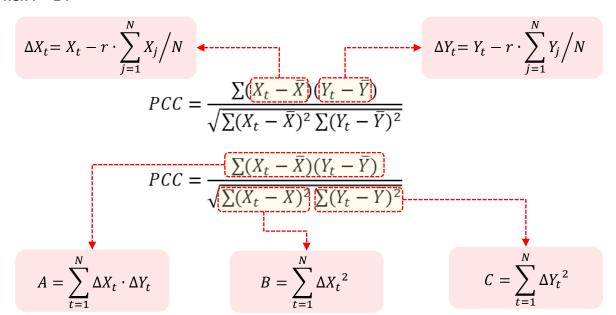
Supp. Figures

Supplementary Figure 1

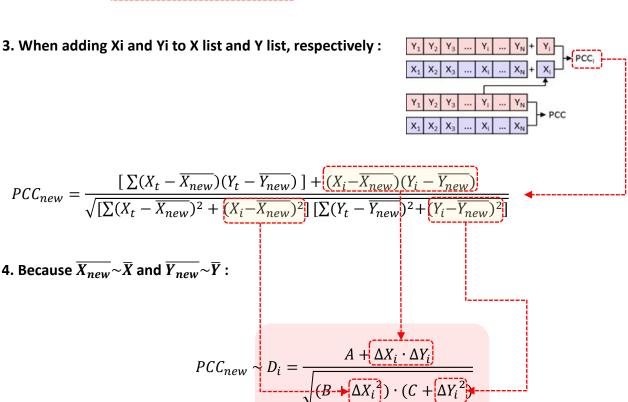
1. The formula of Pearson Correlation Coefficient (PCC):

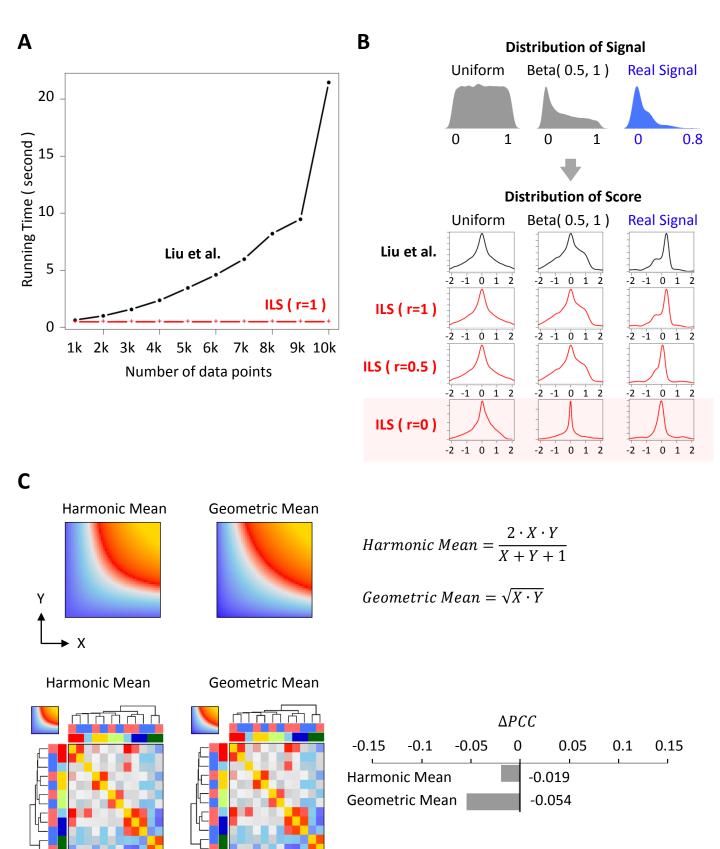
$$PCC = \frac{\sum (X_t - \bar{X})(Y_t - \bar{Y})}{\sqrt{\sum (X_t - \bar{X})^2 \sum (Y_t - \bar{Y})^2}}$$

