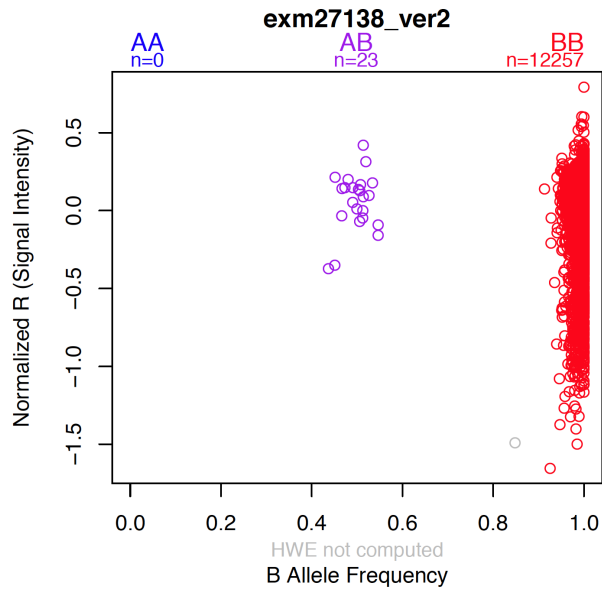
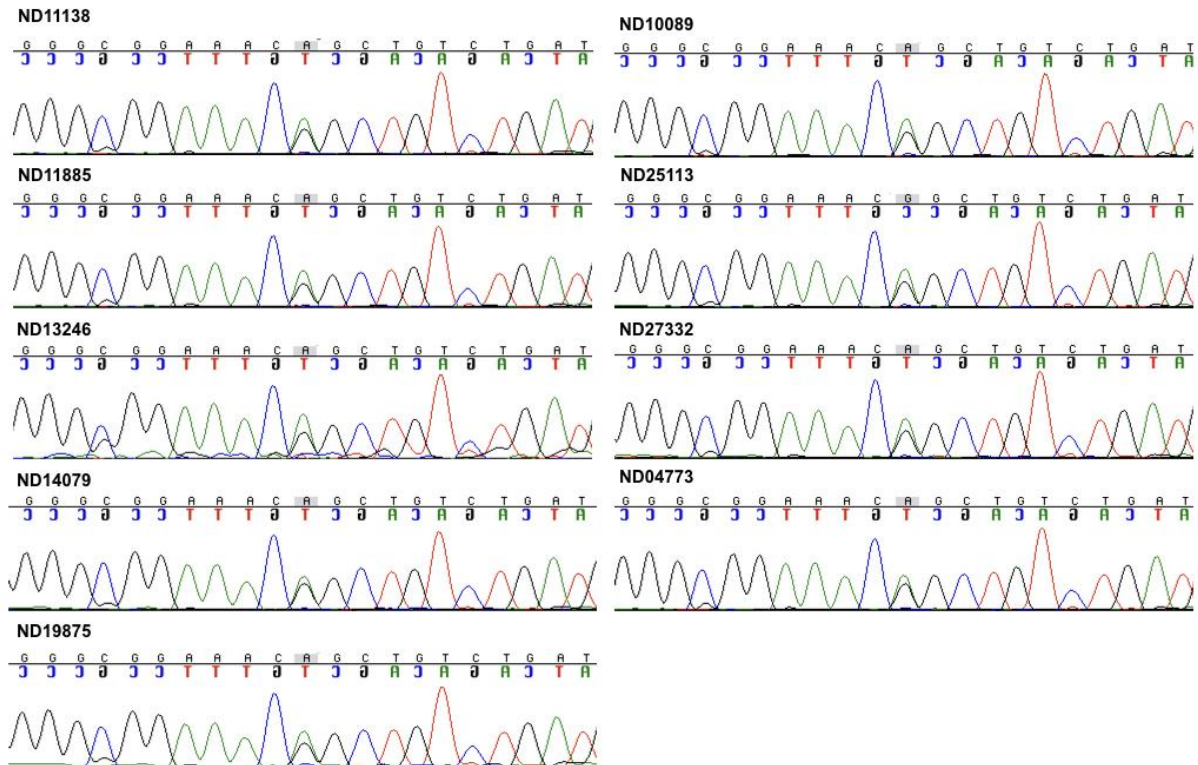


