

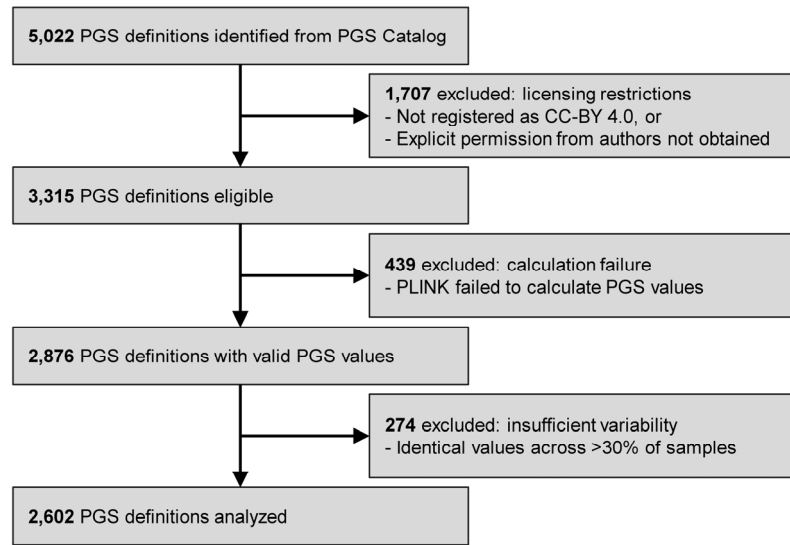


Figure S1. Selection process of PGS definitions.

