
Genetic predictors of lifelong medication-use patterns in cardiometabolic diseases

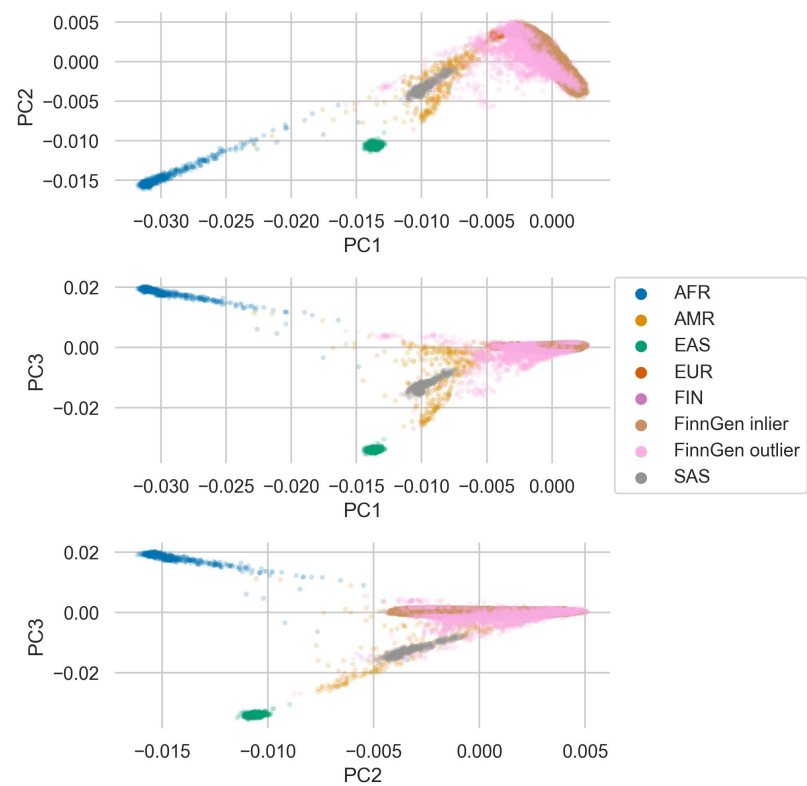
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Supporting Information

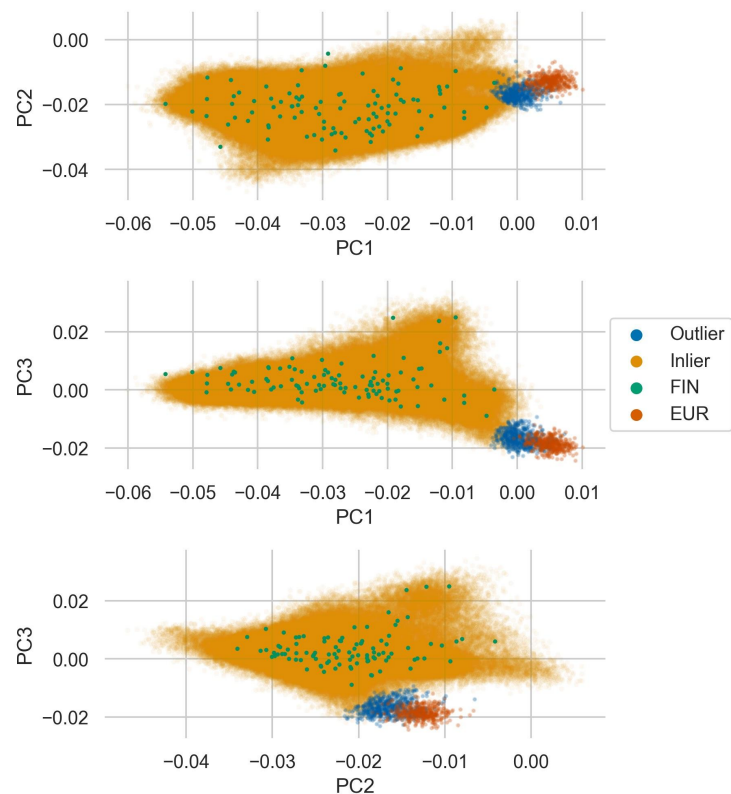
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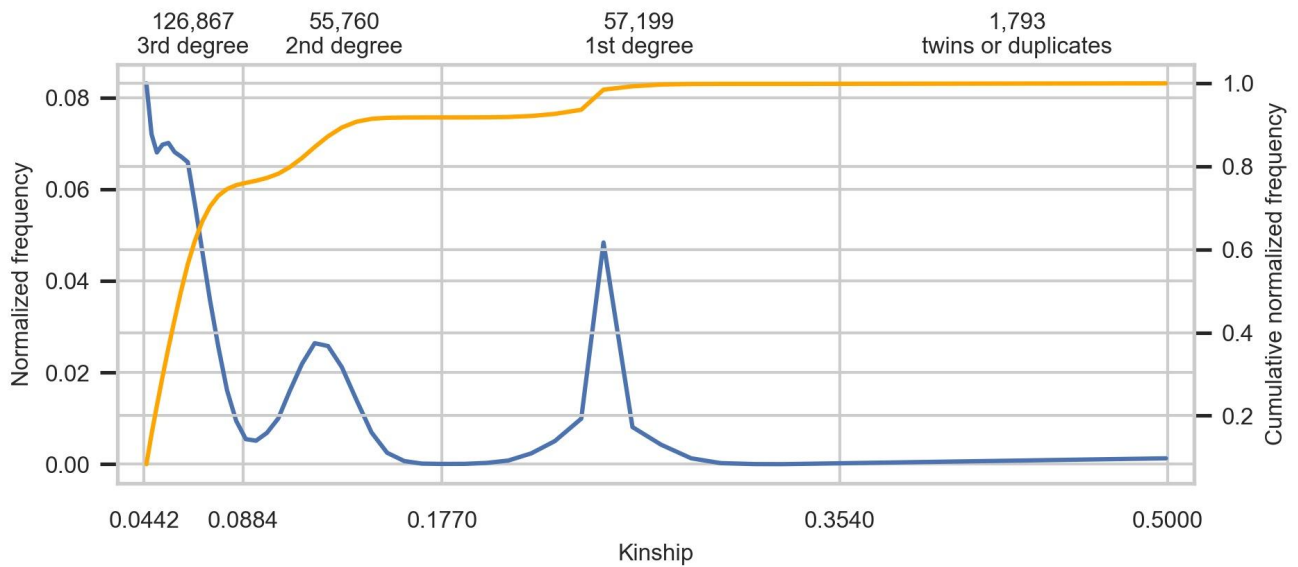
