

	<b>Genotyped</b>	<b>Imputed (any quality)</b>	<b>Imputed (<math>r^2 &gt; 0.8</math>)</b>	<b>Total</b>
<b>Monomorphic</b>	255	3,285	-	3,540
<b>Polymorphic</b>	846	1,909	1,047	2,755
<b>Total</b>	1,101	5,194	1,047	6,295
<b>Only polymorphic sites</b>				
<b>Non-synonymous</b>	9	7	3	16
<b>Synonymous</b>	9	1	1	10
<b>Splice change</b>	0	1	0	1
<b>Loss-of-function</b>	0	0	0	0
<b>Intronic</b>	443	932	455	1,375
<b>Intergenic</b>	382	962	588	1,344
<b>UTRs</b>	3	6	4	9
<b>Total</b>	846	1,909	1,047	2,755

**Table S2:** Summary of imputation data and functional role of SNPs in the 479 kb long *LRRK2* gene region defined as chr12:40,351,601-40,830,814 (hg19).