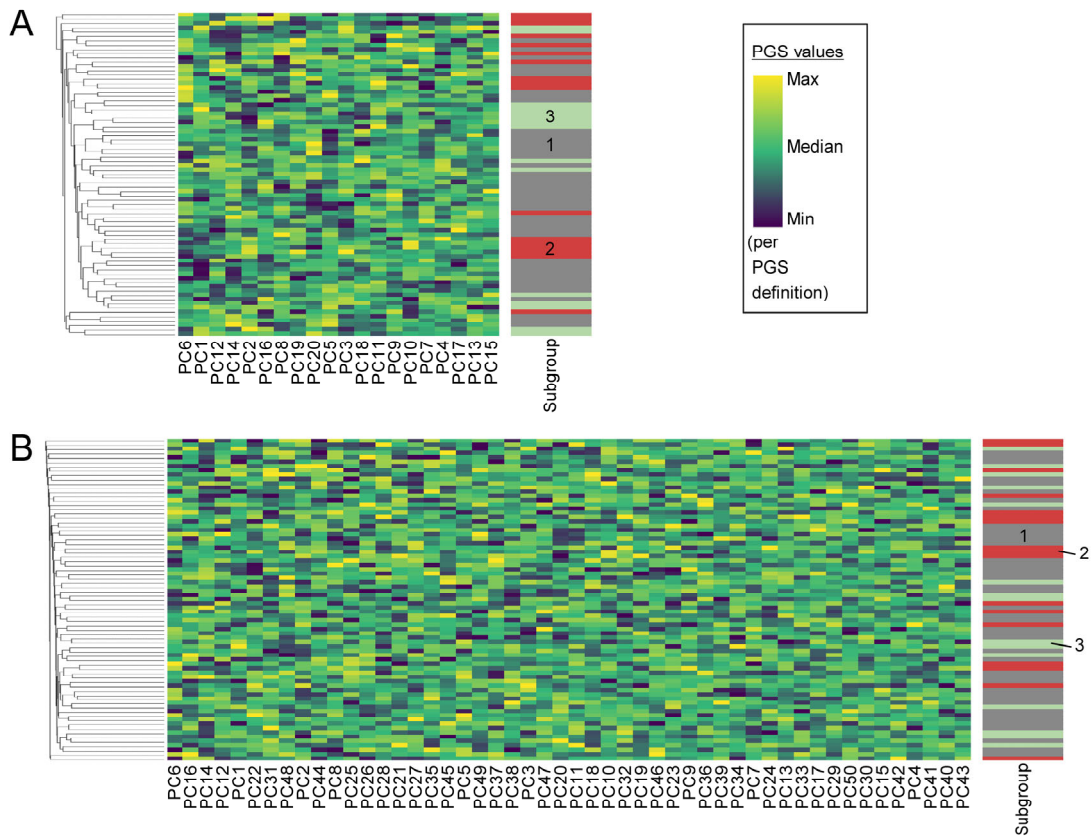


Figure S2. Hierarchical clustering heatmaps of PCA-reduced PGS profiles showed less visually distinct patterns compared to the original PGS space. (A) Heatmap of the top 20 principal components (51.6% of total variance). (B) Heatmap of the top 50 principal components (84.4% of total variance). Dendrogram visualizes Euclidean distance of the PCA-reduced PGS profiles among the individuals. The color bar on the right of each heatmap indicates the three subgroups identified in the original PGS space: subgroup 1 (gray), subgroup 2 (red), and subgroup 3 (green).

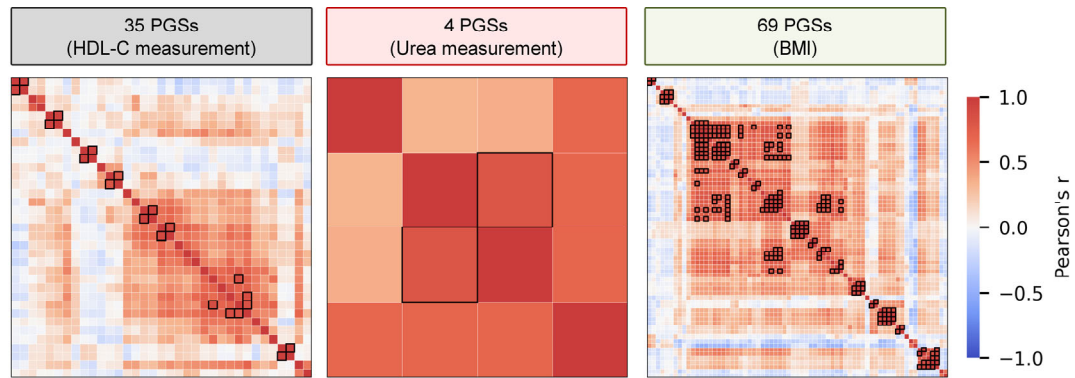


Figure S3. Correlation heatmap documenting PGS redundancy within trait categories. Pairwise Pearson's correlation coefficients between PGSs in trait categories showing significant enrichment (HDL-C measurement, urea measurement, and BMI). Color intensity indicates correlation strength (blue = negative, red = positive; white = minimal correlation). Black boxes outline highly correlated PGS pairs ($|r| > 0.8$) that were removed in the pruning sensitivity analysis.

Table S3. Results of enrichment analyses using the pruned PGS set after removing highly correlated PGS pairs ($|r| > 0.8$).

PGS set	Trait	$N_{\text{mapped}}/N_{\text{all}}$	$q\text{-value}$
Twenty distinctive PGSs in subgroup 1	HDL-C measurement	6/25	8.62×10^{-5}
Twenty distinctive PGSs in subgroup 2	Neuroimaging measurement brain volume measurement	4/28	0.076
	Urea measurement	2/3	0.089
	Cystatin C measurement	2/8	0.461
Twenty distinctive PGSs in subgroup 3	Waist circumference	2/3	0.089
	Hip circumference	2/4	0.118
	Fat body mass	2/4	0.118
	BMI	3/32	0.540

N_{mapped} , number of mapped PGSs in each trait; N_{all} , number of all the PGSs in each trait; $q\text{-value}$, Benjamini-Hochberg corrected $p\text{-value}$. Traits shown are those with $q\text{-value} < 1$. Significance threshold: $q\text{-value} < 0.05$.