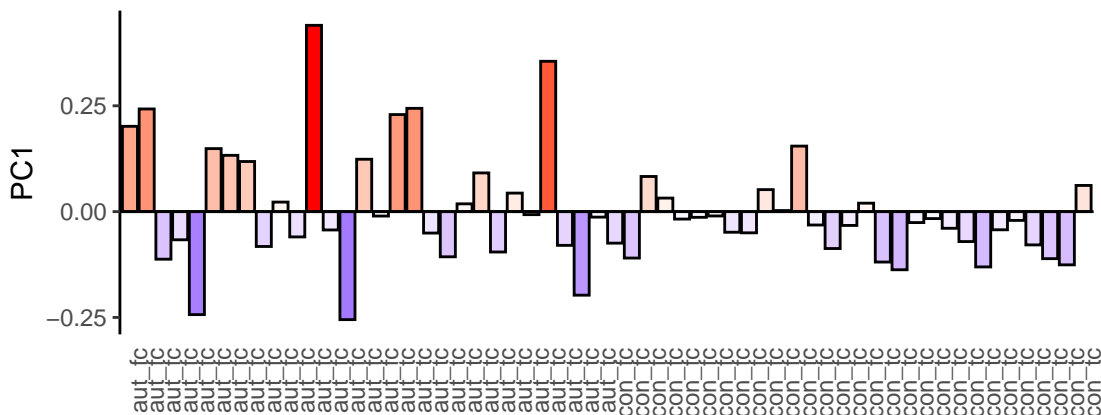
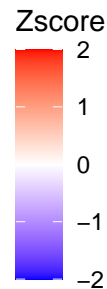
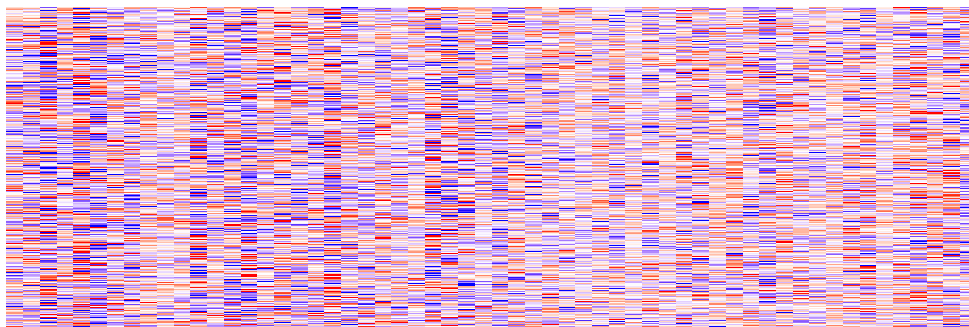
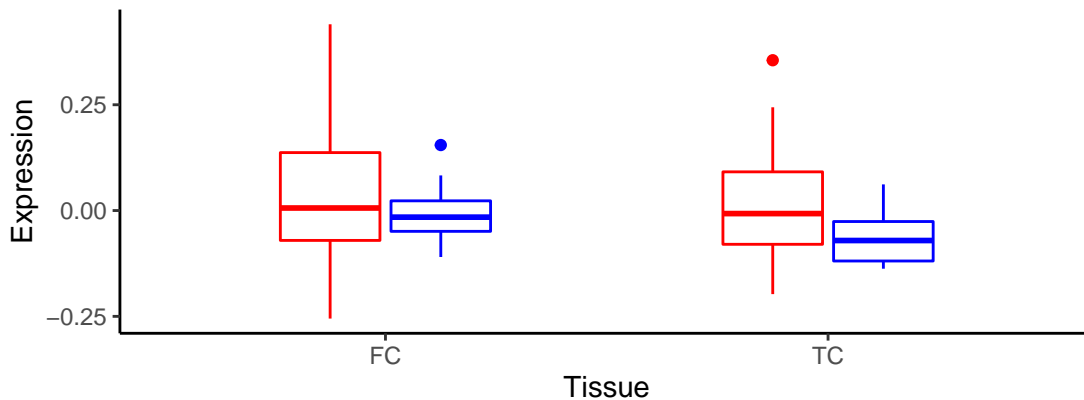


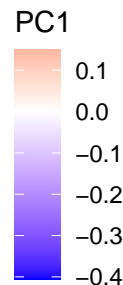
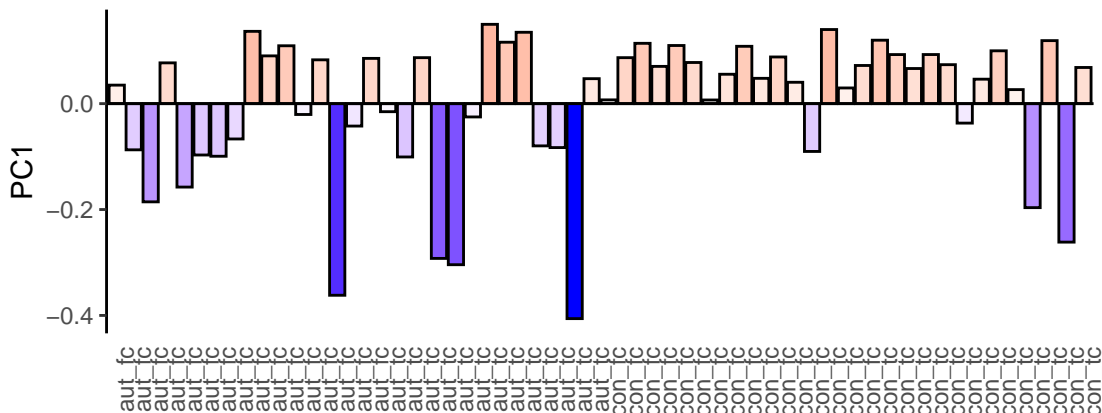
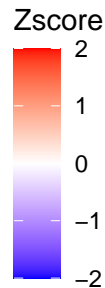
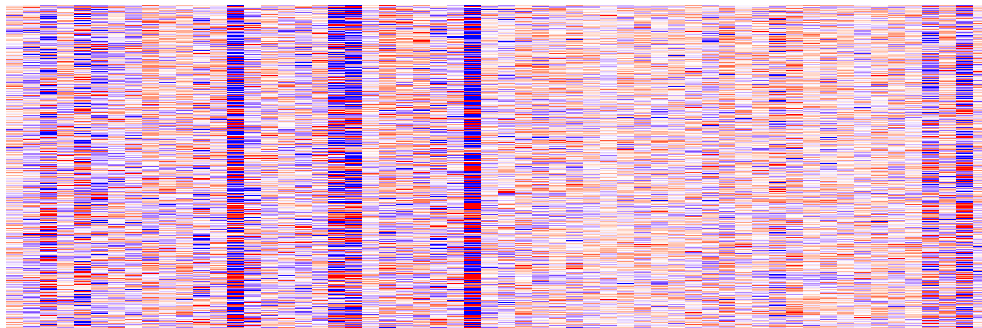
combined\_000



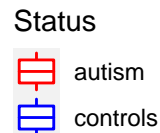
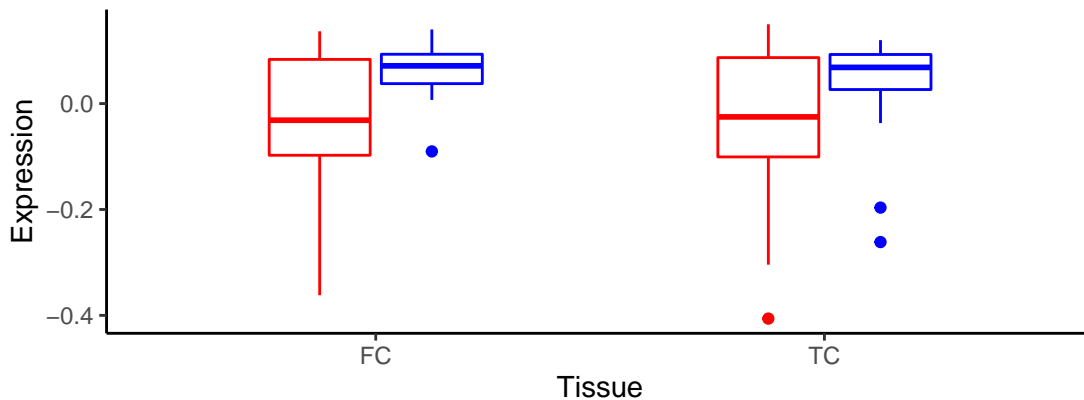
p: Status=0.05, Tissue=0.39, Status\*Tissue=0.42



