | 0.968 | 1.035 | 0.994 | 1.024 | 1.022 | 1.007 | 7.49E-01 |
| cds.Camellia_sinensis.comp36068_c0_seq1_m.43701 | PREDICTED: triosephosphate isomerase, cytosolic [Prunus mume] | 17.268 | 119.61 | 47.5 | 6 | 16 | 6 | 0.986 | 0.965 | 0.964 | 1.08 | 1.006 | 1.028 | 1.068 | 4.20E-02 |
| cds.Camellia_sinensis.comp36069_c0_seq1_m.40367 | PREDICTED: universal stress protein A-like protein [Nicotiana attenuata] | 17.951 | 19.571 | 23.9 | 4 | 7 | 4 | 0.976 | 1.019 | 0.955 | 1.016 | 1.01 | 1.022 | 1.033 | 1.63E-01 |

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| cds.Camellia_sinensis.comp36071_c0_seq1_m.59211 | PREDICTED: reticulon-like protein B1 [Daucus carota subsp. sativus] | 11.192 | 6.7362 | 18.8 | 2 | 2 | 2 | 1.062 | 1.019 | 1.045 | 0.91 | 1.002 | 0.954 | 0.917 | 4.47E-02 |
| cds.Camellia_sinensis.comp36078_c0_seq1_m.57530 | PREDICTED: elongation factor 1-delta-like [Juglans regia] | 12.047 | 3.4778 | 32.5 | 3 | 9 | 1 | 0.917 | 1.081 | 1.012 | 1.108 | 0.895 | 1.007 | 1 | 9.85E-01 |
| cds.Camellia_sinensis.comp36119_c0_seq1_m.23684 | PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein At3g48420 isoform X1 [Theobroma cacao] | 40.503 | 32.846 | 18.5 | 7 | 14 | 7 | 0.956 | 1.017 | 0.996 | 0.973 | 0.983 | 1.003 | 0.997 | 8.85E-01 |
| cds.Camellia_sinensis.comp36132_c0_seq1_m.37343 | PREDICTED: 50S ribosomal protein L11, chloroplastic [Nicotiana tomentosiformis] | 26.731 | 21.071 | 29.8 | 7 | 16 | 7 | 1.017 | 1.015 | 1.009 | 0.975 | 0.981 | 0.978 | 0.965 | 2.64E-04 |

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| cds.Camellia_sinensis.comp36154_c0_seq1_m.40268 | PREDICTED: 60S ribosome subunit biogenesis protein NIP7 homolog [Vitis vinifera] | 20.921 | 8.9644 | 9.1 | 1 | 1 | 1 | 0.855 | 0.963 | 1.21 | 1.027 | 1 | 0.974 | 0.991 | 9.91E-01 |
| cds.Camellia_sinensis.comp36157_c0_seq1_m.18410 | PREDICTED: preprotein translocase subunit SCY1, chloroplastic-like isoform X1 [Populus euphratica] | 59.383 | 14.664 | 16.2 | 8 | 8 | 8 | 0.954 | 0.955 | 0.958 | 1.049 | 1.069 | 1.012 | 1.092 | 3.23E-02 |
| cds.Camellia_sinensis.comp36191_c0_seq1_m.43051 | verprolin [Ananas comosus] | 14.126 | 2.0647 | 6.8 | 1 | 1 | 1 | 0.992 | 0.947 | 1.003 | 1.003 | 1.044 | 1.026 | 1.045 | 1.07E-01 |
| cds.Camellia_sinensis.comp36199_c0_seq1_m.25892 | PREDICTED: very-long-chain 3-oxoacyl-CoA reductase 1 [Juglans regia] | 35.595 | 5.1761 | 11.2 | 4 | 4 | 4 | 1.276 | 1.221 | 1.168 | 0.709 | 0.7 | 0.803 | 0.604 | 5.62E-04 |

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| cds.Camellia_sinensis.comp36262_c0_seq1_m.44784 | transmembrane protein [Arabidopsis thaliana] | 14.622 | 38.584 | 17.3 | 4 | 6 | 4 | 1.009 | 1.026 | 0.981 | 0.946 | 1.015 | 1.037 | 0.994 | 8.41E-01 |
| cds.Camellia_sinensis.comp36281_c0_seq1_m.57270 | PREDICTED: aspartic proteinase-like isoform X1 [Juglans regia] | 12.684 | 13.27 | 20.7 | 2 | 5 | 2 | 0.973 | 1.028 | 1.001 | 0.955 | 1.022 | 1.031 | 1.002 | 9.57E-01 |
| cds.Camellia_sinensis.comp36290_c0_seq1_m.44094 | PREDICTED: protein canopy-1 [Vitis vinifera] | 23.03 | 17.86 | 23.8 | 4 | 7 | 4 | 1.118 | 1.167 | 1.194 | 0.83 | 0.834 | 0.834 | 0.718 | 3.40E-03 |
| cds.Camellia_sinensis.comp36306_c0_seq1_m.27863 | PREDICTED: uridylate kinase-like [Nicotiana tabacum] | 37.36 | 6.6769 | 7.2 | 2 | 2 | 2 | 0.889 | 0.919 | 1.01 | 1.068 | 1.096 | 1.056 | 1.143 | 2.76E-02 |
| cds.Camellia_sinensis.comp36311_c0_seq1_m.37088 | PREDICTED: cytosolic sulfotransferase 15-like [Populus euphratica] | 37.427 | 3.1918 | 9 | 3 | 5 | 2 | 0.922 | 1.043 | 0.965 | 0.962 | 1.029 | 1.096 | 1.054 | 3.74E-01 |

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| cds.Camellia_sinensis.comp36326_c0_seq1_m.11410 | PREDICTED: acyl-coenzyme A oxidase 3, peroxisomal [Vitis vinifera] | 76.486 | 33.514 | 10.2 | 7 | 12 | 7 | 0.983 | 1.026 | 1.029 | 1.008 | 0.958 | 0.97 | 0.966 | 1.84E-01 |
| cds.Camellia_sinensis.comp36355_c0_seq1_m.46734 | PREDICTED: auxin-repressed 12.5 kDa protein [Nelumbo nucifera] | 12.814 | 5.4048 | 21.2 | 2 | 2 | 2 | 0.806 | 0.936 | 1.017 | 1.226 | 1.073 | 1.002 | 1.196 | 1.16E-01 |
| cds.Camellia_sinensis.comp36361_c0_seq1_m.27775 | PREDICTED: protein CIA1 [Ipomoea nil] | 44.375 | 15.979 | 7.3 | 3 | 6 | 3 | 1.01 | 1.04 | 1.016 | 1.006 | 0.979 | 0.954 | 0.959 | 7.49E-02 |
| cds.Camellia_sinensis.comp36377_c0_seq1_m.36798 | pyridoxamine 5'-phosphate oxidase family protein [Medicago truncatula] | 31.796 | 48.93 | 25 | 6 | 12 | 6 | 0.981 | 1.079 | 0.981 | 1.049 | 1 | 0.958 | 0.989 | 8.04E-01 |
| cds.Camellia_sinensis.comp36378_c0_seq1_m.22456 | PREDICTED: phospholipase A1-IIdelta isoform X2 [Solanum tuberosum | 47.548 | 15.938 | 10.3 | 4 | 8 | 4 | 0.969 | 0.975 | 0.955 | 1.013 | 1.022 | 0.988 | 1.043 | 2.42E-02 |

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| cds.Camellia_sinensis.comp36402_c0_seq1_m.27301 | PREDICTED: L-lactate dehydrogenase B-like [Gossypium hirsutum] | 37.778 | 18.094 | 10.3 | 3 | 3 | 3 | 0.987 | 0.991 | 0.997 | 0.952 | 0.987 | 1.094 | 1.019 | 7.15E-01 |
| cds.Camellia_sinensis.comp36409_c0_seq1_m.19147 | PREDICTED: translation initiation factor IF-2-like [Solanum pennellii] | 52.942 | 1.4165 | 2.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp36424_c0_seq1_m.18168 | PREDICTED: protein LURP-one-related 10-like [Nicotiana sylvestris] | 25.015 | 1.57 | 6.3 | 2 | 2 | 2 | 1.002 | 0.955 | 1.003 | 0.968 | 1.098 | 0.987 | 1.031 | 5.23E-01 |
| cds.Camellia_sinensis.comp36431_c0_seq1_m.41059 | FKBP-type peptidyl-prolyl cis-trans isomerase 3 family protein [Populus trichocarpa] | 24.262 | 9.5421 | 13 | 2 | 4 | 2 | 1.033 | 1.072 | 0.976 | 0.953 | 0.961 | 0.96 | 0.933 | 1.29E-01 |

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| cds.Camellia_sinensis.comp36483_c0_seq1_m.36245 | PREDICTED: early nodulin-like protein 1 [Nicotiana attenuata] | 30.285 | 2.1488 | 3.6 | 1 | 1 | 1 | 0.918 | 0.881 | 0.91 | 1.099 | 1.14 | 1.093 | 1.23 | 3.40E-04 |
| cds.Camellia_sinensis.comp36485_c0_seq1_m.31618 | PREDICTED: protein OS-9 homolog [Daucus carota subsp. sativus] | 40.345 | 5.6964 | 8.9 | 3 | 3 | 3 | 0.961 | 0.919 | 1.064 | 1.104 | 0.987 | 0.991 | 1.047 | 4.60E-01 |
| cds.Camellia_sinensis.comp36514_c0_seq1_m.48039 | PREDICTED: glycine-rich RNA-binding protein RZ1B-like [Ziziphus jujuba] | 16.847 | 1.4399 | 4.5 | 1 | 1 | 1 | 1.183 | 1.11 | 1.186 | 0.703 | 0.871 | 0.893 | 0.709 | 1.15E-02 |
| cds.Camellia_sinensis.comp36522_c0_seq1_m.30982 | PREDICTED: replication factor C subunit 2 [Eucalyptus grandis] | 38.637 | 4.6018 | 8.1 | 2 | 2 | 2 | 0.932 | 0.997 | 0.992 | 1.061 | 1.04 | 1.003 | 1.063 | 8.86E-02 |

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| cds.Camellia_sinensis.comp36530_c0_seq1_m.37183 | PREDICTED: LOW QUALITY PROTEIN: tropinone reductase-like 3 [Daucus carota subsp. sativus] | 29.649 | 3.7353 | 6.9 | 2 | 3 | 2 | 1.022 | 1.05 | 1.012 | 1.013 | 0.951 | 0.954 | 0.946 | 7.55E-02 |
| cds.Camellia_sinensis.comp36539_c0_seq1_m.4777 | PREDICTED: mannosylglycoprotein endo-beta-mannosidase [Vitis | 110.57 | 21.426 | 11.1 | 10 | 10 | 10 | 0.982 | 0.996 | 0.994 | 1.028 | 1.008 | 0.982 | 1.015 | 3.38E-01 |
| cds.Camellia_sinensis.comp36549_c0_seq1_m.49530 | PREDICTED: V-type proton ATPase 16 kDa proteolipid subunit [Fragaria vesca subsp. | 14.909 | -2 | 12.1 | 1 | 1 | 1 | 0.835 | 0.897 | 1 | 1.128 | 1.229 | 0.967 | 1.217 | 9.10E-02 |
| cds.Camellia_sinensis.comp36555_c0_seq1_m.57037 | PREDICTED: polyubiquitin, partial [Raphanus sativus] | 13.224 | 117.67 | 74.6 | 6 | 46 | 6 | 1.039 | 1.011 | 1.006 | 0.948 | 0.974 | 0.982 | 0.95 | 2.52E-02 |

