

1 **Appendix**

2 **Supplementary figures..... 1**

3 **Appendix Figure S1: Inactivating BCL11B and NuRD subunits in human T cells. 2**

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6 **Appendix Figure S3: Suppressing mitochondrial fusion inhibits the reprogramming of T**

7 **cells into ITNKs and the antitumor effects of ITNKs..... 4**

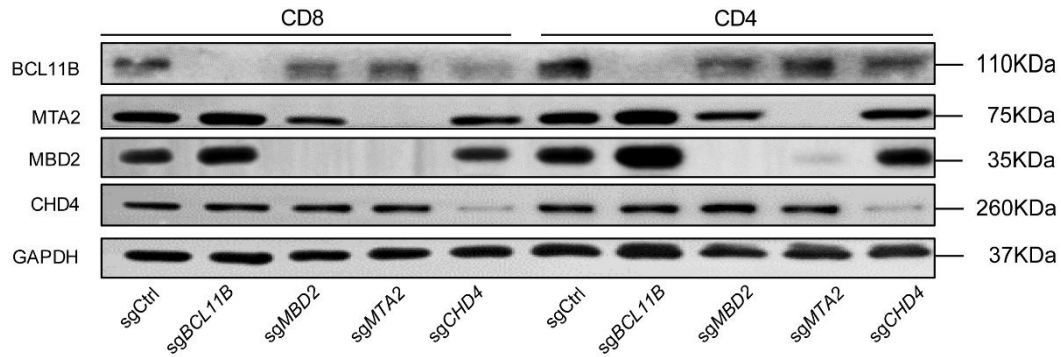
8 **Appendix Figure S4: Related genes express at multiple time points during reprogramming. 5**

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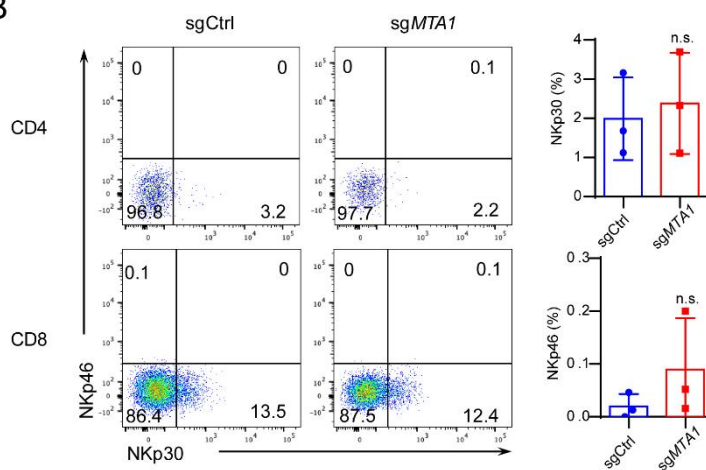
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Appendix Figure S1

A



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2 **Appendix Fig. S1. Inactivating BCL11B and NuRD subunits in human T cells.**