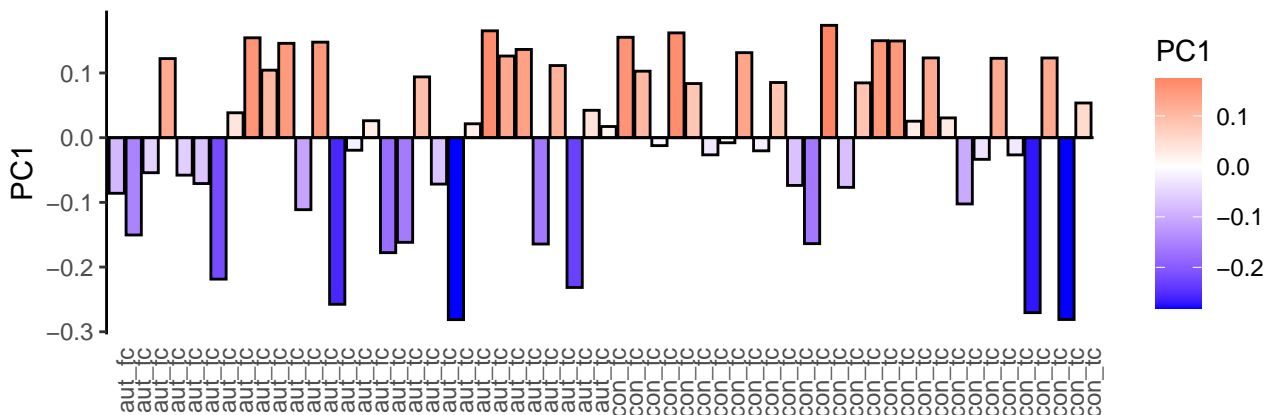
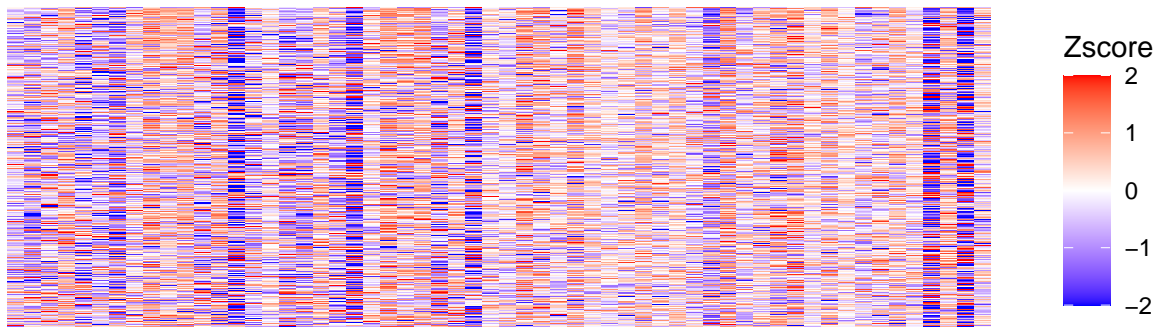
combined\_001



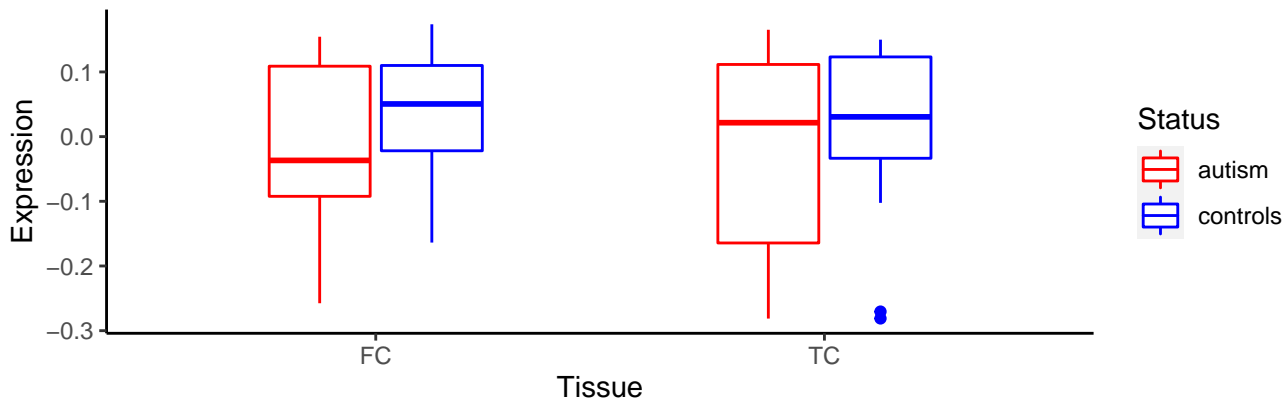
p: Status=0.01, Tissue=0.34, Status\*Tissue=0.9



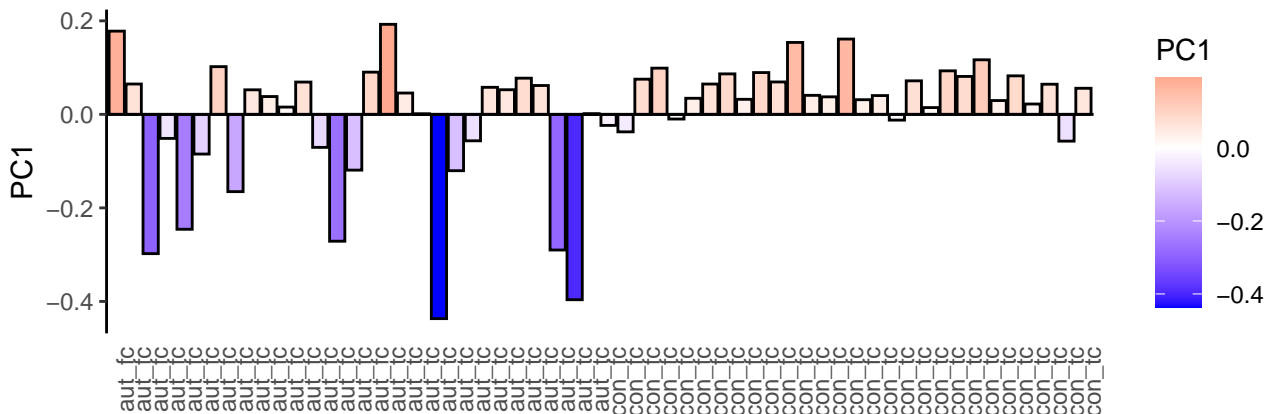
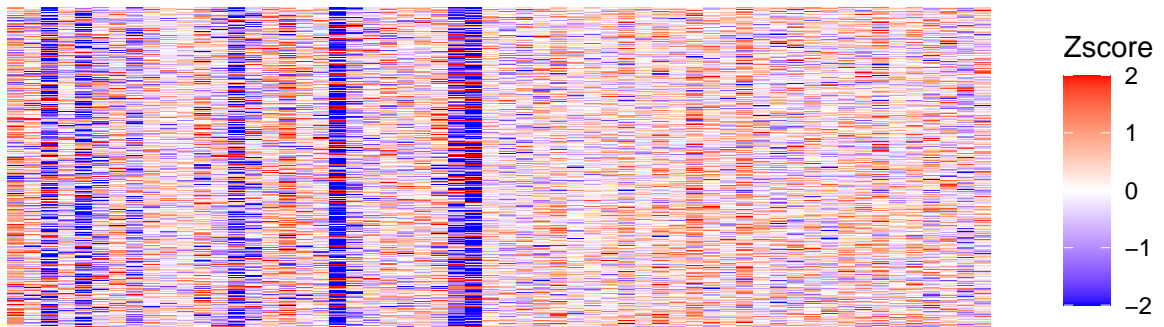
combined\_002



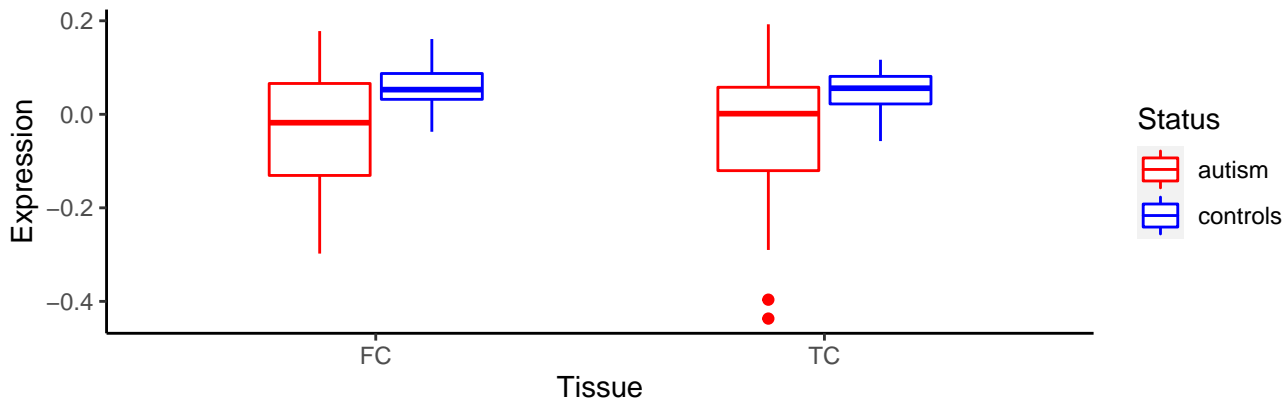
p: Status=0.18, Tissue=0.52, Status\*Tissue=0.76