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| cds.Camellia_sinensis.comp36564_c0_seq1_m.18010 | PREDICTED: protein disulfide isomerase-like 1-4 [Populus euphratica] | 67.5 | 27.807 | 10.8 | 7 | 7 | 7 | 1.04 | 1.014 | 1.06 | 0.973 | 0.957 | 0.921 | 0.916 | 1.30E-02 |
| cds.Camellia_sinensis.comp36568_c0_seq1_m.11790 | PREDICTED: protein SIEVE ELEMENT OCCLUSION B [Ricinus communis] | 83.418 | 263.13 | 38.9 | 26 | 50 | 26 | 0.934 | 0.941 | 0.938 | 1.051 | 1.088 | 1.064 | 1.139 | 2.37E-04 |
| cds.Camellia_sinensis.comp36571_c0_seq1_m.32975 | PREDICTED: casein kinase 1-like protein 2 [Nicotiana attenuata] | 20.561 | 6.7704 | 6.2 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp36576_c0_seq1_m.20868 | PREDICTED: UDP-N-acetylglucosamine diphosphorylase 1 [Citrus sinensis] | 55.479 | 13.619 | 8.6 | 3 | 4 | 3 | 1.05 | 1 | 0.98 | 0.959 | 0.945 | 1.038 | 0.971 | 4.48E-01 |
| cds.Camellia_sinensis.comp36580_c0_seq1_m.17447 | PREDICTED: protein FLX-like 2 [Ziziphus jujuba] | 50.983 | 79.218 | 40.1 | 19 | 26 | 19 | 1.004 | 1.029 | 0.972 | 1.012 | 0.974 | 1.011 | 0.997 | 9.08E-01 |

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| cds.Camellia_sinensis.comp36602_c0_seq1_m.7660 | PREDICTED: carbon catabolite repressor protein 4 homolog 1 [Pyrus x bretschneideri] | 66.865 | 4.0721 | 1.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp36606_c0_seq1_m.29147 | PREDICTED: phosphoglycerate mutase-like protein 1 [Prunus mume] | 39.804 | 20.594 | 15.7 | 5 | 7 | 5 | 1.023 | 1.074 | 1.016 | 0.95 | 0.981 | 0.994 | 0.94 | 4.79E-02 |
| cds.Camellia_sinensis.comp36612_c0_seq1_m.34117 | calcium-dependent phosphotriesterase superfamily protein [Medicago truncatula] | 36.199 | 59.094 | 37 | 9 | 15 | 9 | 0.973 | 0.956 | 1.003 | 1.013 | 1.03 | 1.018 | 1.044 | 4.37E-02 |
| cds.Camellia_sinensis.comp36627_c0_seq1_m.24222 | PREDICTED: chlorophyll synthase, chloroplastic [Prunus mume] | 40.487 | 27.013 | 8.8 | 2 | 2 | 2 | 0.941 | 0.949 | 0.958 | 1.071 | 1.07 | 1.039 | 1.117 | 6.02E-04 |

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| cds.Camellia_sinensis.comp36670_c0_seq1_m.28249 | PREDICTED: replication factor C subunit 3 [Gossypium raimondii] | 41.896 | 6.6658 | 11.7 | 5 | 5 | 5 | 0.973 | 0.972 | 0.932 | 1.023 | 1.053 | 1.048 | 1.086 | 7.94E-03 |
| cds.Camellia_sinensis.comp36696_c0_seq1_m.28755 | PREDICTED: probable pyridoxal 5'-phosphate synthase subunit PDX1 [Daucus carota subsp. sativus] | 37.041 | 3.3632 | 35.2 | 12 | 31 | 2 | 0.952 | 0.948 | 0.955 | 1.059 | 1.047 | 1.061 | 1.109 | 2.21E-05 |
| cds.Camellia_sinensis.comp36700_c0_seq1_m.39603 | sodium/calcium exchanger family protein / calcium-binding EF hand family protein [Arabidopsis thaliana] | 34.335 | 11.168 | 9.8 | 2 | 2 | 2 | 0.883 | 0.923 | 1.071 | 1.15 | 0.965 | 1.045 | 1.098 | 2.88E-01 |

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| cds.Camellia_sinensis.comp36719_c0_seq1_m.52881 | PREDICTED: heat shock 70 kDa protein, mitochondrial-like [Nicotiana tabacum] | 17.549 | 12.197 | 44.7 | 9 | 25 | 3 | 0.905 | 1 | 1.002 | 1.024 | 1.035 | 1.09 | 1.083 | 1.06E-01 |
| cds.Camellia_sinensis.comp36733_c0_seq1_m.44838 | PREDICTED: UPF0426 protein At1g28150, chloroplastic [Prunus mume] | 13.843 | 19.999 | 26.8 | 3 | 4 | 3 | 0.879 | 0.948 | 0.888 | 1.111 | 1.116 | 1.117 | 1.232 | 1.27E-02 |
| cds.Camellia_sinensis.comp36734_c0_seq1_m.26682 | PREDICTED: probable membrane-associated 30 kDa protein, chloroplastic [Nelumbo nucifera] | 36.17 | 255.58 | 57.3 | 18 | 59 | 18 | 1.031 | 1.01 | 0.976 | 0.981 | 0.99 | 1.007 | 0.987 | 5.10E-01 |
| cds.Camellia_sinensis.comp36751_c0_seq1_m.21704 | PREDICTED: protein STRICTOSIDINE SYNTHASE-LIKE 3-like [Jatropha curcas] | 43.85 | 64.193 | 34.1 | 12 | 16 | 12 | 1.091 | 1.116 | 1.058 | 0.871 | 0.886 | 0.92 | 0.82 | 8.95E-04 |

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| cds.Camellia_sinensis.comp36757_c0_seq1_m.20481 | PREDICTED: actin-related protein 4 isoform X1 [Ziziphus jujuba] | 54.079 | 45.258 | 32.4 | 11 | 11 | 11 | 0.965 | 1.095 | 0.948 | 1.053 | 1.003 | 0.994 | 1.014 | 7.65E-01 |
| cds.Camellia_sinensis.comp36769_c0_seq1_m.58934 | PREDICTED: organellar oligopeptidase A, chloroplastic/mitochondrial-like, partial [Nicotiana tabacum] | 11.713 | 7.6225 | 34 | 4 | 7 | 4 | 0.911 | 0.965 | 1.006 | 1.062 | 1.034 | 1.03 | 1.085 | 5.39E-02 |
| cds.Camellia_sinensis.comp36801_c0_seq1_m.55689 | PREDICTED: aldehyde dehydrogenase family 2 member B7, mitochondrial [Eucalyptus grandis] | 14.435 | 56.327 | 53.4 | 5 | 9 | 5 | 0.939 | 0.924 | 0.941 | 1.091 | 1.048 | 1.07 | 1.144 | 4.81E-04 |
| cds.Camellia_sinensis.comp36804_c0_seq1_m.45298 | transmembrane protein, putative [Medicago truncatula] | 17.492 | 24.943 | 23.1 | 3 | 4 | 3 | 0.99 | 0.979 | 0.987 | 1.012 | 1.023 | 1.003 | 1.028 | 1.44E-02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp36845_c0_seq1_m.56300 | probable mitochondrial-processing peptidase subunit beta [Cucumis melo] | 14.372 | 10.274 | 24.8 | 3 | 5 | 1 | 0.958 | 1.025 | 1.031 | 1.045 | 0.953 | 1.003 | 0.996 | 9.06E-01 |
| cds.Camellia_sinensis.comp36862_c0_seq1_m.44499 | PREDICTED: pectin acetylesterase 8-like [Juglans regia] | 27.734 | 8.5182 | 11.8 | 3 | 4 | 3 | 1.013 | 1.032 | 1.043 | 0.988 | 0.966 | 0.961 | 0.944 | 8.74E-03 |
| cds.Camellia_sinensis.comp36945_c0_seq1_m.52410 | PREDICTED: probable phospholipid hydroperoxide glutathione peroxidase [Ricinus communis] | 11.142 | 12.953 | 43 | 5 | 12 | 2 | 0.949 | 0.925 | 0.942 | 1.096 | 1.055 | 1.063 | 1.141 | 6.84E-04 |
| cds.Camellia_sinensis.comp37006_c0_seq1_m.34879 | PREDICTED: pre-mRNA-splicing factor SPF27 homolog [Vitis vinifera] | 30.057 | 12.138 | 16.3 | 5 | 6 | 5 | 0.977 | 1.007 | 1.043 | 0.989 | 1.021 | 0.979 | 0.987 | 6.13E-01 |

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| cds.Camellia_sinensis.comp37024_c0_seq1_m.39511 | PREDICTED: small heat shock protein, chloroplastic-like isoform X2 [Nelumbo nucifera] | 22.449 | 19.429 | 35.2 | 6 | 13 | 6 | 0.975 | 0.953 | 1.013 | 1.047 | 1.035 | 1.02 | 1.055 | 5.04E-02 |
| cds.Camellia_sinensis.comp37091_c0_seq1_m.40308 | PREDICTED: ATP-dependent zinc metalloprotease FTSH 10, mitochondrial [Ricinus communis] | 26.826 | 2.2185 | 4.6 | 1 | 1 | 1 | 1.121 | 1.153 | 0.984 | 0.92 | 0.902 | 0.895 | 0.834 | 2.23E-02 |
| cds.Camellia_sinensis.comp37118_c0_seq1_m.40237 | PREDICTED: eukaryotic translation initiation factor 4B2 [Vitis vinifera] | 33.312 | 2.7258 | 3.3 | 1 | 1 | 1 | 1.038 | 1.117 | 1.147 | 0.874 | 0.969 | 0.839 | 0.812 | 1.61E-02 |
| cds.Camellia_sinensis.comp37124_c0_seq1_m.21044 | PREDICTED: chaperone protein dnaJ 10 [Prunus mume] | 38.789 | 18.414 | 17.5 | 6 | 8 | 6 | 1.043 | 0.984 | 1.023 | 1.048 | 0.966 | 0.98 | 0.982 | 5.68E-01 |

