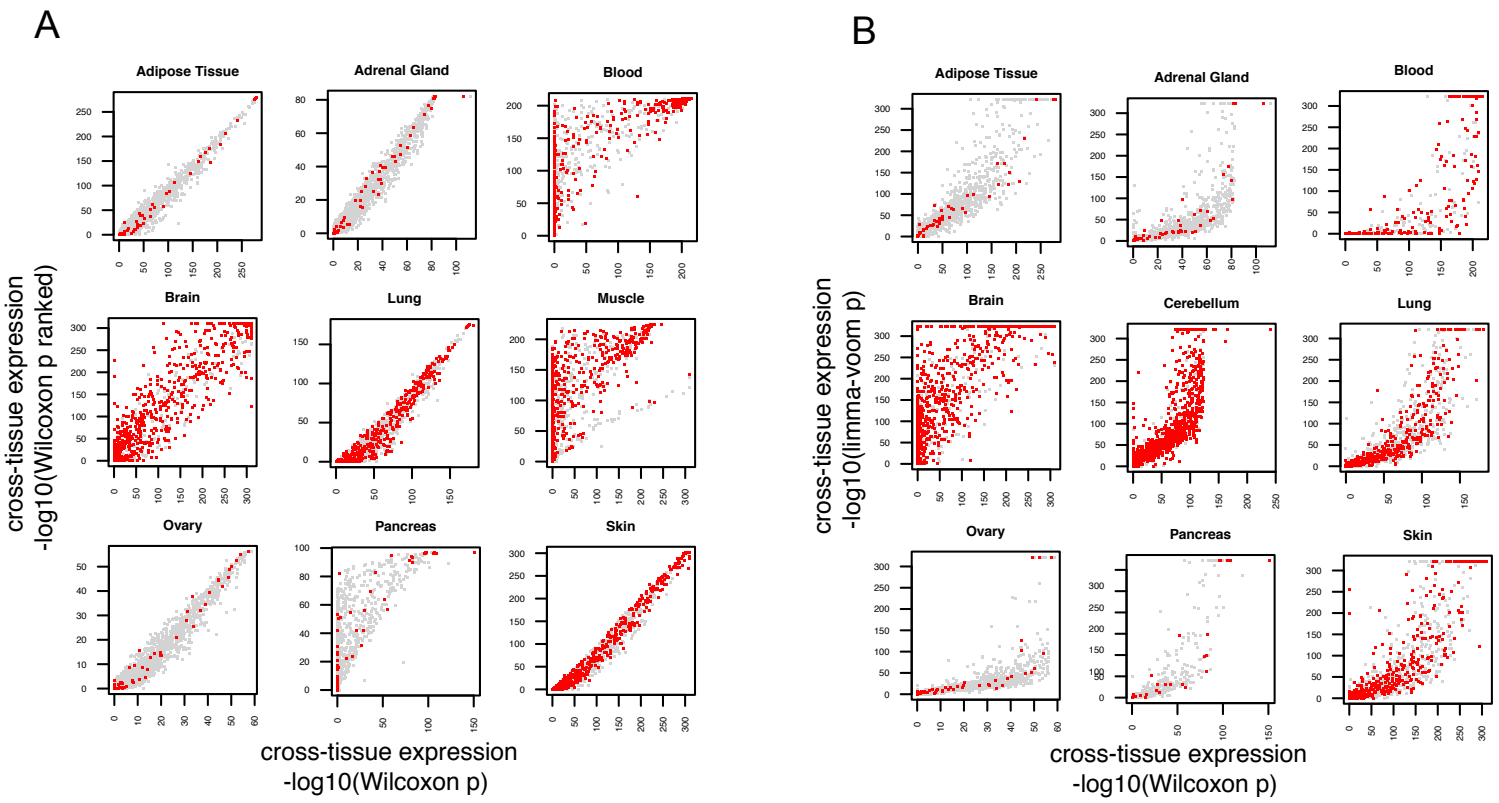