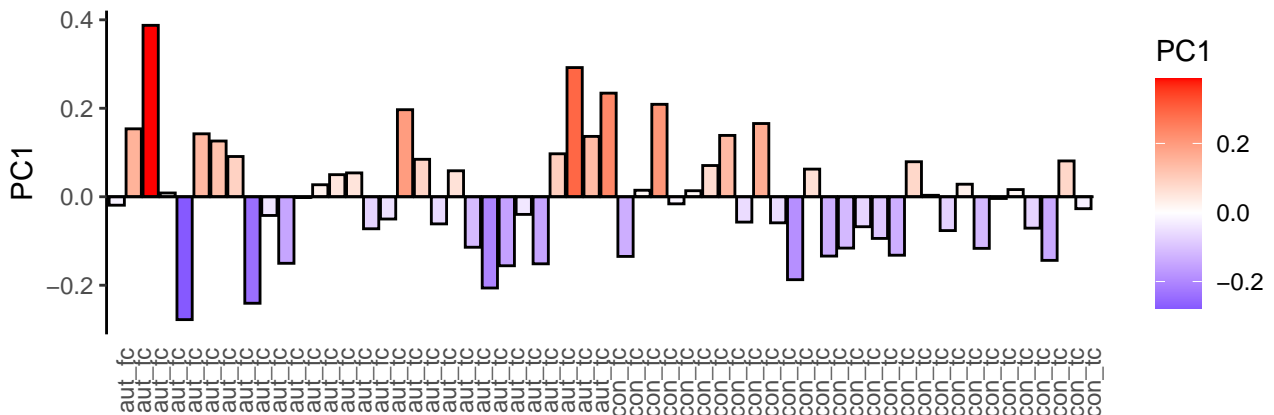
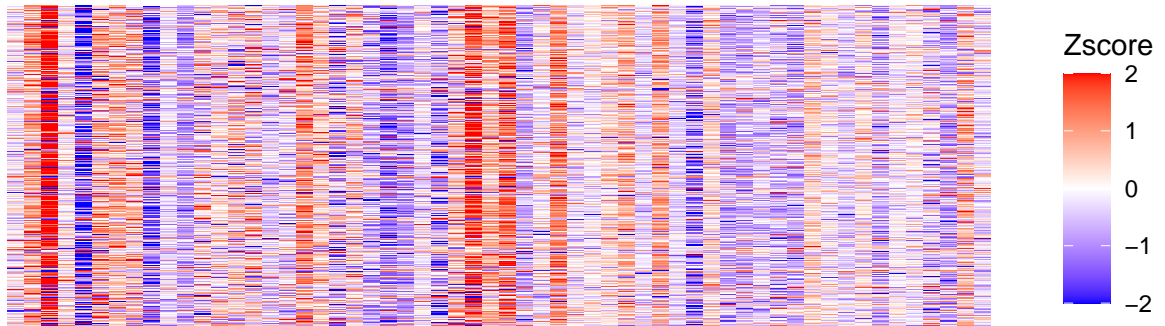
combined\_003



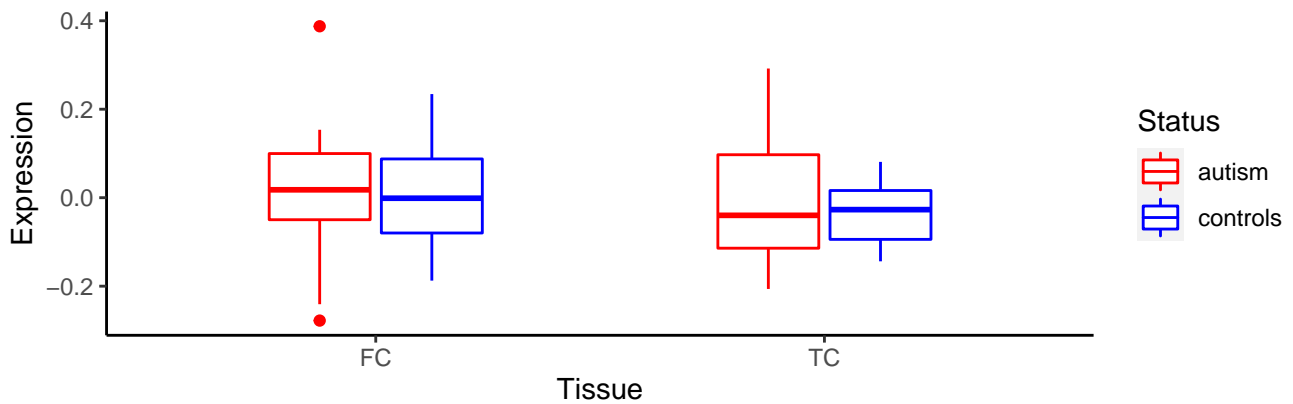
p: Status=0.0023, Tissue=0.66, Status\*Tissue=0.9



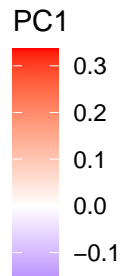
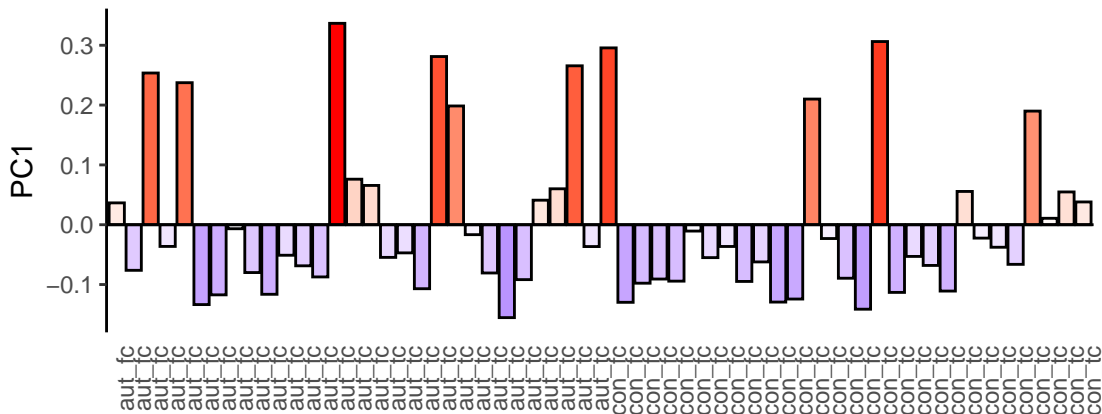
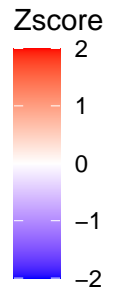
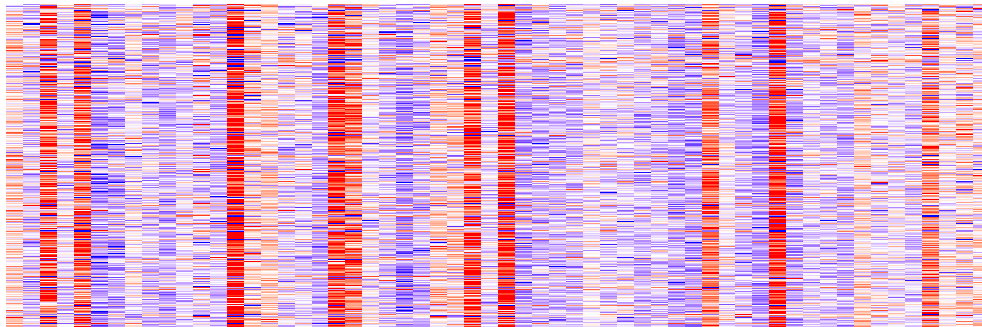
combined\_004



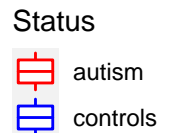
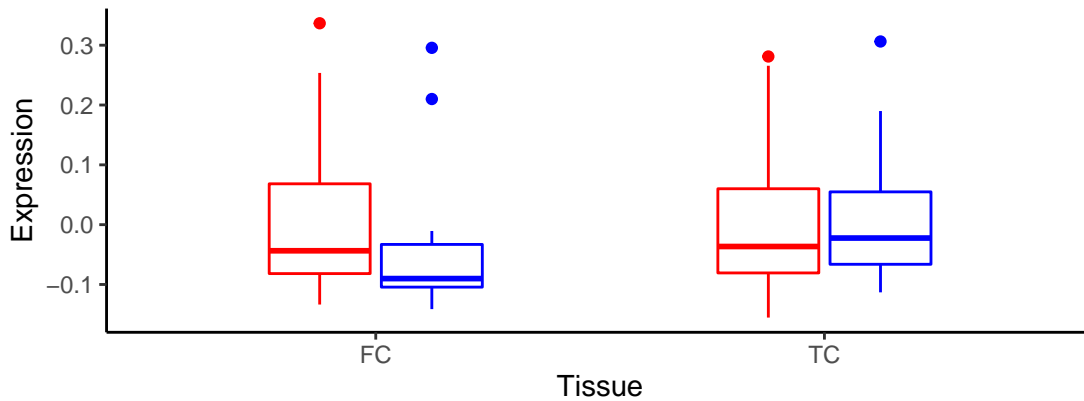
p: Status=0.53, Tissue=0.47, Status\*Tissue=0.62



