**Supplementary Tables**

**Supplementary Table 1** Primers for qRT-PCR of the DEGs

|  |  |  |  |
| --- | --- | --- | --- |
| Gene Name | Gene ID | Primer-F | Primer-R |
| Aspartate Aminotransferase | *Le\_10009629* | GCGACGACAATGATAAGC | AGACCAGTGATAGGCAGAT |
| Hypothetical protein | *Le\_10013468* | CGACGACATTAGGAGAATCT | AGACCAGTGATAGGCAGAT |
| Aminohydrolase | *Le\_10009215* | AACACTGACACTGAGCATT | TTGACAAGAGCAAGTAGCA |
| Hydrophobin 2 | *Le\_10001088* | TATCGCAGCACTGGACAG | AGCAAGTAATCGTCGTTCAA |
| Actin  |  | GGAGAAGATTTGGCATCACACA  | GAAGAGCGAAACCCTCGTAGA |

**Supplementary Table 2** Quality Statistics of filtered reads

Three biological repeats were taken in each treatment.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sample** | **Total Raw Reads (M)** | **Total Clean Reads (M)** | **Total Clean Bases (Gb)** | **Clean Reads Q20 (%)** | **Clean Reads Q30 (%)** |
| **4606-0h-1** | 44.05 | 44.05 | 6.63 | 96.26 | 91.29 |
| **4606-0h-2** | 43.97 | 43.97 | 6.62 | 96.08 | 90.92 |
| **4606-0h-3** | 41.35 | 41.35 | 6.22 | 96.14 | 90.99 |
| **4606-0.5h-1** | 42.12 | 42.12 | 6.34 | 96.25 | 91.2 |
| **4606-0.5h-2** | 47.28 | 47.28 | 7.1 | 96.5 | 91.71 |
| **4606-0.5h-3** | 42.1 | 42.1 | 6.34 | 96.13 | 90.97 |
| **4606-7h-1** | 41.9 | 41.9 | 6.3 | 96.06 | 90.82 |
| **4606-7h-2** | 39.63 | 39.63 | 5.96 | 96.16 | 91.05 |
| **4606-7h-3** | 44.7 | 44.7 | 6.73 | 96.13 | 91.0 |
| **4625-0h-1** | 40.33 | 40.33 | 6.07 | 96.09 | 90.9 |
| **4625-0h-2** | 45.62 | 45.62 | 6.87 | 96.54 | 91.84 |
| **4625-0h-3** | 52.94 | 52.94 | 7.97 | 96.92 | 92.6 |
| **4625-0.5h-1** | 49.92 | 49.91 | 7.51 | 96.9 | 92.57 |
| **4625-0.5h-2** | 40.34 | 40.34 | 6.07 | 96.81 | 92.38 |
| **4625-0.5h-3** | 43.67 | 43.66 | 6.57 | 97.09 | 92.95 |
| **4625-7h-1** | 44.56 | 44.56 | 6.71 | 97.03 | 92.84 |
| **4625-7h-2** | 49.51 | 49.51 | 7.45 | 97.28 | 93.35 |
| **4625-7h-3** | 43.64 | 43.64 | 6.57 | 97.26 | 93.31 |
| **Total**  | 797.63 | 797.61 | 120.03 |  |  |

**Supplementary Table 3** Statistics on mapping of the clean reads

Three biological repeats were taken in each treatment.

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample** | **Total Clean Reads** | **Total Mapping (%)** | **Uniquely Mapping (%)** |
| **4606-0h-1** | 40495996 | 90.22 | 88.26 |
| **4606-0h-2** | 40133320 | 90.2 | 88.22 |
| **4606-0h-3** | 37618644 | 90.21 | 88.11 |
| **4606-0.5h-1** | 38446476 | 90.1 | 88.01 |
| **4606-0.5h-2** | 43528150 | 89.84 | 87.69 |
| **4606-0.5h-3** | 38289894 | 90.14 | 88.03 |
| **4606-7h-1** | 38002160 | 89.83 | 87.77 |
| **4606-7h-2** | 36071198 | 89.86 | 87.72 |
| **4606-7h-3** | 40857366 | 90.35 | 88.19 |
| **4625-0h-1** | 36705782 | 86.89 | 85.13 |
| **4625-0h-2** | 42262972 | 86.18 | 84.52 |
| **4625-0h-3** | 49568612 | 86.65 | 84.91 |
| **4625-0.5h-1** | 46740700 | 86.71 | 84.94 |
| **4625-0.5h-2** | 37660930 | 86.41 | 84.53 |
| **4625-0.5h-3** | 41084088 | 86.23 | 84.52 |
| **4625-7h-1** | 41860420 | 86.64 | 84.92 |
| **4625-7h-2** | 47124066 | 86.62 | 84.98 |
| **4625-7h-3** | 41572454 | 86.5 | 84.82 |