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| cds.Camellia_sinensis.comp37127_c0_seq1_m.43123 | PREDICTED: 30S ribosomal protein 3-1, chloroplastic-like [Populus euphratica] | 22.557 | 4.1082 | 6 | 1 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp37161_c0_seq1_m.54381 | PREDICTED: dynein light chain LC6, flagellar outer arm [Ziziphus | 11.778 | 3.7654 | 22.4 | 2 | 2 | 2 | 0.899 | 0.999 | 0.967 | 1.079 | 1.018 | 1.069 | 1.105 | 4.93E-02 |
| cds.Camellia_sinensis.comp37196_c0_seq1_m.31940 | PREDICTED: cinnamoyl-CoA reductase 2 [Sesamum indicum] | 37.462 | 5.8002 | 8.7 | 3 | 4 | 3 | 0.903 | 0.903 | 0.997 | 1.05 | 1.035 | 1.144 | 1.152 | 3.57E-02 |
| cds.Camellia_sinensis.comp37365_c0_seq1_m.23220 | PREDICTED: tyrosine--tRNA ligase, chloroplastic/mitochondrial-like [Gossypium hirsutum] | 59.345 | 1.7901 | 3.7 | 2 | 2 | 2 | 0.98 | 0.978 | 1.027 | 1.019 | 1.026 | 0.985 | 1.015 | 5.00E-01 |

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| cds.Camellia_sinensis.comp37458_c0_seq1_m.24872 | PREDICTED: sec-independent protein translocase protein TATC, chloroplastic [Ziziphus jujuba] | 39.076 | 19.004 | 10.4 | 2 | 2 | 2 | 1.011 | 1.002 | 1.026 | 0.969 | 0.971 | 1.024 | 0.975 | 2.61E-01 |
| cds.Camellia_sinensis.comp37631_c0_seq1_m.44158 | PREDICTED: mavicyanin-like [Gossypium hirsutum] | 18.427 | 2.0941 | 9.7 | 2 | 2 | 2 | 1.13 | 1.157 | 1.213 | 0.833 | 0.807 | 0.818 | 0.702 | 1.01E-04 |
| cds.Camellia_sinensis.comp37633_c0_seq1_m.16602 | PREDICTED: sucrose transport protein SUC4 [Theobroma cacao] | 54.176 | 1.9145 | 1.6 | 1 | 1 | 1 | 1.047 | 1.007 | 1.07 | 0.957 | 0.936 | 0.978 | 0.919 | 1.81E-02 |
| cds.Camellia_sinensis.comp37744_c0_seq1_m.41489 | PREDICTED: arabinosyltransferase RRA3-like [Nelumbo nucifera] | 32.58 | 6.8766 | 4.8 | 1 | 1 | 1 | 1.043 | 0.934 | 1.031 | 0.96 | 0.992 | 1.041 | 0.995 | 9.23E-01 |
| cds.Camellia_sinensis.comp37907_c0_seq1_m.56509 | PREDICTED: fruit protein pKIWI502-like [Nicotiana tabacum] | 13.301 | 20.582 | 28.7 | 3 | 5 | 2 | 1.178 | 0.977 | 1.112 | 0.877 | 0.985 | 0.844 | 0.828 | 6.03E-02 |

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| cds.Camellia_sinensis.comp38000_c0_seq1_m.28599 | PREDICTED: prostaglandin E synthase 2-like [Jatropha curcas] | 43.273 | 11.411 | 11 | 5 | 7 | 4 | 1.014 | 1.007 | 1.018 | 0.986 | 1.005 | 0.951 | 0.968 | 1.19E-01 |
| cds.Camellia_sinensis.comp38035_c0_seq1_m.22259 | PREDICTED: GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase [Citrus sinensis] | 52.521 | 11.603 | 7.5 | 3 | 4 | 3 | 0.822 | 0.906 | 1.033 | 1.124 | 1.008 | 1.056 | 1.155 | 1.15E-01 |
| cds.Camellia_sinensis.comp38050_c0_seq1_m.42138 | PREDICTED: phenylalanine ammonia-lyase G4 [Ricinus communis] | 26.074 | 3.7057 | 24.1 | 7 | 13 | 3 | 1.227 | 1.231 | 1.292 | 0.762 | 0.75 | 0.707 | 0.592 | 4.47E-05 |
| cds.Camellia_sinensis.comp38095_c0_seq1_m.52871 | PREDICTED: transmembrane protein 120 homolog [Solanum tuberosum | 14.949 | 12.507 | 23.1 | 3 | 5 | 2 | 0.985 | 1.116 | 1.022 | 0.973 | 0.95 | 0.954 | 0.921 | 9.94E-02 |

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| cds.Camellia_sinensis.comp38139_c0_seq1_m.32128 | PREDICTED: D-amino-acid transaminase, chloroplastic [Eucalyptus grandis] | 39.473 | 5.1197 | 7.5 | 3 | 4 | 3 | 1.031 | 1.026 | 0.996 | 1 | 1.006 | 0.945 | 0.967 | 2.05E-01 |
| cds.Camellia_sinensis.comp38204_c0_seq1_m.10632 | PREDICTED: flowering time control protein FY [Vitis vinifera] | 81.936 | 5.6821 | 2.4 | 2 | 2 | 2 | 0.943 | 1.029 | 0.942 | 1.054 | 0.964 | 1.088 | 1.066 | 2.45E-01 |
| cds.Camellia_sinensis.comp38251_c0_seq1_m.43401 | PREDICTED: glycine-rich RNA-binding protein 6, mitochondrial [Prunus | 15.393 | 3.0006 | 9.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp38448_c0_seq1_m.28380 | transmembrane protein, putative [Medicago truncatula] | 37.351 | 3.9296 | 3 | 1 | 1 | 1 | 0.92 | 0.977 | 1.022 | 1.038 | 1.067 | 1.003 | 1.065 | 1.47E-01 |
| cds.Camellia_sinensis.comp38515_c0_seq1_m.33013 | heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] | 33.03 | 8.6961 | 12.8 | 4 | 6 | 4 | 1.004 | 1.024 | 1.059 | 0.955 | 0.964 | 0.994 | 0.944 | 4.24E-02 |

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| cds.Camellia_sinensis.comp38553_c0_seq1_m.49905 | PREDICTED: 10 kDa chaperonin-like [Sesamum indicum] | 11.983 | 3.4024 | 17.4 | 2 | 3 | 2 | 0.991 | 1.005 | 1.05 | 1.004 | 1 | 0.96 | 0.973 | 2.94E-01 |
| cds.Camellia_sinensis.comp38568_c0_seq1_m.40718 | PREDICTED: pantothenate kinase 1 isoform X2 [Ziziphus jujuba] | 20.76 | 16.641 | 24.2 | 3 | 3 | 3 | 0.958 | 0.946 | 1.022 | 0.995 | 1.053 | 1.045 | 1.057 | 1.35E-01 |
| cds.Camellia_sinensis.comp38637_c0_seq1_m.34256 | PREDICTED: pyridoxal 5'-phosphate synthase-like subunit PDX1.2 [Nicotiana tomentosiformis] | 32.845 | 62.895 | 12.1 | 3 | 4 | 2 | 1.025 | 1.002 | 1.082 | 0.953 | 0.969 | 0.968 | 0.93 | 3.63E-02 |

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| cds.Camellia_sinensis.comp38664_c0_seq1_m.43903 | PREDICTED: protein HOMOLOG OF MAMMALIAN LYST-INTERACTING PROTEIN 5-like isoform X2 [Ziziphus jujuba] | 26.14 | 2.2908 | 5.2 | 1 | 1 | 1 | 0.969 | 1.068 | 1.157 | 0.921 | 0.903 | 0.979 | 0.878 | 8.62E-02 |
| cds.Camellia_sinensis.comp38927_c0_seq1_m.45078 | PREDICTED: dihydrolipoyllysine-residue acetyltransferase component 1 of pyruvate dehydrogenase complex,mitochondrial [Prunus mume] | 26.622 | 1.8582 | 9.7 | 2 | 4 | 1 | 1.027 | 0.988 | 1.012 | 1.006 | 0.946 | 1.025 | 0.983 | 5.57E-01 |

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| cds.Camellia_sinensis.comp39032_c0_seq1_m.57934 | PREDICTED: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic-like [Prunus mume] | 12.312 | 15.127 | 9.1 | 1 | 3 | 1 | 1.088 | 1.094 | 1.036 | 0.942 | 0.914 | 0.911 | 0.86 | 1.76E-03 |
| cds.Camellia_sinensis.comp39049_c0_seq1_m.47896 | PREDICTED: acyl-protein thioesterase 2 [Ricinus communis] | 12.752 | 28.227 | 15 | 2 | 2 | 2 | 0.943 | 0.979 | 1.071 | 1.011 | 0.965 | 1.047 | 1.01 | 8.19E-01 |
| cds.Camellia_sinensis.comp39084_c0_seq1_m.17097 | dicarboxylate transporter 2.1, chloroplastic-like [Nicotiana tabacum] | 65.498 | 17.499 | 6.1 | 3 | 6 | 3 | 1.012 | 0.951 | 1.026 | 0.998 | 1.05 | 1.028 | 1.029 | 3.53E-01 |
| cds.Camellia_sinensis.comp39106_c0_seq1_m.45247 | glycine-rich RNA-binding protein 4, mitochondrial [Asparagus officinalis] | 19.515 | 3.1439 | 9.8 | 2 | 2 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp39475_c0_seq1_m.51706 | receptor-interacting protein, putative [Medicago truncatula] | 16.397 | 19.621 | 31.2 | 3 | 3 | 3 | 1.034 | 1.039 | 0.988 | 1.135 | 0.959 | 0.858 | 0.964 | 6.34E-01 |
| cds.Camellia_sinensis.comp39568_c0_seq1_m.46204 | PREDICTED: low-temperature-induced cysteine proteinase-like [Juglans regia] | 21.795 | 2.2803 | 9.9 | 3 | 3 | 2 | 1.108 | 0.971 | 0.991 | 0.946 | 0.998 | 0.977 | 0.951 | 3.33E-01 |
| cds.Camellia_sinensis.comp39622_c0_seq1_m.30228 | PREDICTED: electron transfer flavoprotein subunit alpha, mitochondrial [Juglans regia] | 37.073 | 56.795 | 29.5 | 8 | 10 | 8 | 1.004 | 1.044 | 1.014 | 0.96 | 0.974 | 1.006 | 0.96 | 8.81E-02 |
| cds.Camellia_sinensis.comp39943_c0_seq1_m.53264 | PREDICTED: sorting nexin 2A [Vitis vinifera] | 17.431 | 1.8136 | 7.7 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp39971_c0_seq1_m.51236 | PREDICTED: glycine-rich RNA-binding protein RZ1C isoform X1 [Fragaria vesca subsp. vesca] | 12.197 | 2.0356 | 7.6 | 1 | 1 | 1 | 1.315 | 1.349 | 1.269 | 0.589 | 0.705 | 0.673 | 0.5 | 2.57E-04 |
| cds.Camellia_sinensis.comp401276_c0_seq1_m.59258 | PREDICTED: beta-glucosidase 12-like [Jatropha curcas] | 10.919 | 14.908 | 20 | 2 | 3 | 2 | 1.056 | 1.011 | 1.061 | 0.966 | 0.984 | 0.919 | 0.917 | 2.75E-02 |
| cds.Camellia_sinensis.comp40162_c0_seq1_m.14618 | PREDICTED: aldehyde dehydrogenase family 3 member H1 isoform X1 [Vitis vinifera] | 60.979 | 38.077 | 14.3 | 8 | 10 | 7 | 1.046 | 1.072 | 1.033 | 0.958 | 0.951 | 0.932 | 0.902 | 1.62E-03 |
| cds.Camellia_sinensis.comp40232_c0_seq1_m.33656 | methyltransferase type 11 [Medicago truncatula] | 33.591 | 14.827 | 18 | 5 | 5 | 5 | 1 | 1.021 | 1.025 | 0.991 | 0.968 | 0.987 | 0.967 | 3.40E-02 |