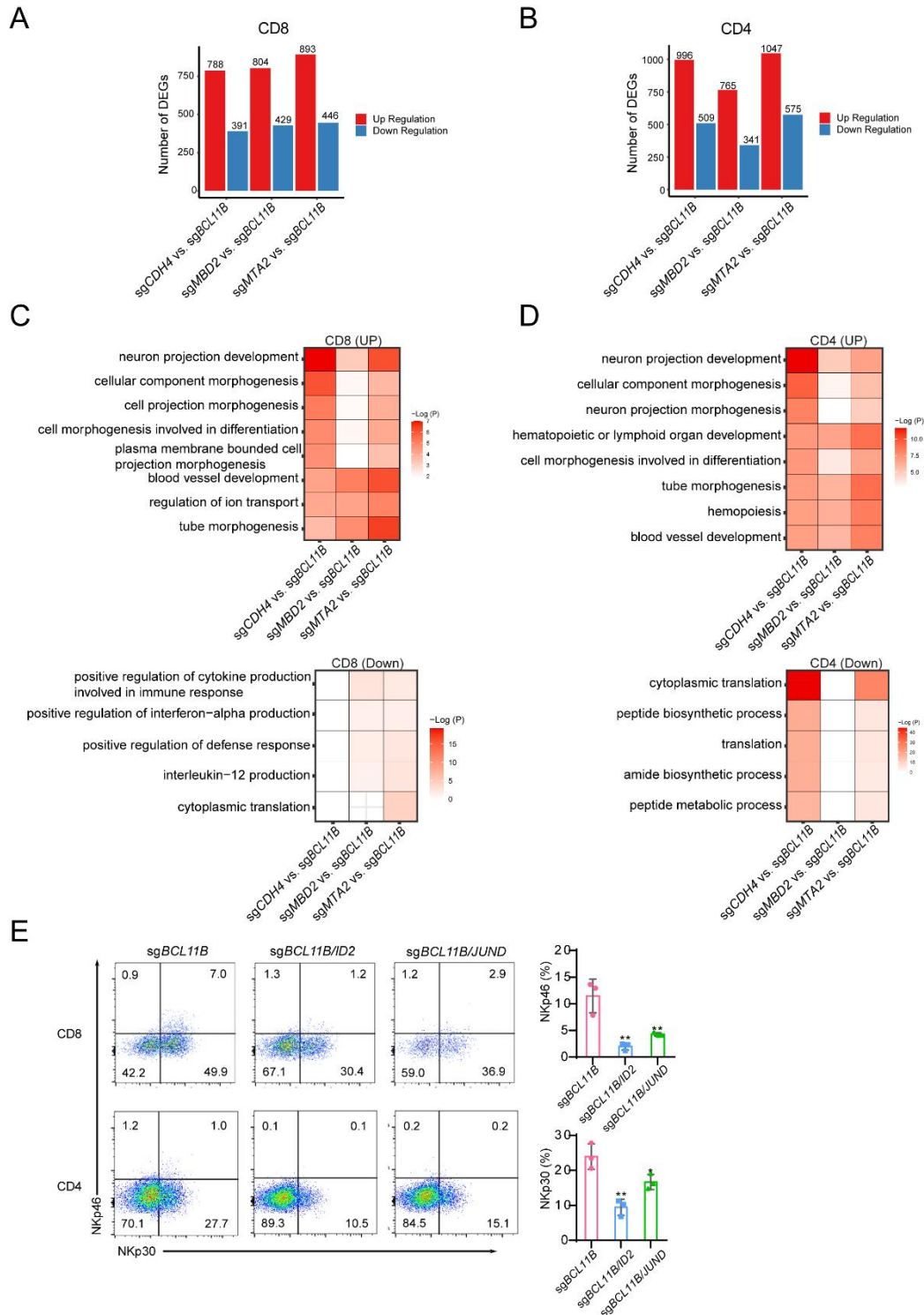
3 A. Representative western blot of BCL11B, MBD2, MTA2, and CHD4 protein levels
 4 in samples of purified CD8⁺ or CD4⁺ PBMC-derived T cells that were transduced
 5 with sgCtrl, sgBCL11B, sgMBD2, sgMTA2, and sgCHD4. The data represents the
 6 efficacy of the knockout experiment from Fig. 1B.

7 B. Representative flow cytometric detection of NKp30 and NKp46 in T cells
 8 transduced with sgCtrl and sgMTA1. Graph summarizing the NKp46⁺ in CD3⁺CD8⁺ T
 9 cells and NKp30⁺ in CD3⁺CD4⁺ T cells transduced with the indicated sgRNAs. Data
 10 were analyzed by two-tailed paired Student's t-test. Data represent mean ± SD (N=3
 11 individual healthy donors).

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Appendix Figure S2



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2 **Appendix Fig. S2. ITNKs derived from NuRD-subunit-deficient cells are**
 3 **different from BCL11B-deleted ITNKs.**

4 A. Bar chart indicating the numbers of up- and down-regulated genes from
 5 differentially expressed genes (DEGs) between NuRD-subunit-deficient CD8⁺ ITNKs

1 and CD8⁺ BCL11B-deficient ITNKs. Gene differential expression analysis was
2 performed by R package DESeq2 (version 1.38.1). The number of differentially
3 expressed genes was counted as visualized by customized R scripts using ggplot2
4 (version 3.4.0).

