# Supplementary Data

**Supplementary Table 1: Expression changes between control and Cushing's disease subjects.** Calculated expression (baseMean), and expression changes for each gene (log2fold change, standard error and *t* statistic) are shown along with raw p values and adjusted p-values (q value).

**Supplementary Table 2: Gene set enrichment analysis of gene ontology and KEGG enrichment categories.** Size is the total size of the GO category, NES is the normalized enrichment score, NOM p-value is the raw p-value and FDR q-value is corrected for multiple observations. Gene details lists the specific genes which led to the enrichment of this category in our data. A negative enrichment score indicates down-regulation of the category in Cushing's disease.

**Supplementary Table 3: Gene set enrichment analysis of transcription factor and miRNA pathways.** These categories indicate that target genes regulated by these factors are altered in Cushing's disease white adipose tissue. Size is the total size of the category, NES is the normalized enrichment score, NOM p-value is the raw p-value and FDR q-value is corrected for multiple observations. Gene details lists the specific genes which led to the enrichment of this category in our data. A negative enrichment score indicates down-regulation of the category in Cushing's disease.

**Supplementary Table 4: Expression changes between control and Cushing's disease subjects whose age are between 40 and 60 years old.** Calculated expression (baseMean), and expression changes for each gene (log2fold change, standard error and *t* statistic) are shown along with raw p values and adjusted p-values (q value).