

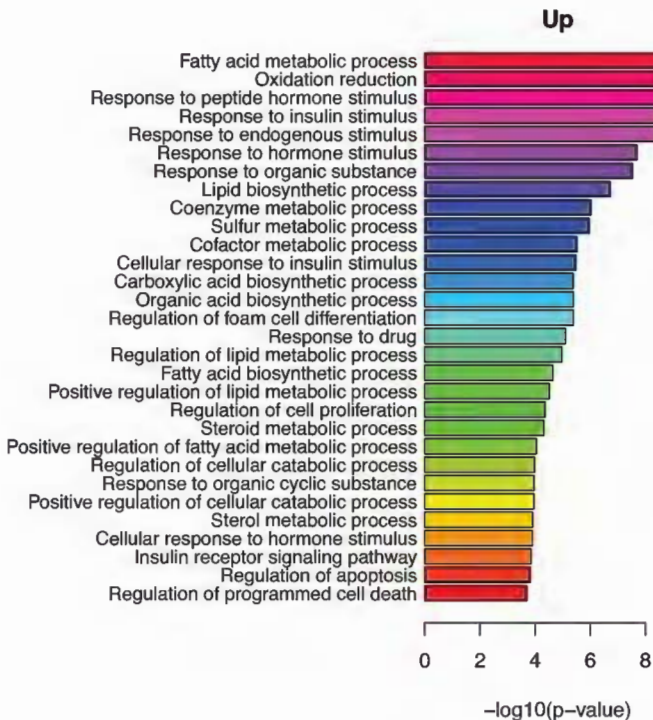
Supplemental Figure Legends

Supplemental Digital Content 1 . Table shows Primer sequences for qRT-PCR analysis.

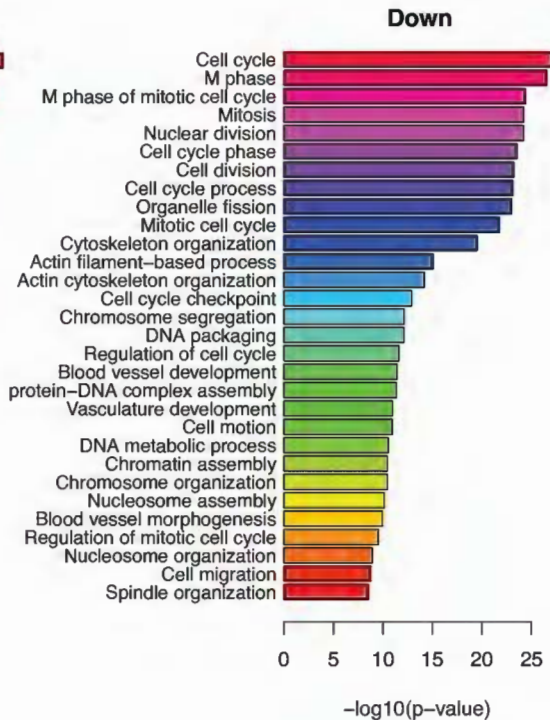
Supplemental Digital Content 2. Figure shows GO term analysis for upregulated and downregulated loci. A) The 30 most highly associated GO terms with upregulated transcripts. Longer bars correspond to greater number of loci associated with specific GO term. B) The 30 most highly associated GO terms with downregulated transcripts. Longer bars correspond to greater number of loci associated with specific GO term.

Supplemental Digital Content 3. Figure shows Guilt-by-association GO term analysis for lncRNA. Number of associated coding genes assigned to each lncRNA corresponding to more GO terms assigned to each specific lncRNA.

Gene	Forward Primer Sequence	Reverse Primer Sequence
<i>HSD17B7P2</i>	GAACTGGAGCCTCTCCTCTG	TTAGATTTCTTGCATTGCG
<i>AQP7P1</i>	CCACTGAGAGTAGGGCACAA	CAAGTCCCATAGGCAACTCA
<i>AQP7P3</i>	GGCACAGGCGAACATACATA	CGTGGTTCCAAGTTAGCATC



(a)



(b)