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Supplemental information

Identifying risk variants for embryo aneuploidy using ultra-low coverage whole-genome sequencing from preimplantation genetic testing

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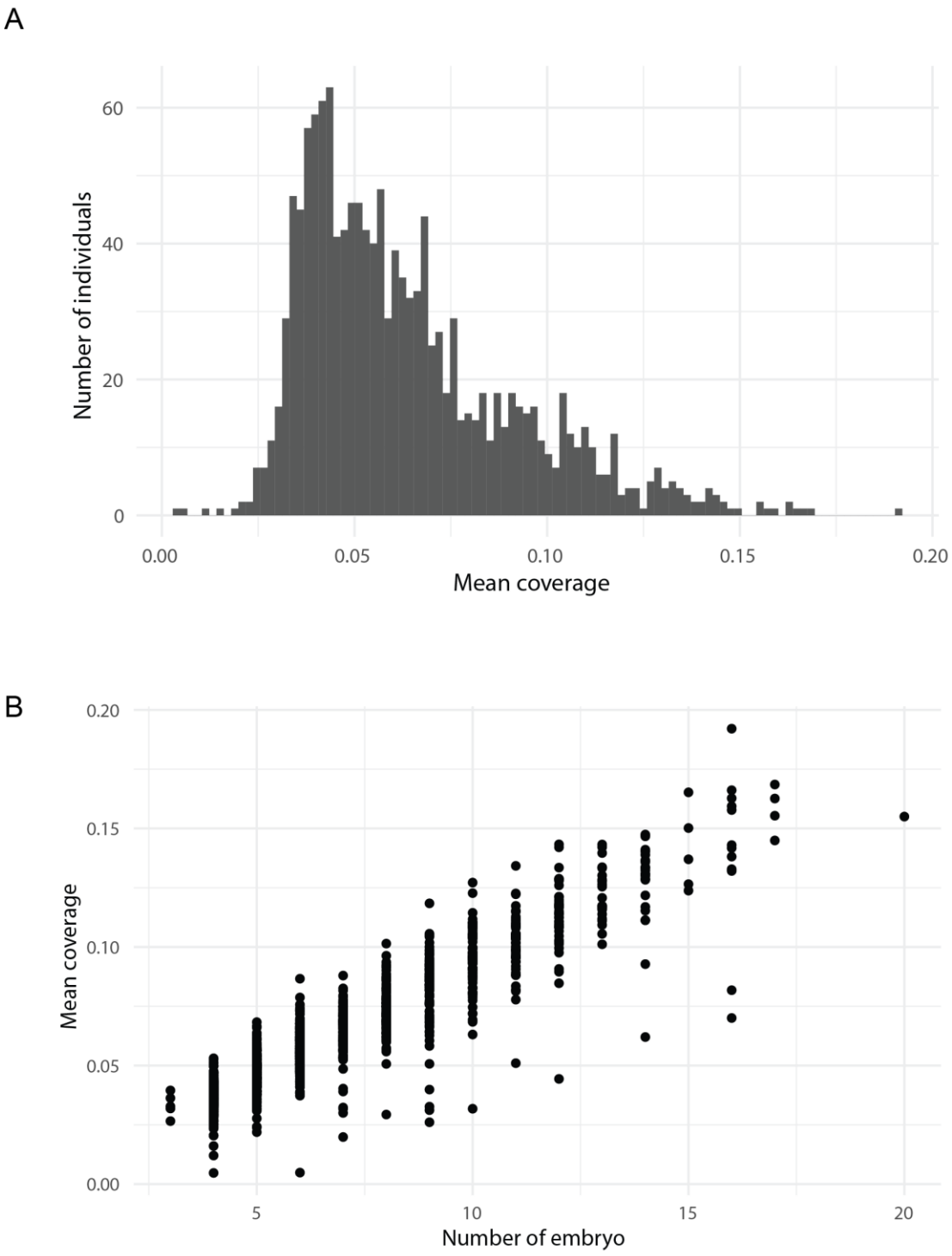

Figure S1. Pooled sequencing coverage across 1,373 individuals. (A) The mean sequence coverage of individuals. **(B)** Individual sequencing coverage correlation with the number of embryos sequenced.

