

Description of Additional Supplementary Files

Supplementary Data	Description
1	DEx (by RNA-seq) and DEn (by CUT&RUN) of genes in pairwise analysis of sorted CD8+ T cell subsets from HD.
2	Integrated RNA-seq and histone mark analyses.
3	DEx and DEn genes in comparison of HD subset-derived CAR-T cells.
4	Differentially enriched transcription factors identified by CUT&RUN (H3K4me2 and H3K27me3) when comparing HD EM- and CM-derived CAR-T.
5	Metascape.org gene ontology analysis of histone mark patterns indicative of EM-derived CAR-T cells in RNA ^{hi} genes.
6	Metascape.org gene ontology analysis of histone mark patterns indicative of CM-derived CAR-T cells in RNA ^{hi} genes.
7	Metascape.org gene ontology analysis of histone mark patterns indicative of EM-derived CAR-T cells in RNA ^{lo} genes.
8	Metascape.org gene ontology analysis of histone mark patterns indicative of CM-derived CAR-T cells in RNA ^{lo} genes.
9	DEx and DEn genes in comparison of HD CM-derived and PT CM-enriched CAR-T cells.
10	Detailed clinical characteristics of patients with large B cell lymphoma undergoing CAR-T cell therapy and used for Analysis of Infusion Product by RNA-seq and CUT&RUN.
11	DEx and DEn genes in comparison of high and low expanding PT CM-enriched CAR-T cells from a clinical trial (NCT01865617).
12	Comparison of Published Positively and Inversely Associated Genesets of CAR-T cell and TIL Exhaustion in Comparison to Low and High Expanding Genesets.
13	KLF7 targets from epigenomic regulome and association with proliferation.
14	Primers used in this study for quantitative RT-PCR.
15	Antibodies used in this study.
16	Packages and Software used in this study.