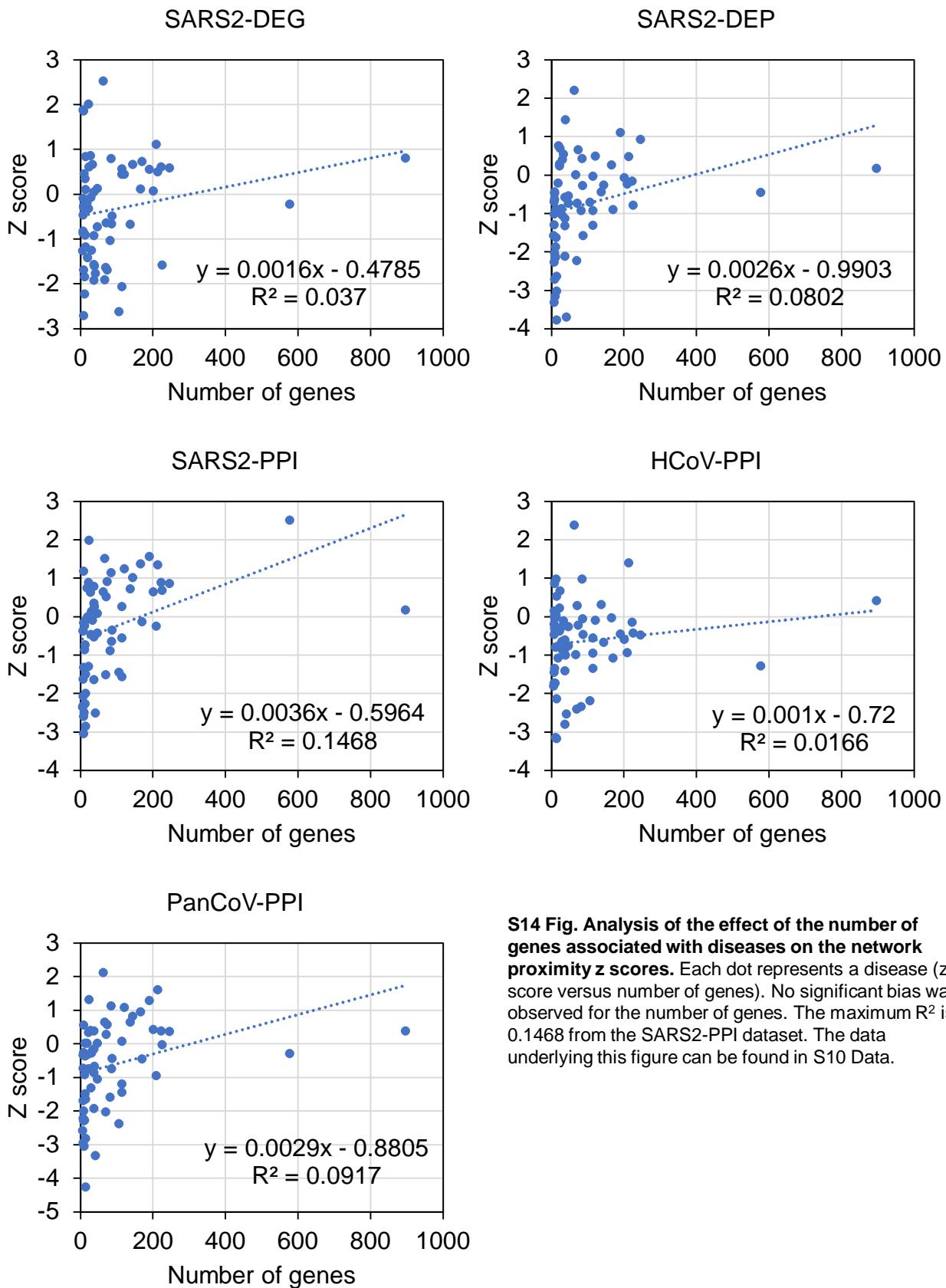


S14 Fig



S14 Fig. Analysis of the effect of the number of genes associated with diseases on the network proximity z scores. Each dot represents a disease (z score versus number of genes). No significant bias was observed for the number of genes. The maximum R^2 is 0.1468 from the SARS2-PPI dataset. The data underlying this figure can be found in S10 Data.