

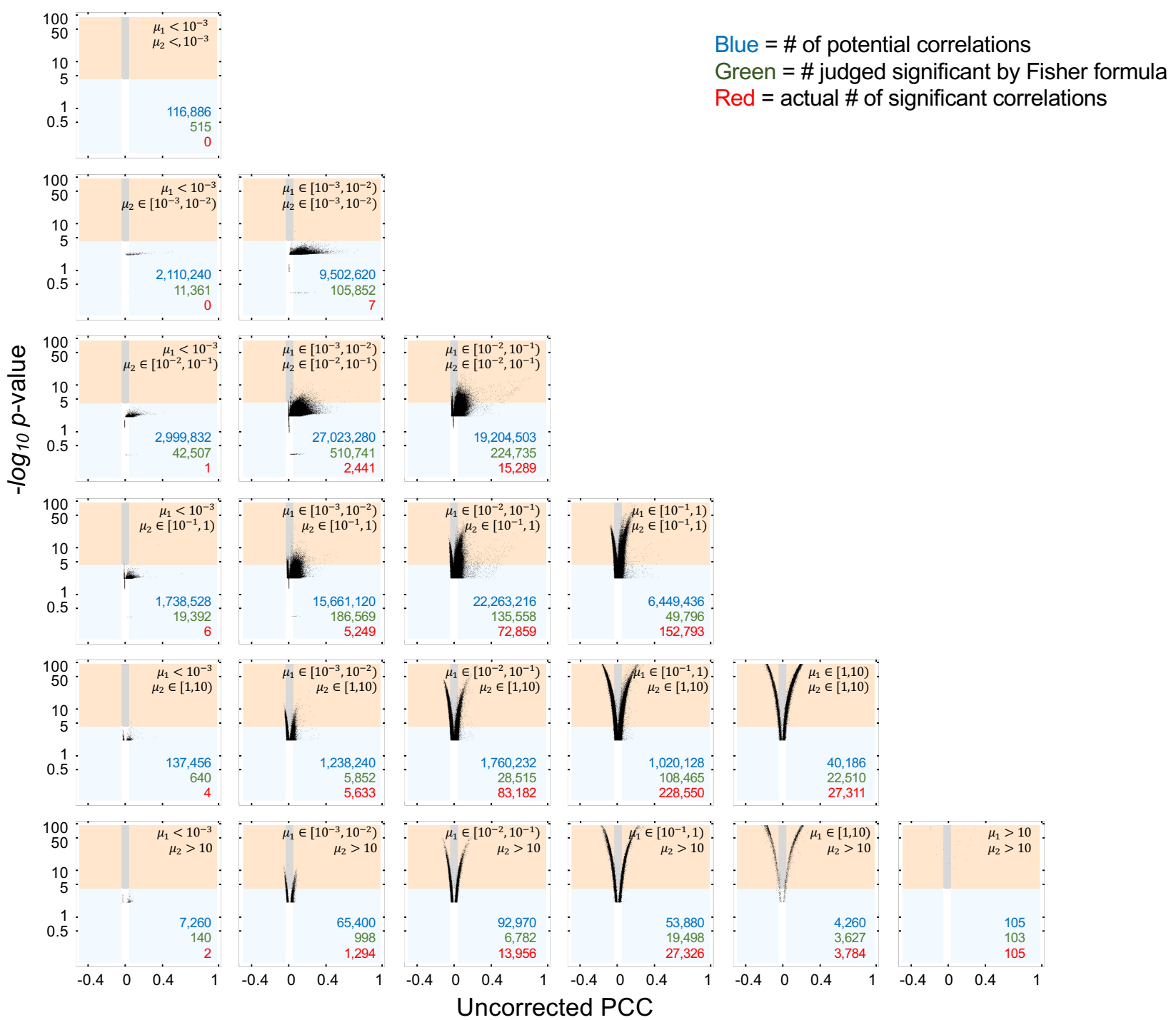


Figure S1. Significance of uncorrected Pearson correlation coefficients (PCC), as calculated by BigSur versus the Fisher formula, binned by gene expression. scRNAseq data were as described in Figure 3. Data points representing pairs of genes were divided into 21 bins based on the mean expression levels of each gene, and the results for each bin were plotted as described in Fig. 3C. The abscissa shows PCC (calculated from default-normalized data) while the ordinate gives the negative $\log_{10}$ of p -values determined by BigSur, i.e., larger values mean greater statistical significance. Orange and gray shading indicate gene pairs judged significant by BigSur ($\text{FDR} < 0.02$). Blue and orange show gene pairs that would have been judged statistically significant by applying the Fisher formula to the PCC, using the same p -value threshold as used by BigSur. The blue region contains gene pairs judged significant by the Fisher formula only, while the unshaded region shows gene pairs not significant by either method. Numbers in the lower right corner of each panel are the total numbers of possible correlations (blue), statistically significant correlations according to the Fisher formula (green), and statistically significant correlations according to BigSur (red).