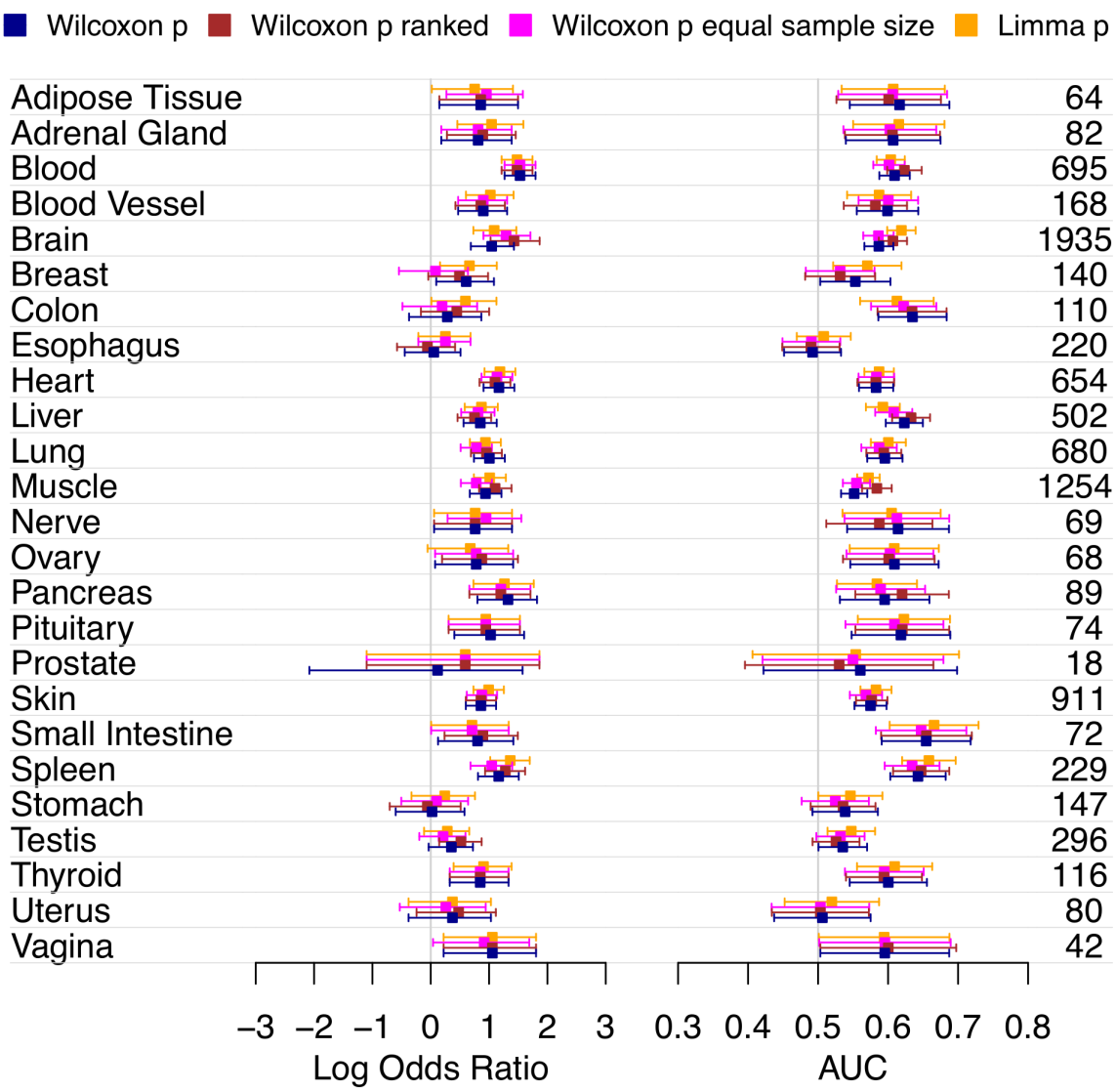
Supplementary Figure S1