5 B. Bar chart indicating the numbers of up- and down-regulated genes from DEGs
6 between NuRD-subunit-deficient CD4⁺ ITNKs and CD4⁺ BCL11B-deficient ITNKs.

7 C. Gene ontology analysis of up- and down-regulated genes from DEGs between
8 NuRD-subunit-deficient CD8⁺ ITNKs and BCL11B-deficient CD8⁺ ITNKs. GO
9 enrichment analysis was performed by R package clusterprofile (version 4.6.2). The
10 was visualized as heatmaps generated by customized R scripts using ggplot2 (version
11 3.4.0).

12 D. Gene ontology analysis of up- and down-regulated genes from DEGs between
13 NuRD-subunit-deficient CD4⁺ ITNKs and BCL11B-deficient CD4⁺ ITNKs.

14 E. Representative flow cytometric detection of NKp30 and NKp46 in PBMC-derived
15 T cells transduced with sgBCL11B, sgBCL11B/ID2, and sgBCL11B/JUND. Graph
16 summarizing the NKp46⁺ in CD3⁺CD8⁺ T cells and NKp30⁺ in CD3⁺CD4⁺ T cells
17 transduced with the indicated sgRNAs. Data were analyzed by one-way ANOVA with
18 Tukey's multiple comparisons test. *P≤0.05 and **P ≤ 0.01. Data represent mean ±
19 SD (N=3 individual healthy donors).

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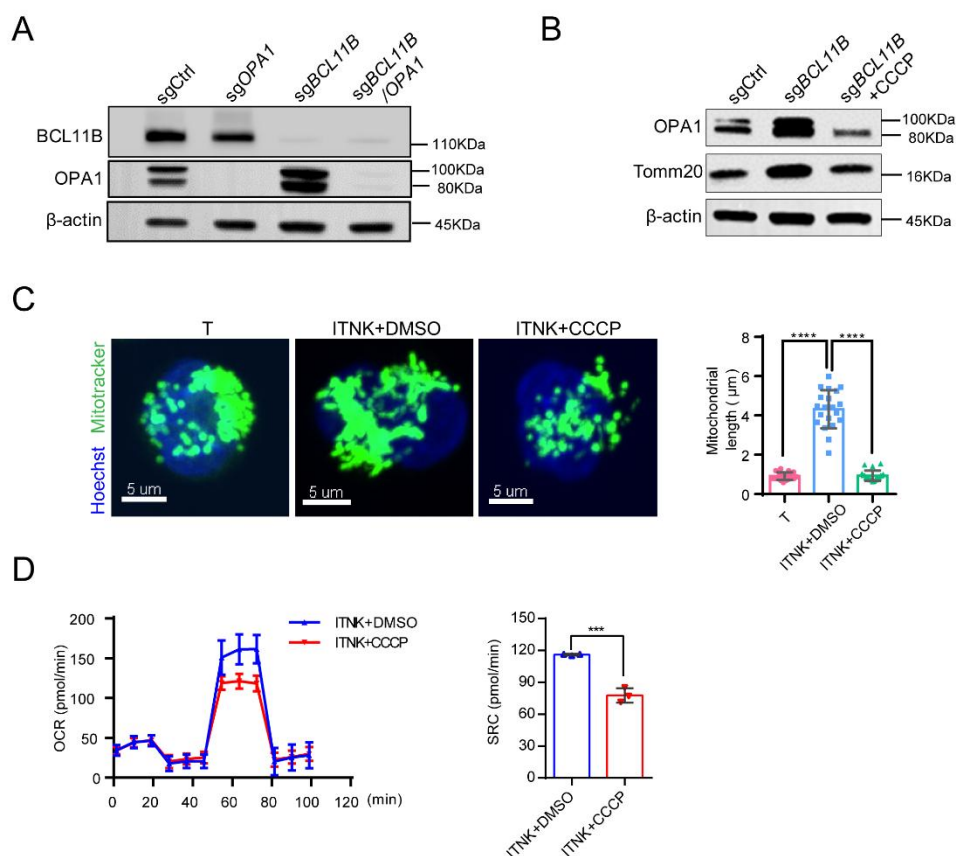
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Appendix Figure S3



