**SUPPLEMENTARY FIGURE LEGENDS**

**Supplemental Figure 1 – Mean and variance of HS rat adipose gene expression**

Mean and variance of HS rat adipose gene expression before transformation, using all 18,353 transcripts analyzed. In general, the variance of each gene increases with the mean, which is expected. There are 28 genes that are considerably more variable than other genes with similar levels of expression (mean expression < 100 and variance > 700; cutoff determined visually). Enrichment analysis suggested that these genes are markers of tissue heterogeneity (Table S1). These 28 genes were used to derive two proxy variables for the muscle and nerve composition of each adipose sample. These proxies were used as covariates for downstream analyses.

**Supplemental Figure 2 Correlations between nerve and muscle tissue proxies and metabolic phenotypes in HS rats.**

Pearson correlations are shown, with blue being a positive correlation and red being a negative correlation. The darker the color, the stronger the correlation. BWg – bodyweight (g); BLcm – body length (cm); EpiFatg – epididymal fat pad weight (g); RetroFatg – retroperitoneal fat pad weight (g); Ins0 – fasting insulin at baseline (ng/ml); InsAUC – insulin area under the curve after glucose challenge; Gluc0 – fasting glucose at baseline (mg/dL); GlucAUC – glucose area under the curve after glucose challenge; Chol – fasting total cholesterol (mg/dL); Trig – fasting triglycerides (mg/dL); NerveProxy – nerve tissue proxy; MuscleProxy – muscle tissue proxy. The nerve and muscle tissue proxies are positively correlated with each other, but negatively correlated with many metabolic phenotypes, and most strongly correlated with RetroFatg, which is the source tissue for gene expression.

**Supplemental Figure 3 – Scale independence and mean connectivity for WGCNA analysis of adipose gene expression**

Different soft thresholding powers were used. The power was set to 5 based on a 0.9 threshold for the scale free topology index.

**Supplemental Figure 4 - Canonical Pathway Enrichment Analysis of the Light Green Module**

Canonical Pathway Enrichment Analysis of the LightGreen module identifies multiple SMAD genes, supporting a role for this module in SMAD phosphorylation. Figure was created using Ingenuity Pathway Analysis software.