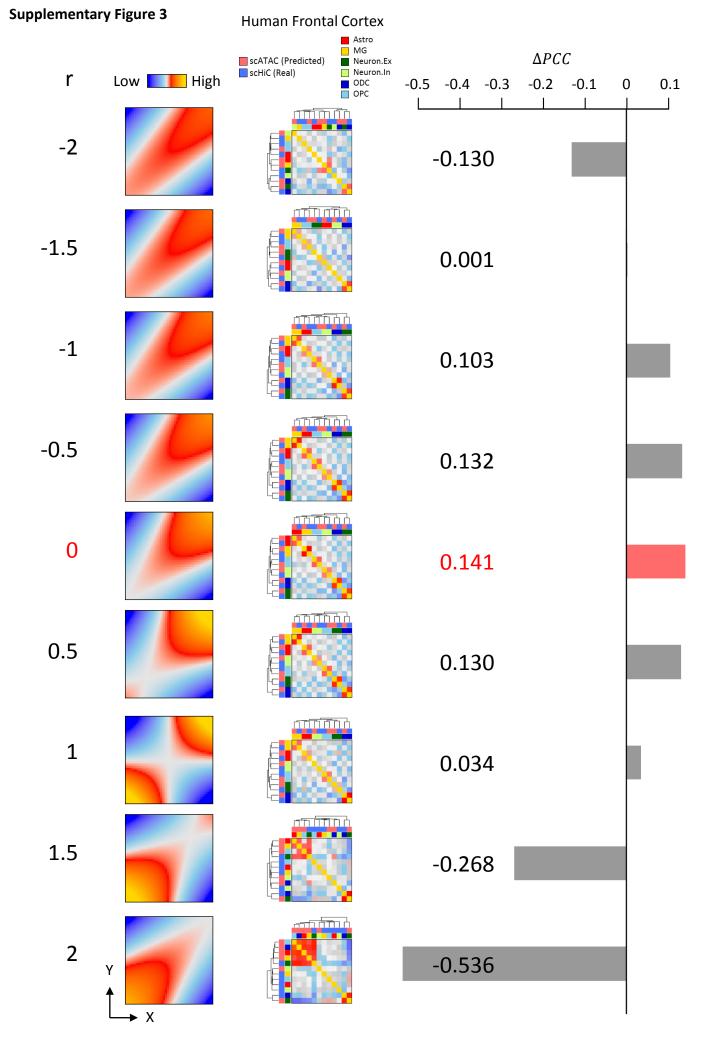
2. When r = 1:



$$PCC = \frac{\sum (X_t - \bar{X})(Y_t - \bar{Y})}{\sqrt{\sum (X_t - \bar{X})^2 \sum (Y_t - \bar{Y})^2}} \longrightarrow D_0 = \frac{A}{\sqrt{B \cdot C}}$$