**Supplementary Table 4** The expression abundance of different expression genes in the KEGG pathways

|  |  |  |
| --- | --- | --- |
| Gene ID (gene\_Lentinula\_edodes\_GLEAN\_X) | Pathway Name | FPKM (Log2 (X+1)) |
| 4606-0h | 4606-0.5h | 4606-7h | 4625-0h | 4625-0.5h | 4625-7h |
| Carbohydrate metabolism |
| *Le\_*10000745 | ko01200//Carbon metabolism; ko00680//Methane metabolism; ko00630//Glyoxylate and dicarboxylate metabolism; | 4.5352  | 7.2076  | 6.5849  | 2.5769  | 3.4078  | 4.0747  |
| *Le\_*10002534 | ko00040//Pentose and glucuronate interconversions; | 1.8979  | 2.1784  | 2.2520  | 4.6167  | 4.4460  | 4.2482  |
| *Le\_*10003459 | ko01230//Biosynthesis of amino acids; ko01200//Carbon metabolism; ko00030//Pentose phosphate pathway; ko00010//Glycolysis / Gluconeogenesis; ko00051//Fructose and mannose metabolism; ko00680//Methane metabolism;ko00710//Carbon fixation in photosynthetic organisms; | 2.4577  | 3.2403  | 3.2570  | 0.0000  | 0.0000  | 0.0000  |
| *Le\_*10003620 | ko00500//Starch and sucrose metabolism; | 4.6377  | 2.8600  | 3.8080  | 1.4222  | 0.7991  | 0.8979  |
| *Le\_*10009137 | ko00520//Amino sugar and nucleotide sugar metabolism; | 3.1705  | 3.2464  | 3.8911  | 1.3353  | 1.4751  | 1.4507  |
| Transport and catabolism |
| *Le\_*10000555 | ko04142//Lysosome; | 10.5293  | 10.6672  | 10.3336  | 7.3199  | 7.1310  | 7.8951  |
| *Le\_*10002334 | ko04142//Lysosome; | 6.4068  | 6.3044  | 6.2351  | 1.5753  | 1.4507  | 2.4785  |
| *Le\_*10002545 | ko04146//Peroxisome; | 4.7996  | 4.8128  | 4.8246  | 0.2829  | 0.0000  | 2.6652  |
| *Le\_*10008653 | ko04142//Lysosome; | 0.4647  | 0.2510  | 0.4889  | 1.8732  | 2.3103  | 1.6229  |
| Signal transduction |
| *Le\_*10000674 | ko04013//MAPK signaling pathway; ko03008//Ribosome biogenesis in eukaryotes;ko03013//RNA transport; | 3.0647  | 3.0715  | 3.3472  | 0.4542  | 0.3859  | 0.5721  |
| *Le\_*10007587 | ko04392//Hippo signaling pathway - multiple species; ko04391//Hippo signaling pathway -fly; ko04011//MAPK signaling pathway - yeast; ko04390//Hippo signaling pathway; | 4.3655  | 4.7551  | 5.1289  | 1.6584  | 2.1932  | 2.5177  |
| *Le\_*10011530 | ko04011//MAPK signaling pathway - yeast; | 5.0118  | 4.7268  | 4.6895  | 2.7232  | 2.6237  | 2.6369  |
| *Le\_*10012891 | ko04011//MAPK signaling pathway - yeast; | 3.3195  | 2.9879  | 1.4594  | 0.0000  | 0.0000  | 0.1287  |
| FoLeing, sorting and degradation |
| *Le\_*10001490 | ko04141//Protein processing in endoplasmic reticulum; | 3.5632  | 1.2408  | 3.2006  | 5.8730  | 5.1775  | 5.3870  |
| *Le\_*10012063 | ko04141//Protein processing in endoplasmic reticulum; | 4.4044  | 4.1249  | 4.7060  | 0.0000  | 0.0000  | 0.0000  |
| *Le\_*10008329 | ko04141//Protein processing in endoplasmic reticulum; | 2.6151  | 2.7463  | 1.8849  | 4.4443  | 4.8391  | 4.5856  |
| *Le\_*10008190 | ko04120//Ubiquitin mediated proteolysis; | 0.5227  | 0.2388  | 0.0000  | 1.8653  | 0.6167  | 2.3065  |
| *Le\_*10005860 | ko04120//Ubiquitin mediated proteolysis; ko04113//Meiosis - yeast; ko04111//Cell cycle - yeast; ko04914//Progesterone-mediated oocyte maturation; ko04110//Cell cycle; ko04114//Oocyte meiosis; | 3.5282  | 2.4186  | 3.0421  | 4.3448  | 4.3650  | 4.3778  |
| *Le\_*10013253 | ko03018//RNA degradation; | 1.0096  | 0.0000  | 0.9758  | 2.6237  | 2.2550  | 2.4033  |
| Lipid metabolism |
| *Le\_*10007938 | ko00062//Fatty acid elongation; ko01040//Biosynthesis of unsaturated fatty acids; ko01212//Fatty acid metabolism; | 0.4612  | 0.2750  | 0.2987  | 2.7662  | 2.5025  | 2.7254  |
| Translation |  |  |  |  |  |  |  |
| *Le\_*10004339 | ko03013//RNA transport; | 0.6198  | 0.1678  | 0.0704  | 1.3467  | 1.3353  | 1.2245  |
| *Le\_*10008377 | ko03010//Ribosome; | 0.2987  | 1.5705  | 0.4222  | 4.0024  | 3.8646  | 3.1133  |

