

Supplementary figure 1: LRRK2 transcription factor binding site prediction.

The CREAD package was employed to identify transcription factor binding sites in 1 Kb proximal promoters of all known human genes. Known genes, their genomic location, and 28 species conservation were obtained from UCSC Genome Browser. For each protein-coding gene, the proximal promoter was defined as 700 bases upstream and 300 bases downstream of the transcription start site. Position weight matrices (PWMs) were obtained from TRANSFAC (v8.2) and JASPAR (v3.0) and each matrix was mapped to a transcription factor. We employed the program STORM for matching PWMs to the promoter sequences with $p < 10e-4$ and $p < 10e-5$. Next we employed multiSTORM and accepted all sites identified in at least four species with the same parameter used in STORM. Finally, the program site-cons was employed to select for sites significantly ($p < 0.05$) more conserved compared to the 100 flanking bases. Image shown was generated using custom tracks in the UCSC genome browser.

Sup figure 1

Prediction of binding sites in LRRK2 promoter region

