Figure S1.Comparison of average expression pattern of six gene groups clustered by hclust approach in maSigPro analysis. Each plot shows the cluster average expression value of experimental group with three replications (Texel and Ujumqin) during five fetal stages (d70, d85, d100, d120, d135).
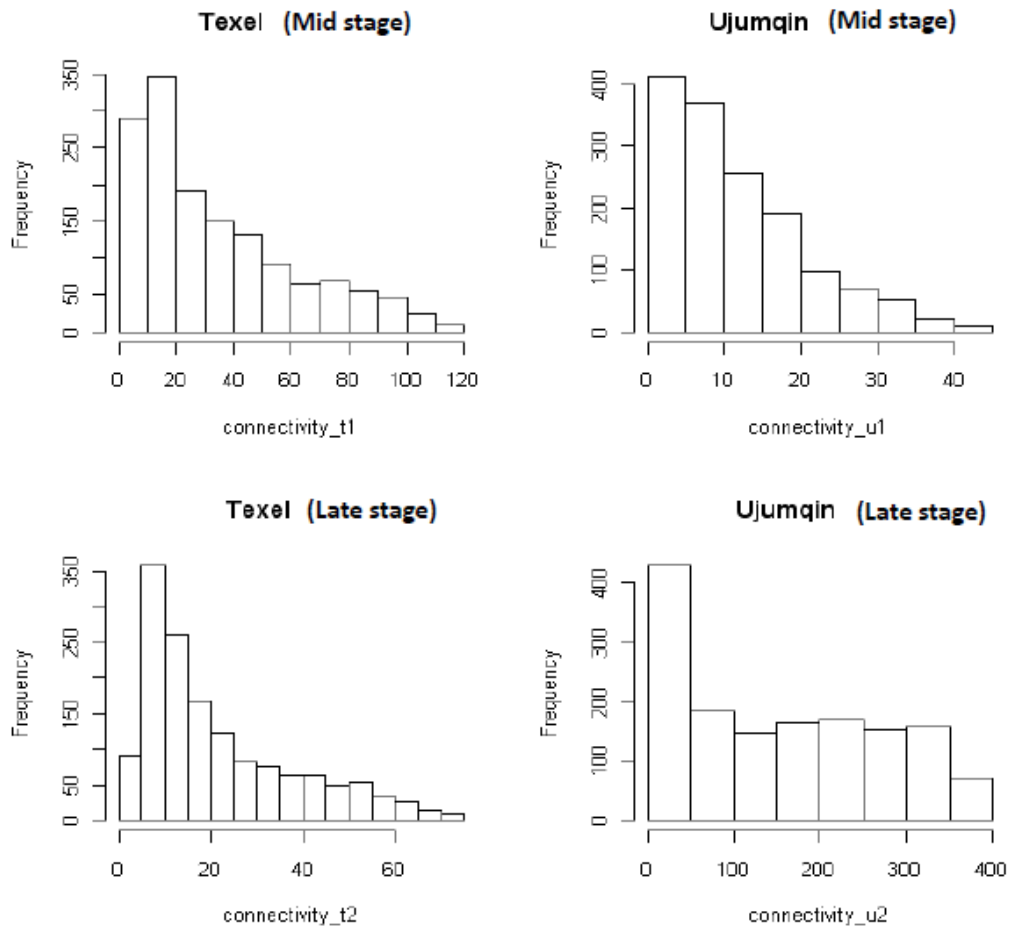
Figure S2. Frequency distribution of genes with different level of connectivity for two sheep (Texel and Ujumqin) breeds at mid and late fetal stages.