**Supplementary Table 5** The expression abundance of DEGs in different GO functions

|  |  |  |
| --- | --- | --- |
| Gene ID (ene\_Lentinula\_edodes\_GLEAN\_X) | GO Term | FPKM (Log2 (X+1)) |
| 4606-0h | 4606-0.5h | 4606-7h | 4625-0h | 4625-0.5h | 4625-7h |
| Binding |
| *Le\_*10000158 | [F]GO:0005507//copper ion binding | 0.0612  | 0.0000  | 0.0000  | 3.6997  | 4.0444  | 4.1160  |
| *Le\_*10001125 | GO:0043169//cation binding | 3.7520  | 4.5229  | 2.9696  | 0.0000  | 0.0000  | 0.0000  |
| *Le\_*10002240 | iron ion binding | 4.3840  | 4.9008  | 4.7738  | 2.3505  | 2.0909  | 2.5599  |
| *Le\_*10002241 | GO:0005506//iron ion binding | 6.3074  | 7.1121  | 7.5190  | 4.4096  | 3.5390  | 4.0347  |
| *Le\_*10002242 | GO:0005506//iron ion binding | 4.6686  | 4.5439  | 4.2245  | 1.8953  | 1.4418  | 2.1021  |
| *Le\_*10002510 | GO:0005506//iron ion binding | 1.1419  | 1.2810  | 1.7341  | 5.6273  | 5.8511  | 5.9013  |
| *Le\_*10002801 | GO:0005506//iron ion binding | 0.4365  | 0.2347  | 0.4820  | 1.4005  | 1.3239  | 1.5311  |
| *Le\_*10003290 | GO:0005506//iron ion binding | 2.6886  | 2.3822  | 2.1689  | 0.0000  | 0.0000  | 0.0000  |
| *Le\_*10005960 | GO:0005506//iron ion binding | 2.9585  | 3.7122  | 4.8895  | 0.0000  | 0.0000  | 0.0000  |
| *Le\_*10007179 | GO:0005506//iron ion binding | 4.3496  | 5.3141  | 4.7899  | 2.3776  | 2.2100  | 3.2245  |
| *Le\_*10007538 | GO:0005506//iron ion binding | 8.1010  | 8.6897  | 7.8551  | 3.7538  | 3.9018  | 4.6180  |
| *Le\_*10007607 | GO:0008270//zinc ion binding | 5.8300  | 6.0198  | 5.6411  | 3.4721  | 3.3785  | 3.8751  |
| *Le\_*10011313 | GO:0005506//iron ion binding | 0.0000  | 0.0931  | 0.2710  | 4.5317  | 3.9803  | 3.0761  |
| *Le\_*10012618 | GO:0008270//zinc ion binding | 5.7409  | 5.4818  | 5.0688  | 2.9069  | 3.0727  | 3.4511  |
| *Le\_*10003230 | [F]GO:0043565//sequence-specific DNA binding; GO:0003700//transcription factor activity, sequence-specific DNA binding; [P]GO:0006355//regulation of transcription, DNA-templated; | 2.8190  | 2.5000  | 2.2479  | 7.9482  | 7.7464  | 7.7759  |
| *Le\_*10003441 | [F]GO:0043565//sequence-specific DNA binding; GO:0008270//zinc ion binding; GO:0003700//transcription factor activity, sequence-specific DNA binding; [P]GO:0006355//regulation of transcription, DNA-templated; | 1.5227  | 3.0012  | 2.9011  | 0.0000  | 0.0000  | 0.0000  |
| *Le\_*10008419 | [F]GO:0043565//sequence-specific DNA binding; GO:0003700//transcription factor activity, sequence-specific DNA binding; [P]GO:0006355//regulation of transcription, DNA-templated; | 2.2006  | 2.3813  | 1.9782  | 4.5181  | 4.7429  | 4.5882  |
| *Le\_*10008353 | [F]GO:0043565//sequence-specific DNA binding; GO:0008270//zinc ion binding; GO:0003700//transcription factor activity, sequence-specific DNA binding; [P]GO:0006355//regulation of transcription, DNA-templated; | 0.8426  | 0.8745  | 0.7570  | 1.9916  | 2.2152  | 2.0670  |
