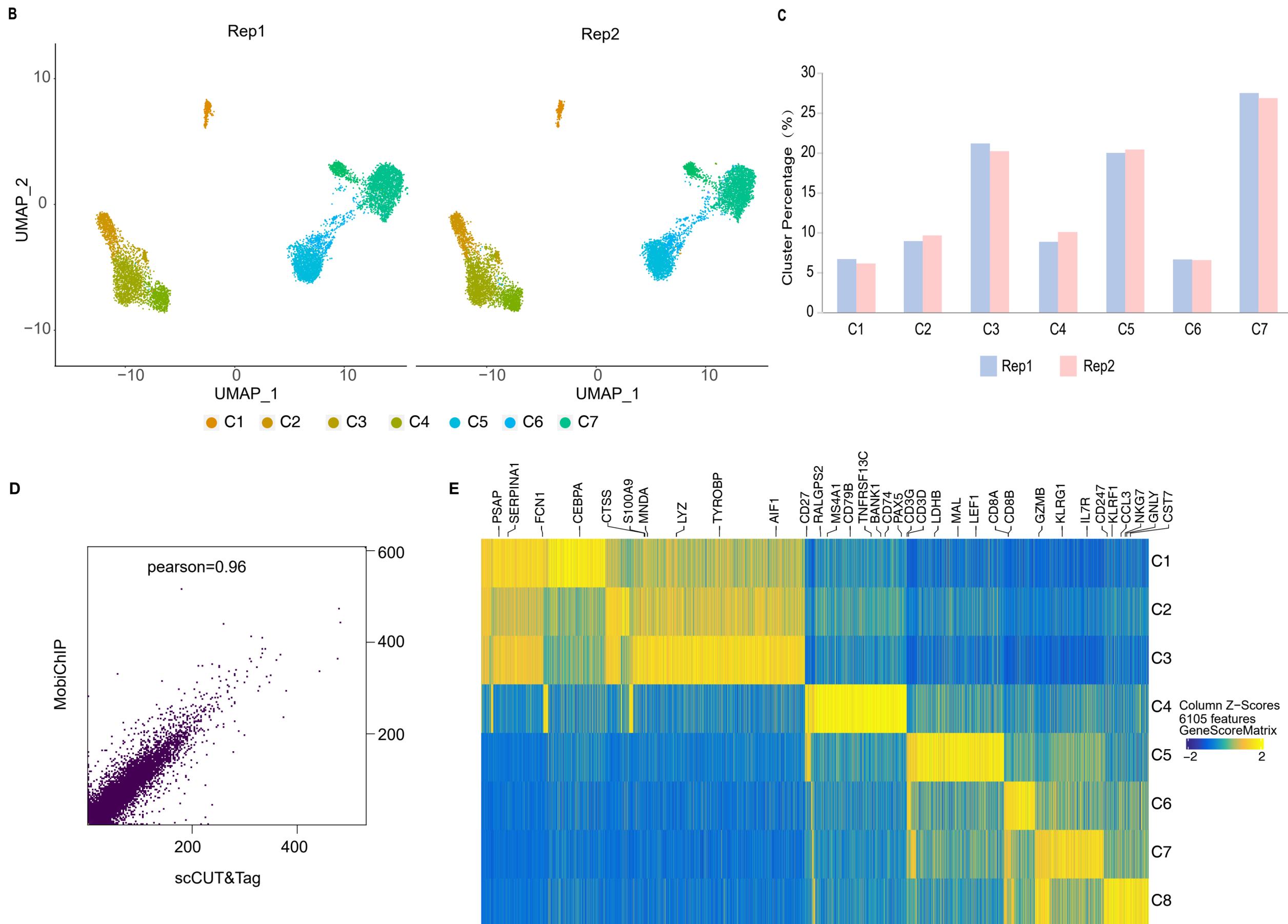


Sample	Epitope	Number of Raw Reads	Number of Valid Reads	Fraction of Valid Reads	Reads mapped to Genome	Non-duplicated Reads	Duplication Rate	Fraction of Fragments in Peaks	Number of Peaks
PBMC	H3K27ac	135,958,787	133,751,514	98.38%	94.74%	44,263,005	57.03%	85.51%	105,832



Extended Data Fig.1 The MobiChIP with PBMCs samples. (A) Table depicting the QC metrics of MobiChIP. (B) UMAP through two biological replicates with H3K27ac in PBMCs samples. The total cells were divided into 7 clusters: C1, C2, C3, C4, C5, C6 and C7. (C) Statistics on the proportion of cells captured by two biological replicates showed in Fig 1B. (D) Global Pearson correlation analysis of MobiChIP and scCUT&Tag with H3K27ac. (E) Heat map of genes with significantly high H3K4me1 signal in each cluster (row). Fold change > 2; $q < 0.05$ (both). Cell-type-specific genes are highlighted.