Supplementary Figure 1. The scatter plots of the genetic components of each FinnGen sample projected onto the first three principal components



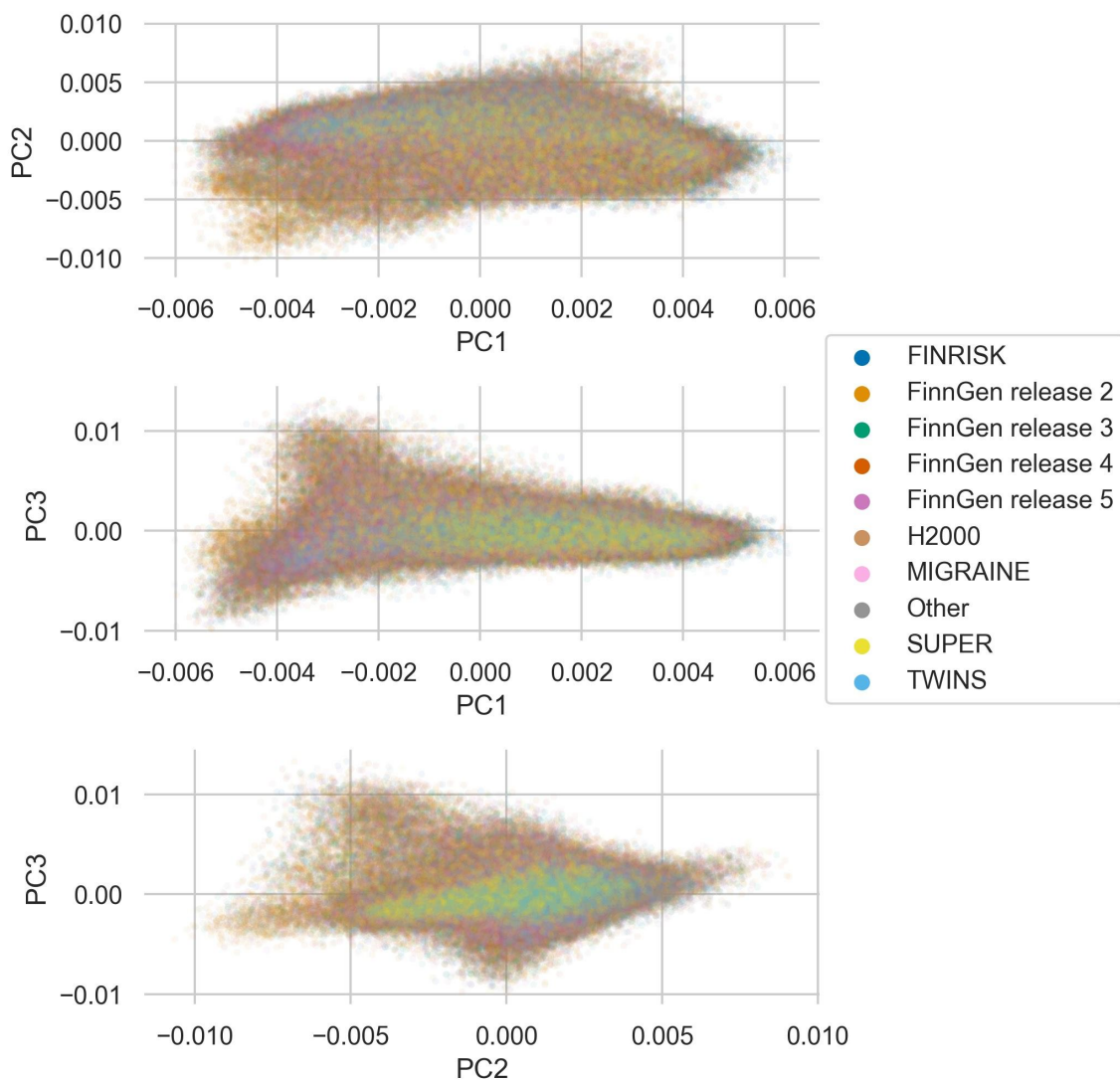
Supplementary Figure 2. The European and Finnish 1000 genomes projected onto the new three-dimensional (principal components 1-3) space



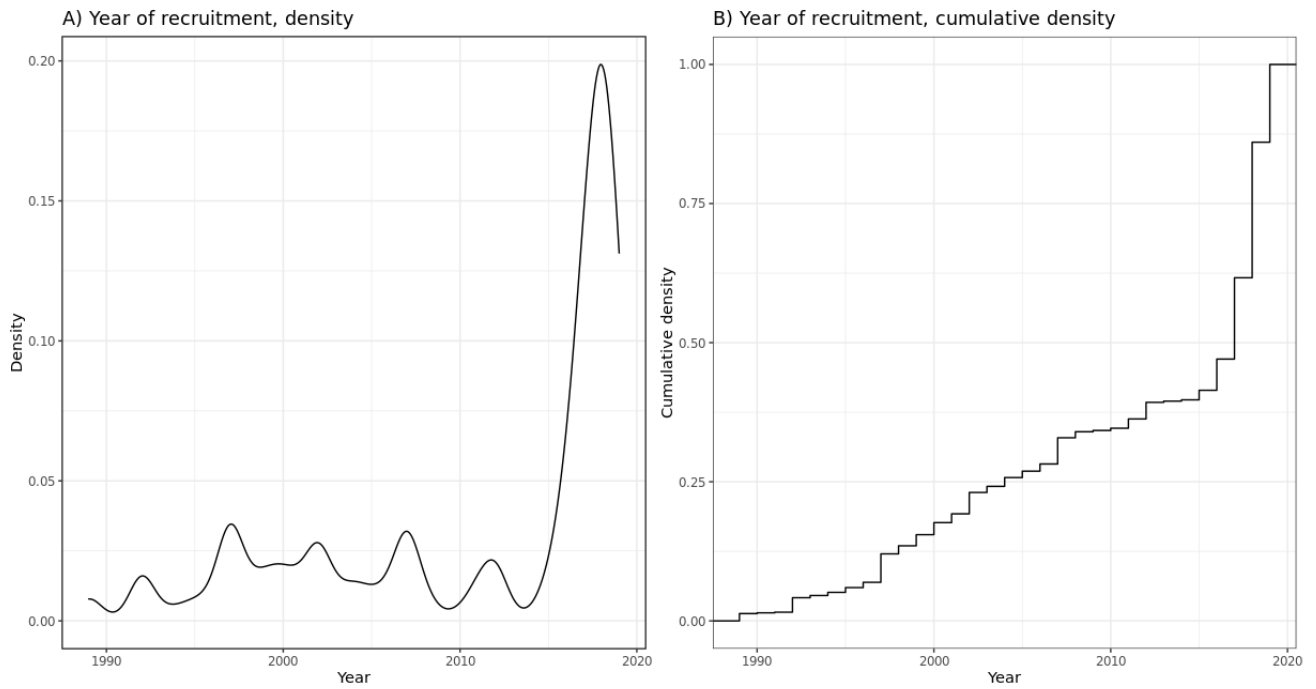