| *Le\_*10003018 | [F]GO:0000981//RNA polymerase II transcription factor activity, sequence-specific DNA binding; GO:0008270//zinc ion binding; [P]GO:0006355//regulation of transcription, DNA-templated; [C]GO:0005634//nucleus; | 1.7239  | 2.5737  | 2.7754  | 0.0000  | 0.0000  | 0.0000  |
| *Le\_*10000608 | [F]catalytic activity;binding; [P]metabolic process;metabolic process; cellular process; | 0.0000  | 1.6260  | 0.0000  | 0.7570  | 1.3084  | 1.5311  |
| *Le\_*10002718 | [F]catalytic activity; binding; [C]organelle; macromolecular complex; organelle; organelle; macromolecular complex; cell; organelle; macromolecular complex; cell; cell part; organelle; macromolecular complex; cell; cell part; organelle part;  | 1.5769  | 0.0000  | 1.2429  | 0.7712  | 0.7627  | 0.0473  |
| *Le\_*10002733 | [F]structural molecule activity; binding; [C]organelle; macromolecular complex; organelle; organelle; macromolecular complex; cell; organelle; macromolecular complex; cell; cell part; organelle; macromolecular complex; cell; cell part; organelle part; [P]metabolic process; metabolic process; cellular process;  | 4.3154  | 0.0000  | 4.1146  | 4.6464  | 3.5977  | 3.8676  |
| *Le\_*10003351 | [F]binding;  | 0.0000  | 2.2449  | 0.9107  | 2.0508  | 2.4436  | 2.2947  |
| *Le\_*10004459 | [F]binding;  | 1.0333  | 2.6841  | 1.0704  | 2.5801  | 2.8271  | 2.1055  |
| *Le\_*10004619 | [F]catalytic activity; binding;  | 0.0000  | 4.9114  | 3.0490  | 4.2658  | 4.4112  | 4.3198  |
| *Le\_*10005960 | [F]catalytic activity; binding; [P]single-organism process; single-organism process; metabolic process;  | 2.9585  | 4.8895  | 3.7122  | 0.0000  | 0.0000  | 0.0000  |
| *Le\_*10009629 | [F]catalytic activity; binding; [P]single-organism process; metabolic process; single-organism process; metabolic process; cellular process;  | 3.0203  | 6.3129  | 4.3142  | 4.3533  | 5.5665  | 1.0473  |
| *Le\_*10010279 | [F]binding;  | 2.5025  | 0.6354  | 1.3315  | 0.1506  | 0.5261  | 0.4294  |
| *Le\_*10010560 | [F]binding;  | 5.1445  | 0.0000  | 1.8600  | 0.0000  | 0.0000  | 3.9474  |
| *Le\_*10011542 | [F]catalytic activity; binding; [P]single-organism process; single-organism process; metabolic process;  | 1.0096  | 3.7141  | 2.2620  | 5.5012  | 5.8857  | 5.8750  |
| *Le\_*10013693 | [F]catalytic activity; binding; [P]single-organism process; single-organism process; metabolic process; single-organism process; metabolic process; cellular process;  | 0.0000  | 2.7775  | 2.1570  | 2.5977  | 2.8339  | 0.5753  |
| Membrane |
| *Le\_*10003014 | [C]GO:0016021//integral component of membrane; [P]GO:0006950//response to stress; | 0.8480  | 0.5850  | 0.3599  | 2.6151  | 2.2987  | 2.3074  |
| *Le\_*10009935 | [F]GO:0004872//receptor activity; [C]GO:0016020//membrane; | 4.3246  | 4.0548  | 4.2785  | 7.1351  | 7.1272  | 6.9119  |
| *Le\_*10004805 | [C]membrane; | 0.0000  | 4.6749  | 2.0096  | 3.1543  | 4.0218  | 2.7071  |
| Extracellular region |  |  |  |  |  |  |  |