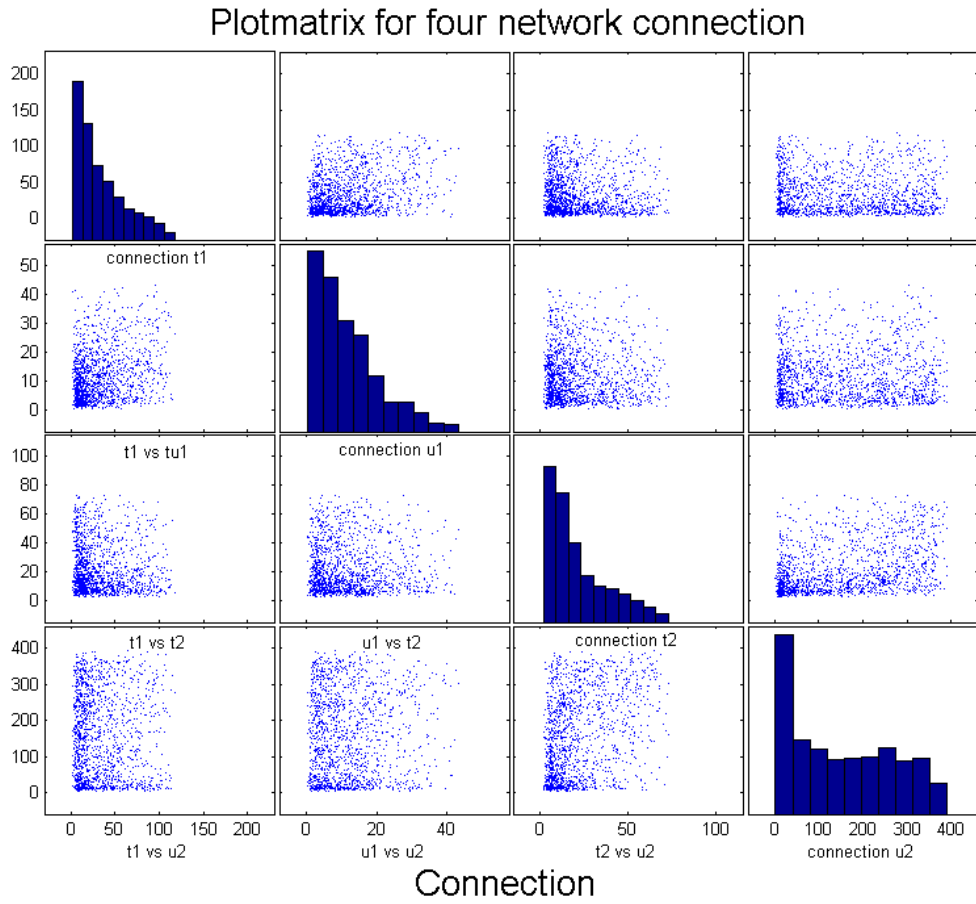
Figure S3. Plot-matrix for the connection of four networks constructed from data sets, Texel mid stage, Ujumuqin mid stage, Texel late stage, Ujumuqin late stage.

t1 vs. u1 (network A vs. network B), t1 vs. t2 (network A vs. network C), u1 vs. t2(network B vs. network C), t1 vs. u2 (network A vs. network D), u1 vs. u2 (network B vs. network D), and t2 vs. u2 (network C vs. network D).
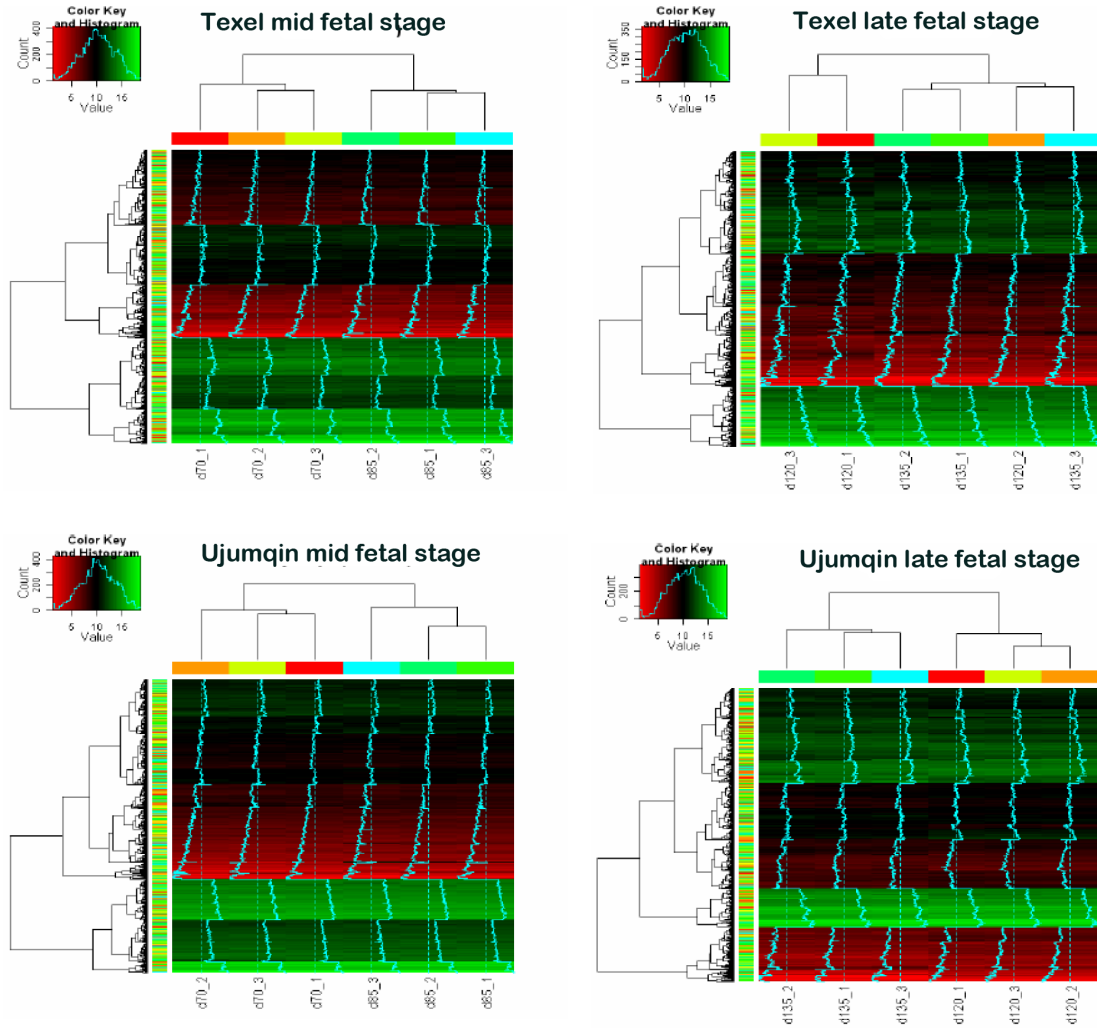
Figure S4. A heatmap (with dendrograms) of genes differentially expressed between the two types of sheep (Texel and Ujumqin) at two stages (mid and late) of fetal development. Red corresponds to low expression and green corresponds to high expression. The heatmap was plotted using the "gplots" heatmap.2 function in R package.
