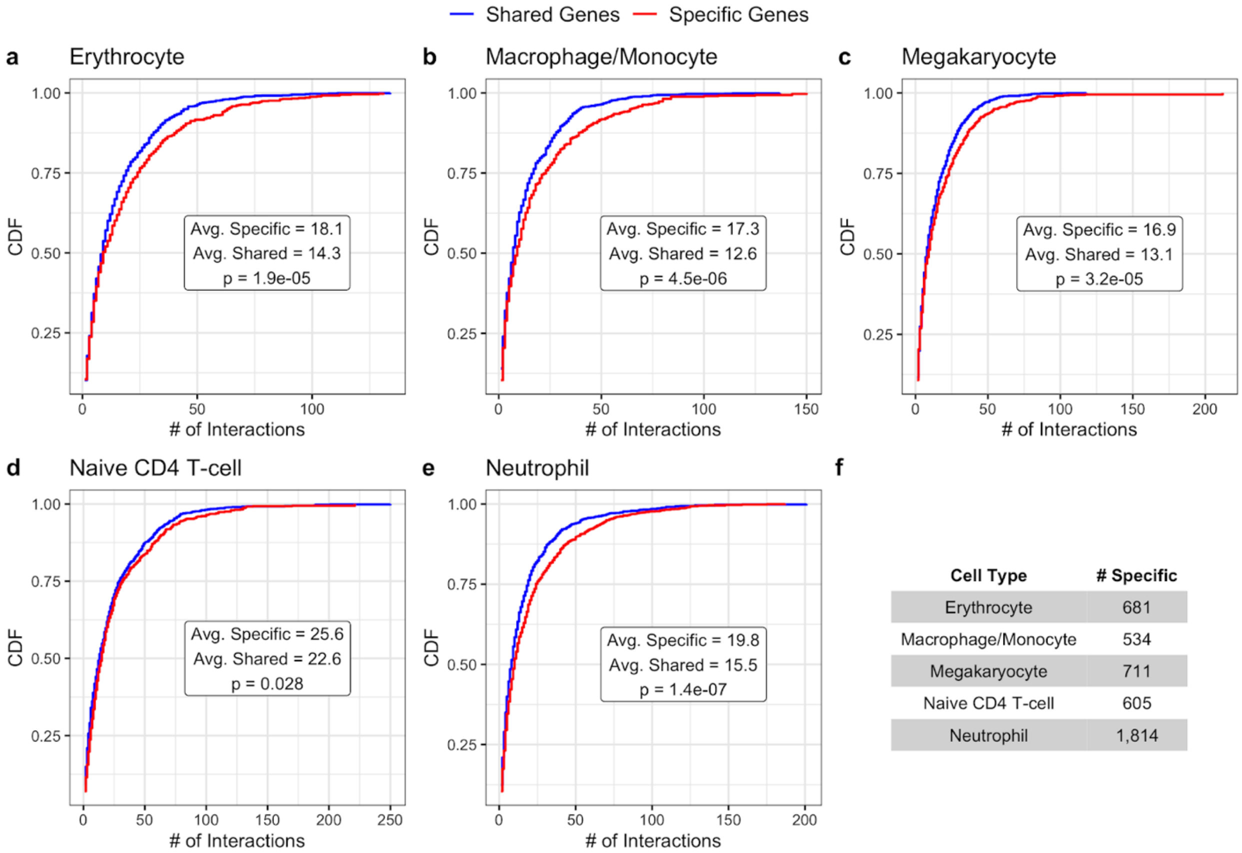

Cell Type	# Specific
Erythrocyte	681
Macrophage/Monocyte	534
Megakaryocyte	711
Naive CD4 T-cell	605
Neutrophil	1,814

S1 Fig. Cell type-specifically expressed genes exhibit higher levels of chromatin interactivity in the corresponding cell type. Each panel displays the empirical cumulative distribution function (CDF) of the number of significant pcHi-C interactions for shared versus cell type-specific genes in **(A)** erythrocytes, **(B)** macrophages/monocytes, **(C)** megakaryocytes, **(D)** naive CD4 T-cells, and **(E)** neutrophils. The average number of interactions for specific and shared genes within each cell type is reported along with the corresponding two-sided *t*-test *p*-value. **(F)** The number of specific genes per cell type.