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| cds.Camellia_sinensis.comp40300_c0_seq1_m.49352 | Tetratricopeptide repeat (TPR)-like superfamily protein [Arabidopsis thaliana] | 18.842 | -2 | 4.2 | 1 | 2 | 1 | 0.752 | 1.032 | 1.266 | 1.178 | 0.958 | 0.863 | 0.983 | 9.88E-01 |
| cds.Camellia_sinensis.comp40740_c0_seq1_m.48580 | PREDICTED: kxDL motif-containing protein 1-like [Juglans regia] | 15.205 | 6.0489 | 9 | 1 | 1 | 1 | 0.946 | 0.876 | 1.056 | 1.028 | 1.084 | 1.037 | 1.094 | 1.77E-01 |
| cds.Camellia_sinensis.comp40827_c0_seq1_m.36639 | PREDICTED: thaumatin-like protein [Vitis vinifera] | 29.404 | 8.7214 | 9 | 2 | 2 | 2 | 1.067 | 1.067 | 1.015 | 0.971 | 0.933 | 0.939 | 0.903 | 7.92E-03 |
| cds.Camellia_sinensis.comp41274_c0_seq1_m.27135 | PREDICTED: omega-hydroxypalmitate O-feruloyl transferase [Vitis vinifera] | 50.195 | 15.876 | 13.3 | 6 | 10 | 6 | 1.296 | 1.24 | 1.31 | 0.678 | 0.725 | 0.652 | 0.534 | 5.93E-05 |

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| cds.Camellia_sinensis.comp41282_c0_seq1_m.25530 | PREDICTED: probable acyl-activating enzyme 1, peroxisomal isoform X1 [Vitis vinifera] | 52.393 | 1.1559 | 1.9 | 1 | 1 | 1 | 0.945 | 0.963 | 0.951 | 1.076 | 1.082 | 1.011 | 1.108 | 1.03E-02 |
| cds.Camellia_sinensis.comp41324_c0_seq1_m.36863 | Acid phosphatase 1 [Morus notabilis] | 29.104 | 12.726 | 15.6 | 3 | 4 | 3 | 0.974 | 1.012 | 0.934 | 1.163 | 0.997 | 0.945 | 1.063 | 4.31E-01 |
| cds.Camellia_sinensis.comp41457_c0_seq1_m.43683 | PREDICTED: germin-like protein 11-1 [Vitis vinifera] | 26.058 | 6.9438 | 13.7 | 3 | 3 | 3 | 1.088 | 1.097 | 1.005 | 0.938 | 0.93 | 0.927 | 0.876 | 4.29E-02 |
| cds.Camellia_sinensis.comp414583_c0_seq1_m.57860 | PREDICTED: galactinol synthase 2-like [Citrus sinensis] | 13.069 | 4.5376 | 19.8 | 2 | 3 | 2 | 0.952 | 0.929 | 0.777 | 1.122 | 1.075 | 1.181 | 1.271 | 2.50E-02 |
| cds.Camellia_sinensis.comp42092_c0_seq1_m.36103 | transmembrane protein [Arabidopsis thaliana] | 33.844 | 6.4069 | 9.5 | 3 | 4 | 3 | 0.915 | 1.086 | 0.981 | 1.051 | 1.023 | 0.966 | 1.019 | 7.23E-01 |

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| cds.Camellia_sinensis.comp421310_c0_seq1_m.58720 | PREDICTED: subtilisin-like protease SBT1.7 [Vitis vinifera] | 11.108 | 2.5143 | 16.3 | 2 | 3 | 2 | 0.892 | 0.951 | 0.96 | 1.028 | 1.11 | 1.093 | 1.153 | 1.25E-02 |
| cds.Camellia_sinensis.comp42486_c0_seq1_m.42101 | PREDICTED: calponin homology domain-containing protein DDB_G0272472 isoform X2 [Populus euphratica] | 28.725 | 6.6258 | 16.6 | 4 | 4 | 3 | | | | | | | | |
| cds.Camellia_sinensis.comp42499_c0_seq1_m.34886 | transmembrane protein, putative [Medicago truncatula] | 37.405 | 4.2894 | 7.6 | 3 | 5 | 3 | 1.014 | 1.002 | 0.989 | 1.034 | 1.009 | 0.963 | 1 | 9.98E-01 |
| cds.Camellia_sinensis.comp42843_c0_seq1_m.45117 | PREDICTED: protein RETICULATA-RELATED 1, chloroplastic-like [Nicotiana tabacum] | 21.168 | 21.174 | 17.5 | 3 | 4 | 3 | 0.954 | 1.01 | 1.015 | 0.991 | 0.969 | 1.046 | 1.009 | 7.83E-01 |

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| cds.Camellia_sinensis.comp42942_c0_seq1_m.42302 | PREDICTED: protein FAM136A [Vitis vinifera] | 20.553 | 10.436 | 20 | 3 | 3 | 3 | 1.022 | 0.956 | 0.962 | 1.019 | 1.089 | 0.965 | 1.045 | 3.48E-01 |
| cds.Camellia_sinensis.comp43060_c0_seq1_m.14223 | PREDICTED: ATPase family AAA domain-containing protein 3C-like [Nicotiana tabacum] | 69.453 | 16.508 | 11.8 | 9 | 10 | 8 | 0.959 | 0.962 | 0.945 | 1.028 | 0.994 | 1.046 | 1.07 | 1.31E-02 |
| cds.Camellia_sinensis.comp43546_c0_seq1_m.36228 | PREDICTED: BTB/POZ and MATH domain-containing protein 3-like isoform X1 [Vigna radiata var. radiata] | 35.6 | 1.9894 | 2.9 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp4412_c0_seq1_m.47742 | PREDICTED: dammarenediol II synthase-like [Daucus carota subsp. sativus] | 25.26 | -2 | 6 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp44218_c0_seq1_m.46187 | SNARE-associated family protein [Populus trichocarpa] | 17.607 | 6.242 | 9.9 | 1 | 1 | 1 | | 1.046 | 1.009 | 1.069 | | 0.953 | 0.984 | 7.97E-01 |
| cds.Camellia_sinensis.comp45076_c0_seq1_m.42729 | PREDICTED: acetylornithine aminotransferase, mitochondrial [Theobroma cacao] | 22.025 | 1.6269 | 16.3 | 3 | 4 | 2 | 0.974 | 1.12 | 1.013 | 0.942 | 0.993 | 0.96 | 0.932 | 1.94E-01 |
| cds.Camellia_sinensis.comp45314_c0_seq1_m.27017 | PREDICTED: DUF21 domain-containing protein At4g14240 [Vitis vinifera] | 45.073 | 4.306 | 7.2 | 2 | 2 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp45372_c0_seq1_m.42279 | PREDICTED: CCG-binding protein 1 [Juglans regia] | 24.55 | 2.6584 | 10.2 | 2 | 2 | 2 | 0.865 | 0.993 | 0.944 | 1.041 | 1.047 | 1.145 | 1.154 | 4.72E-02 |
| cds.Camellia_sinensis.comp4543_c0_seq1_m.35900 | PREDICTED: ricin-like [Elaeis guineensis | 36.078 | 50.212 | 6.5 | 2 | 4 | 2 | 0.848 | 0.856 | 0.848 | 1.113 | 1.174 | 1.204 | 1.368 | 5.54E-03 |
| cds.Camellia_sinensis.comp45686_c0_seq1_m.44193 | PREDICTED: homeobox protein BEL1 homolog [Juglans regia] | 22.13 | 1.7117 | 5.3 | 1 | 1 | 1 | 1.095 | 1 | 1.01 | 0.937 | 0.954 | 0.993 | 0.929 | 9.37E-02 |
| cds.Camellia_sinensis.comp45943_c0_seq1_m.50866 | PREDICTED: endo-1,3;1,4-beta-D-glucanase-like [Juglans regia] | 19.354 | 28.42 | 22.7 | 4 | 4 | 4 | 1.014 | 0.948 | 1.1 | 0.973 | 0.967 | 0.998 | 0.96 | 4.20E-01 |
| cds.Camellia_sinensis.comp46107_c0_seq1_m.13891 | PREDICTED: putative BPI/LBP family protein At1g04970 isoform X1 [Nelumbo nucifera] | 53.95 | 40.69 | 13.5 | 6 | 7 | 6 | 1.071 | 1.02 | 1.033 | 0.949 | 0.937 | 0.963 | 0.912 | 5.20E-03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| cds.Camellia_sinensis.comp46125_c0_seq1_m.54741 | | 11.837 | -2 | 7.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp46723_c0_seq1_m.58684 | PREDICTED: plasma membrane Ca2+-ATPase isoform X1 [Glycine max] | 11.241 | -2 | 18.1 | 2 | 3 | 1 | 0.937 | 0.935 | 0.986 | 1.044 | 1.021 | 1.102 | 1.108 | 2.30E-02 |
| cds.Camellia_sinensis.comp47152_c0_seq1_m.29533 | alpha/beta hydrolase family protein [Medicago truncatula] | 40.689 | 52.657 | 35.6 | 10 | 15 | 10 | 1.017 | 1.04 | 1.013 | 0.967 | 0.957 | 0.977 | 0.945 | 5.04E-03 |
| cds.Camellia_sinensis.comp47520_c0_seq1_m.36626 | PREDICTED: probable sarcosine oxidase [Vitis vinifera] | 39.465 | 3.6348 | 4 | 1 | 1 | 1 | 1.137 | 1.074 | 1.18 | 1.099 | 0.677 | 0.812 | 0.763 | 1.14E-01 |
| cds.Camellia_sinensis.comp47551_c0_seq1_m.50882 | | 14.053 | 7.1958 | 19.2 | 3 | 4 | 3 | 1.016 | 0.969 | 1.031 | 0.96 | 1.028 | 0.996 | 0.989 | 7.14E-01 |