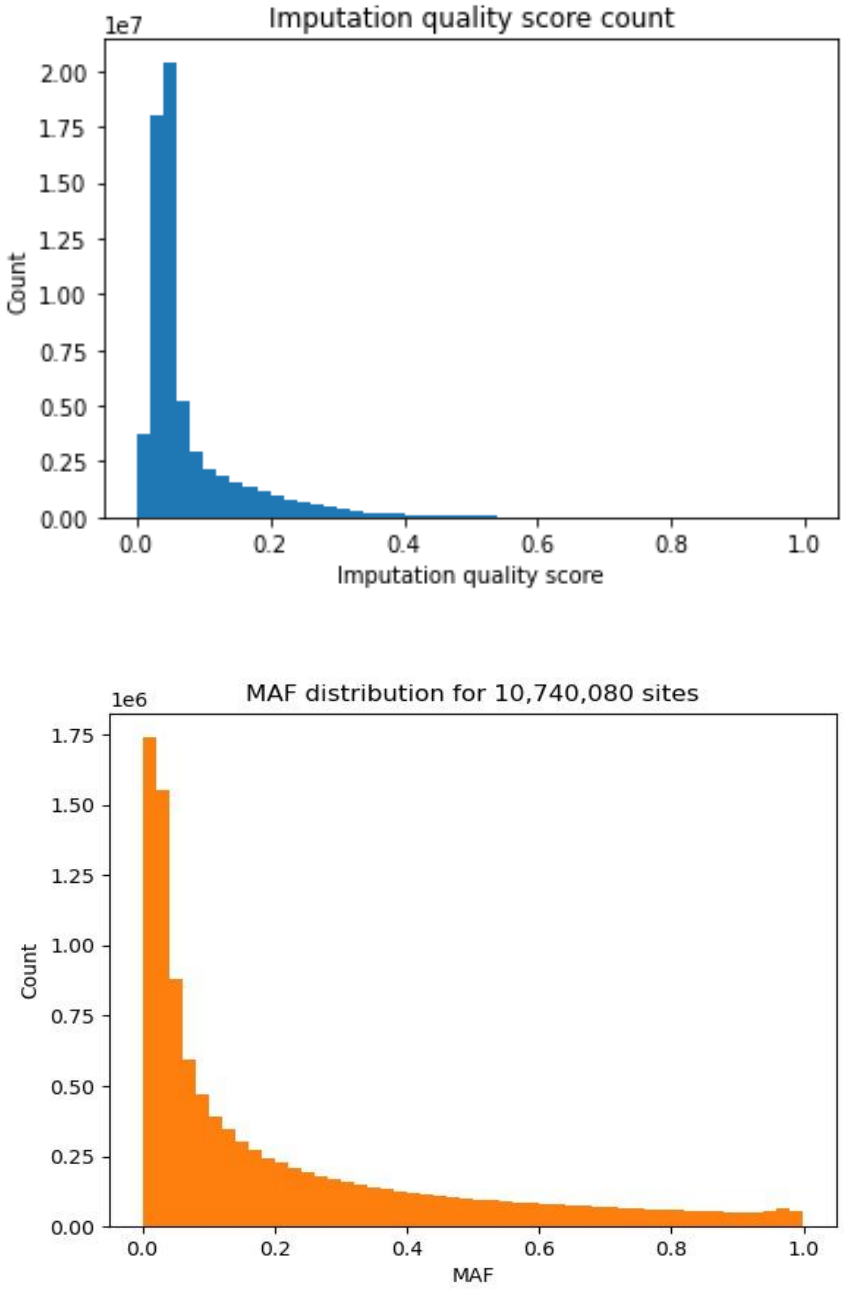

Figure S2. Variant QC and distribution across chromosomes. (A) Imputation quality score distribution of variants before filtering. **(B)** Minor allele frequency (MAF) distribution of variants before filtering.

