|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **rsid** | **chr12 position**  **(hg19)** | **description** | **rs11175518** | **rs117762348** | **rs10784428** | **rs1491942** | **rs1491938** | **rs10784486** | **rs3761863** | **rs11564258** |
| **rs11175518** | 40,580,318 | liver eQTL, 110kb 5’ of *LRRK2* | - | - | - | - | - | - | - | - |
| **rs117762348** | 40,597,612 | best PD SNP, 91 kb 5’ of *LRRK2* | 0.0041 | - | - | - | - | - | - | - |
| **rs10784428** | 40,604,608 | monocyte eQTL, 84 kb 5’ of *LRRK2* | 0.032 | 0.0496 | - | - | - | - | - | - |
| **rs1491942** | 40,620,808 | GWAS SNP, 78 kb 5’ of *LRRK2* | 0.204 | 0.313 | 0.166 | - | - | - | - | - |
| **rs1491938** | 40,645,630 | Leprosy, 43 kb upstream of *LRRK2* | 0.0128 | 0.0444 | 0.301 | 0.002 | - | - | - | - |
| **rs10784486** | 40,677,029 | brain eQTL, exon 32-33, 12 kb upstream of *LRRK2* | 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 *LRRK2* | 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 r2) 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.