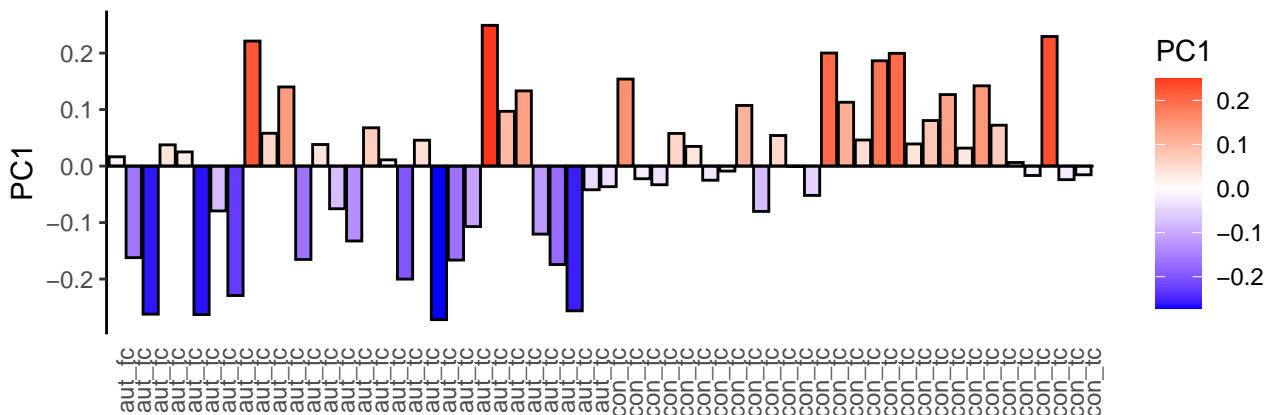
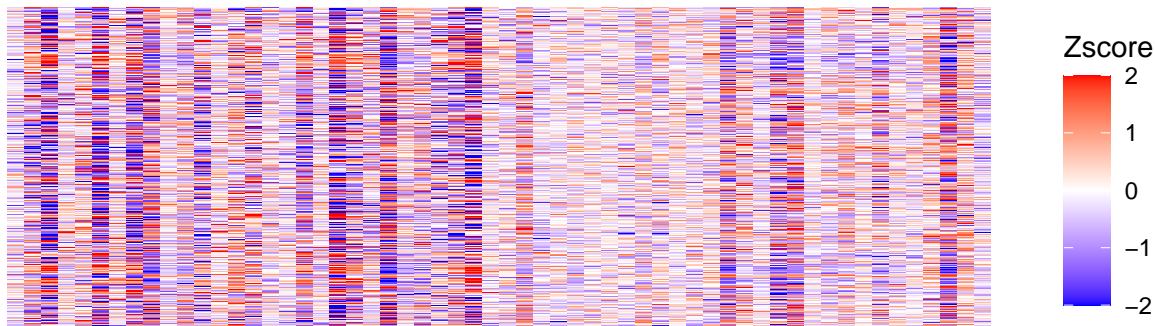
combined\_005



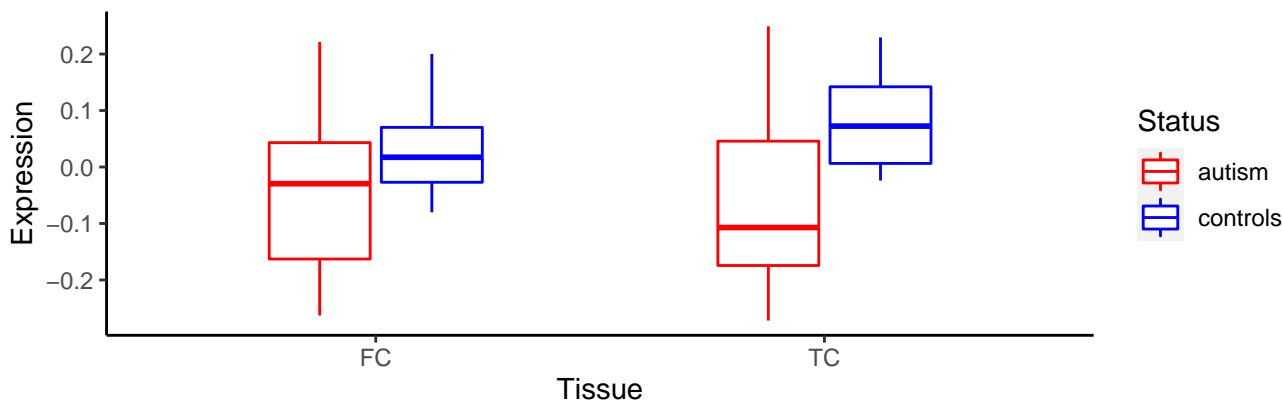
p: Status=0.34, Tissue=0.38, Status\*Tissue=0.47



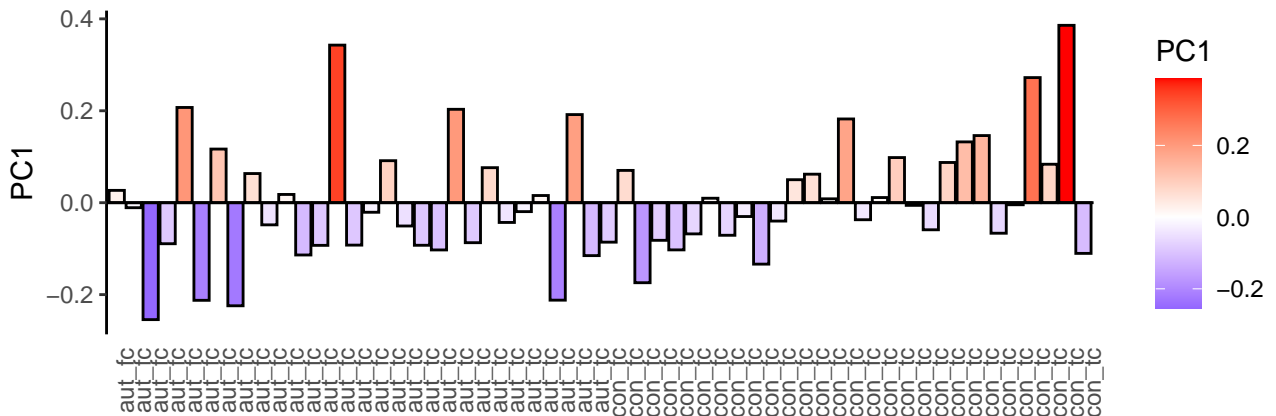
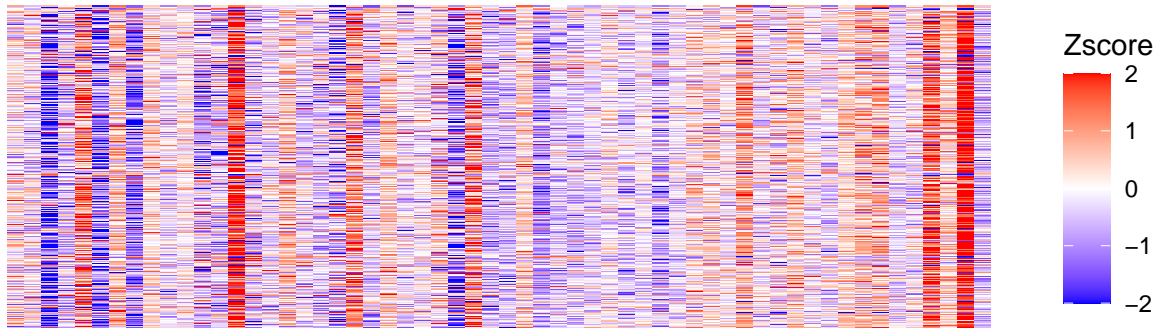
combined\_006



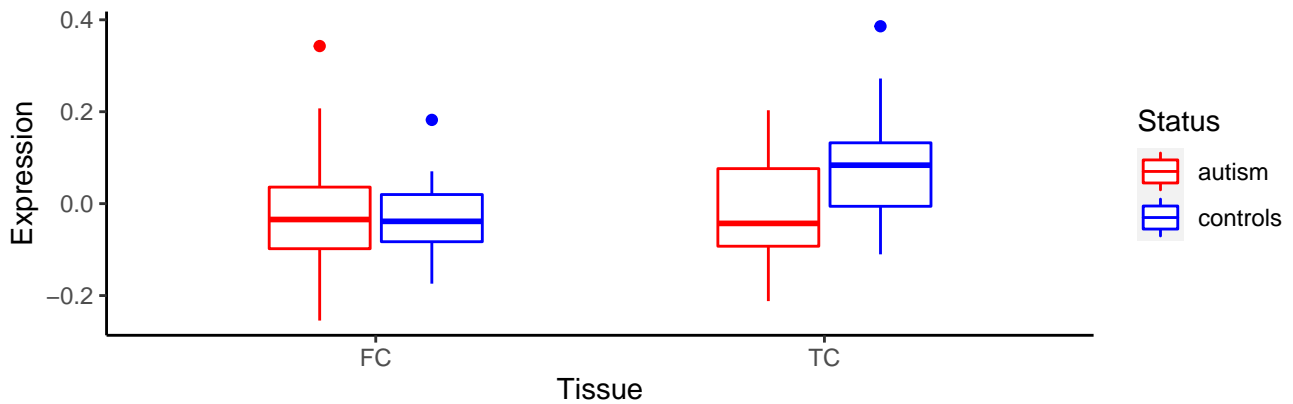
p: Status=0.0014, Tissue=0.58, Status\*Tissue=0.33