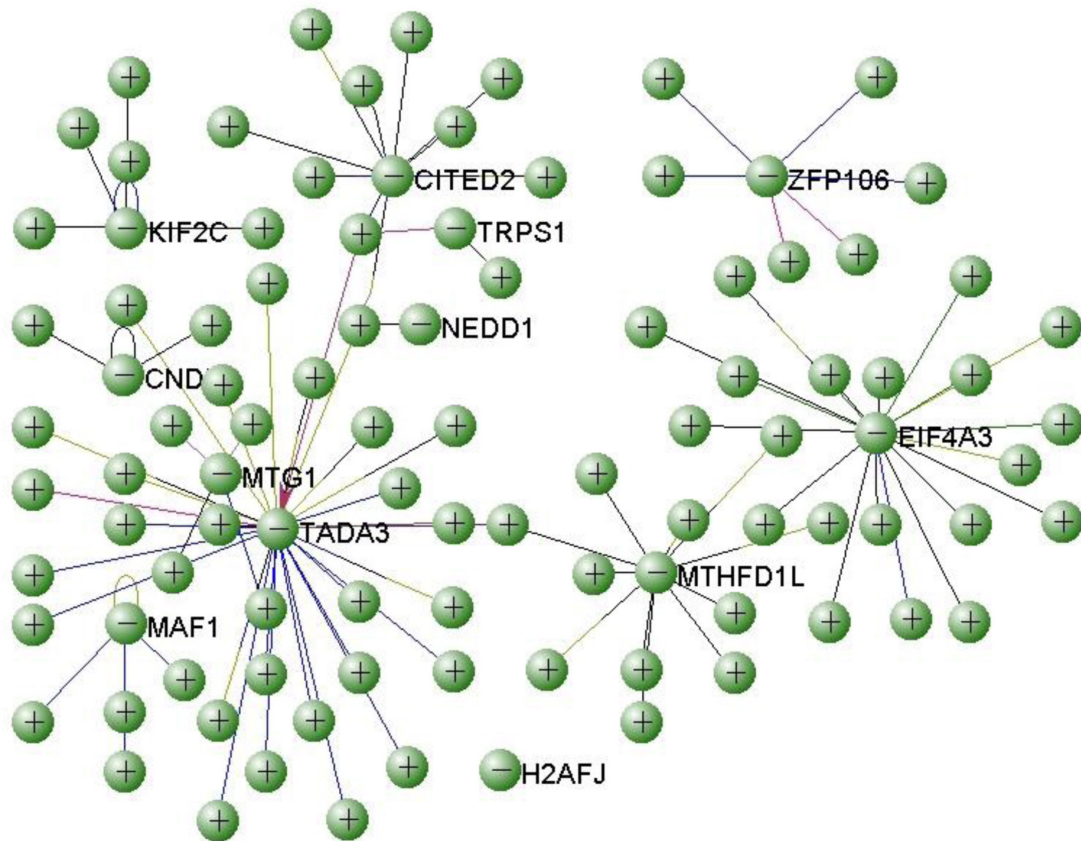
Figure S5. Visualization network using key genes with gene significant (GS) values > 0.8 (positive connected with fetal weight) in the mid fetal stage. Dots correspond to genes and lines correspond to connections. The sign "-" in the node indicates that the node is fully expanded (i.e., all connections are shown), whereas "+" indicates that some links have not yet been displayed. Correlations between nodes are indicated by connecting lines (edges), and different colors correspond to different experimental methods. Edges between transcription factors and the products of the genes they regulate are represented by arrows to indicate causal direction, and all other edges were currently undirected.