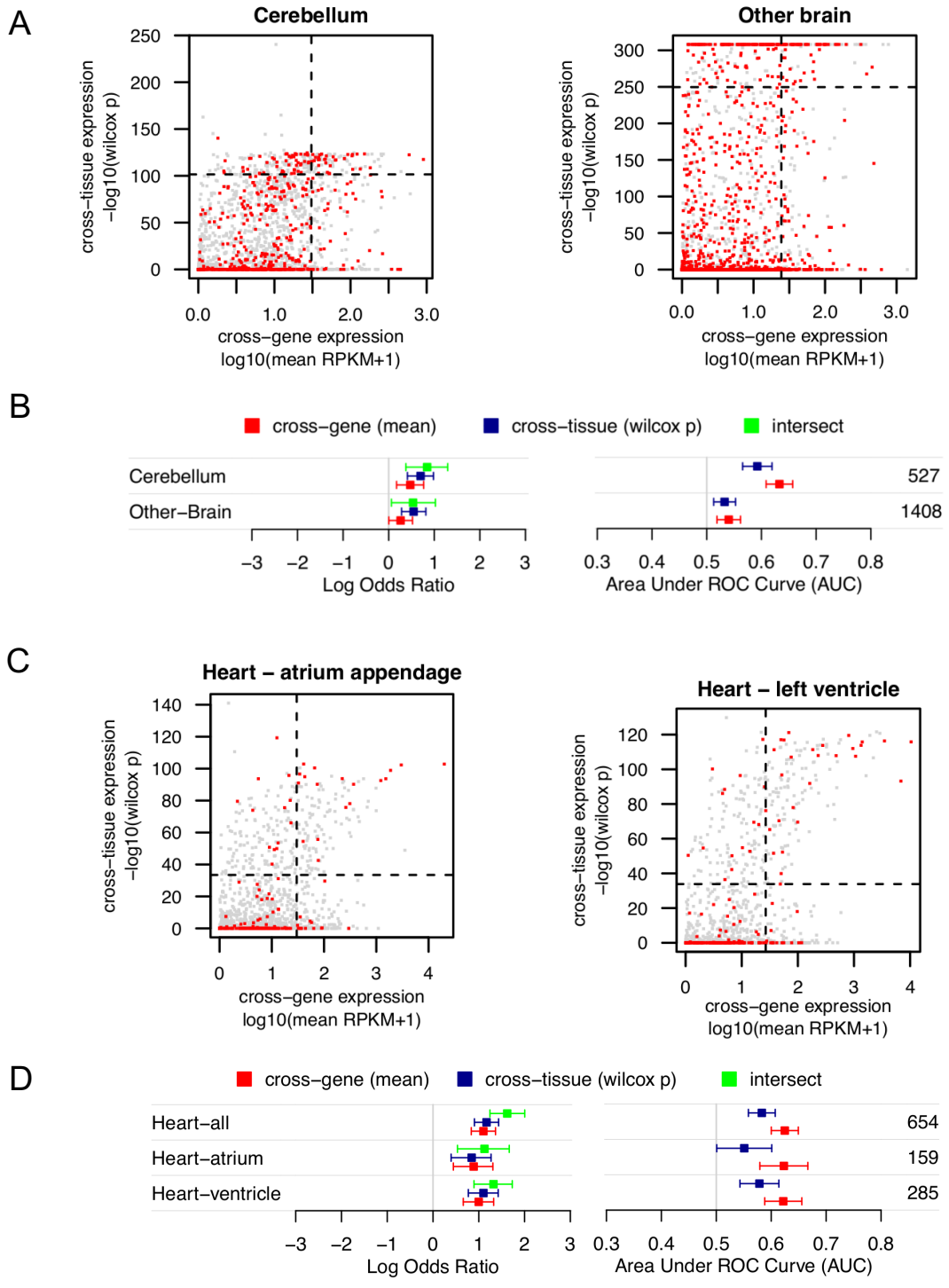
Supplementary Figure S1. Related to Figure 3. Comparison of cross-tissue expression measures. Cross-tissue expression measures are compared for 2,747 disease genes across tissues. P-values computed using a Wilcoxon rank sum test on RPKM expression values are compared with p-values from the same test on ranked expression values (A) and with p-values from limma-voom (B). For the comparison with limma-voom we included cerebellum as a separate brain region. Disease genes associated with phenotypes affecting each tissue are colored red; other disease genes are colored grey. Values on the axes correspond to the –log10(p-value) derived from each method. Plots are shown for a representative subset of tissues.