combined\_007

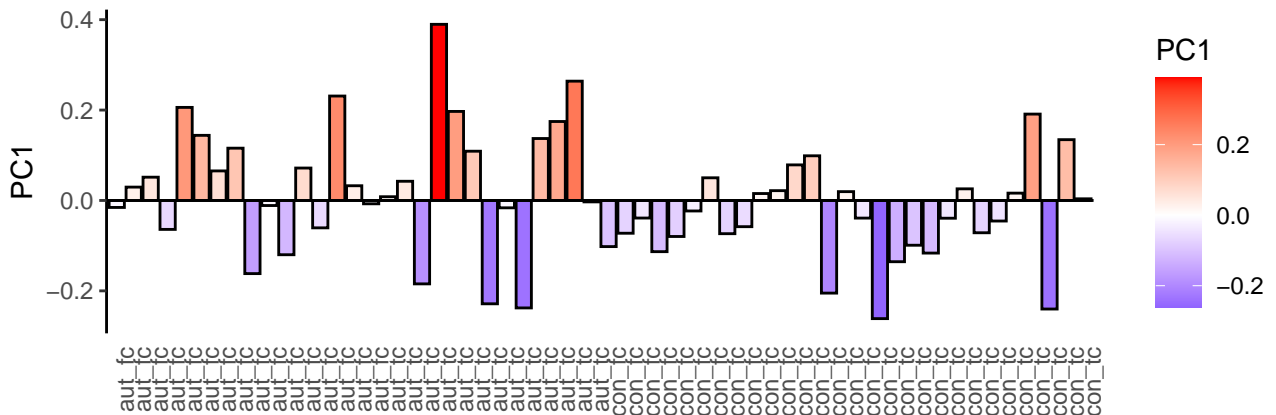
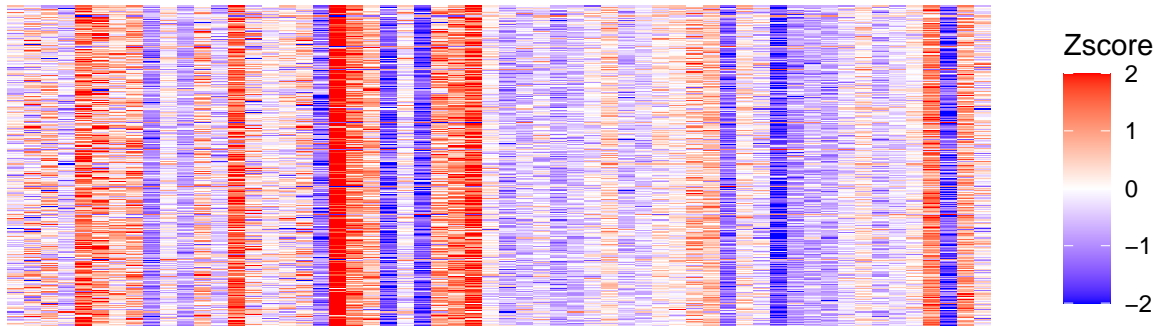


p: Status=0.29, Tissue=0.1, Status\*Tissue=0.2

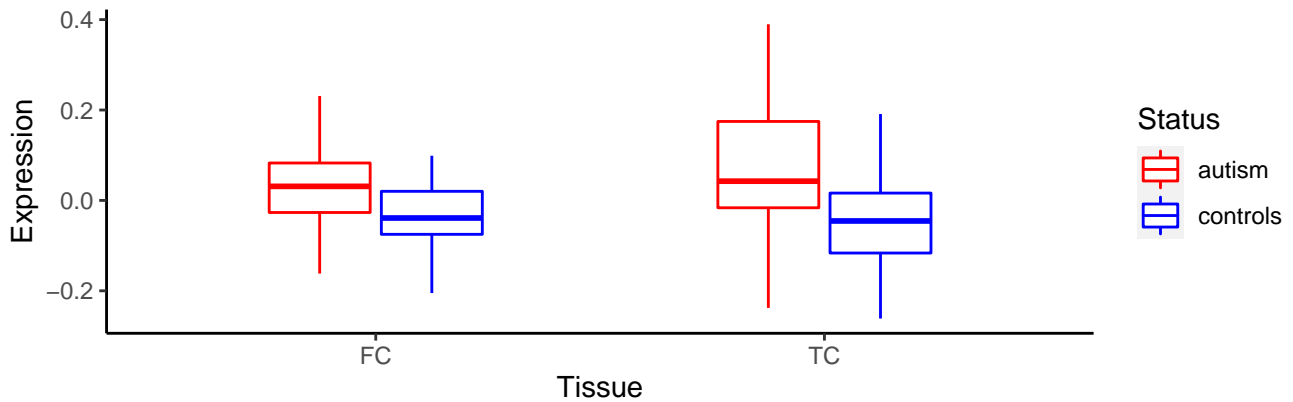




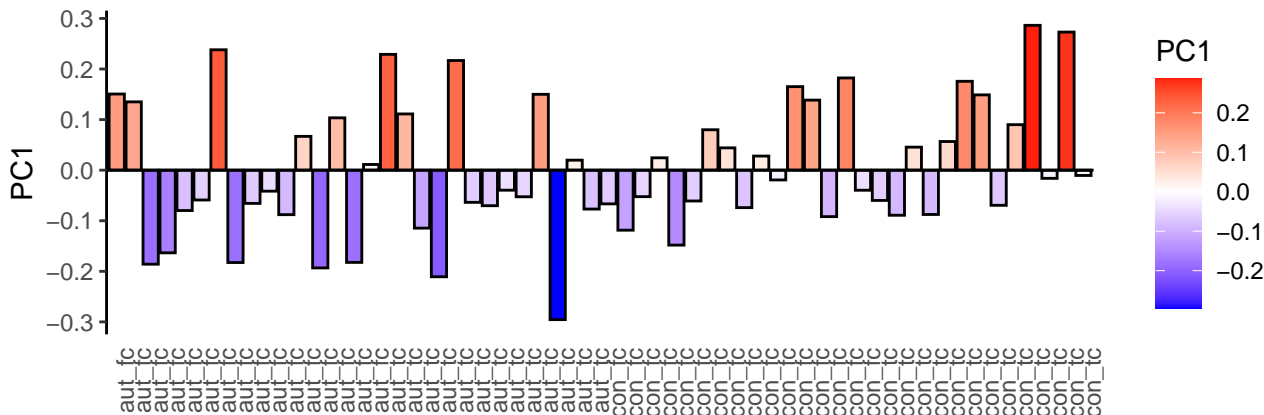
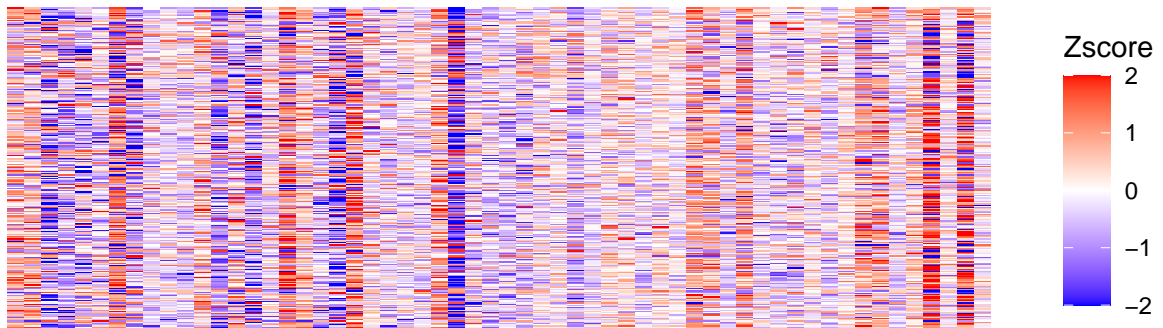
combined\_008



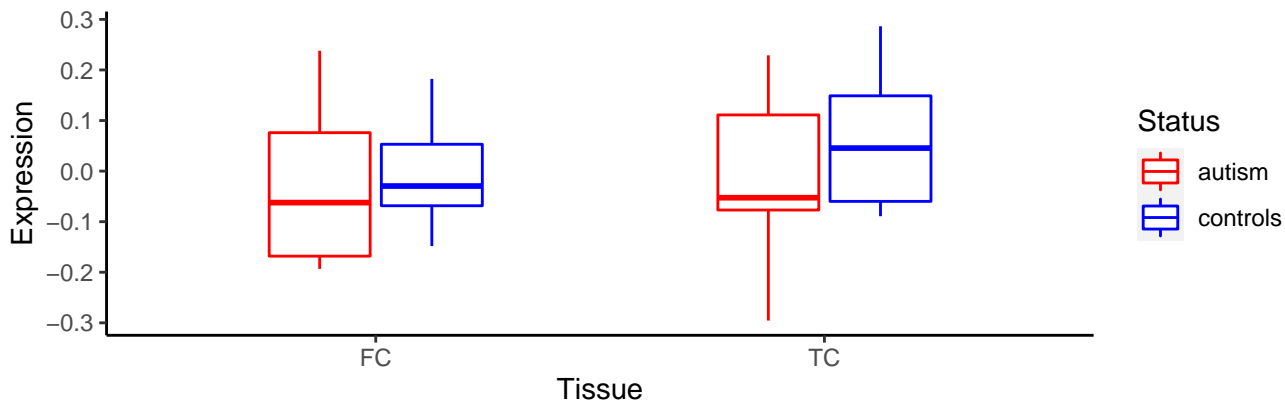
p: Status=0.021, Tissue=0.98, Status\*Tissue=0.61



