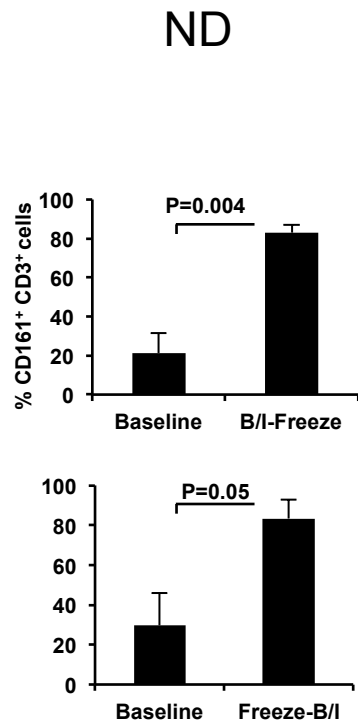
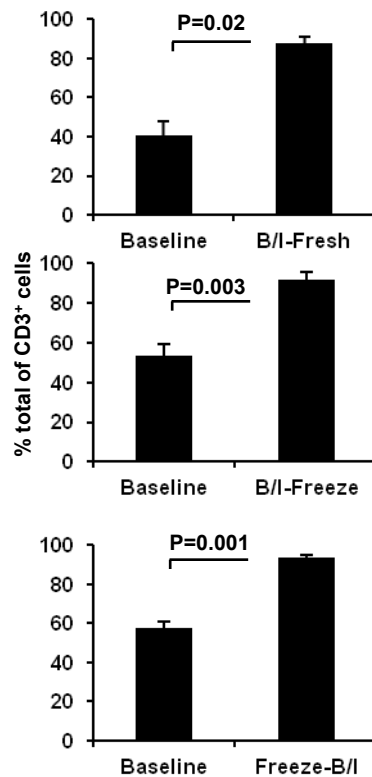