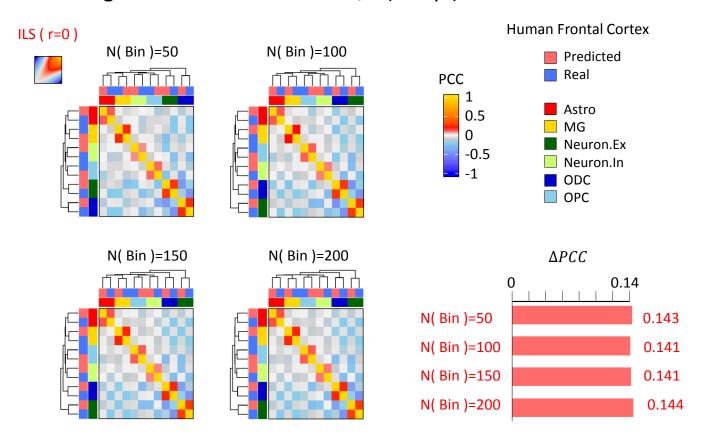




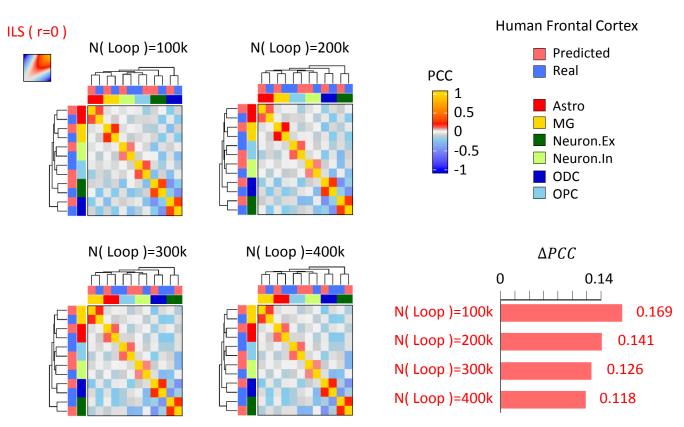


Α

Using different number of bins, N(Loop)=200k

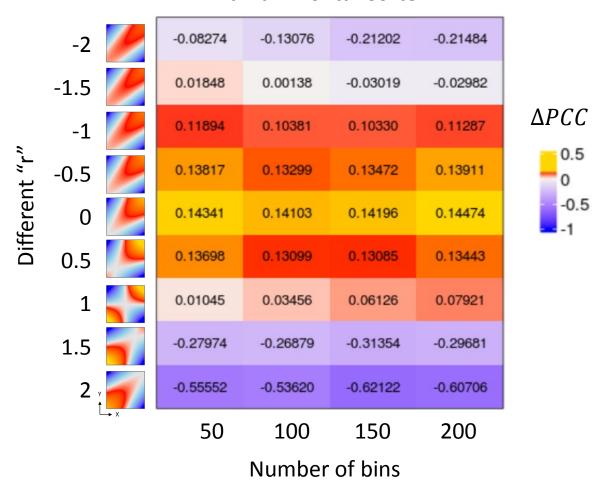


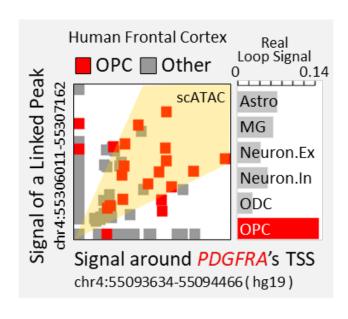
B Using different number of top loops of Cicero, N(Bin)=100

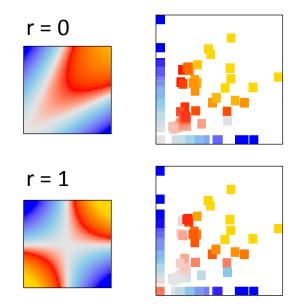


Number of bins & different "r"

Human Frontal Cortex



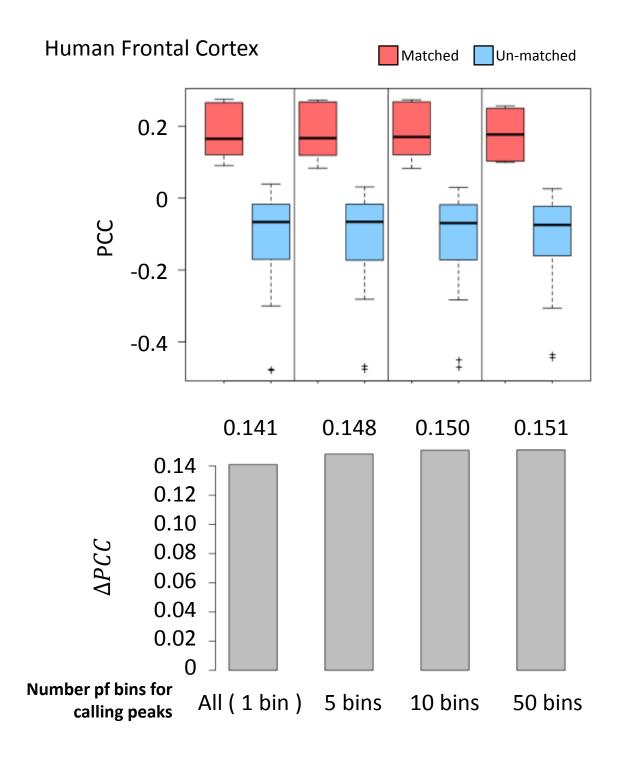




Number of bins & peak calling

Peaks are called independently on each bin of cells and then combined:

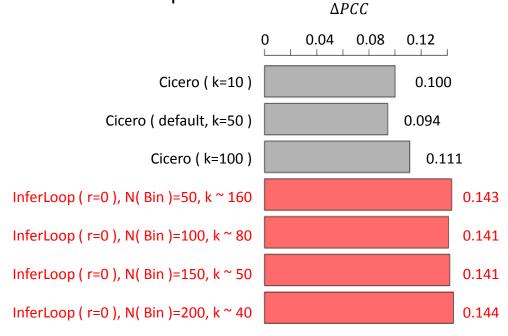
CallPeaks(..., group.by="bin", ...) in Signac

