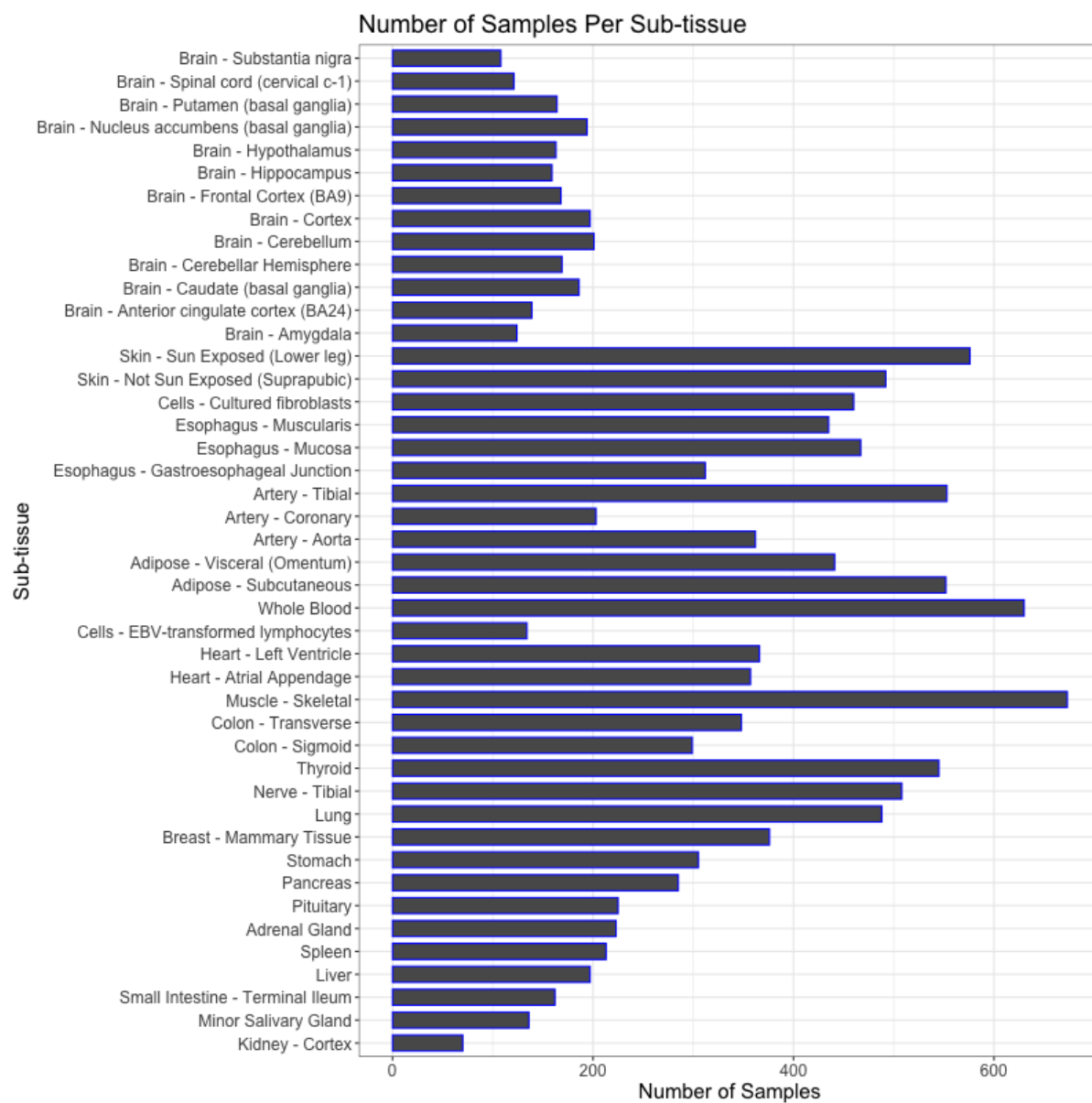
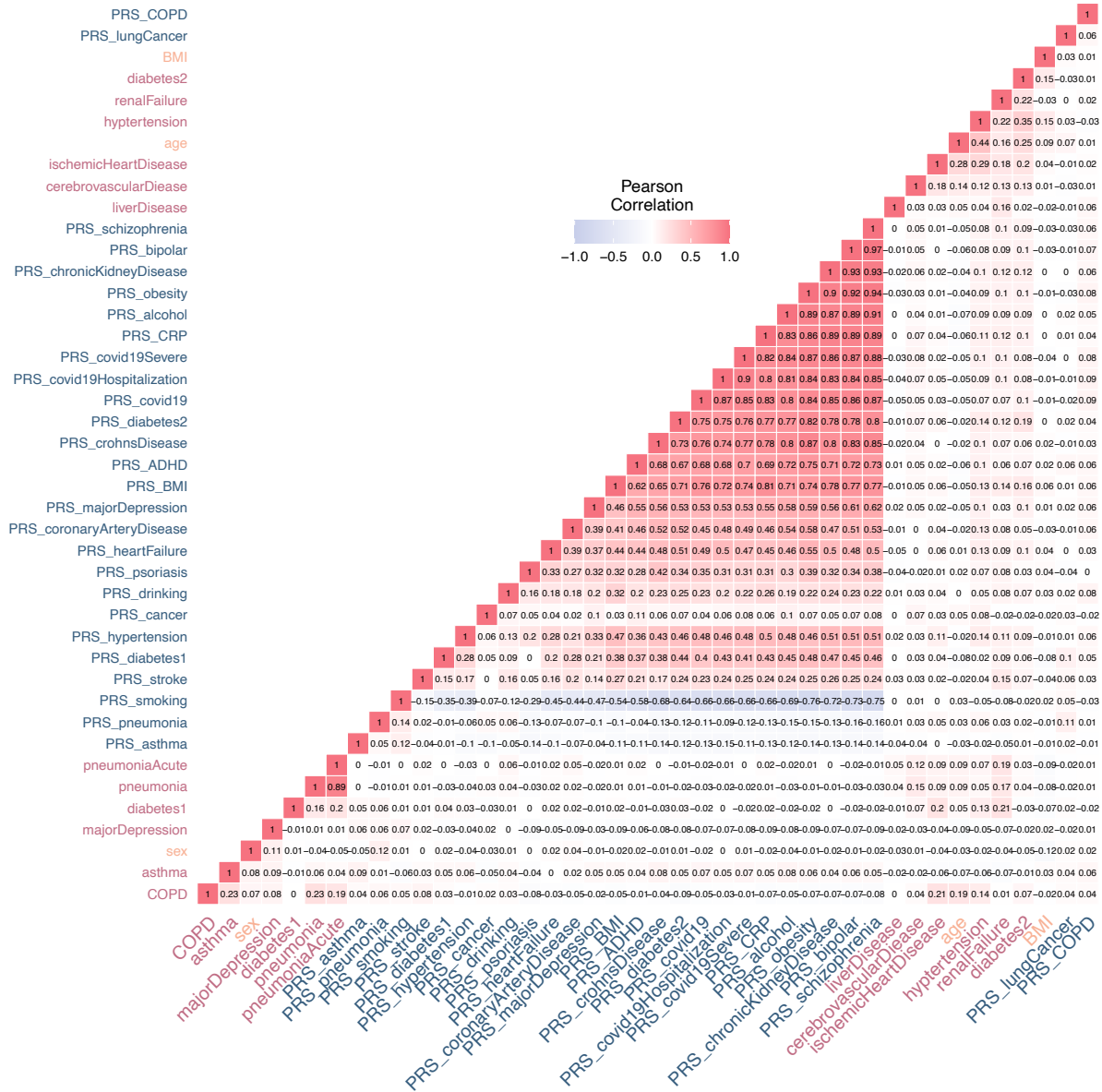


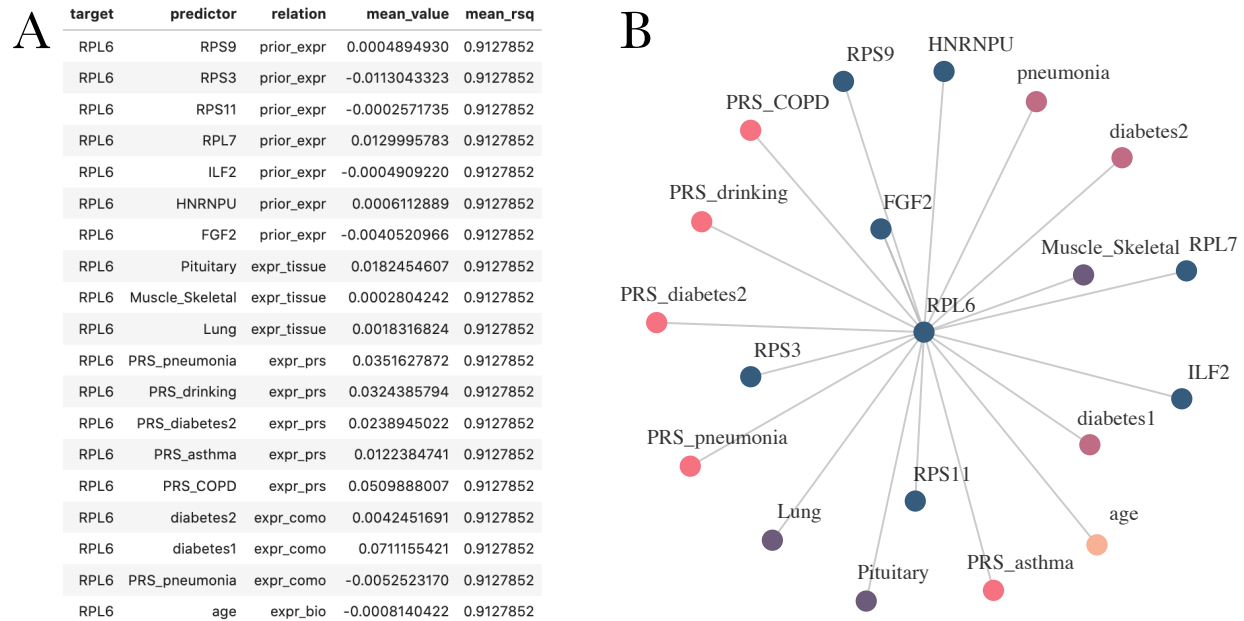
Supplementary Material



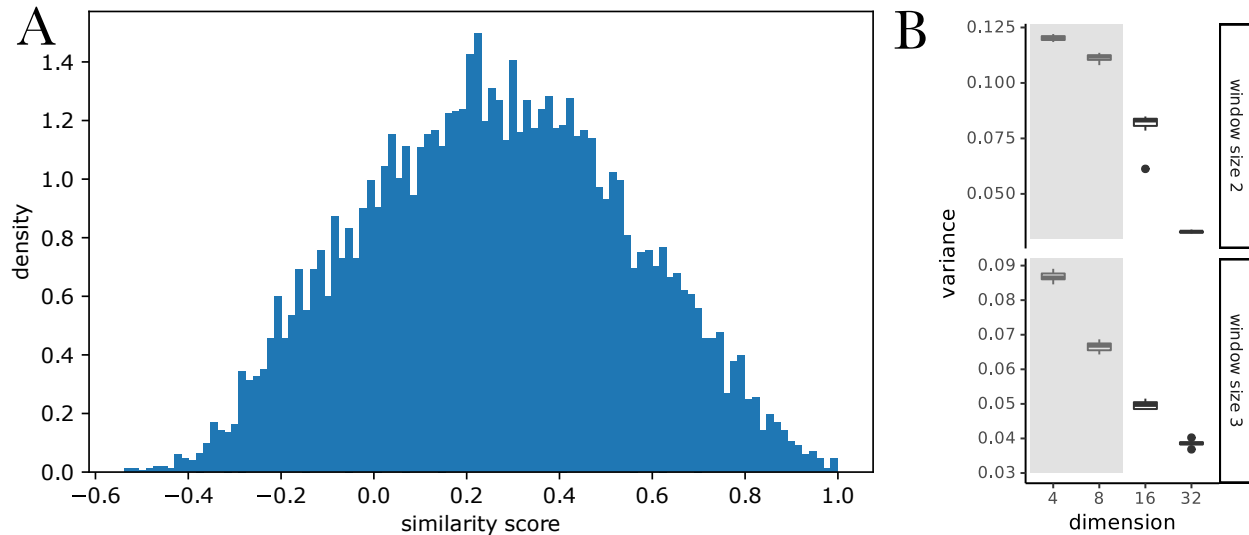
Supplementary Figure 1: Number of samples per sub-tissue type from the GTEx consortium used for the network inference



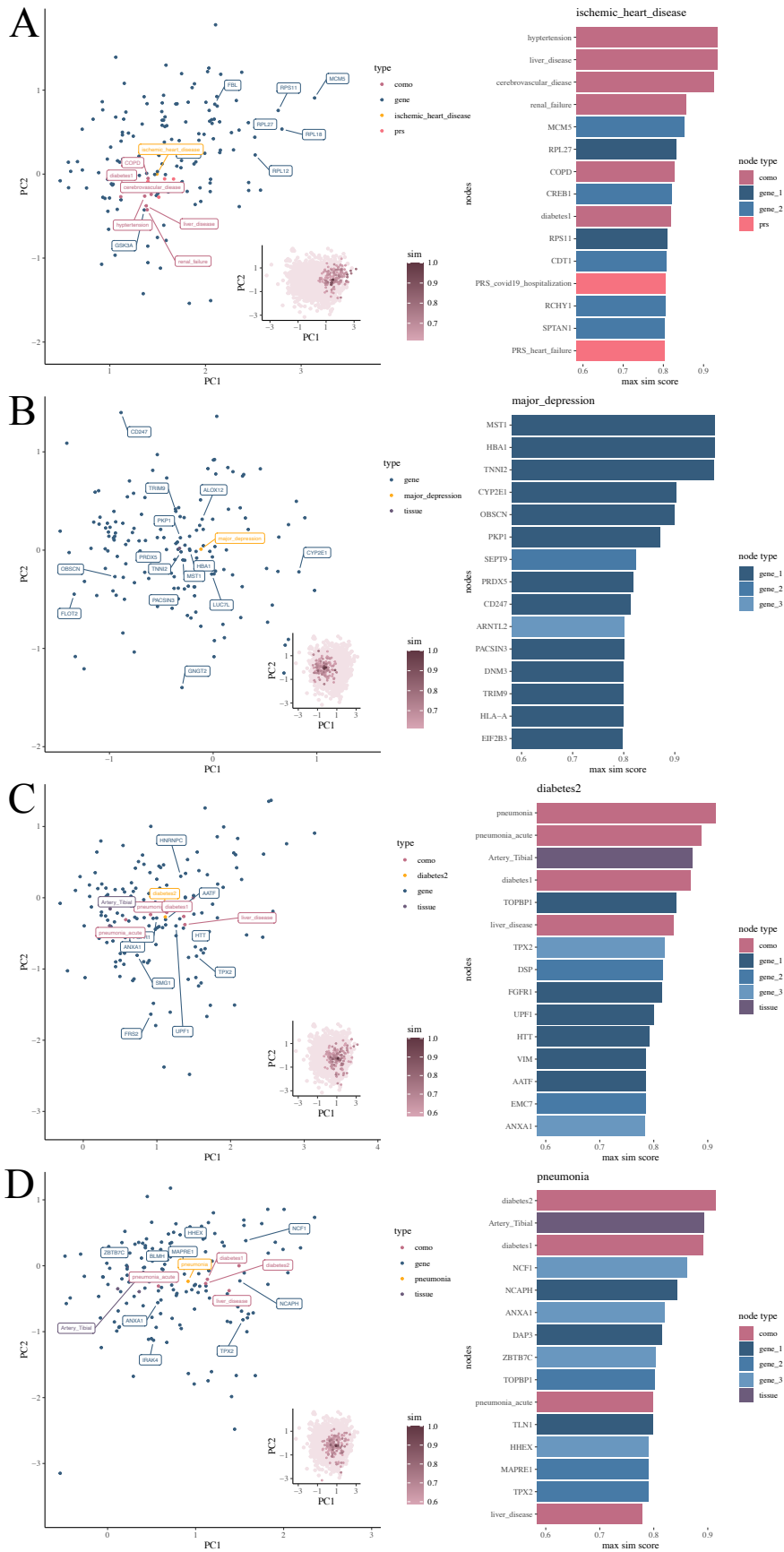