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| cds.Camellia_sinensis.comp47557_c0_seq1_m.46952 | PREDICTED: phosphoenolpyruvate carboxylase [Capsicum annuum] | 16.262 | -2 | 30.3 | 4 | 6 | 0 | | | | | | | | |
| cds.Camellia_sinensis.comp48384_c0_seq1_m.47721 | PREDICTED: acetylornithine aminotransferase, mitochondrial [Populus euphratica] | 15.282 | 9.8073 | 12.8 | 2 | 3 | 2 | 1.058 | 1.079 | 0.991 | 0.919 | 0.979 | 0.928 | 0.903 | 3.52E-02 |
| cds.Camellia_sinensis.comp48392_c0_seq1_m.51039 | PREDICTED: gibberellin-regulated protein 1-like isoform X2 [Nicotiana sylvestris] | 12.635 | 3.2003 | 18.1 | 2 | 3 | 2 | 1.053 | 1.023 | 1.001 | 1.062 | 0.983 | 0.993 | 0.987 | 6.67E-01 |
| cds.Camellia_sinensis.comp492684_c0_seq1_m.58839 | PREDICTED: translationally-controlled tumor protein homolog [Gossypium hirsutum] | 11.776 | 11.42 | 38.5 | 6 | 16 | 3 | 1.012 | 0.95 | 1.018 | 0.997 | 1.03 | 1.001 | 1.016 | 5.39E-01 |

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| cds.Camellia_sinensis.comp49969_c0_seq1_m.40407 | PREDICTED: heat shock 70 kDa protein [Nelumbo nucifera] | 33.991 | 1.8236 | 20.1 | 7 | 22 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp51268_c0_seq1_m.48530 | PREDICTED: clathrin heavy chain 1-like [Oryza brachyantha] | 20.307 | 16.54 | 18.9 | 2 | 3 | 1 | 1.01 | 0.912 | 0.919 | 1.032 | 1.043 | 1.103 | 1.119 | 4.38E-02 |
| cds.Camellia_sinensis.comp52650_c0_seq1_m.46280 | PREDICTED: probable calcium-binding protein CML29 [Theobroma cacao] | 17.113 | 40.119 | 10.1 | 1 | 4 | 1 | 0.888 | 1.064 | 1.105 | 1.036 | 0.941 | 0.973 | 0.965 | 6.85E-01 |
| cds.Camellia_sinensis.comp53351_c0_seq1_m.53378 | PREDICTED: serine carboxypeptidase-like [Erythranthe guttata] | 17.209 | 1.7211 | 5.2 | 1 | 1 | 1 | 1.168 | 1.141 | 1.092 | 0.89 | 0.828 | 0.843 | 0.753 | 6.39E-04 |
| cds.Camellia_sinensis.comp53621_c0_seq1_m.37575 | PREDICTED: cannabidiolic acid synthase-like 1 [Citrus sinensis] | 34.518 | 5.1177 | 10.8 | 3 | 3 | 3 | 0.623 | 0.613 | 0.553 | 1.402 | 1.527 | 1.424 | 2.433 | 4.04E-05 |

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| cds.Camellia_sinensis.comp53961_c0_seq1_m.41267 | PREDICTED: protein PLASTID REDOX INSENSITIVE 2 [Nicotiana attenuata] | 23.337 | 4.1696 | 12.2 | 2 | 2 | 2 | 0.941 | 0.941 | 0.975 | 1.049 | 1.019 | 1.101 | 1.109 | 1.55E-02 |
| cds.Camellia_sinensis.comp54424_c0_seq1_m.57834 | PREDICTED: nucleoporin NUP152-like [Juglans | 11.825 | 2.1357 | 8.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp55332_c0_seq1_m.45185 | | 26.423 | 4.4742 | 7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp56153_c0_seq1_m.55980 | | 11.726 | 16.486 | 11 | 2 | 3 | 2 | 1.016 | 0.932 | 0.906 | 1.083 | 1.095 | 1.064 | 1.136 | 2.22E-02 |
| cds.Camellia_sinensis.comp57239_c0_seq1_m.48520 | PREDICTED: shikimate O-hydroxycinnamoyltransferase [Citrus sinensis] | 15.275 | 3.059 | 8.8 | 1 | 1 | 1 | 1.064 | 1.051 | 1.022 | 0.953 | 0.966 | 0.936 | 0.91 | 3.30E-03 |

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| cds.Camellia_sinensis.comp57924_c0_seq1_m.44234 | Aldolase-type TIM barrel family protein [Arabidopsis thaliana] | 22.123 | 120.89 | 36.9 | 6 | 13 | 6 | 0.935 | 0.984 | 0.968 | 1.008 | 1.065 | 1.08 | 1.092 | 2.74E-02 |
| cds.Camellia_sinensis.comp59003_c0_seq1_m.33995 | PREDICTED: protein SCO1 homolog 2, mitochondrial isoform X2 | 31.166 | 1.7285 | 5.8 | 2 | 2 | 2 | 1.011 | 1.045 | 1.013 | 0.986 | 1 | 0.949 | 0.956 | 7.75E-02 |
| cds.Camellia_sinensis.comp59169_c0_seq1_m.58685 | PREDICTED: cysteine-rich repeat secretory protein 60-like [Populus euphratica] | 10.862 | 3.2851 | 13.3 | 1 | 1 | 1 | 0.915 | 0.945 | 0.92 | 1.034 | 1.094 | 1.123 | 1.169 | 4.06E-03 |
| cds.Camellia_sinensis.comp6175_c0_seq1_m.49015 | PREDICTED: protein ASPARTIC PROTEASE IN GUARD CELL 2 [Citrus sinensis] | 19.549 | 5.8724 | 14 | 2 | 3 | 2 | 1.061 | 1.041 | 1.059 | 1.077 | 0.949 | 0.86 | 0.913 | 2.83E-01 |

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| cds.Camellia_sinensis.comp63389_c0_seq1_m.43336 | putative mannitol dehydrogenase [Morus notabilis] | 27.064 | 47.983 | 28.6 | 7 | 12 | 7 | 0.841 | 0.852 | 0.832 | 1.159 | 1.155 | 1.19 | 1.388 | 4.78E-06 |
| cds.Camellia_sinensis.comp66358_c0_seq1_m.30735 | PREDICTED: CLIP-associated protein-like [Nicotiana attenuata] | 37.671 | 1.1765 | 2.5 | 1 | 1 | 1 | 0.883 | 0.842 | 0.972 | 1.114 | 1.112 | 1.123 | 1.242 | 3.56E-02 |
| cds.Camellia_sinensis.comp66891_c0_seq1_m.58005 | PREDICTED: BEL1-like homeodomain protein 9 [Vitis vinifera] | 12.246 | 1.5614 | 7.3 | 1 | 1 | 1 | 1.034 | 1.004 | 1.068 | 0.974 | 0.908 | 1.009 | 0.931 | 1.13E-01 |
| cds.Camellia_sinensis.comp6690_c0_seq1_m.53308 | PREDICTED: golgin subfamily A member 1 isoform X1 [Theobroma cacao] | 18.257 | -2 | 5.8 | 1 | 1 | 1 | 1.079 | 0.971 | 1.026 | 0.941 | 1.008 | 0.97 | 0.949 | 2.27E-01 |
| cds.Camellia_sinensis.comp67036_c0_seq1_m.38292 | PREDICTED: reticuline oxidase-like protein [Eucalyptus grandis] | 36.396 | 5.7183 | 6.9 | 2 | 6 | 1 | 0.921 | 0.924 | 0.929 | 1.074 | 1.06 | 1.124 | 1.174 | 1.23E-02 |

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| cds.Camellia_sinensis.comp67181_c0_seq1_m.57359 | PREDICTED: zeatin O-xylosyltransferase-like [Nicotiana attenuata] | 11.895 | 12.544 | 8.2 | 1 | 1 | 1 | 1.09 | 1.072 | 1.005 | 0.952 | 0.947 | 0.921 | 0.89 | 1.25E-02 |
| cds.Camellia_sinensis.comp67295_c0_seq1_m.36148 | PREDICTED: peroxisomal 2,4-dienoyl-CoA reductase [Vitis vinifera] | 33.097 | 1.2639 | 2.6 | 1 | 1 | 1 | 0.949 | 0.995 | 0.957 | 1.018 | 1.041 | 1.06 | 1.075 | 1.78E-02 |
| cds.Camellia_sinensis.comp69681_c0_seq1_m.38233 | PREDICTED: vestitone reductase-like [Vitis vinifera] | 37.026 | 3.26 | 8.7 | 3 | 3 | 3 | 0.884 | 0.869 | 0.893 | 1.15 | 1.176 | 1.082 | 1.288 | 6.41E-04 |
| cds.Camellia_sinensis.comp7043_c0_seq1_m.43597 | PREDICTED: probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 2 isoform X1 [Vitis vinifera] | 19.226 | 1.5844 | 4.1 | 1 | 3 | 1 | 0.96 | 0.909 | 0.979 | 1.021 | 1.045 | 1.068 | 1.1 | 2.02E-02 |

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| cds.Camellia_sinensis.comp7156_c0_seq1_m.36164 | PREDICTED: tryptophan aminotransferase-related protein 2 [Vitis vinifera] | 36.233 | 1.5395 | 2.8 | 1 | 1 | 1 | 0.444 | 1.522 | 1.425 | 1.148 | 0.853 | 0.667 | 0.787 | 7.78E-01 |
| cds.Camellia_sinensis.comp72738_c0_seq1_m.34175 | PREDICTED: hexose carrier protein HEX6-like [Gossypium raimondii] | 40.021 | 2.3306 | 3.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp7306_c0_seq1_m.21311 | PREDICTED: pectinesterase-like [Gossypium hirsutum] | 56.944 | 99.605 | 20.4 | 8 | 22 | 8 | 1.19 | 1.181 | 1.217 | 0.809 | 0.786 | 0.78 | 0.662 | 4.30E-06 |
| cds.Camellia_sinensis.comp7329_c0_seq1_m.36717 | PREDICTED: clathrin heavy chain 1-like, partial [Nicotiana tabacum] | 38.859 | 7.1565 | 25.2 | 10 | 13 | 2 | 1.047 | 0.982 | 0.918 | 1.015 | 0.956 | 1.086 | 1.037 | 5.26E-01 |

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| cds.Camellia_sinensis.comp7370_c0_seq1_m.2142 | PREDICTED: sister chromatid cohesion 1 protein 4 [Vitis vinifera] | 146.01 | 2.1265 | 1.3 | 2 | 2 | 2 | 1.001 | 1.031 | 1.138 | 1.048 | 0.849 | 0.935 | 0.893 | 1.86E-01 |
| cds.Camellia_sinensis.comp7398_c0_seq1_m.51903 | PREDICTED: aldehyde dehydrogenase family 2 member C4 [Ricinus communis] | 19.086 | 6.2598 | 17.6 | 3 | 3 | 2 | 1.043 | 0.977 | 0.989 | 0.952 | 1.035 | 1.006 | 0.995 | 8.70E-01 |
| cds.Camellia_sinensis.comp7414_c0_seq1_m.23149 | PREDICTED: endoplasmic reticulum-Golgi intermediate compartment protein 3-like [Nelumbo nucifera] | 43.668 | 3.4285 | 9.1 | 5 | 5 | 5 | 0.965 | 0.964 | 0.964 | 1.055 | 1.019 | 1.055 | 1.082 | 2.12E-02 |
| cds.Camellia_sinensis.comp7442_c0_seq1_m.31191 | PREDICTED: protein DETOXIFICATION 27-like [Ziziphus jujuba] | 44.466 | 2.5815 | 3.2 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |

