**Supplementary Figures**

**Supplementary Figure 1. Number of non-coding variants imputed with info > 0.7.**

This figure shows the number of well-imputed (info > 0.7) variants with three different minor allele count (MAC) ranges (10-30, 30-70, 70-110) for each of the tested panels. 1000G: 1000 Genomes panel (N = 1,092); HRC: Haplotype reference Consortium panel (N = 32,488); Local panel: Combined Finnish low-pass whole genome sequence and high-pass whole exome sequence panel (N = 6,873).



**Supplementary Figure 2. Imputation of masked variants (non-coding variation included)**

This figure shows the imputation results for the masked variation. Each of the masked variants falls into one of four groups for each of the panels; white = not covered by the panel, light grey = info < 0.7, dark grey = concordance < 0.8, colored = concordance > 0.8. 1000G: 1000 Genomes panel (N = 1,092); HRC: Haplotype reference Consortium panel (N = 32,488); Local panel: Combined Finnish low-pass whole genome sequence and high-pass whole exome sequence panel (N = 6,873).

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**Supplementary Tables**

**Supplementary Table 1**. Number of false positive calls after imputation when using info threshold 0.7 (A) and 0.9 (B). Best guess genotypes based on genotype posterior probability of 0.9.

|  |  |
| --- | --- |
| AReference Panel | Best guess MAC bins in the imputed dataset |
| <10 | 10-30 | 30-70 | 70-110 | 110-200 | >=200 |
| 1000G | 35 | 14 | 6 | 3 | 2 | 3 |
| HRC | 65 | 1 | 0 | 0 | 0 | 2 |
| Local panel | 3 | 4 | 0 | 0 | 0 | 2 |
| 1000G + LP-WGS | 151 | 80 | 30 | 7 | 1 | 10 |

|  |  |
| --- | --- |
| BReference Panel | Best guess MAC bins in the imputed dataset |
| <10 | 10-30 | 30-70 | 70-110 | 110-200 | >=200 |
| 1000G | 7 | 7 | 2 | 1 | 0 | 2 |
| HRC | 4 | 0 | 0 | 0 | 0 | 2 |
| Local panel | 1 | 1 | 0 | 0 | 0 | 2 |
| 1000G + LP-WGS | 28 | 17 | 6 | 1 | 0 | 4 |

MAC: Minor allele count; 1000G: 1000 Genomes panel; HRC: Haplotype reference Consortium panel; Local panel: Finnish low-pass whole genome sequences with Finnish high-pass whole exome extension; LP-WGS: Finnish low-pass whole genome sequences; 1000G + LP-WGS: Finnish whole genome sequence panel combined with 1000G panel;