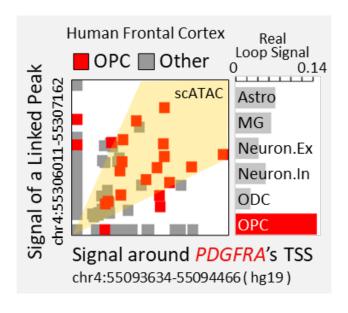


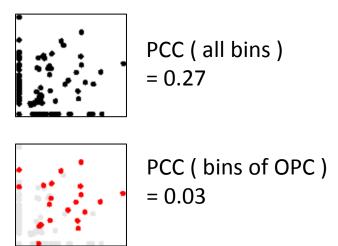
Using different k to run Cicero

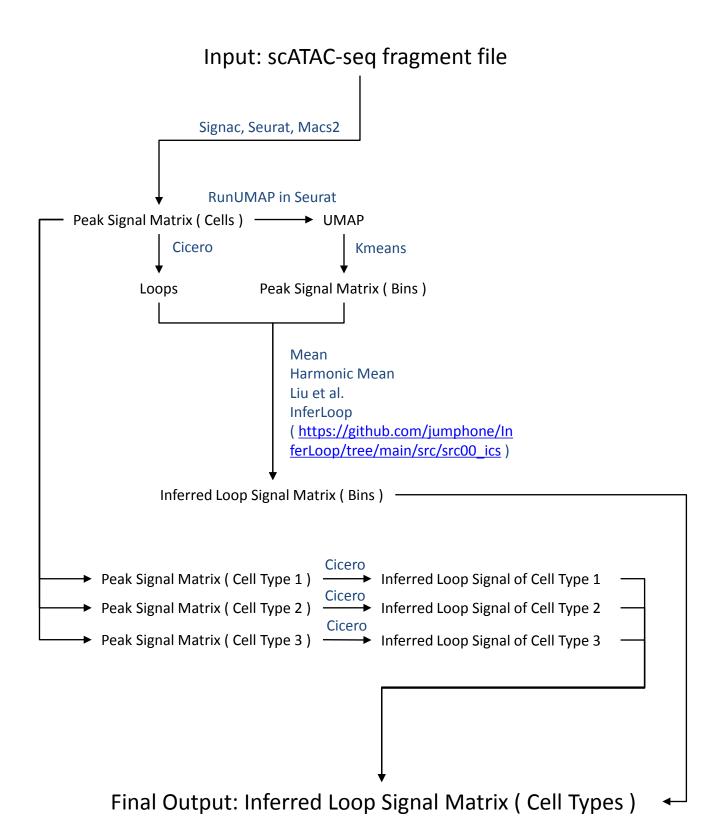
Human Frontal Cortex: ~8000 cells

k: number of cells per bin

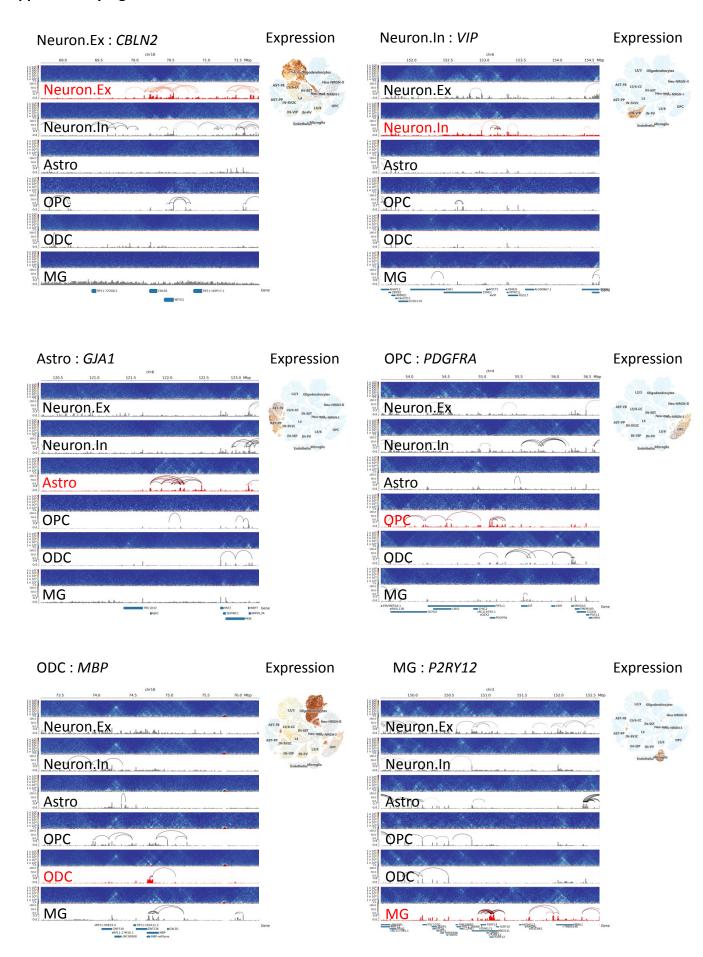