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| cds.Camellia_sinensis.comp7457_c0_seq1_m.29704 | PREDICTED: glucan endo-1,3-beta-glucosidase 5 [Sesamum | 48.901 | 3.5188 | 4.6 | 2 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp7459_c0_seq1_m.59126 | PREDICTED: protein transport protein SEC23-like [Nicotiana tabacum] | 10.585 | 34.392 | 27.5 | 3 | 4 | 3 | 0.957 | 0.956 | 0.923 | 1.195 | 1.005 | 1 | 1.128 | 1.21E-01 |
| cds.Camellia_sinensis.comp74698_c0_seq1_m.45845 | PREDICTED: cysteine-rich repeat secretory protein 55-like [Gossypium hirsutum] | 26.69 | 7.2489 | 12.1 | 2 | 2 | 2 | 1.047 | 1.295 | 1.01 | 0.964 | 0.734 | 0.925 | 0.783 | 9.90E-02 |
| cds.Camellia_sinensis.comp7481_c0_seq1_m.25260 | PREDICTED: protein disulfide-isomerase [Nelumbo nucifera] | 48.994 | 1.2802 | 4.1 | 3 | 4 | 1 | 1.015 | 0.926 | 0.952 | 0.888 | 1.169 | 1.06 | 1.077 | 4.62E-01 |

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| cds.Camellia_sinensis.comp7486_c0_seq1_m.13209 | PREDICTED: ferrochelatase-2, chloroplastic [Vitis vinifera] | 57.912 | 13.033 | 7.5 | 4 | 6 | 4 | 1.054 | 1.074 | 0.994 | 0.927 | 0.945 | 0.942 | 0.901 | 1.27E-02 |
| cds.Camellia_sinensis.comp74925_c0_seq1_m.19313 | PREDICTED: probable acyl-activating enzyme 2 [Juglans regia] | 65.575 | 12.883 | 8.1 | 4 | 5 | 4 | 0.981 | 1.04 | 0.985 | 1.071 | 0.927 | 1.014 | 1.002 | 9.90E-01 |
| cds.Camellia_sinensis.comp7507_c0_seq1_m.52448 | PREDICTED: phospholipase D alpha 1-like [Juglans regia] | 18.715 | 14.699 | 19.5 | 3 | 4 | 2 | 0.947 | 0.884 | 0.954 | 1.045 | 1.095 | 1.105 | 1.165 | 6.80E-03 |
| cds.Camellia_sinensis.comp7540_c0_seq1_m.42081 | PREDICTED: acylphosphatase-like isoform X1 [Nicotiana tabacum] | 25.436 | 6.4602 | 8.8 | 2 | 4 | 2 | 0.926 | 0.967 | 0.951 | 1.035 | 1.038 | 1.047 | 1.097 | 2.08E-03 |
| cds.Camellia_sinensis.comp7544_c0_seq2_m.47755 | PREDICTED: calcineurin subunit B-like [Nicotiana tabacum] | 21.778 | 6.1985 | 9.8 | 2 | 3 | 1 | 0.918 | 0.949 | 0.873 | 1.094 | 1.142 | 1.062 | 1.204 | 4.48E-03 |

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| cds.Camellia_sinensis.comp7575_c0_seq1_m.43805 | plant/MOJ10-14 protein [Medicago truncatula] | 21.256 | 11.112 | 16.2 | 3 | 3 | 3 | 0.969 | 1.05 | 1.002 | 1.028 | 1.008 | 0.958 | 0.991 | 7.91E-01 |
| cds.Camellia_sinensis.comp7627_c0_seq1_m.12093 | PREDICTED: root phototropism protein 3 [Citrus sinensis] | 73.688 | 10.098 | 7.8 | 4 | 5 | 4 | 1.052 | 0.898 | 1.144 | 1.031 | 0.947 | 0.932 | 0.941 | 5.01E-01 |
| cds.Camellia_sinensis.comp7655_c0_seq2_m.28124 | PREDICTED: 50S ribosomal protein L15 isoform X1 [Daucus carota subsp. sativus] | 30.729 | 5.6863 | 3.9 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp7756_c0_seq1_m.19701 | PREDICTED: probable 2-carboxy-D-arabinitol-1-phosphatase [Theobroma cacao] | 59.893 | 191.09 | 29.8 | 15 | 35 | 15 | 0.981 | 0.981 | 0.999 | 1.016 | 1.012 | 1.007 | 1.025 | 1.99E-02 |
| cds.Camellia_sinensis.comp7765_c0_seq1_m.49699 | PREDICTED: tubulin alpha-3 chain-like [Malus domestica] | 15.45 | 7.7989 | 44.9 | 5 | 9 | 2 | 1.1 | 1.09 | 1.325 | 0.765 | 0.856 | 0.823 | 0.695 | 7.32E-03 |

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| cds.Camellia_sinensis.comp7790_c0_seq1_m.36728 | embryo-abundant family protein [Populus trichocarpa] | 30.556 | 89.831 | 42.2 | 11 | 21 | 11 | 1.032 | 0.959 | 0.985 | 0.971 | 1.06 | 0.996 | 1.017 | 6.45E-01 |
| cds.Camellia_sinensis.comp7843_c0_seq1_m.37966 | PREDICTED: isoleucine--tRNA ligase, cytoplasmic-like [Nicotiana tabacum] | 23.995 | 2.5024 | 9.7 | 1 | 2 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp7873_c0_seq1_m.33440 | PREDICTED: exosome complex component RRP42 [Ziziphus jujuba] | 29.914 | 3.5615 | 9.1 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp7911_c0_seq1_m.48286 | PREDICTED: HVA22-like protein f [Daucus carota subsp. sativus] | 18.385 | 10.847 | 18.8 | 3 | 3 | 3 | 0.943 | 0.935 | 0.947 | 1.089 | 1.064 | 1.035 | 1.128 | 1.36E-03 |
| cds.Camellia_sinensis.comp7916_c0_seq2_m.4146 | LETM1-like protein [Medicago truncatula] | 103.16 | 3.8131 | 2.2 | 2 | 2 | 2 | 0.992 | 1.1 | 1.041 | 0.962 | 0.918 | 0.985 | 0.914 | 7.05E-02 |

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| cds.Camellia_sinensis.comp7948_c0_seq1_m.50183 | PREDICTED: protein SPA, chloroplastic isoform X1 [Citrus sinensis] | 12.787 | 5.1659 | 12.3 | 1 | 2 | 1 | 1.006 | 1.028 | 1.063 | 1.03 | 0.898 | 0.98 | 0.939 | 2.11E-01 |
| cds.Camellia_sinensis.comp7974_c0_seq1_m.52825 | PREDICTED: coatomer subunit zeta-1-like [Juglans regia] | 18.477 | 9.455 | 14.5 | 3 | 6 | 3 | 1.053 | 1.014 | 0.983 | 0.992 | 1.023 | 0.937 | 0.968 | 3.69E-01 |
| cds.Camellia_sinensis.comp7976_c0_seq1_m.40429 | PREDICTED: thioredoxin M3, chloroplastic-like [Ipomoea nil] | 19.762 | 39.591 | 28.8 | 4 | 5 | 4 | 0.98 | 1.046 | 1.011 | 1.005 | 0.998 | 0.97 | 0.979 | 3.87E-01 |
| cds.Camellia_sinensis.comp7984_c0_seq1_m.25603 | PREDICTED: maspardin [Theobroma cacao] | 46.59 | 1.7325 | 2.9 | 1 | 1 | 1 |  |  |  |  |  |  |  |  |
| cds.Camellia_sinensis.comp8031_c0_seq1_m.49811 | PREDICTED: alcohol dehydrogenase class-3-like isoform X2 [Capsicum annuum] | 13.113 | 2.2441 | 18.5 | 2 | 2 | 2 | 1.036 | 0.965 | 1.075 | 0.927 | 0.999 | 0.996 | 0.95 | 2.72E-01 |

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| cds.Camellia_sinensis.comp8059_c0_seq1_m.38917 | | 19.822 | 1.7826 | 6.5 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp8060_c0_seq2_m.27832 | PREDICTED: ferredoxin--NADP reductase, root isozyme, chloroplastic [Cicer arietinum] | 42.626 | 44.229 | 27.2 | 10 | 15 | 10 | 1.025 | 1.004 | 0.981 | 0.995 | 0.99 | 1.004 | 0.993 | 6.34E-01 |
| cds.Camellia_sinensis.comp80684_c0_seq1_m.42619 | PREDICTED: bifunctional epoxide hydrolase 2-like [Erythranthe guttata] | 31.406 | 4.6848 | 10.5 | 2 | 2 | 2 | 0.9 | 0.998 | 0.839 | 1.094 | 1.016 | 1.187 | 1.205 | 5.06E-02 |
| cds.Camellia_sinensis.comp80707_c0_seq1_m.24397 | transferring glycosyl group transferase [Medicago truncatula] | 53.175 | 1.1743 | 1.9 | 1 | 1 | 1 | 1.024 | 1.069 | 1.004 | 0.985 | 0.963 | 0.955 | 0.937 | 3.58E-02 |
| cds.Camellia_sinensis.comp80858_c0_seq1_m.39939 | PREDICTED: phosphomannomutase/phosphoglucomutase isoform X2 [Ziziphus jujuba] | 34.189 | 37.016 | 19 | 6 | 7 | 6 | 1.017 | 1.052 | 1.057 | 0.973 | 0.925 | 0.969 | 0.917 | 1.29E-02 |

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| cds.Camellia_sinensis.comp8105_c0_seq1_m.8660 | PREDICTED: copper amine oxidase 1-like isoform X2 [Populus euphratica] | 26.139 | 2.1693 | 4.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp81312_c0_seq1_m.23202 | PREDICTED: aspartic proteinase Asp1 isoform X3 [Fragaria vesca subsp. vesca] | 51.099 | 2.1335 | 2.8 | 1 | 1 | 1 | 0.957 | 1.379 | 0.937 | 1.033 | 0.837 | 0.851 | 0.831 | 2.91E-01 |
| cds.Camellia_sinensis.comp81846_c0_seq1_m.59305 | PREDICTED: pectinesterase 2.2-like [Juglans regia] | 11.322 | 11.57 | 27.7 | 2 | 2 | 2 | 0.954 | 0.967 | 0.995 | 1.119 | 0.954 | 1.036 | 1.066 | 2.63E-01 |