| *Le\_*10010320 | [P]GO:0009405//pathogenesis; [C]GO:0005576//extracellular region; | 7.5476  | 7.0234  | 7.6590  | 3.4423  | 3.8859  | 3.9721  |
| *Le\_*10010322 | [P]GO:0009405//pathogenesis; [C]GO:0005576//extracellular region; | 0.0000  | 0.8319  | 0.0000  | 4.4603  | 4.7488  | 3.8768  |
| Localization |
| *Le\_*10001950 | [F]GO:0022857//transmembrane transporter activity; [P]GO:0055085//transmembrane transport; [C]GO:0016021//integral component of membrane; | 3.1032  | 3.1232  | 3.1662  | 0.0473  | 0.0426  | 0.5025  |
| *Le\_*10002462 | [F]GO:0005215//transporter activity; [P]GO:0055085//transmembrane transport; [C]GO:0016021//integral component of membrane; | 4.1029  | 3.1331  | 4.1312  | 0.2790  | 0.1066  | 0.1848  |
| *Le\_*10006364 | [F]GO:0022857//transmembrane transporter activity; [P]GO:0055085//transmembrane transport; [C]GO:0016021//integral component of membrane; | 4.9067  | 5.7391  | 5.3683  | 2.0886  | 1.6338  | 2.5882  |
| *Le\_*10006934 | [P]GO:0055085//transmembrane transport; [C]GO:0016021//integral component of membrane; | 2.6773  | 2.6900  | 2.8453  | 5.2780  | 5.1221  | 5.6895  |
| *Le\_*10007614 | [P]GO:0055085//transmembrane transport; | 1.2947  | 1.2610  | 1.7852  | 0.0886  | 0.2058  | 0.0566  |
| *Le\_*10009468 | [F]GO:0022857//transmembrane transporter activity; [P]GO:0055085//transmembrane transport; [C]GO:0016021//integral component of membrane; | 3.3128  | 2.0179  | 3.0350  | 0.1066  | 0.0000  | 0.1419  |
| *Le\_*10012169 | [P]GO:0055085//transmembrane transport; [C]GO:0016021//integral component of membrane; | 4.0403  | 3.5615  | 3.3089  | 6.7409  | 6.4826  | 6.7214  |
| *Le\_*10013475 | [F]GO:0022857//transmembrane transporter activity; [P]GO:0055085//transmembrane transport; [C]GO:0016020//membrane;GO:0016021//integral component of membrane; | 6.6362  | 6.9865  | 6.9838  | 2.4708  | 2.5785  | 4.4256  |
| *Le\_*10003609 | [F]GO:0022857//transmembrane transporter activity; [P]GO:0055085//transmembrane transport; [C]GO:0016021//integral component of membrane; | 1.6260  | 1.6900  | 1.0772  | 1.1419  | 0.4471  | 0.8074  |
| *Le\_*10006404 | [F]GO:0022857//transmembrane transporter activity; [P]GO:0055085//transmembrane transport; [C]GO:0016020//membrane;GO:0016021//integral component of membrane; | 1.6945  | 1.6477  | 1.0215  | 1.6104  | 0.5327  | 1.1419  |
| *Le\_*10009268 | [P]GO:0055085//transmembrane transport; [C]GO:0016021//integral component of membrane; | 1.6151  | 2.4276  | 1.0356  | 1.1995  | 0.7684  | 1.1506  |
| *Le\_*10009463 | [P]GO:0055085//transmembrane transport; [C]GO:0016021//integral component of membrane; | 1.0589  | 1.8600  | 1.7880  | 0.9411  | 1.1656  | 0.4471  |
| *Le\_*10014087 | [F]GO:0015095//magnesium ion transmembrane transporter activity; [C]GO:0016021//integral component of membrane; [P]GO:0015693//magnesium ion transport; | 0.2469  | 1.6292  | 0.0000  | 1.0024  | 1.6120  | 1.2750  |