Supplementary Figure S2



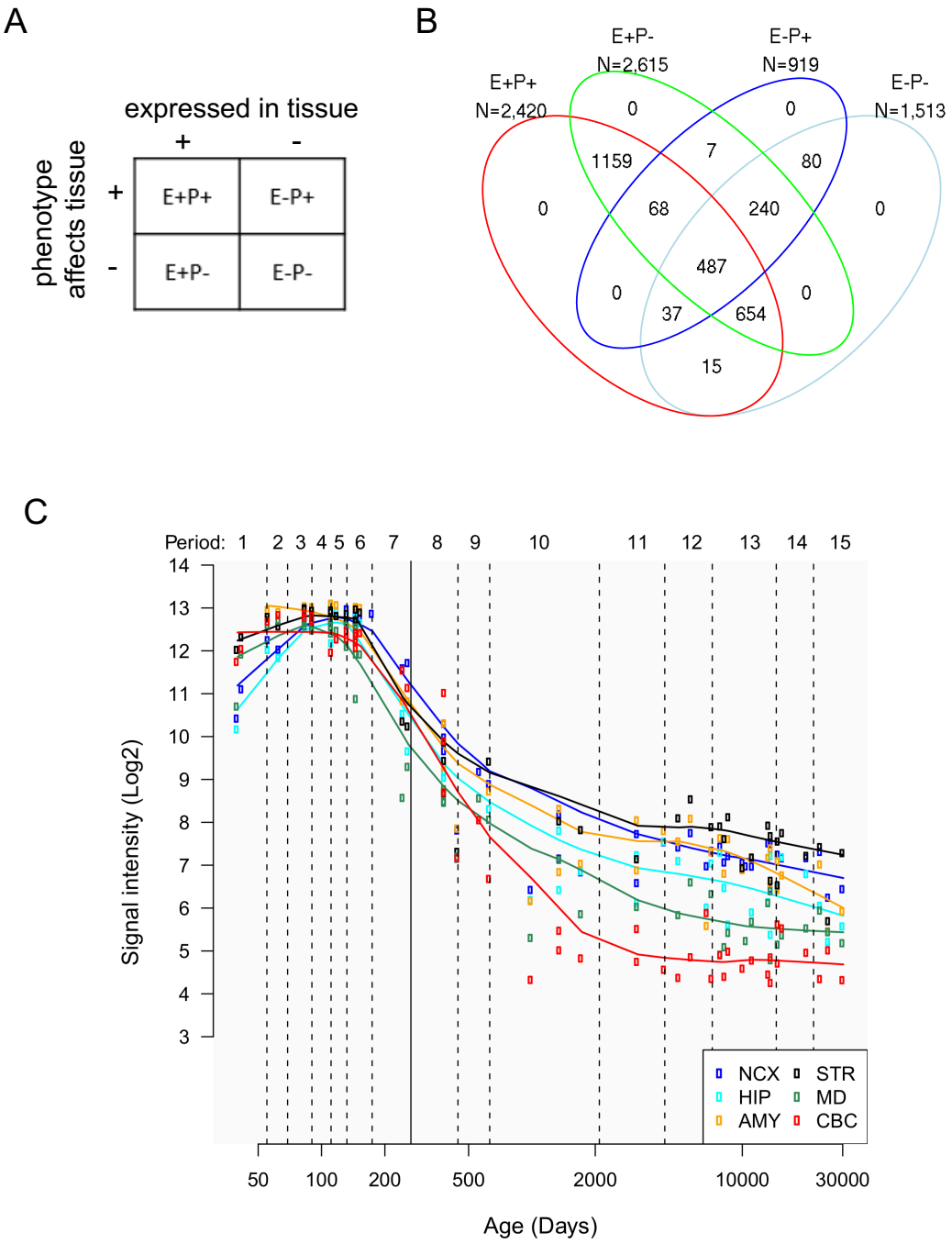
Supplementary Figure S2. Related to Figures 3 and 4. Linking expression and phenotype – comparison of cross-tissue expression measures. Odds ratios representing enrichment of genes associated with phenotypes in each tissue versus those that are not, are computed using the top 10% of genes using three different cross-tissue expression measures described in the main text. Briefly, we compared expression of a gene in GTEx samples from one tissue to all other tissues using a Wilcoxon rank sum test on the original (colored dark blue) and ranked (colored brown) expression values, and using limma-voom (colored orange). Similarly, the relationship between cross-tissue expression levels and phenotypes are quantified via ROC curves (AUCs) in each tissue for the three measures. The number of genes associated with a phenotype in each tissue are shown on the right.

Supplementary Figure S3



Supplementary Figure S3. Linking expression and phenotype in brain and Heart sub-regions. Related to Figures 3 and 4. (A, C) Cross-gene and cross-tissue expression measures computed using cerebellum samples and other brain regions separately (A) or atrial appendage and left ventricle samples separately (C) are plotted for 2,747 disease genes. Genes associated with diseases in each sub-region are colored red; other disease genes are colored grey. Horizontal and vertical dashed lines mark the top 10% value on each axis, dividing the plot into quadrants. **(B, D)** Odds ratios representing enrichment of genes associated with phenotypes in each sub-region versus those that are not, are computed using the top 10% of genes on the cross-gene axis (colored red), cross-tissue axis (colored dark blue) and their intersect (colored green). Similarly, the relationship between expression levels and phenotypes are quantified via ROC curves (AUCs) for cross-gene (colored red) and cross-tissue (colored dark blue) measures. The number of genes associated with a phenotype in each tissue sub-region are listed on the right.

Supplementary Figure S4



Supplementary Figure S4. Related to Figure 1. Categorizing disease genes by expression and phenotype. (**A)** Illustrating the division of 2,747 disease genes into four groups for each tissue based on mean expression > 1 RPKM (+/-) and associated phenotype (+/-). (**B)** Venn diagram summarizing the intersection between four gene groups across all tissues. **(C)** Expression of the *DCX* gene is shown beginning at early development, in 6 brain regions (cerebellar cortex (CBC), mediodorsal nucleus of the thalamus (MD), striatum (STR), amygdala (AMY), hippocampus (HIP) and neocortex (NCX)). The *DCX* gene is implicated in X-linked lissencephaly-1 (OMIM ID: 300067). This figure was reproduced from the Human Brain Transcriptome (HBT) project http://hbatlas.org.