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| cds.Camellia_sinensis.comp8216_c0_seq1_m.31089 | PREDICTED: biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplastic-like [Gossypium raimondii] | 29.807 | 7.1227 | 13.1 | 4 | 10 | 4 | 1.037 | 1.057 | 1.008 | 0.986 | 0.974 | 1.005 | 0.956 | 5.27E-02 |
| cds.Camellia_sinensis.comp8275_c0_seq1_m.49996 | PREDICTED: protein lava lamp isoform X5 [Vitis vinifera] | 21.74 | 2.7562 | 11 | 2 | 2 | 2 | 1.087 | 1.008 | 1.098 | 1.018 | 0.854 | 0.926 | 0.876 | 8.03E-02 |
| cds.Camellia_sinensis.comp8320_c0_seq1_m.49805 | PREDICTED: SPX domain-containing protein 1-like [Jatropha curcas] | 22.306 | 1.203 | 7.3 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp8340_c0_seq1_m.48112 | PREDICTED: mitochondrial phosphate carrier protein 3, mitochondrial [Vitis vinifera] | 14.185 | 7.2687 | 16.5 | 2 | 4 | 1 | 0.982 | 0.899 | 0.882 | 0.979 | 1.09 | 1.188 | 1.179 | 6.68E-02 |

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| cds.Camellia_sinensis.comp8370_c0_seq1_m.39819 | PREDICTED: probable glutathione S-transferase [Vitis vinifera] | 26.244 | 45.45 | 39.2 | 8 | 13 | 8 | 0.918 | 0.892 | 0.888 | 1.128 | 1.139 | 1.046 | 1.228 | 2.08E-03 |
| cds.Camellia_sinensis.comp8436_c0_seq1_m.50373 | PREDICTED: pectin acetylesterase 10 [Nelumbo nucifera] | 20.935 | 6.1345 | 6.4 | 1 | 1 | 1 | 1 | 1.156 | 1.139 | 0.951 | 0.847 | 0.897 | 0.818 | 2.46E-02 |
| cds.Camellia_sinensis.comp8468_c0_seq1_m.37024 | glyoxalase/bleomycin resistance protein/dioxygenase [Medicago truncatula] | 22.623 | 15.368 | 22.7 | 4 | 6 | 4 | 1.039 | 1.063 | 1.022 | 0.952 | 0.953 | 0.988 | 0.926 | 1.00E-02 |
| cds.Camellia_sinensis.comp8505_c0_seq1_m.28563 | PREDICTED: putative invertase inhibitor [Ziziphus jujuba] | 21.54 | 2.1267 | 5.1 | 1 | 1 | 1 | 0.984 | 1.102 | 1.233 | 0.884 | 0.953 | 0.834 | 0.805 | 4.72E-02 |
| cds.Camellia_sinensis.comp85250_c0_seq1_m.59355 | phosphoenolpyruvate carboxylase-like [Malus domestica] | 11.762 | -2 | 24 | 3 | 4 | 1 | 0.848 | 0.975 | 0.967 | 1.14 | 1.114 | 1.004 | 1.168 | 5.98E-02 |
| cds.Camellia_sinensis.comp8548_c0_seq1_m.30661 | Protein ApaG [Morus notabilis] | 21.503 | 7.6426 | 10.5 | 2 | 2 | 2 | 0.902 | 1.09 | 1.057 | 1.056 | 1.009 | 0.908 | 0.975 | 7.63E-01 |

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| cds.Camellia_sinensis.comp85536_c0_seq1_m.58933 | stress up-regulated Nod 19 protein [Medicago truncatula] | 11.674 | 3.4634 | 10.7 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp8559_c0_seq1_m.31734 | transmembrane protein, putative [Medicago truncatula] | 18.39 | 2.1378 | 9.6 | 1 | 1 | 1 | 0.978 | 0.945 | 0.932 | 1.193 | 0.937 | 1.044 | 1.112 | 2.29E-01 |
| cds.Camellia_sinensis.comp8571_c0_seq1_m.30552 | PREDICTED: protein MEMO1 [Vitis vinifera] | 32.687 | 4.0276 | 6.5 | 2 | 2 | 2 | 0.928 | 1.013 | 1.025 | 1.022 | 0.991 | 1.041 | 1.03 | 4.33E-01 |
| cds.Camellia_sinensis.comp8673_c0_seq1_m.10797 | 26S proteasome non-ATPase regulatory subunit 5 [Morus notabilis] | 21.633 | 31.4 | 41.7 | 7 | 7 | 7 | 0.981 | 1.018 | 1.082 | 0.985 | 0.982 | 0.962 | 0.951 | 1.67E-01 |
| cds.Camellia_sinensis.comp8726_c0_seq1_m.43781 | PREDICTED: UPF0160 protein-like [Populus euphratica] | 13.611 | 7.49 | 11.4 | 1 | 2 | 1 | 0.999 | 0.948 | 0.973 | 1.026 | 1.031 | 1.039 | 1.06 | 1.95E-02 |

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| cds.Camellia_sinensis.comp8740_c0_seq1_m.36201 | SMP-30/gluconolaconase/LRE-like region protein [Medicago truncatula] | 39.718 | 4.3274 | 5.9 | 2 | 2 | 2 | 1.035 | 0.989 | 0.977 | 1.029 | 0.937 | 1.038 | 1.001 | 9.95E-01 |
| cds.Camellia_sinensis.comp8761_c0_seq1_m.42795 | PREDICTED: 15 kDa selenoprotein-like isoform X2 [Juglans regia] | 20.876 | 4.5007 | 9.8 | 2 | 2 | 2 | 1.008 | 1.043 | 0.934 | 1.092 | 0.936 | 0.998 | 1.014 | 8.30E-01 |
| cds.Camellia_sinensis.comp8839_c0_seq1_m.30938 | PREDICTED: mitochondrial outer membrane protein porin 4 [Juglans regia] | 29.662 | 46.409 | 31.9 | 9 | 15 | 8 | 1.08 | 1.023 | 1.033 | 0.939 | 0.953 | 1.001 | 0.923 | 3.41E-02 |
| cds.Camellia_sinensis.comp8848_c0_seq1_m.38628 | latex abundant protein 1 [Populus trichocarpa] | 25.275 | 3.9751 | 5.8 | 1 | 2 | 1 | 1.073 | 0.956 | 0.938 | 1.011 | 0.92 | 1.102 | 1.022 | 7.69E-01 |
| cds.Camellia_sinensis.comp8891_c1_seq1_m.56602 | tropinone reductase homolog At5g06060-like [Ananas comosus] | 13.052 | 15.253 | 23 | 3 | 8 | 2 | 0.994 | 0.953 | 0.98 | 1.008 | 0.994 | 1.037 | 1.038 | 9.93E-02 |

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| cds.Camellia_sinensis.comp8892_c0_seq1_m.2156 | PREDICTED: kinesin-like protein KIN-14B [Vitis vinifera] | 142.71 | 312.9 | 36.1 | 41 | 60 | 41 | 1.048 | 1.038 | 1.032 | 0.959 | 0.961 | 0.962 | 0.924 | 6.36E-05 |
| cds.Camellia_sinensis.comp8914_c0_seq1_m.15133 | PREDICTED: probable RNA-binding protein 46 isoform X3 [Vitis vinifera] | 62.649 | 67.809 | 25.8 | 13 | 15 | 13 | 0.993 | 0.964 | 0.977 | 1.025 | 1.002 | 1.028 | 1.041 | 2.66E-02 |
| cds.Camellia_sinensis.comp8916_c0_seq1_m.36632 | PREDICTED: putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 3 isoform X2 [Ricinus communis] | 17.69 | 21.263 | 30.1 | 5 | 6 | 4 | 0.98 | 1.023 | 0.971 | 1.05 | 1.014 | 1.021 | 1.037 | 1.29E-01 |
| cds.Camellia_sinensis.comp8921_c0_seq1_m.29053 | PREDICTED: inositol-tetrakisphosphate 1-kinase 1 [Vitis vinifera] | 35.903 | 14.876 | 14 | 4 | 5 | 4 | 1.09 | 1.037 | 1.02 | 0.946 | 1.01 | 0.897 | 0.907 | 6.74E-02 |

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| cds.Camellia_sinensis.comp8966_c0_seq1_m.22522 | PREDICTED: uncharacterized hydrolase YugF-like [Ziziphus jujuba] | 45.77 | 2.0702 | 3.4 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp8972_c0_seq1_m.42754 | PREDICTED: cytochrome c6, chloroplastic [Vitis vinifera] | 18.845 | 5.6472 | 19 | 4 | 5 | 4 | 0.915 | 0.958 | 0.97 | 1.06 | 1.083 | 1.042 | 1.12 | 5.60E-03 |
| cds.Camellia_sinensis.comp90284_c0_seq1_m.38720 | PREDICTED: D-3-phosphoglycerate dehydrogenase 3, chloroplastic-like [Jatropha curcas] | 34.008 | 16.57 | 12 | 4 | 5 | 4 | 0.918 | 0.952 | 1.002 | 1.012 | 1.063 | 1.119 | 1.112 | 5.13E-02 |
| cds.Camellia_sinensis.comp9057_c0_seq1_m.42253 | PREDICTED: purple acid phosphatase [Eucalyptus grandis] | 32.811 | 4.3972 | 3.9 | 1 | 1 | 1 | 1.029 | 1.138 | 0.984 | 0.965 | 0.966 | 0.913 | 0.903 | 9.74E-02 |
| cds.Camellia_sinensis.comp9149_c0_seq1_m.50925 | PREDICTED: basic blue protein [Arachis ipaensis] | 12.843 | 2.3989 | 10.6 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp9166_c0_seq1_m.26212 | PREDICTED: protein SRG1 [Theobroma cacao] | 43.278 | 95.806 | 28.3 | 10 | 16 | 10 | 0.96 | 0.965 | 0.991 | 1.044 | 1.09 | 1.046 | 1.091 | 7.26E-03 |
| cds.Camellia_sinensis.comp9179_c0_seq1_m.26764 | PREDICTED: protein DJ-1 homolog D [Musa acuminata subsp. malaccensis] | 43.787 | 59.101 | 16.7 | 6 | 17 | 6 | 0.925 | 0.947 | 0.939 | 1.084 | 1.036 | 1.055 | 1.129 | 1.20E-03 |
| cds.Camellia_sinensis.comp9186_c0_seq1_m.31693 | PREDICTED: peroxisomal trans-2-enoyl-CoA reductase [Sesamum indicum] | 29.245 | 4.4668 | 3.8 | 1 | 2 | 1 | 0.896 | 1.47 | 0.922 | 0.901 | 0.882 | 0.918 | 0.821 | 4.02E-01 |
| cds.Camellia_sinensis.comp9249_c0_seq1_m.13569 | PREDICTED: cysteine--tRNA ligase, chloroplastic/mitochondrial isoform X2 [Vitis vinifera] | 53.618 | 7.5102 | 5.7 | 3 | 5 | 3 | 0.966 | 1.013 | 1.01 | 0.984 | 0.972 | 1.069 | 1.012 | 7.53E-01 |

