

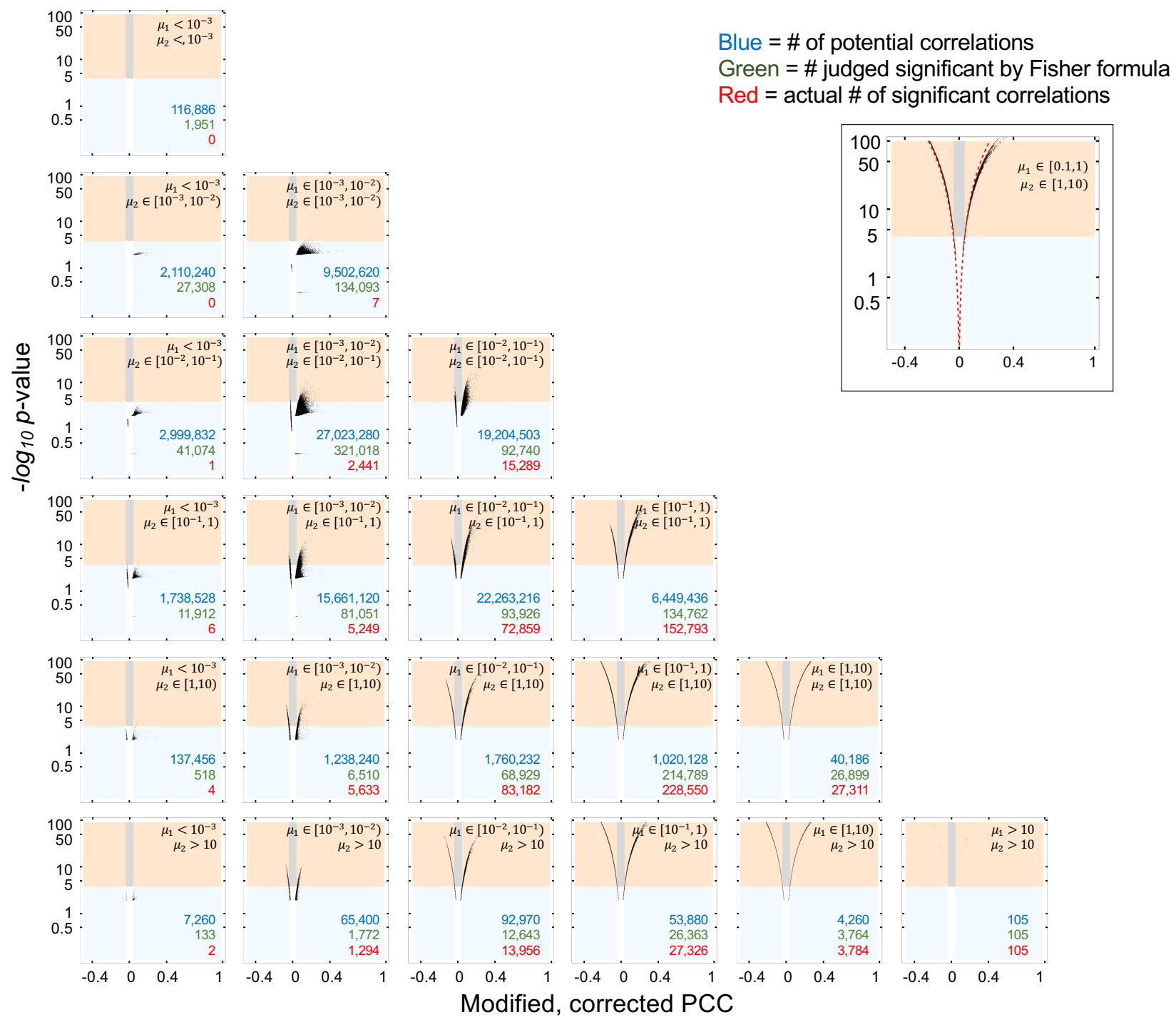


Figure S2. Significance of modified corrected Pearson correlation coefficients, (PCC'), as calculated by BigSur versus the Fisher formula, binned by gene expression. scRNAseq data were as described in Figure 3. Data points representing pairs of genes were divided into 21 bins based on the mean expression levels of each gene, and the results for each bin were plotted as in Fig. S1. The inset compares the PCC' - p -value relationship determined by BigSur (for genes with relatively high expression levels) with that predicted by the Fisher formula (dashed red line), showing that, for highly expressed genes, the two methods agree well.