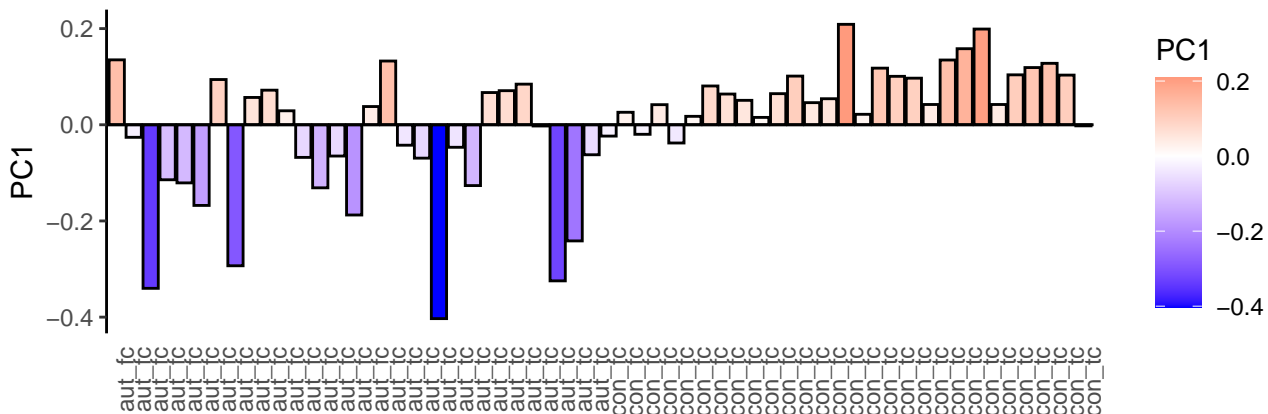
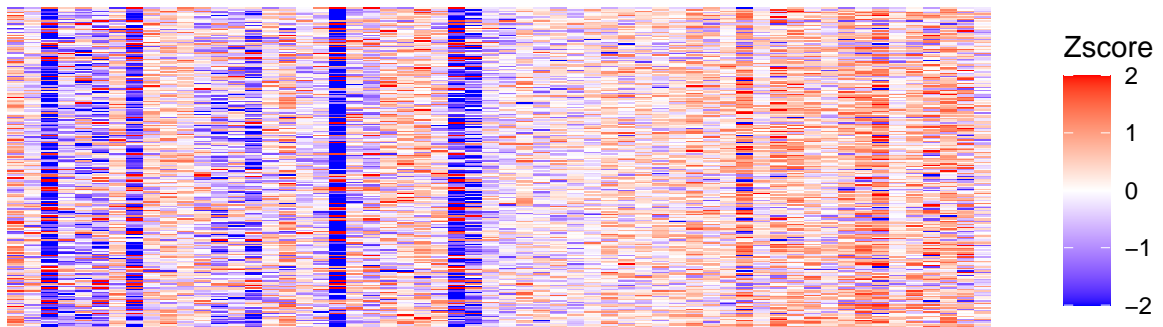
combined\_009



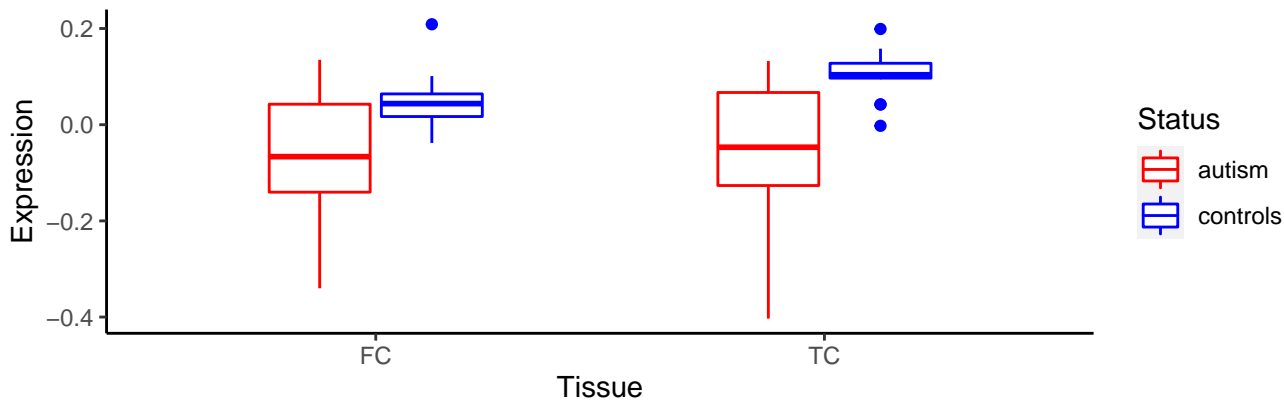
p: Status=0.15, Tissue=0.28, Status\*Tissue=0.57



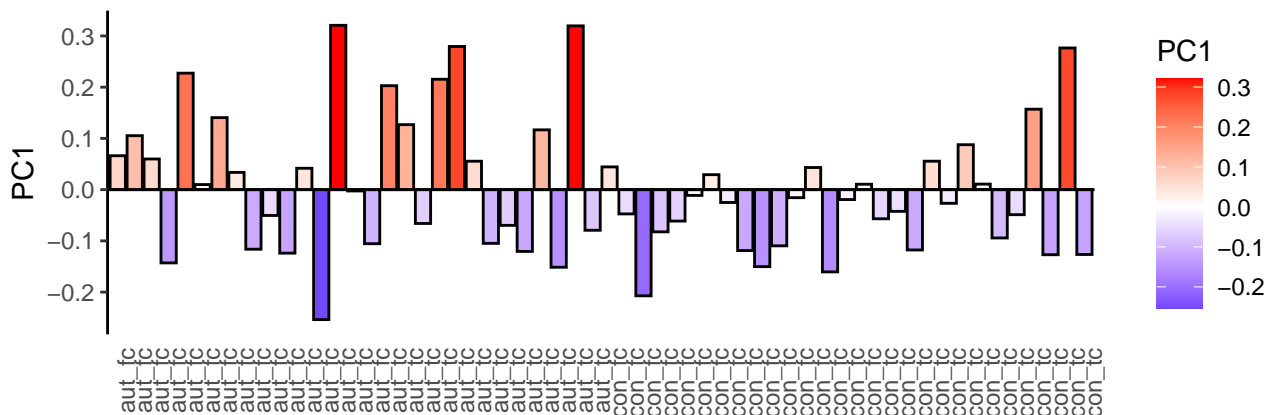
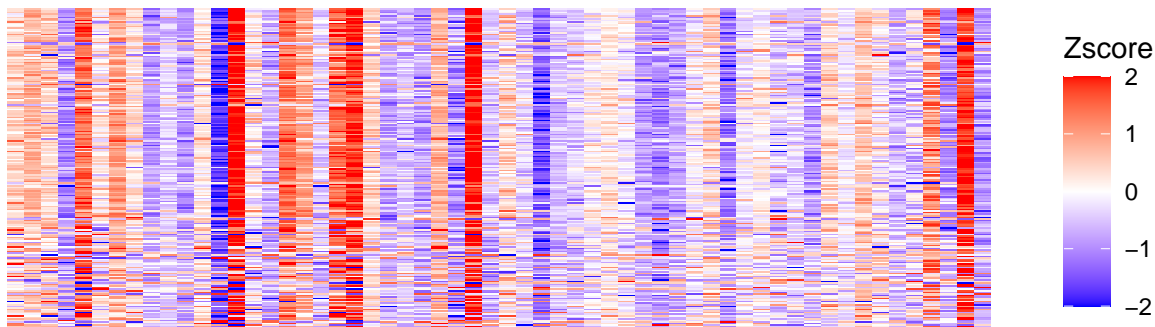
combined\_010



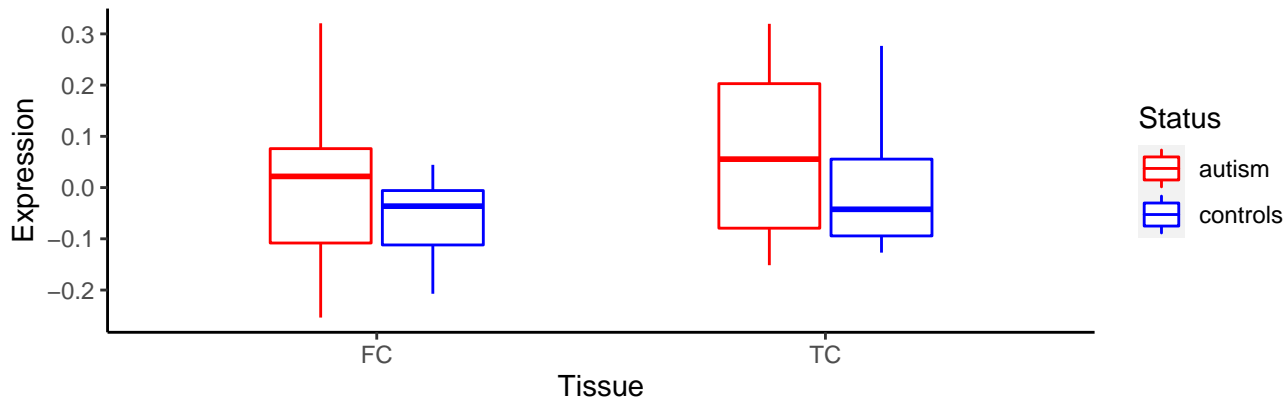
p: Status=1.3e-05, Tissue=0.38, Status\*Tissue=0.28



