# 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 when controlled for BMI.** 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). The suffixes for those mentioned statistics are BMIxDisease – the interaction between BMI and the disease status (Cushing’s vs Control); Obese\_vs\_notObese – indicating the comparison between obese subjects to non-obese subjects; Cushing\_vs\_Con – indicating the comparison between Cushing’s and control.

**Supplementary Table 5: Cushing’s effect on gene expression in obese and non-obese subjects.** Expression changes for each gene (log2fold change and standard error) are shown along with raw p values and adjusted p-values (q value). The suffix NotObese indicating the comparison between Cushing’s vs Control among non-obese subjects while the suffix Obese indicating the same comparison but within obese subjects.

**Supplementary Table 6: Expression changes between control and Cushing's disease subjects when controlled for both BMI and age.** 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). Suffixes: CushingvsControl – designated for the comparison between Cushing’s vs Control; Age.MidvsYoung – designated for the comparison between subjects whose ages were (40,60] vs those were (0,40]; Age.OldvsYoung – designated for the comparison between subjects whose ages are (60,100] vs those were (0,40]; BMI.ObesevsNotObese – designated for the comparison between obese and non-obese subjects.