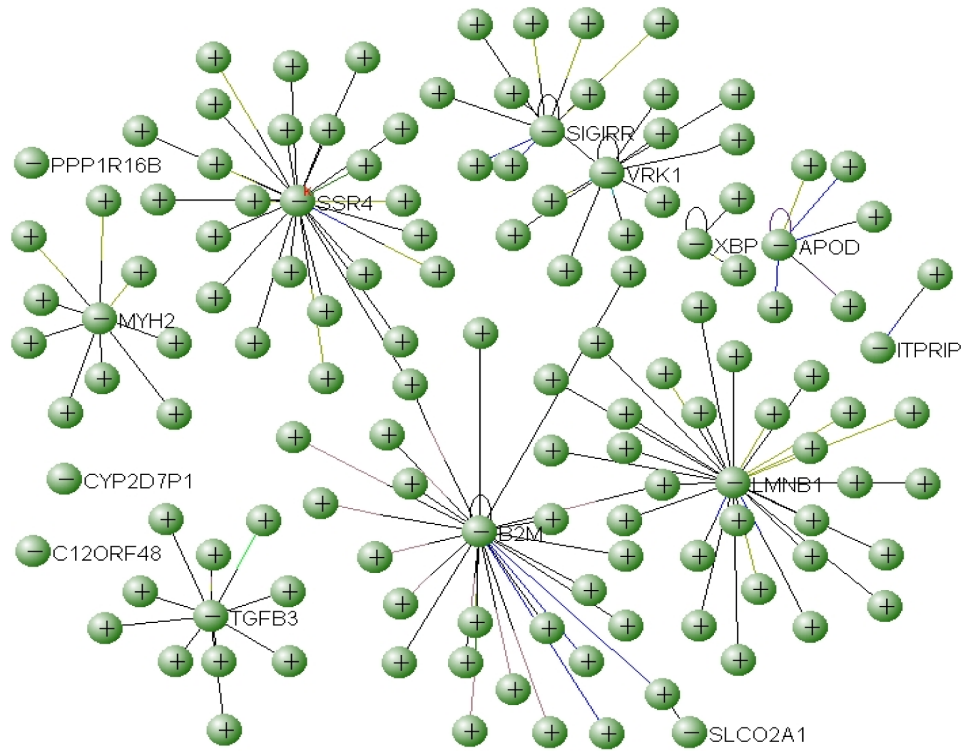
Figure S6. Visualization network using key genes with gene significant (GS) values <
-0.8 (negative connected with fetal weight) at mid stage. Dots correspond to genes
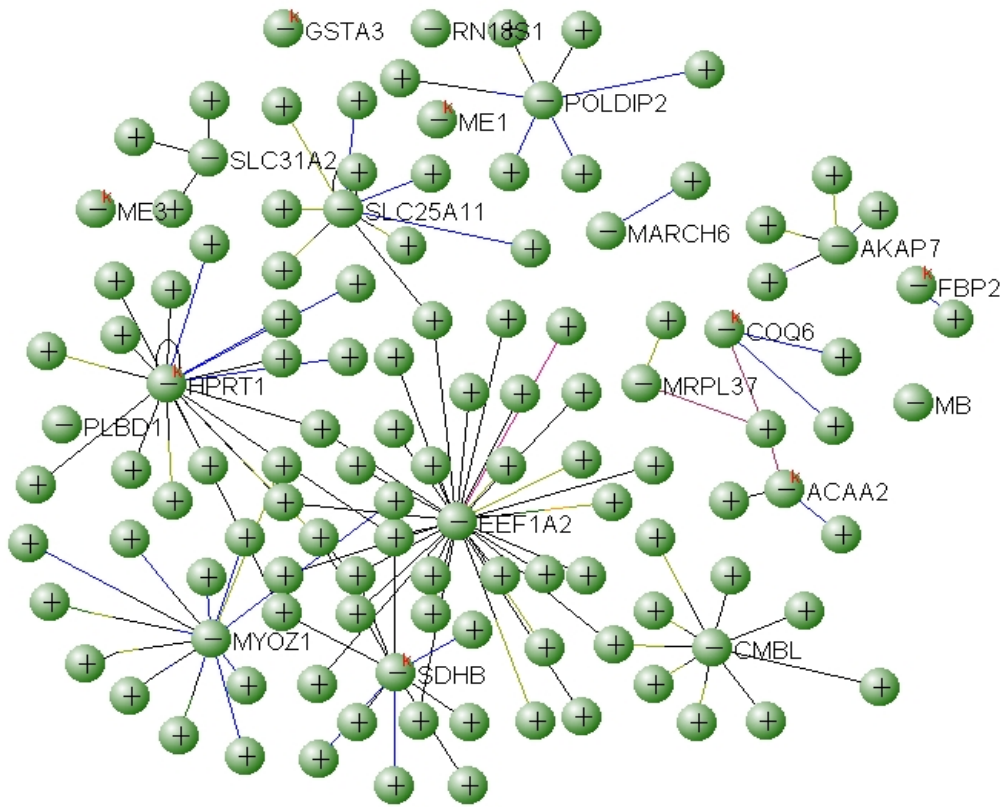and lines to correspond to connections. Symbols are similarly defined in Figure S5.