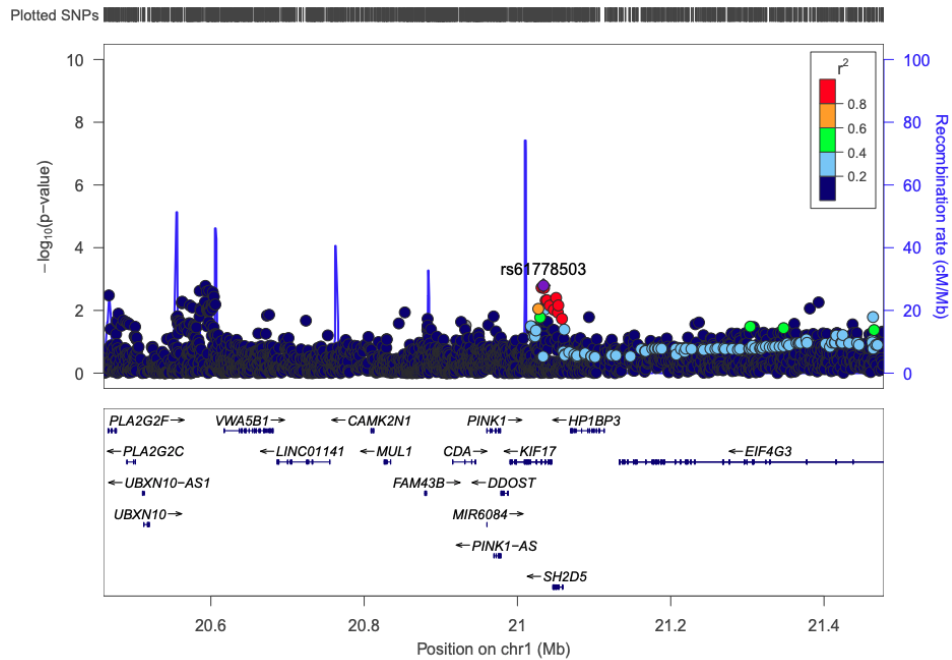
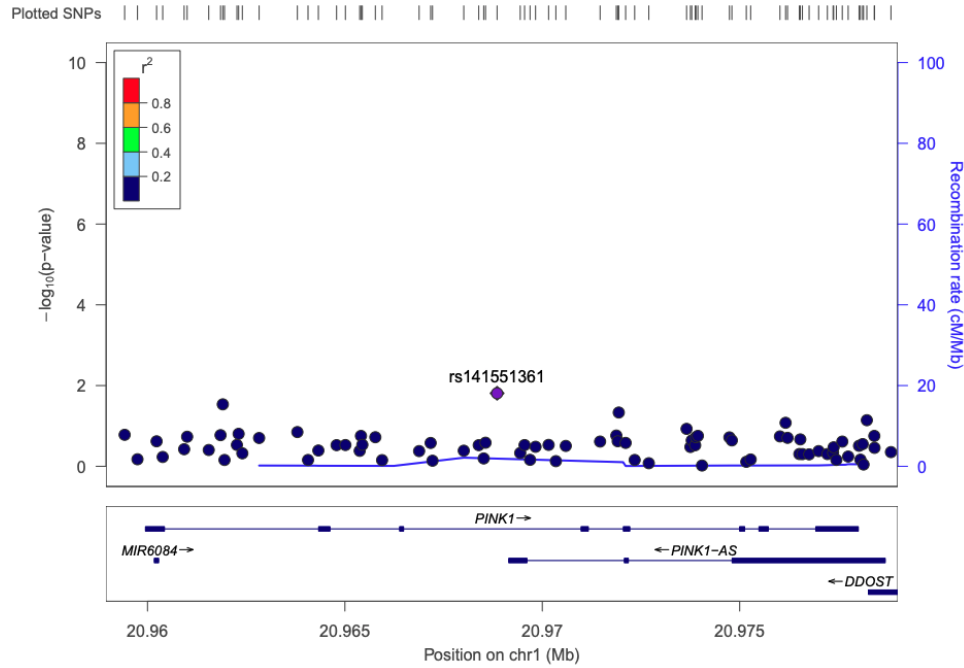
## Supplementary Figures



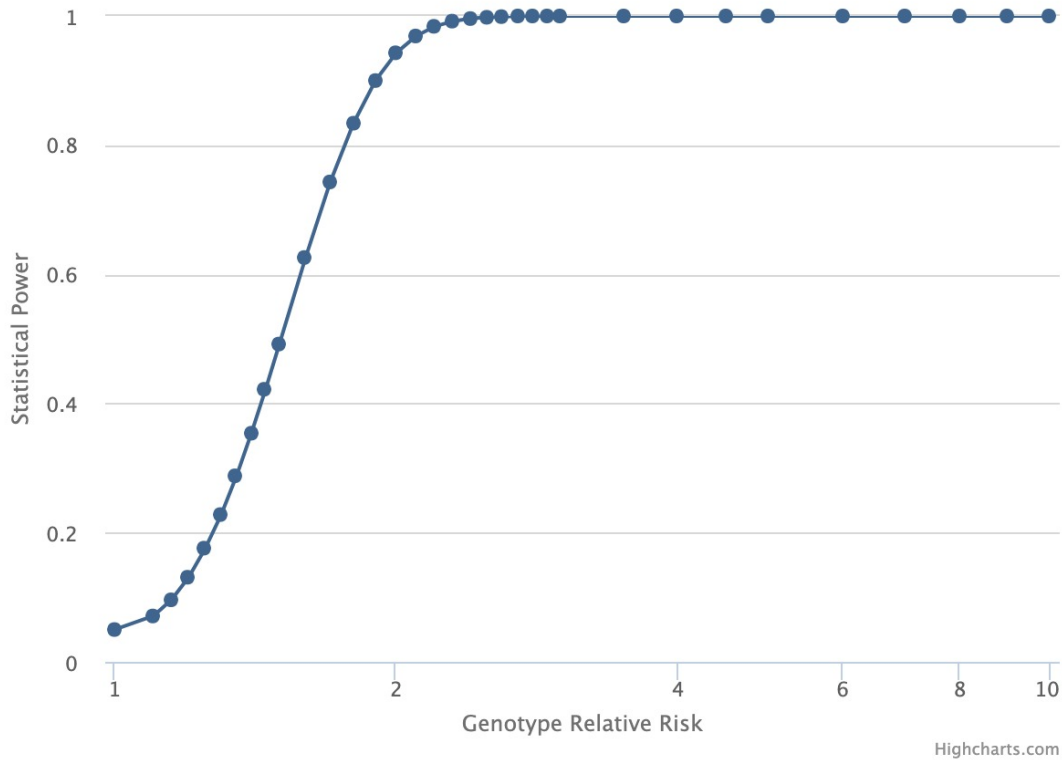
**Supplementary Figure 1:** NeuroX cluster plot of the exm27138\_ver2 probe showing good separation between the homozygous reference cluster (red) and the heterozygous cluster (purple)



