**Electronic Supplementary Materials**

**Table S1** Expression of genes between samples related to different signal transduction pathways.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KEGG Pathways | Number of genes annotated | BVT\_3dpi vs CK | BVT\_6dpi vs CK | BVT\_6dpi vs BVT\_3dpi |
| Up | Down | Up | Down | Up | Down |
| Neuroactive ligand-receptor interaction | 85 | 6 | 5 | 4 | 8 | 3 | 8 |
| MAPK signaling pathway | 134 | 1 | 2 | 0 | 1 | 0 | 1 |
| Two-component system | 13 | 1 | 0 | 0 | 0 | 0 | 0 |
| Calcium signaling pathway | 80 | 0 | 1 | 0 | 1 | 0 | 0 |
| mTOR signaling pathway | 50 | 0 | 1 | 0 | 0 | 0 | 0 |
| Wnt signaling pathway | 81 | 0 | 2 | 0 | 0 | 1 | 0 |
| Notch signaling pathway | 48 | 0 | 1 | 0 | 1 | 0 | 1 |
| TGF-beta signaling pathway | 37 | 0 | 2 | 0 | 0 | 1 | 0 |
| VEGF signaling pathway | 43 | 1 | 0 | 0 | 0 | 0 | 0 |
| ECM-receptor interaction | 51 | 1 | 0 | 1 | 0 | 1 | 2 |
| Jak-STAT signaling pathway | 26 | 0 | 1 | 0 | 0 | 0 | 0 |

**Table S2** List of Forward and Reverse primers used in quantitative RT-PCR analysis.

|  |  |  |  |
| --- | --- | --- | --- |
| Unigene ID | Annotation | Forward primer | Reverse primer |
| comp15682\_c0  | Trypsin | GGCTGGTAAAATGGCAACGG | CACGACCGCCCTCCTTATAG |
|  |  |  |  |
| comp19542\_c0  | Lipoprotein lipase  | ATGTTGTTGGAGTCGCTGGT | CGTTGGGGTAAAAGTCAGCG |
| comp9968\_c0  | Stearoyl-CoA desaturase  | GGCAGCAGAACACTTCGACT | TACTGGTGTACCGTCGCCTA |
| comp17951\_c0  | Attacin  | GCCCTCGGTAGTGTTGGTAT | CCGGCACCAGTCAACTTAGA |
| comp16005\_c0  | Gloverin precursor  | TGGCATACACAAACGCCCAA | AGTTGTCCGCCACCAAAGTT |
| comp13751\_c0  | Phosphatidyllinositol 4 phosphate 5 kinase  | ACGGAGCAGGCGAGATTTTA | ATGACGAGCAGTTCCGTGAC |
| comp15533\_c0  | Glucoronosyl transferase  | ACGTGCTATATGGTGGACCG | AATCTGTATGCGGGTAGCGT |
| comp7919\_c0  | UDP- glycosyltransferase | CGACACCTGTGCCTAGTCTG | GAGGCAGAGCATCGACACTT |
| comp14600\_c0 | Chymotrypsin | CAACACAAACGCACCTCCAG | CACAAGGGAAGCCCCATGAT |
|  | Actin (Reference gene)  | GGGAAATCGTGCGTGAC | GAAGGAAGGCTGGAAGAG |
|  | GAPDH (Reference gene)  | CTGTCGCTAATGTATCC GTTGTC | AACCTGCTCCTCAGTGTAGTCAAG |



**Figure S1** GC content distribution in the unigenes.



**Figure S2** Length distribution of the unigenes.



**Figure S3** KOG functional classification of *L. dispar* transcriptome. Y-axis represents a number of unigenes involved and X-axis denotes different categories of KOG functional groups.



**Figure S4** Validation of RNA-Seq data analysis by RT-qPCR. The nine genes differentially expressed at all time points were validated for their expression by RT-qPCR for CK, BVT\_3dpi and BVT\_6dpi. Overall, all time points showed consistency between the two methods in their expression trends.