

### **Supplemental Figure Legends:**

**Dataset S1.** Master list for gene expression values. RNA sequencing was performed as described in supplemental materials and methods section. Genes with an RPKM value of 1 were expressed at non-quantifiable levels and those genes displaying 1 in all three samples were not characterized as changing in downstream analysis. Genes are sorted based on descending comparable RPKM values between samples.

**Dataset S2.** List of genes upregulated in both HG and LG+GNS samples compared to LG. RNA-sequencing was performed as described in supplemental materials and methods section. 2-fold changes were the lower limit for genes considered to be significantly influenced between samples. Genes are sorted based on descending comparable RPKM values between samples.

**Dataset S3.** List of genes downregulated in both HG and LG+GNS samples compared to LG. RNA-sequencing was performed as described in supplemental materials and methods section. 2-fold changes were the lower limit for gene considered to be significantly influenced between samples. Genes are sorted based on descending comparable RPKM values between samples.