**Supplementary Figure 2:** Sanger sequencing chromatograms confirming the presence of PINK1 p.G411S variant in nine carriers.

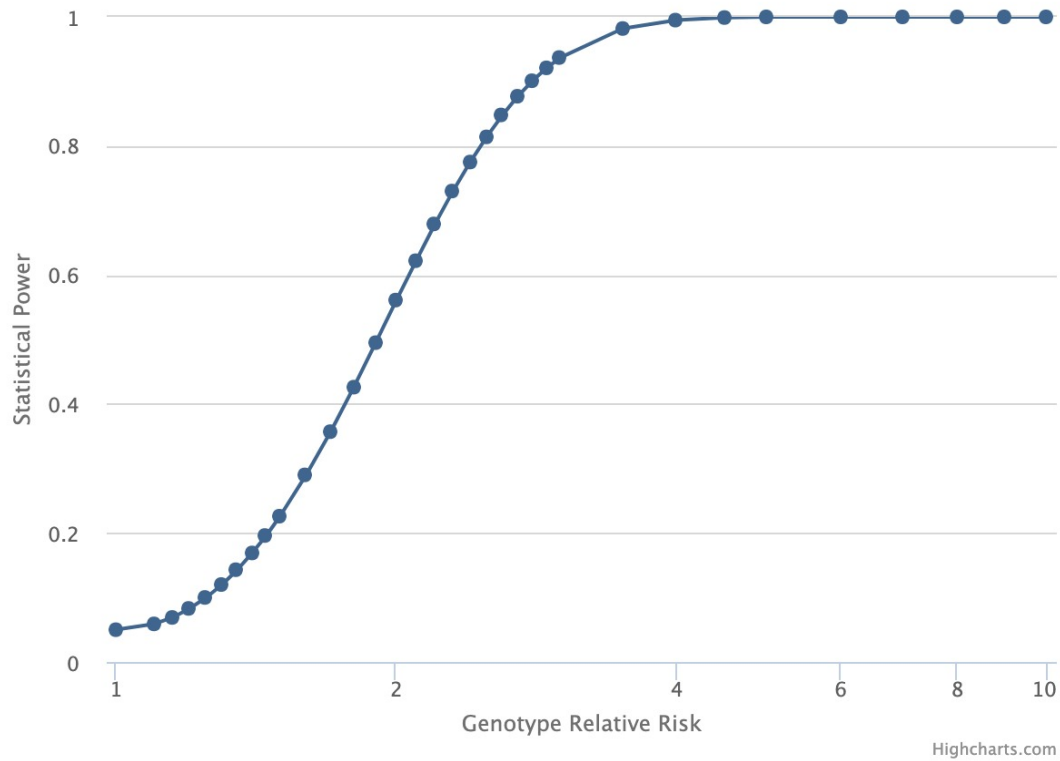


**Supplementary Figure 3:** GWAS data from Nalls et al 2019. A) When looking only at the *PINK1* region no signal of interest is identified. B) Zooming-out more no signals of interest are detected.



**Supplementary Figure 4: Power calculation using GAS Power Calculator for *PINK1* p.G411S.** Cases were set to 12166, controls to 12489, significance level to 0.05, prevalence to 0.01 and Disease Allele Frequency to 0.0015.

[http://csg.sph.umich.edu/abecasis/cats/gas\\_power\\_calculator/](http://csg.sph.umich.edu/abecasis/cats/gas_power_calculator/)



**Supplementary Figure 5: Power calculation using GAS Power Calculator for *PINK1* pathogenic variants.** Cases were set to 6712, controls to 45113, significance level to 0.05, prevalence to 0.01 and Disease Allele Frequency to 0.0007.  
[http://csg.sph.umich.edu/abecasis/cats/gas\\_power\\_calculator/](http://csg.sph.umich.edu/abecasis/cats/gas_power_calculator/)