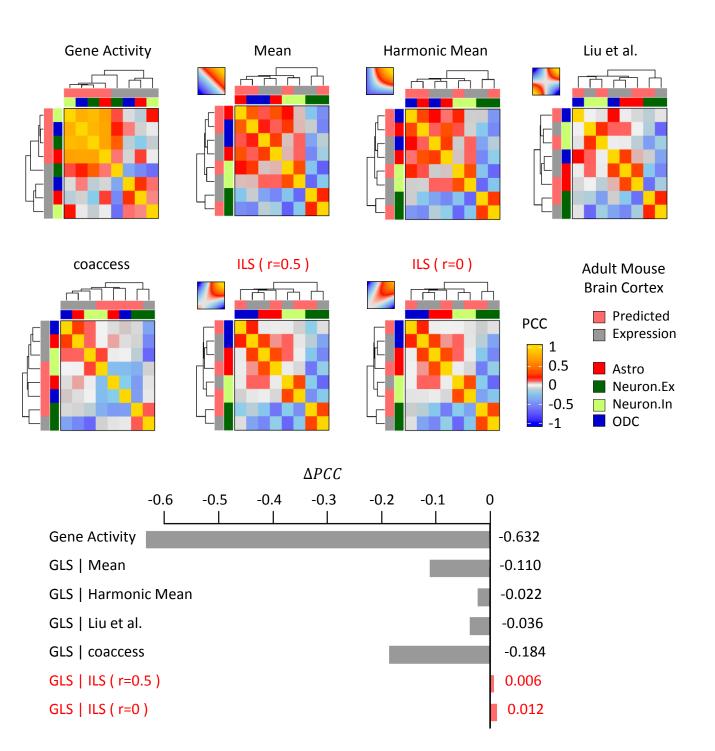


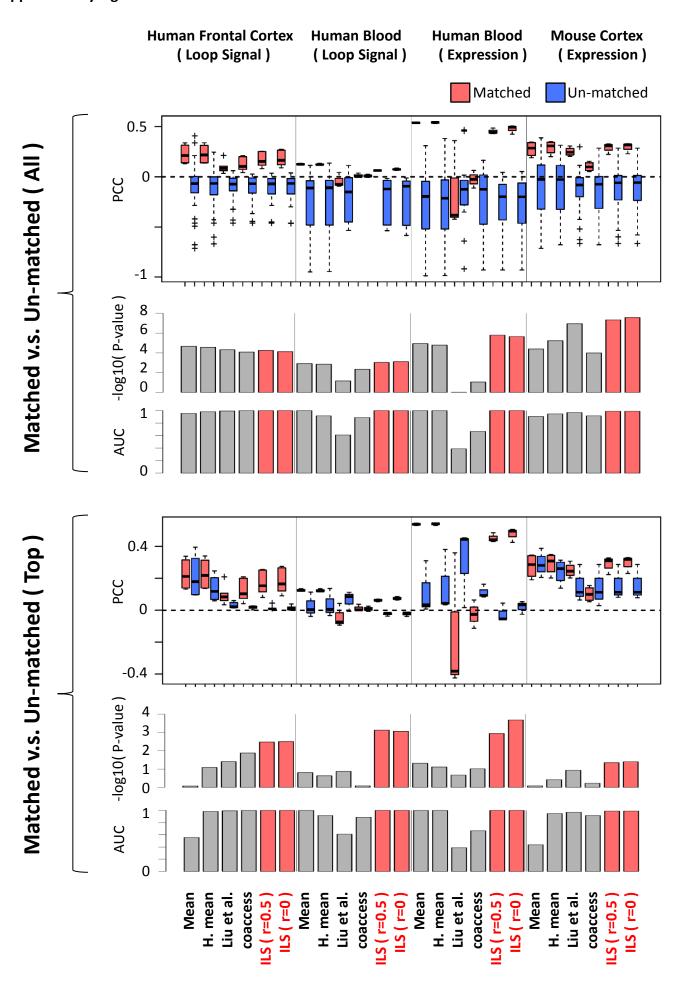


Supplementary Figure 9



Supplementary Figure 10

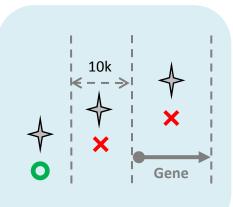




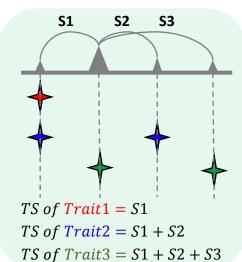
SNPs & Traits in GWAS Catalog Trait 1 SNP

Trait 2

