**Supplementary data.**

**Supplementary Table 1** – Summary results of the largest previous genome-wide association study for IPF using SNPs reported in (Allen et al., 2020) showing IPF common variant signals and the effect sizes observed.



**Supplementary Table 2.1**: Number of loci called as percentage of total in catalogue for GangSTR and HipSTR and ExpansionHunter, and call concordance as function of sequence length

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Tool | Sample | No of loci in catalogue bed file | No. of calls at 2x150 bp | No. of calls at 2x250 bp | Calls in both | Identical by allele length (%) | Identical by allele sequence (%) |
| HipSTR.v0.6.2 | HG002 | 790661 | 96.1 | 94.1 | 93.5 | 99.6 | 99.8 |
|  | HG003 | 790661 | 96.1 | 93.8 | 93.8 | 99.6 | 99.8 |
|  | HG004 | 790661 | 95.8 | 93.9 | 93.5 | 99.6 | 99.8 |
|  |  |  |  |  |  |  |  |
| GangSTR.v2.5.4 | HG002 | 790661 | 99.7 | 96.1 | 96.1 | 99.4 | x |
|  | HG003 | 790661 | 99.7 | 95.8 | 95.8 | 99.4 | x |
|  | HG004 | 790661 | 99.2 | 96.8 | 96.8 | 99.4 | x |
|  |  |  |  |  |  |  |  |
| ExpansionHunter.v5.0.0 | HG002 | 790661 | 99.8 | 99.3 | 99.3 | 97.6 | x |
|  | HG003 | 790661 | 99.8 | 99.8 | 99.8 | 97.5 | x |
|  | HG004 | 790661 | 99.3 | 99.4 | 99.3 | 97.3 | x |

**Supplementary Figure 4.1**: distribution of HWE P values estimated for loci genotype by GangSTR for discovery and replication cohorts

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**Supplementary Figure 4.2**: Visualisation of read alignments for the *FUT8-CCDC196* and *LOC102723769* loci using Nanopore long-read sequencing data, along with randomly selected cases/controls sequenced suing Illumina.

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**Supplementary Figure 5.2**: Visualisation of read alignments for the *DOK6, TXK, MINDY3-PTER*, and *LOC101927815, LOC101927815, RPL23AP87, GPATCH2L-ESRRB, SLC15A4, RPH3AL, PPP6R3* and *MICA* loci using Nanopore long-read sequencing data.

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