Supplementary Figure 3. The distribution of kinship values of the FinnGen Study samples



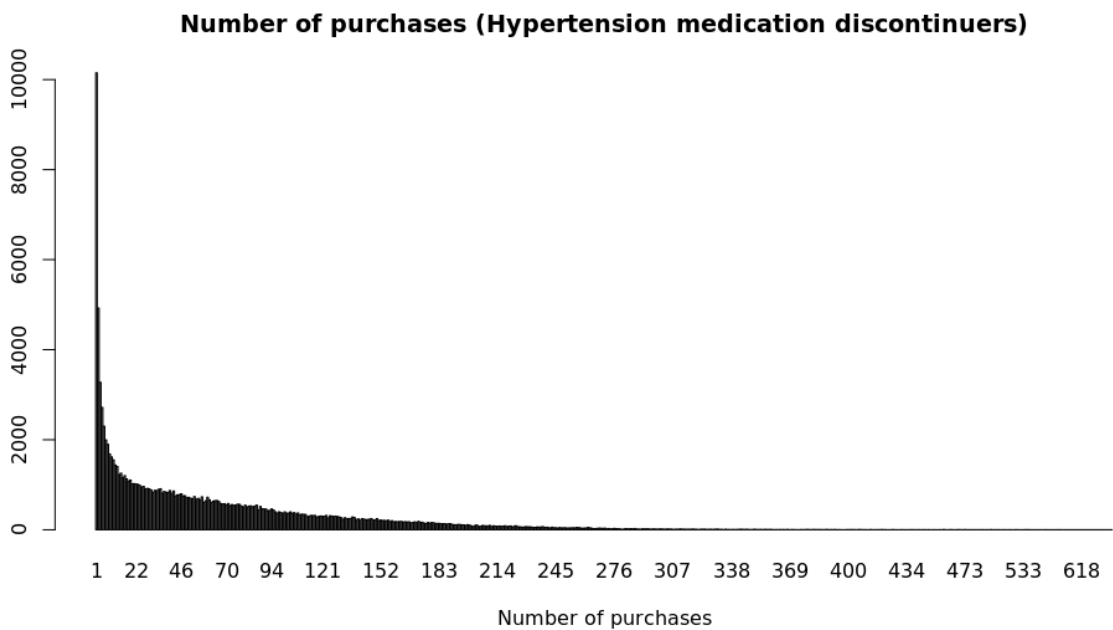
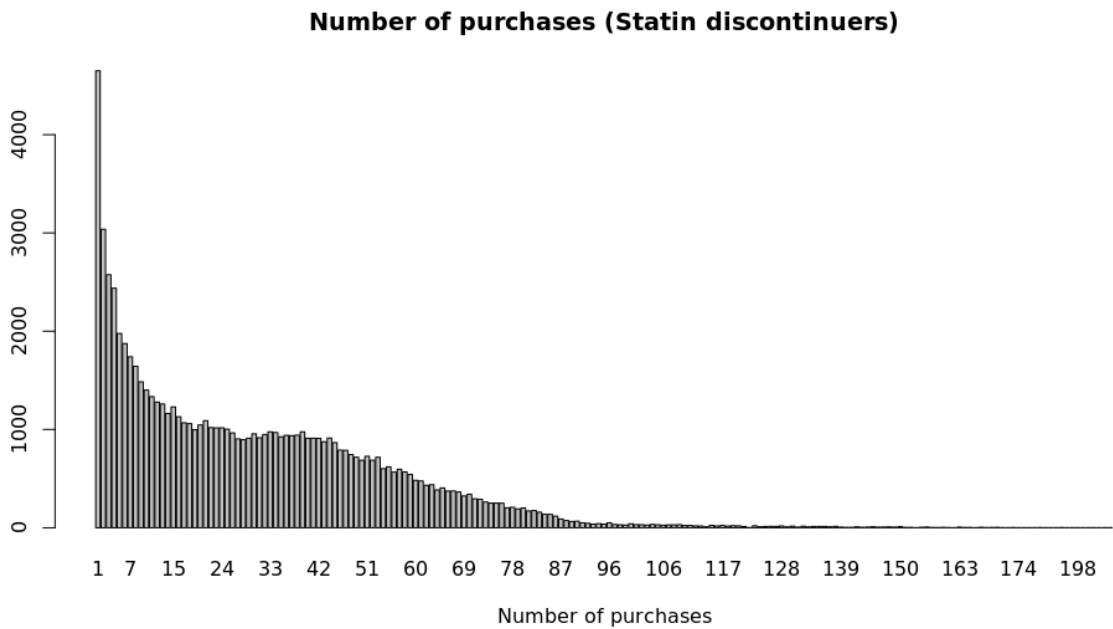
Supplementary Figure 4. Population covariates for 218,957 FinnGen samples from a principal components (PC) analysis performed for the 156,977 unrelated samples after which the 61,980 samples in the second set were projected onto the same multidimensional space, the first 3 PCs are shown