Figure S7.Visualization network using the key genes in the GS Module with values higher than 0.8 in late stage. Symbols are similarly defined in Figure S5.
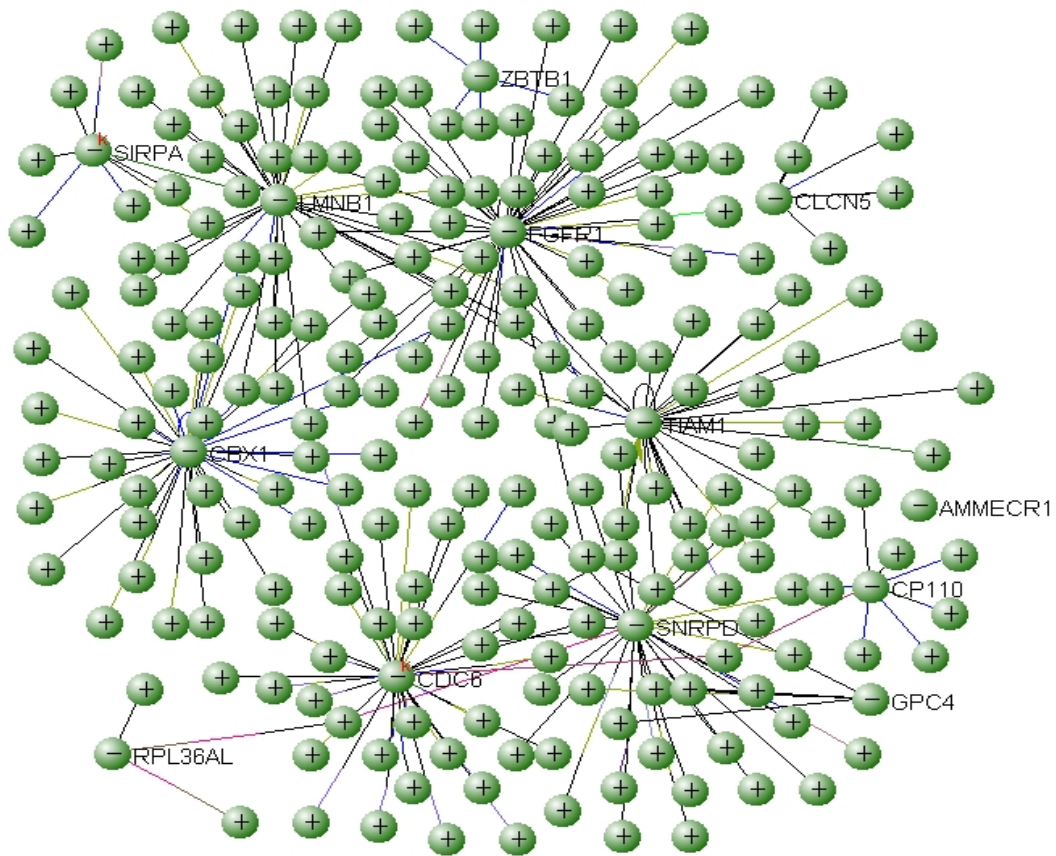
Figure S8. Visualization network using the key genes in the GS Module with values lower than -0.8 in late stage. Symbols are similarly defined in Figure S5