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2 **Appendix Fig. S3. Suppressing mitochondrial fusion inhibits the reprogramming**
 3 **of T cells into ITNKs and the antitumor effects of ITNKs.**

4 A. Representative western blots of BCL11B and OPA1 protein levels in samples of T
 5 cells transduced with sgCtrl, sgOPA1, sgBCL11B, or the combination of sgBCL11B
 6 and sgOPA1.

7 B. CCCP (5 μM, mitochondrial fission inducer) was added to a culture of sgBCL11B-
 8 transduced human T cells derived from PBMCs 24 hours after electroporation. OPA1
 9 protein, Tomm20, and β-actin were detected by western blot assay.

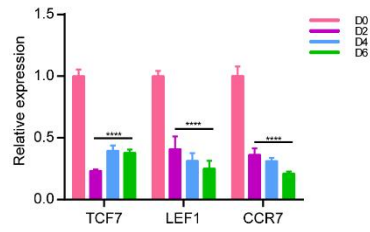
10 C. Confocal microscopy images showing T cells, ITNK cells, and ITNK cells treated
 11 with CCCP in which the mitochondria (MitoTracker, green) and nuclei (Hoechst; blue)
 12 are stained. Scale bars: 5 μm. Relative lengths of the mitochondria, as analyzed by
 13 confocal microscopy, are shown. The images were digitized using ImageJ software.
 14 Each dot represents the mean relative length of the mitochondria in a sample.

15 ****P≤0.0001, one-way ANOVA with Tukey's multiple comparisons test.

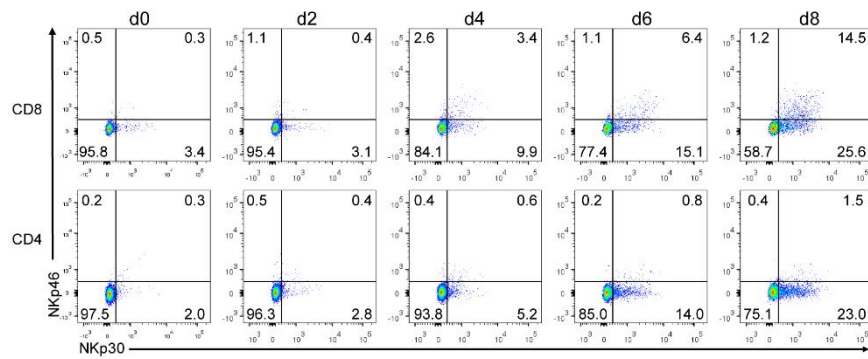
1 D. OXPHOS (OCR: O₂ consumption rate) assays were performed in ITNKs and
2 ITNKs treated with CCCP. The maximum OCR values were achieved after FCCP
3 uncoupling (maximum respiration). The curves represent the mean \pm SD (N=5
4 individual healthy donors). ***P \leq 0.001, two-tailed paired Student's t-test.
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Appendix Figure S4

A



B



1

2 **Appendix Fig. S4. Related genes express at multiple time points during**
 3 **reprogramming.**

4 A. Time course of T cell-related genes expression by RT-qPCR. The results represent
 5 mean \pm SD (N=4 individual healthy donors); ****P \leq 0.0001, two-way ANOVA with
 6 Dunnett's multiple comparisons test.

7 B. T cells transduced sgBCL11B (from (Fig. 6A)) were cultured in vitro. The makers
 8 (NKp30 and NKp46) of CD4⁺ and CD8⁺ ITNKs were detected using flow cytometry
 9 at multiple timepoints.

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