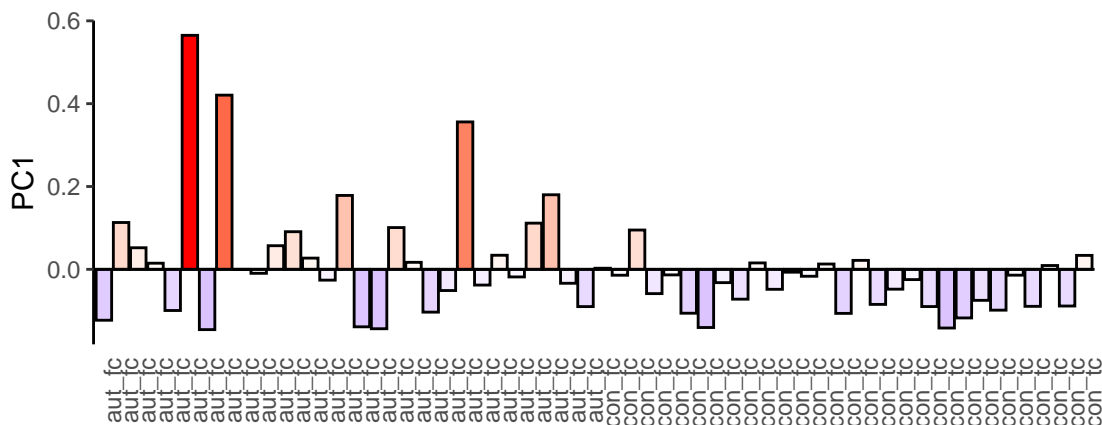
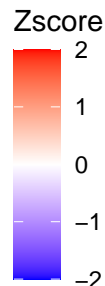
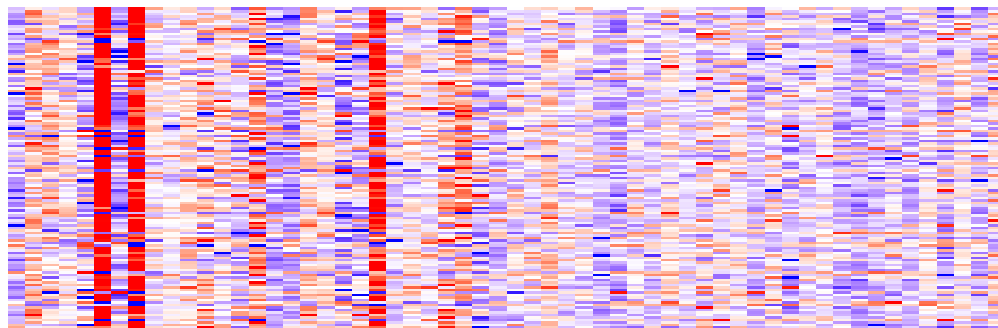
combined\_011



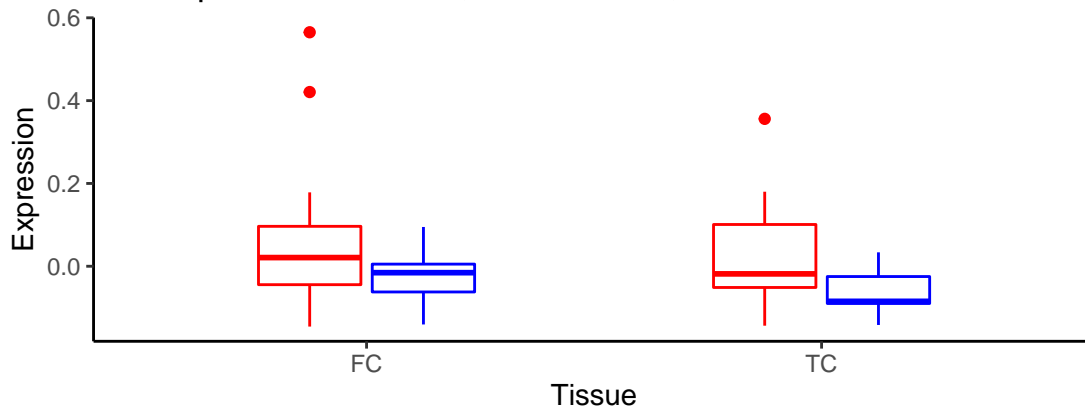
p: Status=0.061, Tissue=0.17, Status\*Tissue=0.9



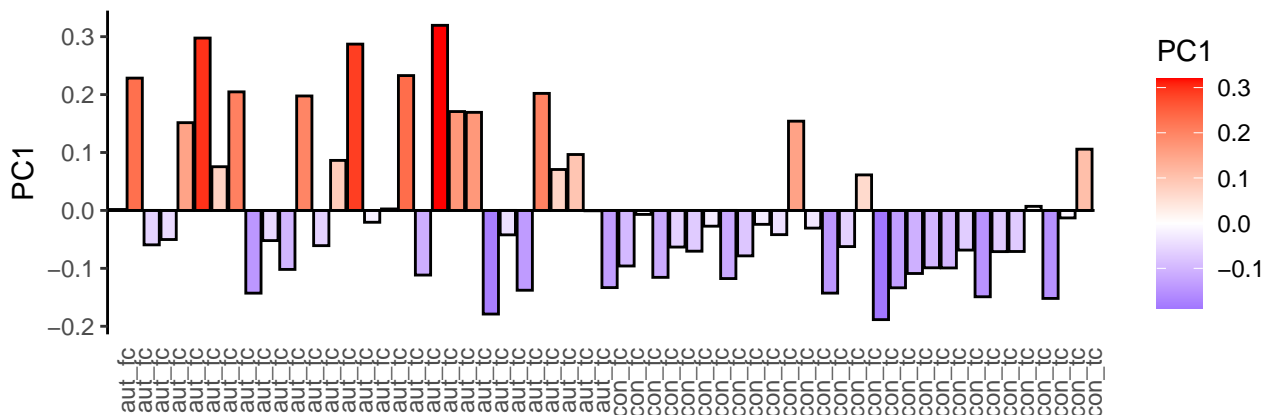
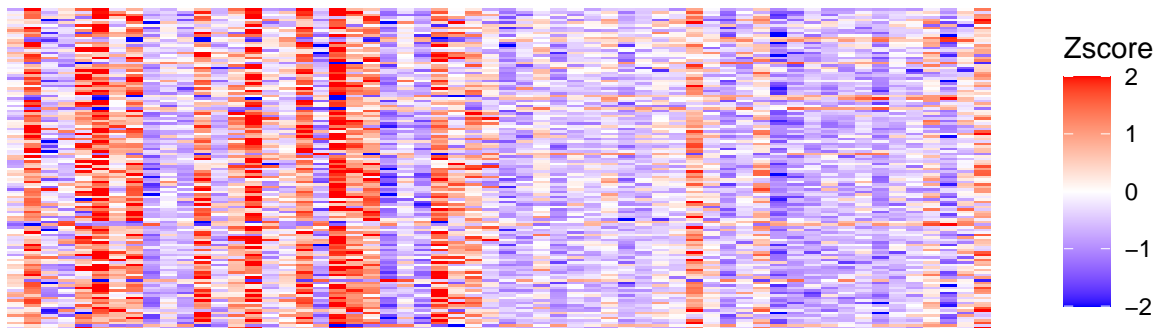
combined\_012