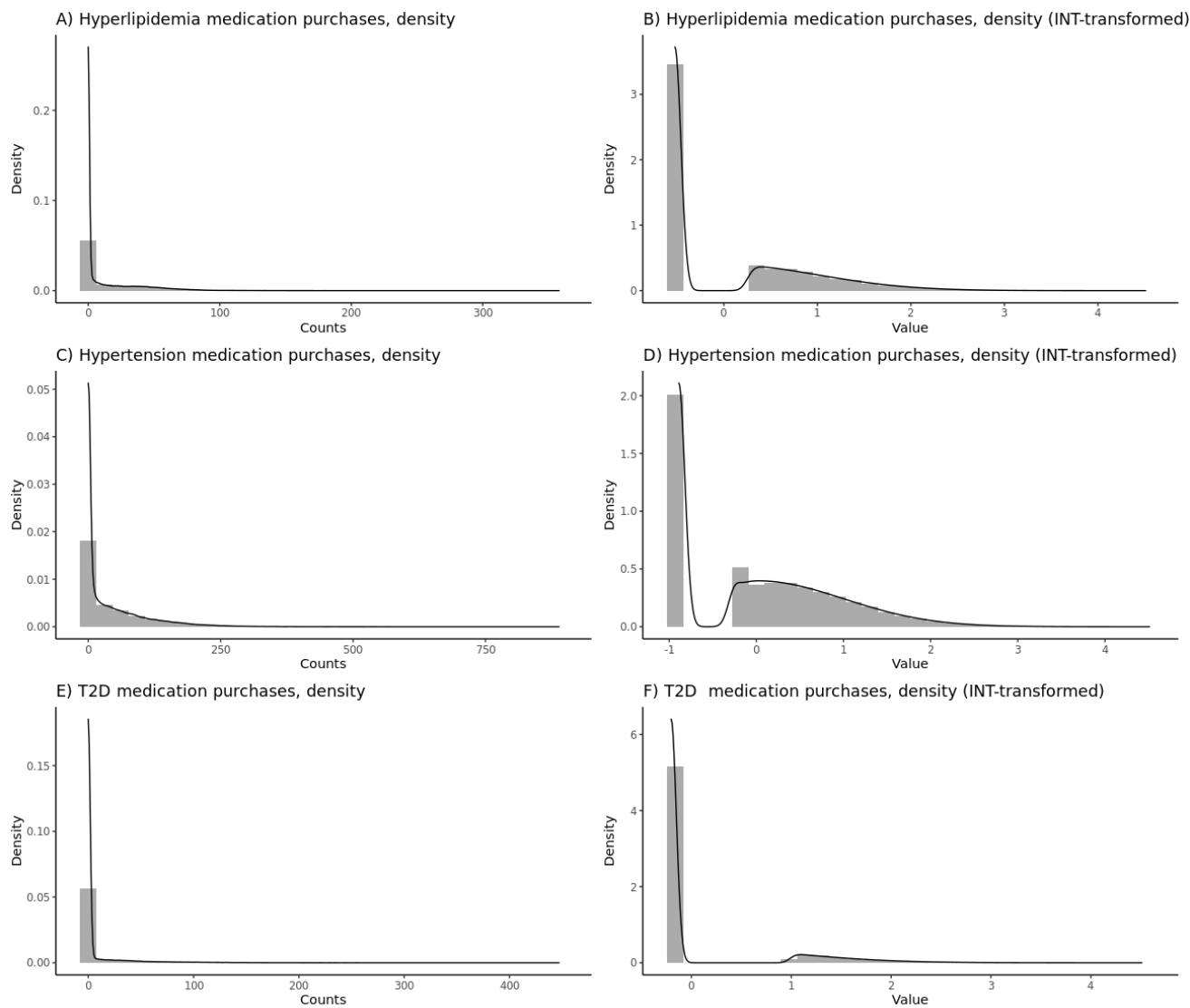
Supplementary Figure 5. Density plots for the year of the recruitment in FinnGen. A significant proportion of the FinnGen R5 participants (n=218,792) are from legacy cohorts collected prior to the FinnGen study and have thus been recruited prior to the official FinnGen study launch in autumn 2017. A) Density plot. B) Cumulative density plot.



Supplementary Figure 6. Medication purchases before discontinuation. Histograms display the number of individuals for each number of medication purchases before medication discontinuation. Discontinuation here has been defined as having recorded the last purchase at least 1 year before the end of follow-up.



Supplementary Figure 7. The raw and the transformed quantitative phenotypes. Histograms displaying the densities of the raw (A, C, D) and the rank-based inverse normal transformed phenotypes for the total number of purchases of medications used in hyperlipidemia (A-B), hypertension (B-D), and type 2 diabetes (E-F).



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