

rsid	chr12 position (hg19)	description	rs11175518	rs117762348	rs10784428	rs1491942	rs1491938	rs10784486	rs3761863	rs11564258
rs11175518	40,580,318	liver eQTL, 110kb 5' of <i>LRRK2</i>	-	-	-	-	-	-	-	-
rs117762348	40,597,612	best PD SNP, 91 kb 5' of <i>LRRK2</i>	0.0041	-	-	-	-	-	-	-
rs10784428	40,604,608	monocyte eQTL, 84 kb 5' of <i>LRRK2</i>	0.032	0.0496	-	-	-	-	-	-
rs1491942	40,620,808	GWAS SNP, 78 kb 5' of <i>LRRK2</i>	0.204	0.313	0.166	-	-	-	-	-
rs1491938	40,645,630	Leprosy, 43 kb upstream of <i>LRRK2</i>	0.0128	0.0444	0.301	0.002	-	-	-	-
rs10784486	40,677,029	brain eQTL, exon 32-33, 12 kb upstream of <i>LRRK2</i>	0.0037	0.0112	0.0187	0.0003	0.121	-	-	-
rs3761863	40,758,652	common nsSNP, Crohn signal 2, exon 49	0.0034	0.004	0.0268	0.0178	0.105	0.7	-	-
rs11564258	40,792,300	Crohn signal 1, 29 kb 3' of <i>LRRK2</i>	0.0013	0.0037	0.0098	0.08	0.0065	0.01	0.053	-

Table S3: Summary of the pattern of linkage disequilibrium (correlation coefficient r^2) between the SNPs mentioned throughout the text. Linkage disequilibrium was computed in the brain gene expression dataset, including imputation data for SNPs that were not directly genotyped.