Supplementary Figure 2: Pearson correlation of different data modalities of Polygenic Risk Scores (PRS) in blue, comorbidities in purple and phenotypes in orange. Correlation was generally low across the different data modalities, making the integration of information very important in order to get a holistic view of ranging from genetic predisposition to actual comorbidity being influence by environmental effects. Higher correlations were observed between PRS



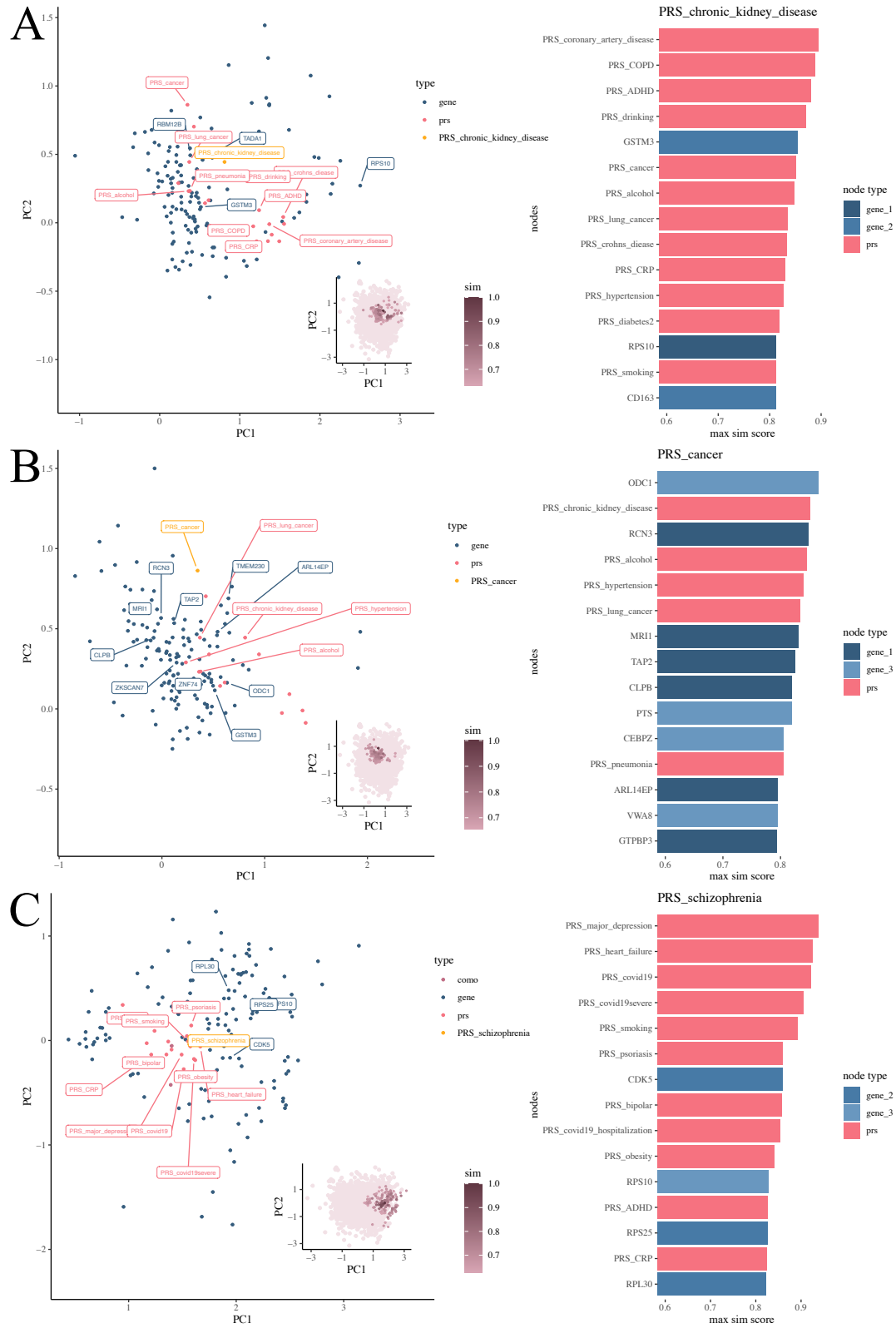
Supplementary Figure 3: Illustration of KiMONo's gene models A) from the sparse group lasso output with a R^2 of 0.912 and the mean beta coefficients over 30 runs of stability selection and B) the statistical associations displayed as edges between RPL6 and its explanatory variables from different modalities of genes, phenotypes, tissues, disease states and PRS



Supplementary Figure 4: Grid search of optimal parameters on small subnetwork of brain samples A) Similarity score distribution of one run with window size = 2 and embedding dimensionality = 16 between 10,000 random node pairs; variance = 0.080. B) variance of 10,000 random node pair similarities with window size [2,3] and dimensionality of embedding [4, 8,16, 32] over 10 embedding repetitions. Distributions that were not normally distributed are overlaid with gray background and thus discarded for parameter selection.



Supplementary Figure 5: Embedding space of comorbidities A) ischemic heart disease, B) major depression, C) Diabetes Type II and D) pneumonia



Supplementary Figure 6: Embedding space of PRS for A) chronic kidney disease, B) cancer and C) schizophrenia