| *Le\_*10001594 | [F]transporter activity; [C]membrane; [P]localization; | 1.6229  | 3.6956  | 2.4418  | 4.5630  | 4.6114  | 4.8943  |
| *Le\_*10001689 | [P]localization; [C]membrane;membrane;membrane part; | 2.3730  | 0.0000  | 0.9235  | 2.7648  | 0.7627  | 2.1088  |
| *Le\_*10002245 | [P]localization; [C]membrane;membrane;membrane part; | 0.0000  | 4.1974  | 4.5940  | 0.6135  | 2.2957  | 0.1243  |
| *Le\_*10008273 | [P]localization; [C]membrane;membrane;membrane part; | 0.0000  | 3.8898  | 3.2580  | 3.3780  | 3.8507  | 3.3368  |
| *Le\_*10010327 | [F]transporter activity; [P]localization; [C]membrane; | 0.0000  | 3.9117  | 1.6736  | 2.7232  | 2.9075  | 1.1953  |
| Antioxidant activity |
| *Le\_*10000923 | [F]GO:0004601//peroxidase activity; | 1.0072  | 0.9461  | 0.9209  | 3.1795  | 3.2172  | 3.0993  |
| *Le\_*10000926 | [F]GO:0004601//peroxidase activity; | 0.0000  | 0.0000  | 0.0520  | 2.5501  | 2.6485  | 2.2908  |
| *Le\_*10004084 | [F]GO:0020037//heme binding; GO:0004601//peroxidase activity; [P]GO:0006979//response to oxidative stress;GO:0055114//oxidation-reduction process; | 0.0000  | 0.0000  | 0.0000  | 3.9669  | 3.6724  | 4.7097  |
| *Le\_*10008662 |  |  |  |  |  |  |  |
| Catalytic activity |
| *Le\_*10011064 | [F]GO:0004222//metalloendopeptidase activity; | 0.1549  | 0.0000  | 0.0000  | 4.3067  | 4.4083  | 4.4575  |
| *Le\_*10008442 | [F]GO:0016491//oxidoreductase activity; [P]GO:0008152//metabolic process; | 0.0000  | 0.0380  | 0.1806  | 2.9739  | 3.2126  | 3.0920  |
| *Le\_*10008994 | [F]GO:0016491//oxidoreductase activity; [P]GO:0055114//oxidation-reduction process; | 5.3108  | 5.5472  | 5.6448  | 8.9356  | 8.9287  | 8.6236  |
| *Le\_*10012258 | [F]GO:0016491//oxidoreductase activity; [P]GO:0055114//oxidation-reduction process; | 0.1419  | 0.0426  | 0.0426  | 2.8940  | 2.5882  | 4.1353  |
| *Le\_*10007938 | [F]GO:0016627//oxidoreductase activity, acting on the CH-CH group of donors; [P]GO:0006629//lipid metabolic process; [C]GO:0016021//integral component of membrane;GO:0005737//cytoplasm; | 0.4612  | 0.2750  | 0.2987  | 2.7662  | 2.5025  | 2.7254  |
| *Le\_*10002534 | [F]GO:0030599//pectinesterase activity; [P]GO:0042545//cell wall modification; [C]GO:0005618//cell wall; | 0.0000  | 0.0000  | 0.0000  | 2.1155  | 1.7181  | 1.5930  |
| *Le\_*10008178 | [F]GO:0030599//pectinesterase activity; [P]GO:0042545//cell wall modification; [C]GO:0005618//cell wall; | 1.9733  | 2.2540  | 2.6096  | 0.3969  | 0.7796  | 0.3142  |
| *Le\_*10010877 | [F]GO:0016491//oxidoreductase activity; [P]GO:0055114//oxidation-reduction process; | 1.6781  | 0.8823  | 1.5737  | 1.0473  | 0.4577  | 0.5753  |
| Signal transduction |  |  |  |  |  |  |  |
| *Le\_*10009735 | [F]GO:0004435//phosphatidylinositol phospholipase C activity; [P]GO:0007165//signal transduction; GO:0035556//intracellular signal transduction;GO:0006629//lipid metabolic process; | 1.8745 | 4.9991 | 3.7276 | 1.8169 | 2.9702 | 0.1679 |