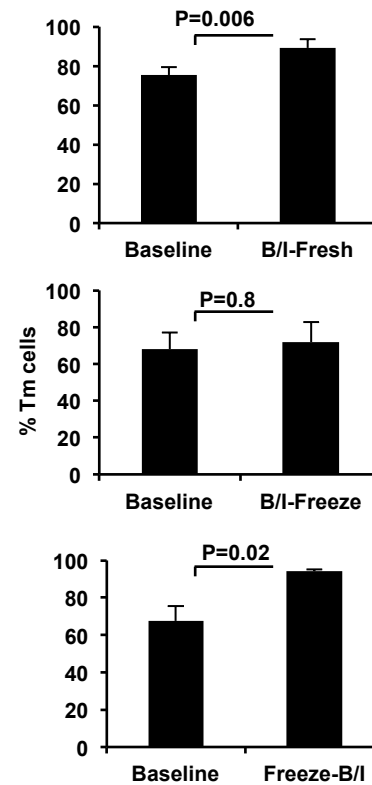
E. Activated CD161+ NKT



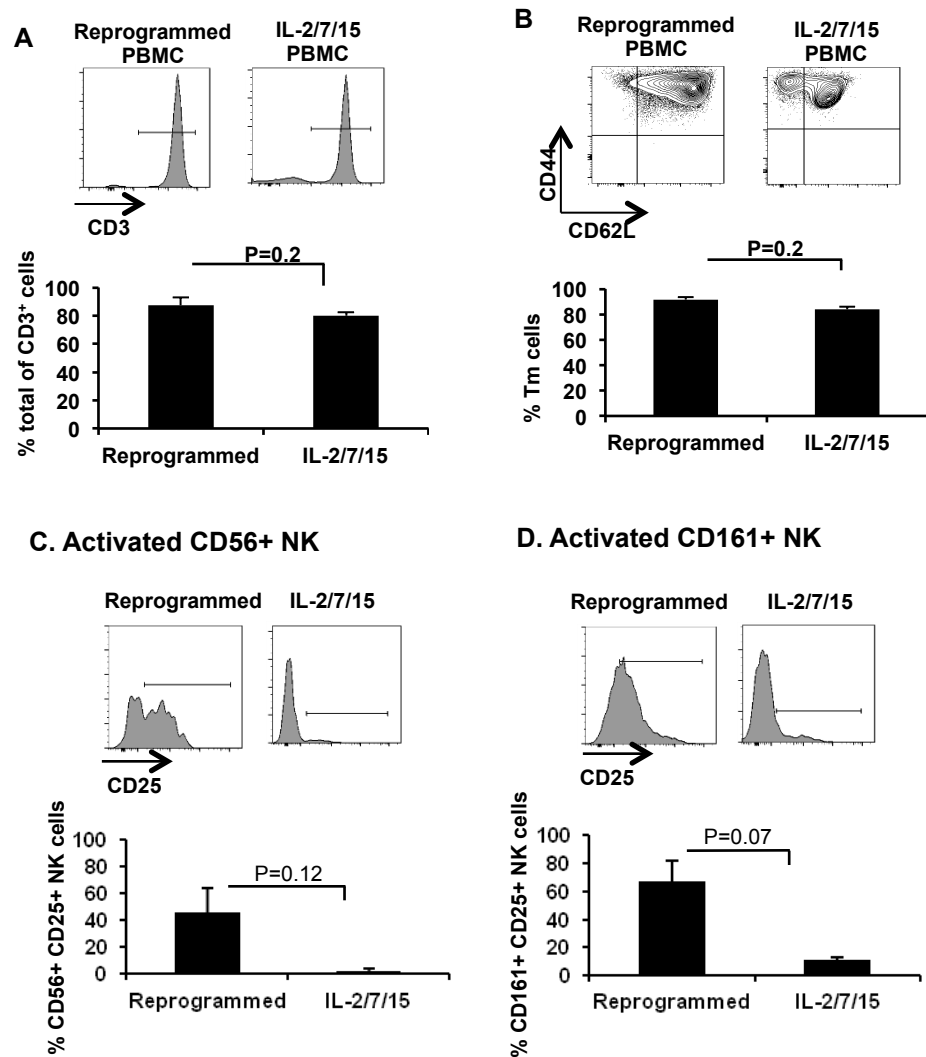
F. CD3+ Cells



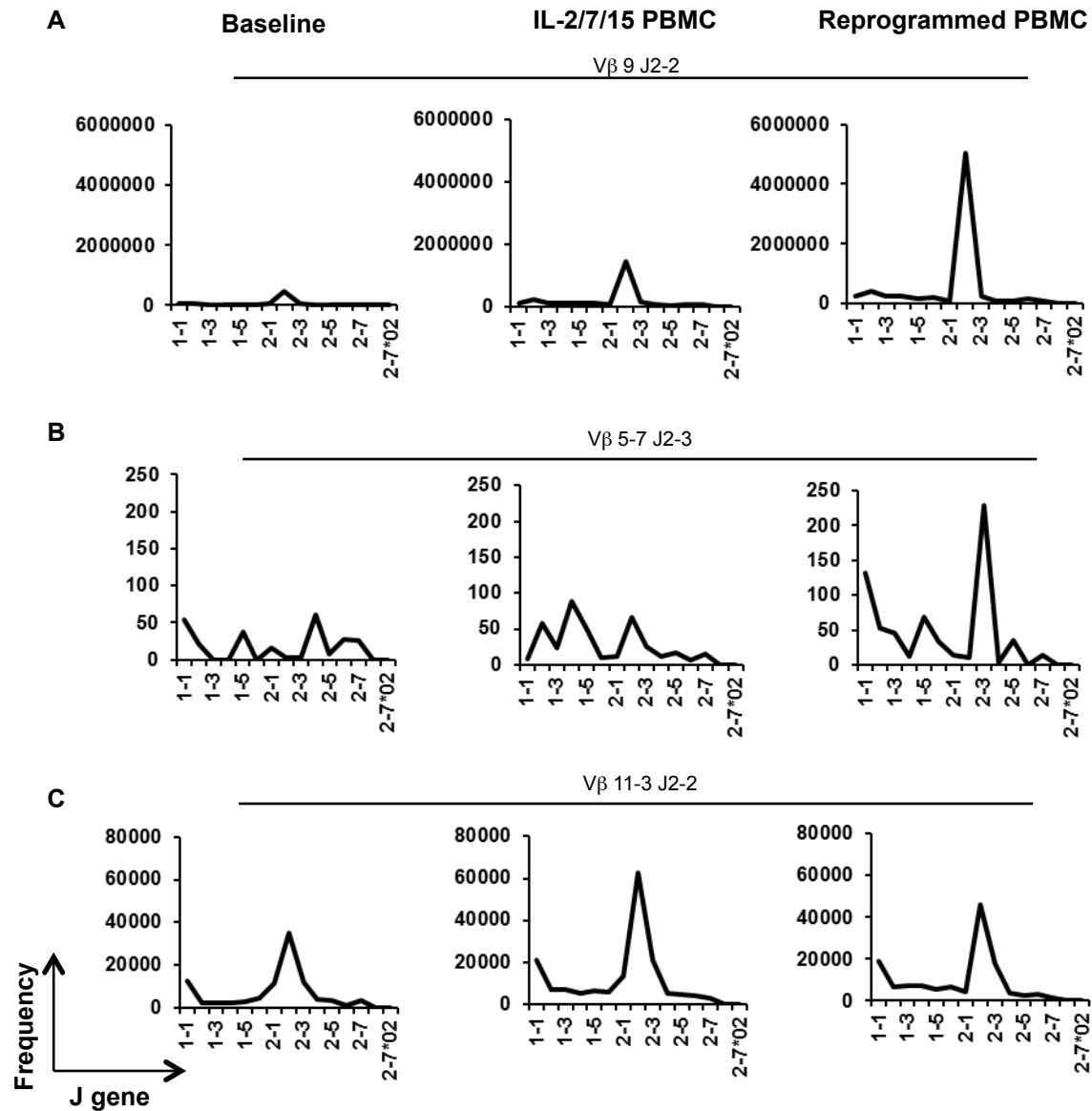
G. Tm cells



Supplemental Figure 1. Determination of cryosensitivity of the reprogrammed cells. A) Fold expansion compared to day one of IL-2 (n=13), B/I-Fresh (n=16) and Freeze-B/I (n=11) PBMCs. Cell counts were performed using trypan blue exclusion. Data represent Least Squares Means \pm SEM. B) The percentage of activated CD56+ NK cells was determined in reprogrammed cells which included B/I-Fresh (n=6), B/I-Freeze (n=9), and Freeze-B/I (n=8). C) The percentage of activated CD161+ NK cells was determined in B/I-Freeze (n=5), and Freeze-B/I (n=3). D) The percentage of activated CD56+ NKT cells was determined in B/I-Fresh (n=6), B/I-Freeze (n=9), and Freeze-B/I (n=8). E) The percentage of activated CD161+ NKT cells was determined in B/I-Freeze (n=5), and Freeze-B/I (n=3). F) The percentage of total CD3+ cells on gated lymphocyte region was determined in B/I-Fresh (n=5), B/I-Freeze (n=7), and Freeze-B/I PBMCs (n=8). G) The percentage of Tm cells was determined in B/I-Fresh (n=5), B/I-Freeze (n=7), and Freeze-B/I PBMCs (n=8). Data represent Mean \pm SEM. ND = not done.



Supplemental Figure 2. Determination of the role of B/I in cellular reprogramming. PBMCs (n=3) were split into two groups and then subjected to reprogramming protocol in the presence (Reprogrammed PBMC) or absence (IL-2/7/15 PBMC) of B/I. The frequency of (A) total CD3⁺ cells, (B) Tm cells, (C) activated CD56⁺ NK cells, and (D) activated CD161⁺ NK cells was determined in Reprogrammed and IL2/7/15 PBMCs using flow cytometry. Data represent Mean \pm SEM.



Supplemental Figure 3. Bryostatins 1 and Ionomycin selectively expand specific T cell clones. High-throughput sequencing of TcR V β was performed from one patient's PBMCs at baseline, after culture with γ -c cytokines only (IL-2/7/15 PBMC), or after reprogramming with B/I and γ -c cytokines (Reprogrammed PBMC). Representative data for the effect of reprogramming on the expansion of dominant clone (A), skewed clonality (B), or no impact on specific clones (C).