**Additional file 1** Sequences for real-time PCR primers

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| Genes1 | Primer sequence2(5′-3′) | Accession no. |
| β-Actin | F: GAGAAATTGTGCGTGACATCA | L08165 |
|  | R: CCTGAACCTCTCATTGCCA |  |
| GYS2 | F: ATCGCCTTCTGTCTCTCAGC | XM\_015291547.1 |
|  | R: TTTTGCCTATCCCTTTCAGC |  |
| INSR | F: CTCCCTTCTGTAACCGTGGT  | XM\_001233398.4 |
|  | R: TCTGTAGTGACGAGGATGCC |  |
| Claudin-2 | F: CCTGCTCACCCTCATTGGAG | NM\_001277622.1 |
|  | R: GCTGAACTCACTCTTGGGCT |  |
| SOD3 | F: TTGTGATCCATGAGCAGGAA | XM\_015285700.2 |
|  | R: TTGTTGCAGATCCCAATCAC |  |
| FABP1 | F: GGGGAAGAGTGTGAGATGGA | NM\_204192 |
|  | R: GTTGAGTTCGGTCACGGATT |  |
| FABP2 | F: TGGCATTTAACGGTACTTGGA | NM\_001007923 |
|  | R: TCAGATTATCGTGGGCTCCT |  |
| LPL | F: ACTTGAAGACCCGTGCTCAG | NM\_205282 |
|  | R: GGCTGGTCTACCTTGGTCAC |  |
| APOA1 | F: GTGACCCTCGCTGTGCTCTT | NM 205525 |
|  | R: CACTCAGCGTGTCCAGGTTGT |  |
| TXN | F: GATTTCTCTGCCACATGGTGT | NM\_205453.1 |
|  | R: ATCTTGGGCATCATCCACAT |  |
| NDUFS6 | F: ACGGCAAAAGGAGGTGAACA | XM 419061 |
|  | R: CAACCTCACTCACAGGCTGC |  |
| GSTM2 | F: GGCAACCTGAGCCAATTCCT | NM\_205090.1 |
|  | R: CCACCCCCCTCACTCTTTCT |  |
| GSTA3 | F: TTGGATAAGGCCGCAAACAGATA | NM\_001001777.1 |
|  | R: TTTCCAGTAAATGCACGTCTGCTC |  |

 1 GYS2, glycogen synthase 2; INSR, insulin receptor; SOD3, extracellular superoxide dismutase; FABP, fatty acid-binding protein; LPL, lipoprotein lipase; APOA1, apolipoprotein A1; TXN, thioredoxin; NDUFS6, NADH dehydrogenase (ubiquinone) iron-sulfur protein 6; GST, glutathione S-transferase.

2 F, forward; R, reverse.



**Additional file 2** Principal component analysis (PCA) plot of gene expression profile of the layer intestine between groups.



**Additional file 3** Clusters of Orthologous Genes (COG) classification of differentially expressed genes of the layer intestine between groups.



**Additional file 4** Sketch map of peroxisome proliferators-activated receptors **(**PPAR) signaling pathway.



**Additional file 5** Sketch map of oxidative phosphorylation pathway.



**Additional file 6** Sketch map of glutathione metabolism pathway.



**Additional file 7** Sketch map of metabolism of xenobiotics by cytochrome P450.