Filtering of GWAS SNPs



Calculating Trait Score (TS)



Using Key Words to Select Target Traits

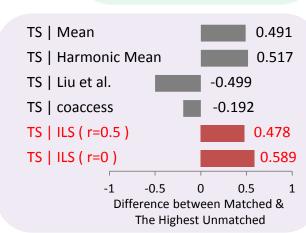
Trait 3

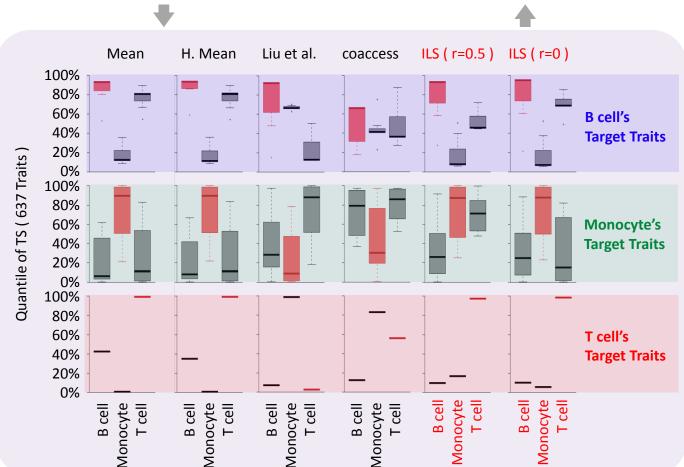
Cell Type	Key Word in Trait Name
B cell	"B CELL"
Monocyte	"MONOCYTE"
T cell	"T CELL"

