

Supplemental Figures

KIR gene content imputation from single-nucleotide polymorphisms in the Finnish population

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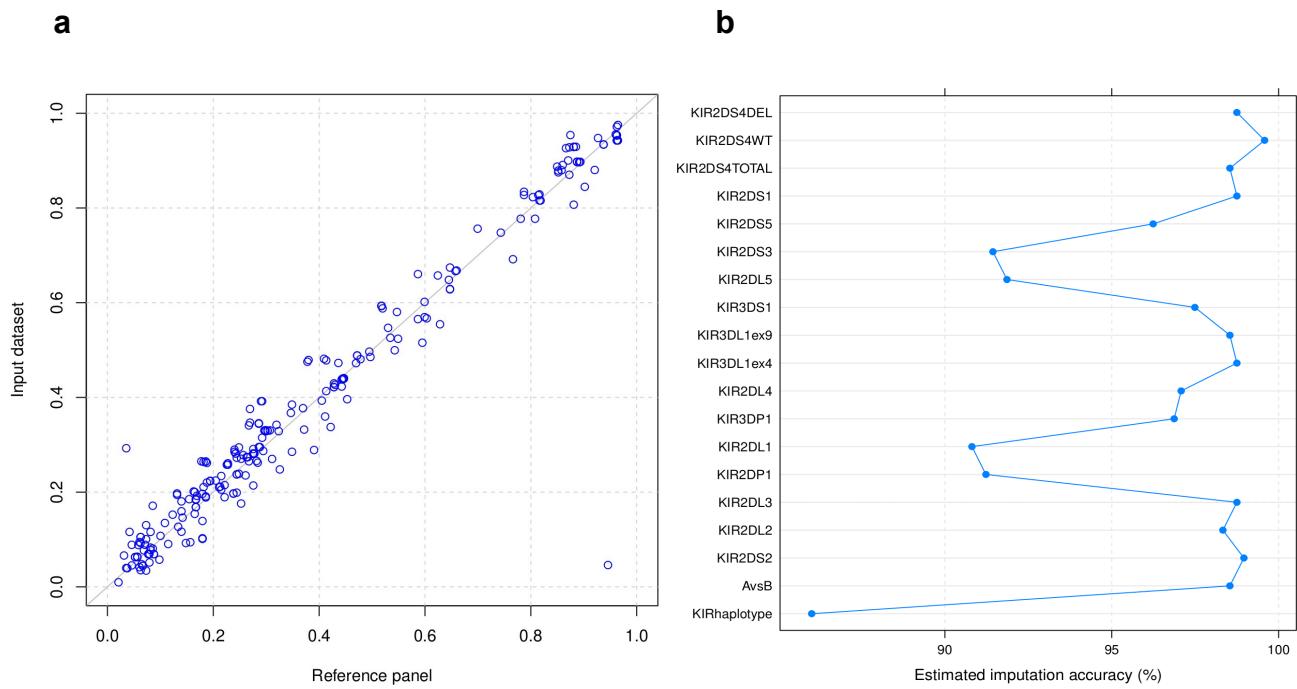


Figure S1. KIR*IMP input data validity check. (A) Scatterplot showing the SNP allele frequencies in the KIR*IMP reference panel (x-axis) and in the input data (y-axis). (B) KIR*IMP imputation accuracy estimate based on SNPs present in the input data.