# Single Nucleotide Polymorphism (SNP)

## Description

Subjects were genotyped for selected polymorphisms in a small set of genes representing immune and central nervous system functions, particularly hypothalamic-pituitary adrenal (HPA) axis to identify genetic variants associated with CFS or quantitative measures of major domains of CFS.

## Study Sample

222 participants

## Data Collection Methods

The details of SNP selection and genotyping assays are described in publications listed under the reference section below. Briefly, there are a total of 168 polymorphisms (166 SNPs and 2 variable number of tandem repeats [VNTR] in the data set. SNPS, identified by their rs IDs, were selected from the SNP database (dbSNP) of National Center for Biotechnology Information database, Applied Biosystem's SNPBrowser™ or from the literature. Of the two VNTRs, one is in gene MAOA (designated as MAOA-VNTR in column DZ in the SNP spreadsheet) and the second one is in serotonin transporter gene (SLC6A4) designated as 5-HTTLPR in column EZ in the SNP spreadsheet). DNA was extracted from the peripheral blood mononuclear cells by Trizol extraction (Invitrogen, Carlsbad, CA). Genomic DNA was amplified using the Genomiphi DNA amplification kit (Amersham Biosciences, Piscataway, NJ). Amplified DNA was quantified by TaqMan PCR with primers and probe for β-globin (2 copies of β-globin/cell and 5 pg DNA per cell) prior to genotyping. Most SNPs (158 out of 166) were genotyped using validated TaqMan genotyping assay kits (Applied Biosystems, CA) and the 7900 Sequence detection system (Applied Biosystems). Eight SNPs were genotyped by pyrosequencing. The two VNTRs were genotyped using gel based assays. All SNP genotype calls were made automatically by the TaqMan and Pyrosequencing platforms, whereas VNTR genotype calls were made manually based on the expected size of the PCR products. Genotypes calls corresponding to each polymorphisms are provided in the dataset.

## Reference

Rajeevan MS, Smith AK, Dimulescu I, Unger ER, Vernon SD, Heim C, Reeves WC. 2007. Glucocorticoid receptor polymorphisms and haplotypes associated with chronic fatigue syndrome. *Genes Brain and Behavior* 6: 167:176: PMID: 16740143

Smith AK, Falkenberg VR, Dimulescu I, Narasimhan S, Heim C, Vernon SD, Rajeevan MS. 2008. Genetic evaluation of the serotonergic system in chronic fatigue syndrome. *Psychoneuroendocrinology* 33: 188-197. PMID: 18079067

Smith AK, Maloney EM, Falkenberg VR, Dimulescu I, Rajeevan MS. 2009. An angiotensin converting enzyme polymorphism is associated with allostatic load mediated by C- reactive protein, interleukin 6 and cortisol. *Psychoneuroendocrinology* 34: 597-606. PMID: 19081678