p: Status=0.0088, Tissue=0.29, Status\*Tissue=0.98



combined\_013



p: Status=0.00014, Tissue=0.58, Status\*Tissue=0.68

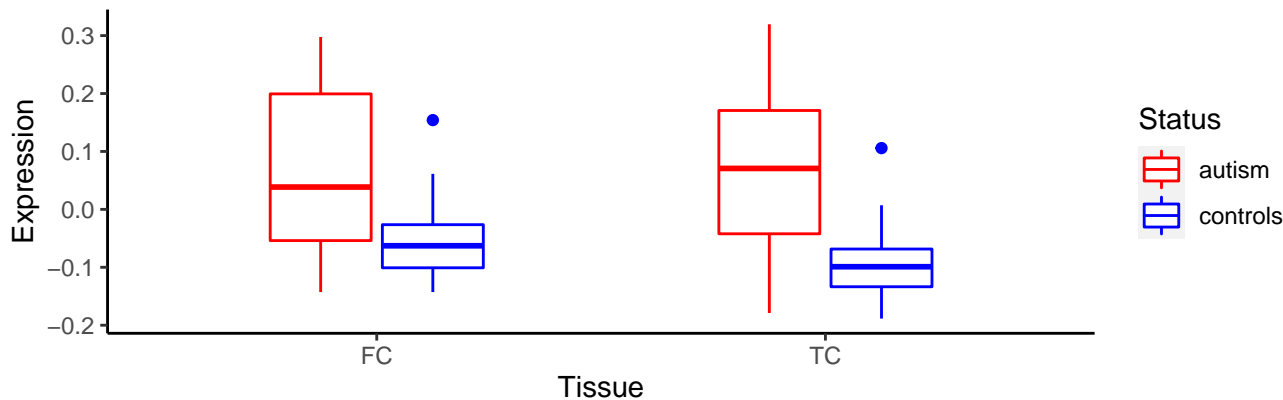
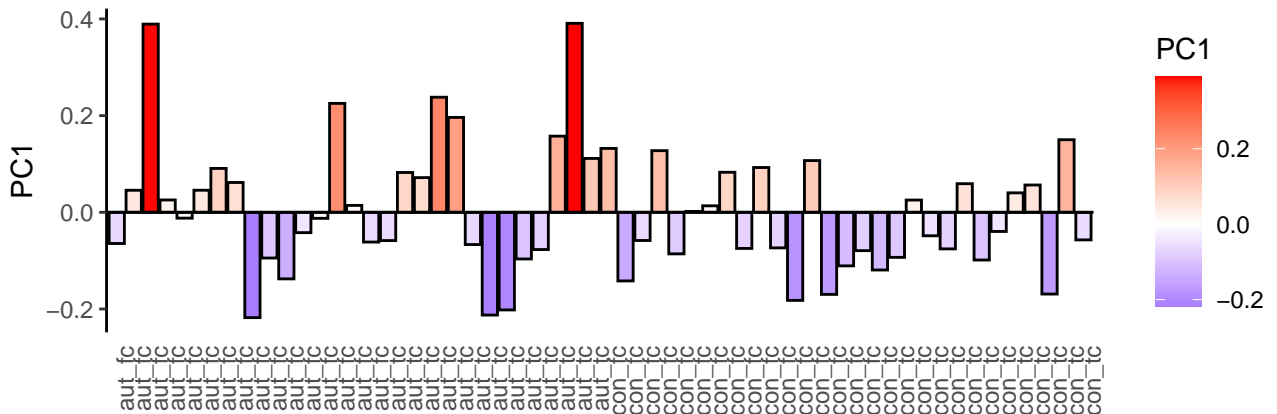
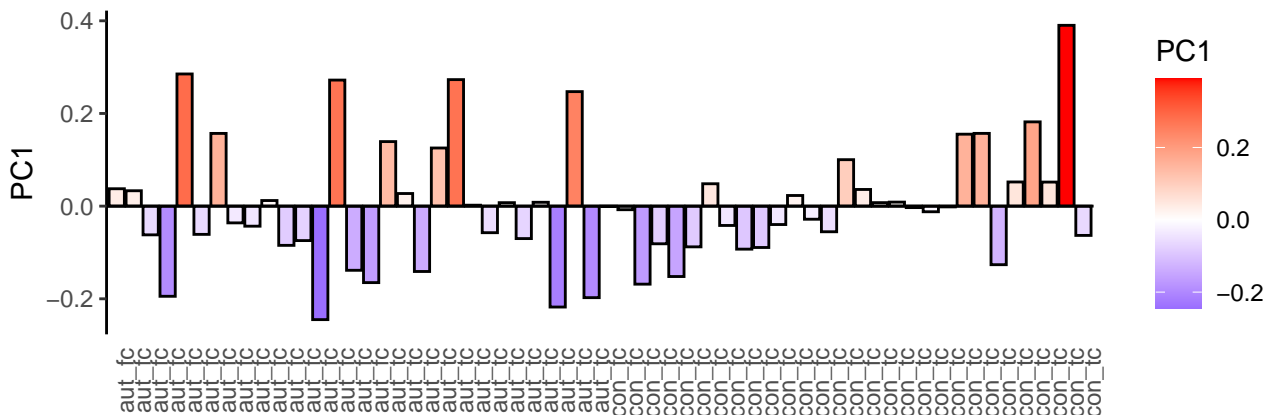
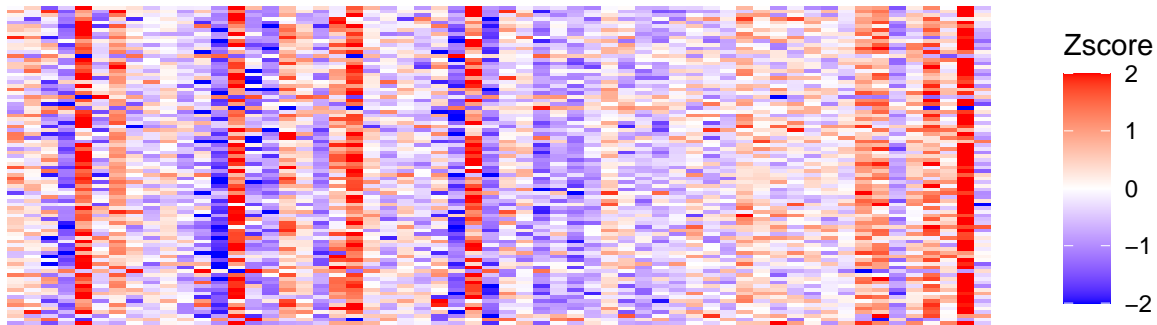


Figure 1. The effect of the number of iterations on the accuracy of the proposed algorithm. The accuracy of the proposed algorithm increases with the number of iterations. The accuracy of the proposed algorithm is 0.95 after 100 iterations.

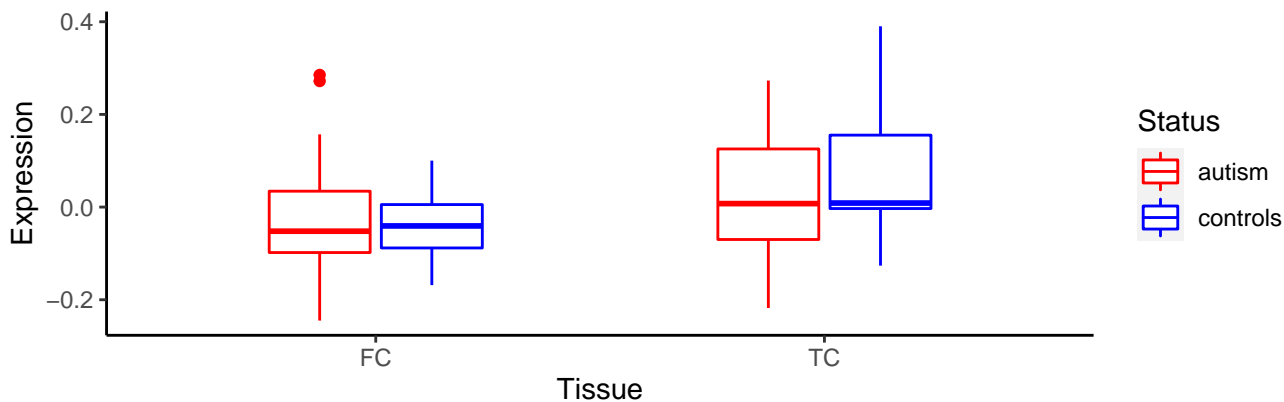


A box plot comparing the expression levels of the top 100 genes in two tissues, FC (Fibrous Connective) and TC (Tendons), for two groups: autism (red) and controls (blue). The y-axis represents 'Expression' levels, ranging from -0.2 to 0.4. The x-axis is labeled 'Tissue' with categories FC and TC. For each tissue, there are two box plots: a red one for autism and a blue one for controls. In the FC tissue, the autism group shows a median expression near 0.0, while the controls group shows a median expression slightly below -0.1. In the TC tissue, the autism group shows a median expression slightly above 0.0, while the controls group shows a median expression slightly below -0.1. Outliers are present for the autism group in the FC tissue, with two points at approximately 0.22 and 0.38. The legend on the right indicates 'Status' with 'autism' in red and 'controls' in blue.

combined\_015

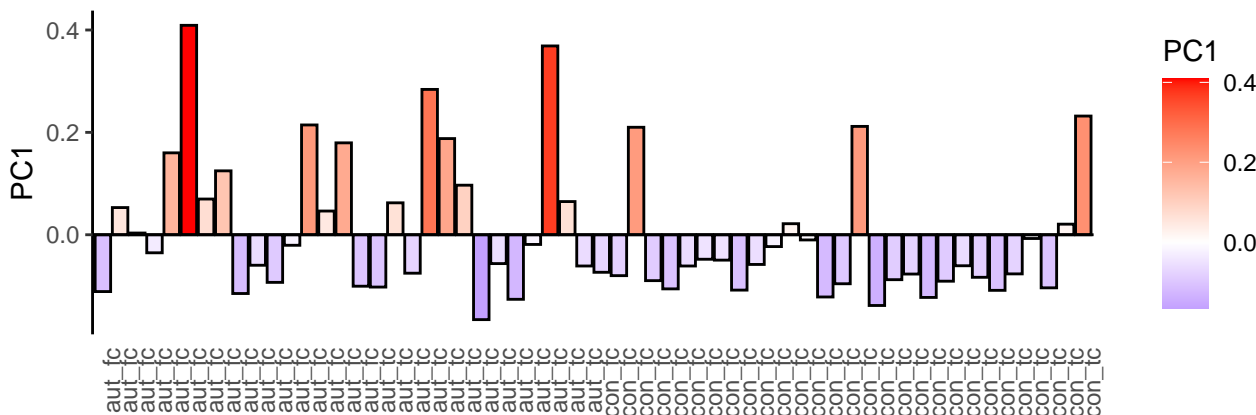
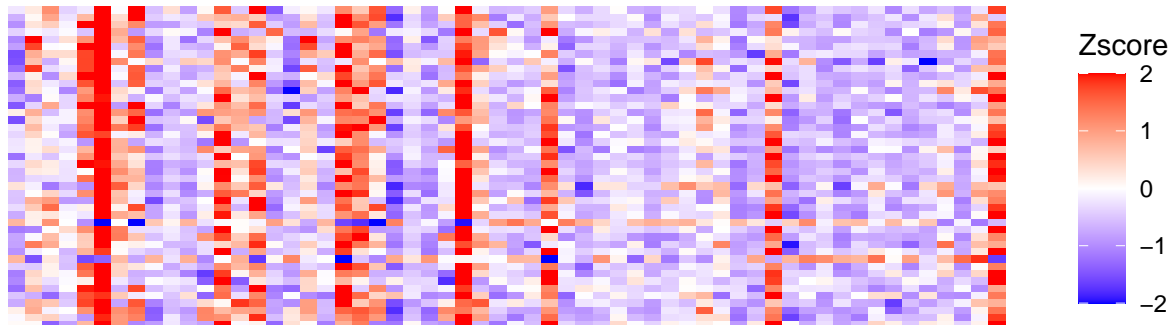


p: Status=0.75, Tissue=0.061, Status\*Tissue=0.31





combined\_016



p: Status=0.018, Tissue=0.62, Status\*Tissue=0.84