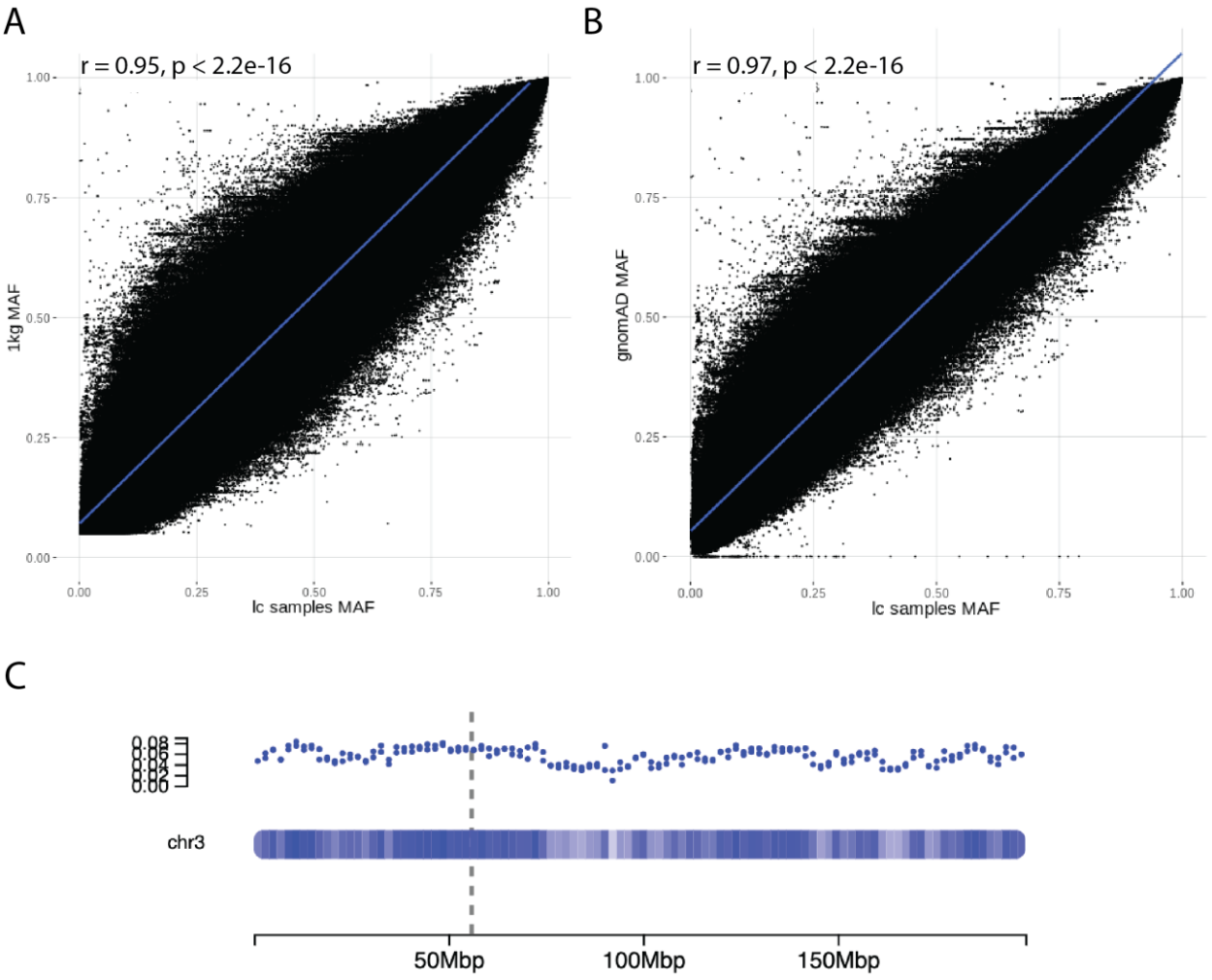

Figure S3. Variant MAF correlation and sequencing depth distribution on chromosome 3. The correlation of variant MAF distribution between the PGT-A samples and the 1000 Genomes **(A)** and gnomAD **(B)** samples. **(C)** The median sequencing depth on chromosome 3. The sequencing depth was calculated for non-overlapping one million base-pair regions across the chromosome.

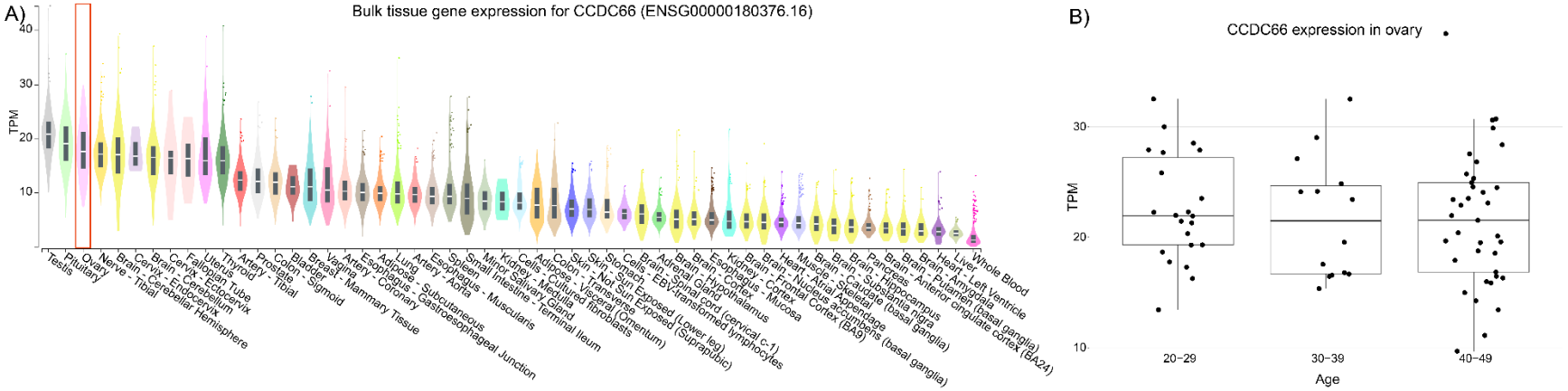

Figure S4. *CCDC66* expression in GTEx samples. (A) *CCDC66* expression in different tissues in GTEx samples. Ovary is labelled with a red box. **(B)** *CCDC66* expression in ovary in different age groups among GTEx samples. The whiskers in the box-whisker plot span a range that is 1.5 times the interquartile range (IQR). The data used for the analyses described in the figure were obtained from: the GTEx Portal on 09/21/23 and dbGaP accession number phs000424.v8.p2 on 09/21/23.