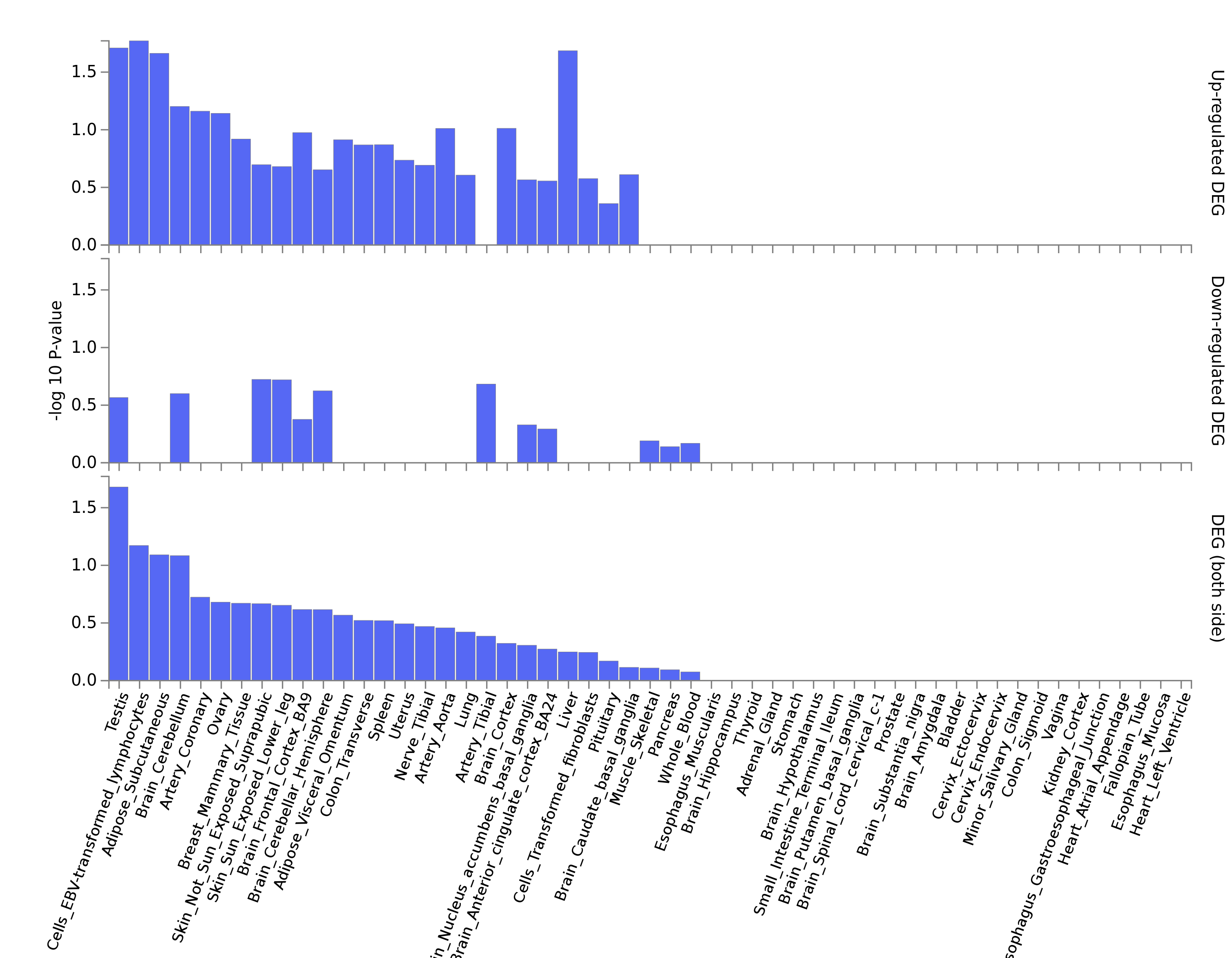
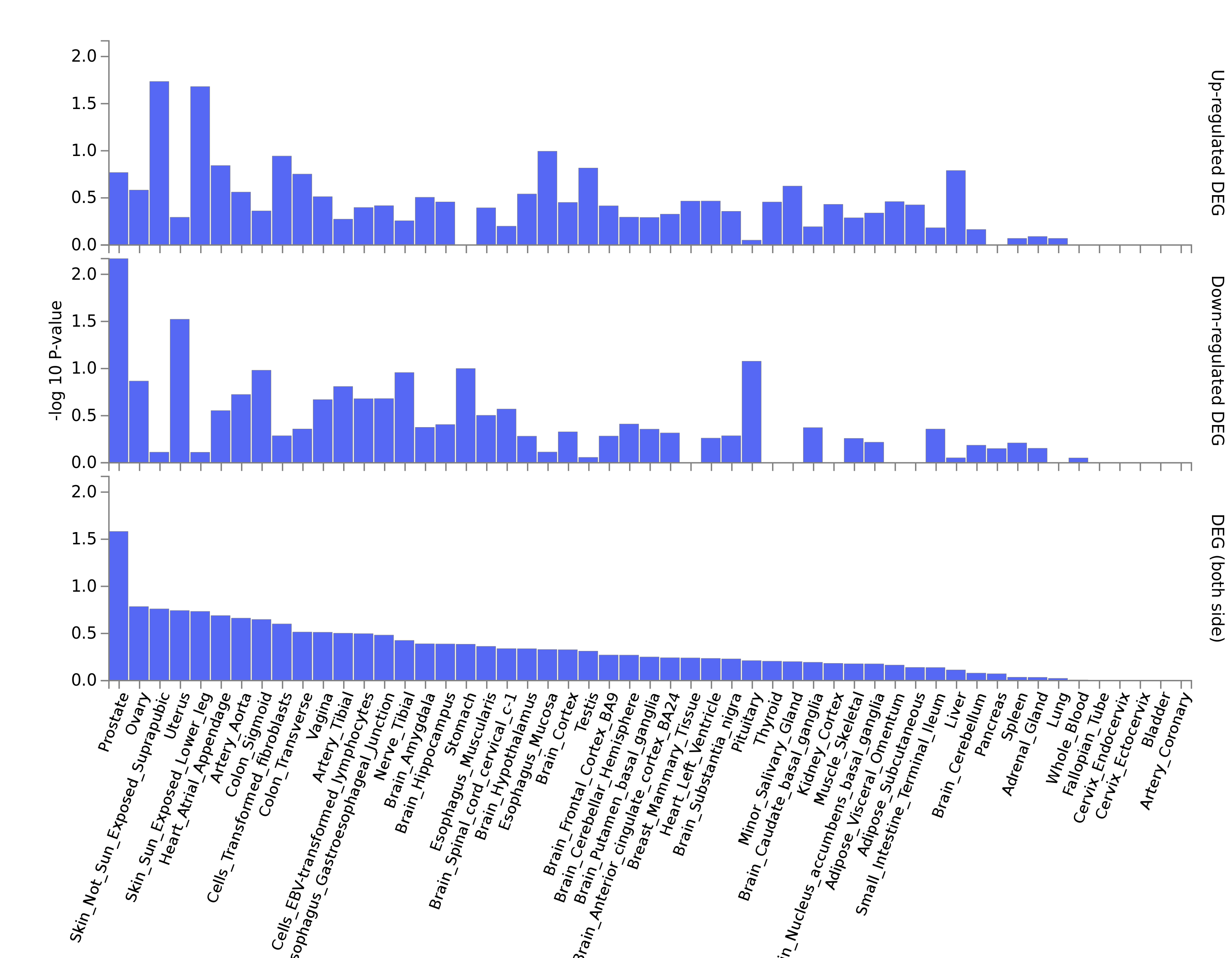
**Supplementary Figure 2**: Differentially Expressed Gene (DEG) Sets considering genes in regions of SNPs with suggestive p values (p<5e-06) for association with the phenotypes of interest in the GSRD sample. DEG sets were pre-calculated by performing two-sided t-test for any one of labels against all others. For this, expression values were normalized (zero-mean) following to a log 2 transformation of expression value. Genes which with P-value ≤ 0.05 after Bonferroni correction and absolute log fold change ≥ 0.58 were defined as differentially expressed genes in a given label compared to others. On top of DEG, up-regulated DEG and down-regulated DEG were also pre-calculated by taking sign of t-statistics into account (Watanabe et al., 2017).

**TRD vs. responders**



**Symptom improvement in TRD and responders**



**TRD vs. responders + non-responders**

