

Table S3. KEGG significant pathway enrichment analysis of the DE lncRNA target genes.

| Pathway ID | Name | Cluster frequency | Genome frequency of use | P-value | Q-value | Genes |
|------------|--------------------------|-------------------|-------------------------|------------|-----------|--|
| ko04390 | Hippo signalling pathway | 8/109 | 314/9593 | 0.02635468 | 0.7375082 | MTCONS_00108259 MTCONS_00051711 MTCONS_00078810 MTCONS_00131568 MTCONS_00153178 MTCONS_00155163 MTCONS_00110762 MTCONS_00026808 |

Table S3. KEGG enrichment analysis showed that the DE lncRNA-targeted mRNAs were only significantly enriched in the Hippo signalling pathway.