**Supplementary Table 3**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chr** | **Coordinate** | **R** | **A** | **Gene** | **Nucleotide change** | **AA Change** | **Zygosity** | **AF\*** | **dbSNP** | **Polyphen2\*\*** | **CADD \*\*\*** | **Comment** |
| chr6 | 162683775 | C | T | PARK2 | exon3:c.G194A  (NM\_004562) | p.S65N | hom | 8.179e-6 | rs754604402 | D | 25.5 | Novel |
| chr15 | 89873364 | C | G | POLG | exon3:c.G803C  (NM\_001126131) | p.G268A | het | 0.0034 | rs61752784 | D | 26.6 | Linked to AR/sporadic PEO (1,2) |
| chr16 | 89986091 | G | A | MC1R | exon1:c.G425A  (NM\_002386) | p.R142H | het | 0.0051 | rs11547464 | D | 28.6 | Likely not disease-linked |
| chr1 | 155205634 | T | C | GBA | exon10:c.A1226G  (NM\_001005741) | p.N409S | het | 0.0022 | rs76763715 | B | 23.7 | Risk variant for late-onset PD (also named N370S) (3) |

Chr:chromosome, R:reference nucleotide, A:alternate nucleotide, AA:amino acid, het:heterozygous, hom:homozygous, AF:allele frequency, dbSNP:the Single Nucleotide Polymorphism Database reference, D:Probably damaging, B:Benign. \*gnomAD total allele frequency, \*\*Polyphen2 (HVAR-based) prediction, \*\*\*CADD-C Score v1.4 (PHRED)

**References**

1. Di Fonzo, Bordoni *et al*. (2003)
2. Graziewicz, Longley *et al*. (2006)
3. Sidransky, Nalls *et al*. (2009)