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| cds.Camellia_sinensis.comp9258_c0_seq1_m.13017 | PREDICTED: MICOS complex subunit MIC60 [Nelumbo nucifera] | 74.337 | 109.42 | 30.2 | 18 | 25 | 18 | 1.017 | 0.999 | 0.991 | 1.026 | 0.998 | 0.985 | 1.001 | 9.70E-01 |
| cds.Camellia_sinensis.comp9365_c0_seq1_m.15477 | PREDICTED: vacuolar protein sorting-associated protein 45 homolog [Theobroma cacao] | 64.82 | 2.6308 | 2.1 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp93901_c0_seq1_m.56272 | PREDICTED: 1-aminocyclopropane-1-carboxylate oxidase homolog 1-like [Jatropha curcas] | 13.59 | 4.3057 | 8.2 | 1 | 1 | 1 | 1.086 | 0.986 | 1.016 | 0.942 | 0.907 | 1.052 | 0.939 | 2.95E-01 |
| cds.Camellia_sinensis.comp9404_c0_seq1_m.46471 | DUF1680 domain protein [Medicago truncatula] | 14.004 | 9.3763 | 16.3 | 1 | 1 | 1 | | | | | | | | |

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| cds.Camellia_sinensis.comp9406_c0_seq1_m.55002 | PREDICTED: protein ABCI7, chloroplastic-like isoform X2 [Ipomoea nil] | 14.823 | 13.542 | 24.1 | 3 | 6 | 3 | 1.076 | 1.043 | 0.992 | 0.94 | 0.96 | 1.009 | 0.935 | 1.02E-01 |
| cds.Camellia_sinensis.comp9428_c0_seq1_m.53920 | PREDICTED: calcium-transporting ATPase 10, plasma membrane-type [Erythranthe guttata] | 16.319 | -2 | 7.4 | 1 | 1 | 1 | 1.048 | 1.074 | 1.049 | 0.938 | 0.905 | 0.975 | 0.889 | 6.70E-03 |
| cds.Camellia_sinensis.comp9438_c0_seq1_m.15474 | PREDICTED: aldehyde dehydrogenase family 7 member A1 [Nelumbo nucifera] | 56.082 | 32.538 | 18.3 | 9 | 15 | 9 | 0.973 | 0.998 | 0.993 | 0.996 | 1.018 | 1.027 | 1.026 | 9.89E-02 |
| cds.Camellia_sinensis.comp9443_c0_seq1_m.43794 | PREDICTED: dnaJ homolog 1, mitochondrial-like [Sesamum | 19.311 | 4.4 | 28.7 | 6 | 14 | 1 | 1.034 | 1.032 | 1.065 | 0.91 | 0.948 | 1.003 | 0.914 | 3.88E-02 |

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| cds.Camellia_sinensis.comp9451_c0_seq1_m.34591 | PREDICTED: pyrroline-5-carboxylate reductase [Erythranthe guttata] | 28.647 | 1.7665 | 9.7 | 3 | 3 | 3 | 0.963 | 1.054 | 0.98 | 1.036 | 0.986 | 0.996 | 1.007 | 8.23E-01 |
| cds.Camellia_sinensis.comp9469_c0_seq1_m.45143 | PREDICTED: protein TIC 55, chloroplastic [Solanum tuberosum | 17.791 | 2.1189 | 5.8 | 1 | 1 | 1 | 0.968 | 1.126 | 1.06 | 0.906 | 1.004 | 0.935 | 0.902 | 1.29E-01 |
| cds.Camellia_sinensis.comp946_c0_seq1_m.50226 | PREDICTED: carboxylesterase 1-like [Juglans regia] | 20.971 | 2.2902 | 6.4 | 1 | 1 | 1 | 0.982 | 0.994 | 0.879 | 1.008 | 1.137 | 1.021 | 1.109 | 1.31E-01 |
| cds.Camellia_sinensis.comp9477_c0_seq1_m.27406 | PREDICTED: phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic [Ricinus | 45.922 | 33.978 | 27.1 | 10 | 13 | 10 | 0.991 | 0.974 | 1.005 | 0.957 | 1.033 | 1.012 | 1.011 | 6.97E-01 |

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| cds.Camellia_sinensis.comp9536_c0_seq2_m.35214 | Nuclear transport factor 2 (NTF2) family protein [Arabidopsis thaliana] | 29.351 | 22.84 | 21.5 | 5 | 7 | 5 | 1.002 | 1.033 | 1.041 | 0.996 | 0.999 | 0.968 | 0.963 | 7.20E-02 |
| cds.Camellia_sinensis.comp9540_c0_seq1_m.46800 | PREDICTED: small nuclear ribonucleoprotein E-like [Populus euphratica] | 14.937 | 3.0596 | 9.4 | 1 | 3 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp9560_c0_seq1_m.38151 | PREDICTED: UPF0678 fatty acid-binding protein-like protein At1g79260 [Vitis vinifera] | 20.389 | 7.7577 | 10.3 | 2 | 3 | 2 | 0.973 | 0.943 | 0.942 | 1.022 | 1.047 | 1.093 | 1.106 | 1.07E-02 |
| cds.Camellia_sinensis.comp9565_c0_seq1_m.53859 | PREDICTED: protein ROOT HAIR DEFECTIVE 3-like [Malus domestica] | 16.407 | 7.8304 | 20.3 | 2 | 2 | 2 | | | | | | | | |

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| cds.Camellia_sinensis.comp9596_c0_seq1_m.33351 | PREDICTED: probable enoyl-CoA hydratase 1, peroxisomal [Juglans regia] | 29.042 | 25.078 | 28.6 | 7 | 9 | 7 | 0.948 | 0.987 | 0.973 | 1.044 | 1.045 | 1.076 | 1.088 | 5.34E-03 |
| cds.Camellia_sinensis.comp9641_c0_seq1_m.41860 | PREDICTED: cellulose synthase-like protein E6, partial [Vitis vinifera] | 33.443 | 2.0846 | 7.4 | 2 | 2 | 2 | 1.038 | 1.123 | 0.97 | 0.866 | 1.003 | 0.988 | 0.912 | 2.18E-01 |
| cds.Camellia_sinensis.comp9643_c0_seq1_m.39066 | PREDICTED: protein DCL, chloroplastic [Vitis vinifera] | 24.25 | 4.4331 | 4.8 | 1 | 1 | 1 | 1.07 | 0.992 | 1.016 | 0.881 | 1.041 | 0.992 | 0.947 | 3.56E-01 |
| cds.Camellia_sinensis.comp9669_c0_seq1_m.35880 | PREDICTED: PITH domain-containing protein 1 [Juglans regia] | 22.44 | 28.824 | 17.6 | 3 | 4 | 3 | 0.941 | 1.015 | 1.007 | 0.997 | 1.064 | 0.996 | 1.032 | 3.89E-01 |

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| cds.Camellia_sinensis.comp9690_c0_seq1_m.30320 | PREDICTED: acetolactate synthase small subunit 2, chloroplastic [Vitis vinifera] | 35.374 | 14.053 | 15.2 | 5 | 6 | 5 | 0.93 | 0.971 | 0.909 | 1.093 | 1.052 | 1.076 | 1.146 | 3.58E-03 |
| cds.Camellia_sinensis.comp9719_c0_seq1_m.15955 | PREDICTED: translation initiation factor eIF-2B subunit gamma [Nelumbo nucifera] | 49.73 | 13.029 | 11 | 4 | 6 | 4 | 0.913 | 1.029 | 0.999 | 1.027 | 0.987 | 1.082 | 1.053 | 3.10E-01 |
| cds.Camellia_sinensis.comp9790_c0_seq1_m.23760 | PREDICTED: acyl-CoA thioesterase 2-like isoform X1 [Nicotiana tabacum] | 48.149 | 9.933 | 9.8 | 4 | 6 | 4 | 1.025 | 1.049 | 1.019 | 1.008 | 0.964 | 0.992 | 0.958 | 5.37E-02 |
| cds.Camellia_sinensis.comp9808_c0_seq2_m.22340 | PREDICTED: serine carboxypeptidase-like 45 isoform X1 [Theobroma cacao] | 55.567 | 10.927 | 9.1 | 4 | 5 | 4 | 0.922 | 0.964 | 0.955 | 1.051 | 1.055 | 1.04 | 1.107 | 1.98E-03 |

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| cds.Camellia_sinensis.comp9835_c0_seq1_m.44238 | PREDICTED: cytochrome P450 CYP72A219-like [Nicotiana tabacum] | 29.72 | 8.2084 | 24.5 | 7 | 8 | 6 | 1.066 | 1.09 | 1.042 | 1.019 | 0.911 | 0.883 | 0.88 | 4.57E-02 |
| cds.Camellia_sinensis.comp9846_c0_seq1_m.9208 | PREDICTED: MAR-binding filament-like protein 1-1 isoform X1 [Fragaria vesca subsp. vesca] | 66.879 | 60.388 | 32 | 18 | 20 | 18 | 1.057 | 1.066 | 1.078 | 0.9 | 0.938 | 0.927 | 0.864 | 4.18E-04 |
| cds.Camellia_sinensis.comp98529_c0_seq1_m.53511 | PREDICTED: glycerophosphodiester phosphodiesterase GDPD1, chloroplastic [Vitis vinifera] | 13.38 | 2.6605 | 8.1 | 1 | 1 | 1 | 1.015 | 1.2 | 1.033 | 0.908 | 0.901 | 0.93 | 0.843 | 3.60E-02 |
| cds.Camellia_sinensis.comp9879_c0_seq1_m.20633 | PREDICTED: monothiol glutaredoxin-S17 isoform X1 [Vitis vinifera] | 54.981 | 48.971 | 14.6 | 6 | 8 | 6 | 0.97 | 1.01 | 1.035 | 1.043 | 0.94 | 1.008 | 0.992 | 8.23E-01 |

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| cds.Camellia_sinensis.comp9908_c0_seq1_m.26455 | PREDICTED: probable polygalacturonase [Eucalyptus grandis] | 26.271 | 3.3251 | 12.3 | 2 | 2 | 2 | | | | | | | | |
| cds.Camellia_sinensis.comp9913_c0_seq1_m.57107 | PREDICTED: pre-mRNA-processing factor 19-like, partial [Nicotiana tomentosiformis] | 12.677 | 2.9441 | 12.8 | 1 | 1 | 1 | | | | | | | | |
| cds.Camellia_sinensis.comp9962_c0_seq1_m.50653 | PREDICTED: RNA-binding protein 1-like [Juglans regia] | 19.996 | 106.01 | 54.6 | 7 | 12 | 7 | 0.965 | 1.018 | 0.993 | 0.997 | 0.968 | 1.011 | 1 | 9.97E-01 |
| cds.Camellia_sinensis.comp9991_c0_seq1_m.48761 | PREDICTED: 60S acidic ribosomal protein P2B-like [Populus euphratica] | 11.319 | 15.089 | 22.1 | 3 | 7 | 3 | 1.036 | 1.046 | 1.061 | 0.974 | 0.975 | 0.922 | 0.913 | 1.00E-02 |
| cds.Camellia_sinensis.comp9994_c0_seq1_m.38016 | PREDICTED: adenylate kinase 4 [Oryza sativa Japonica Group] | 28.4 | 14.865 | 42.6 | 10 | 21 | 6 | 1.023 | 1.071 | 1.069 | 0.918 | 0.917 | 0.974 | 0.888 | 8.84E-03 |