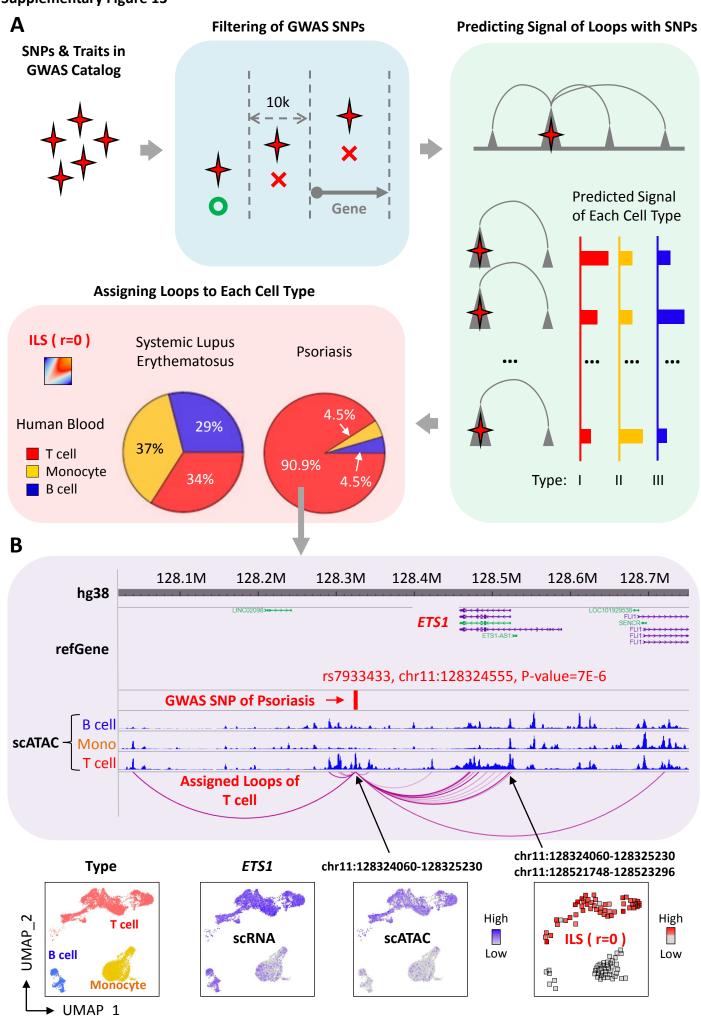
B CELL %CD3- LYMPHOCYTE
CD24 ON UNSWITCHED MEMORY B CELL
CD24 ON IGD- CD38- B CELL
CD24 ON IGD+ CD38- B CELL
CD24 ON IGD+ CD34- B CELL
CD20 ON IGD- CD38DIM B CELL
CD20 ON UNSWITCHED MEMORY B CELL

MONOCYTE PERCENTAGE OF WHITE CELLS MONOCYTE COUNT LYMPHOCYTE-TO-MONOCYTE RATIO CX3CR1 ON CD14- CD16+ MONOCYTE SSC-A ON CD14+ MONOCYTE SSC-A ON MONOCYTE CD86 ON MONOCYTE

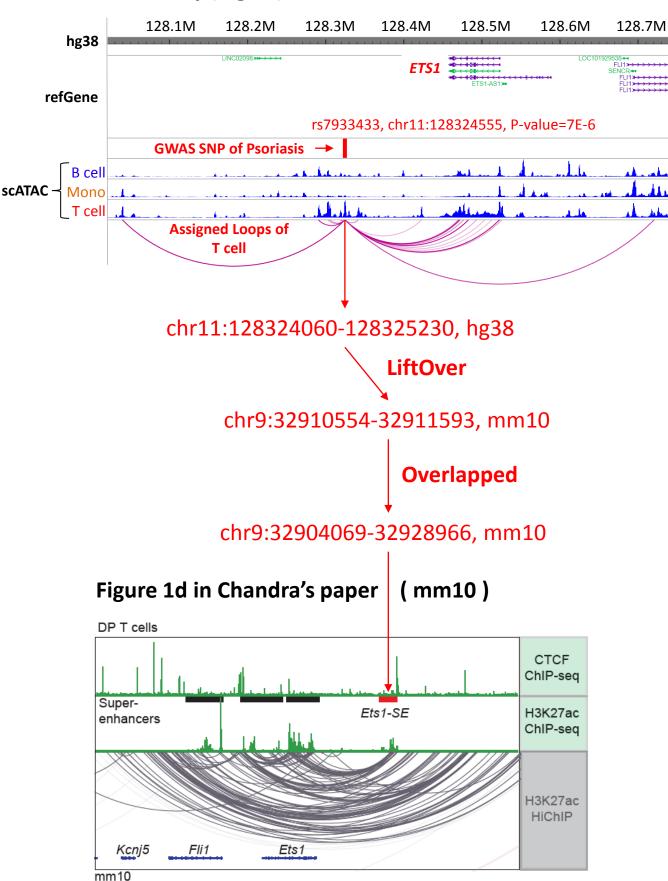
CENTRAL MEMORY CD4+ T CELL %T CELL
CENTRAL MEMORY CD4+ T CELL %CD4+ T CELL







Our study (hg38)



A multi-enhancer hub at the Ets1 locus controls T cell differentiation and allergic inflammation through 3D genome topology, *bioRxiv*, 2022.10.28, https://doi.org/10.1101/2022.10.28.514213