



Supplementary Figure 3 Characterization of neoantigen-reactive lymphocytes isolated from the circulating CD8⁺PD1⁺ subset of subjects NCI-3784, and 3903. Enriched populations of TMG-reactive cells were generated by selecting 4-1BB⁺ lymphocytes and expanding the cells *in vitro* for 15 d. **(a–c)** NCI-3784 TMG3- (top), TMG5- (middle), and TMG8-reactive (bottom) lymphocytes, recognizing FLNA_{R>C}, KIF16B_{L>P}, or SON_{R>C}, respectively, were cocultured with DCs transfected with the indicated TMGs **(a)**. IFN- γ ELISPOT assay and flow cytometry detection of 4-1BB upregulation at 20 h are shown. Data are gated on CD3⁺CD8⁺ cells. **(b)** TRB deep sequencing of the TMG-enriched populations. Data show the frequency of the top five TRB clonotypes (unique V-D-J sequences) for each population. **(c)** TMG3-, TMG5- and TMG8-reactive lymphocytes were co-incubated with COS7 cotransfected with the corresponding constructs expressing the indicated TMG and individual HLA alleles encoding the HLA class I molecules indicated on the x axis (such as HLA-A*01:01). Flow cytometry detection of 4-1BB at 20 h after the coculture is shown. Data are gated on CD3⁺CD8⁺. **(d–f)** NCI-3903 TMG9-reactive cells were cocultured with DCs transfected with the indicated TMGs **(d)**, DCs pulsed with the individual 25-mers encoded by 3903 TMG9 **(e)**, or COS7 cells co-transfected with TMG9 and DNA constructs encoding for the HLA-I molecules indicated in the x axis **(f)**. IFN- γ ELISPOT assay and or flow cytometry detection of 4-1BB upregulation are shown. Data are gated on CD3⁺CD8⁺ cells. “>” denotes greater than 500 spots /2 $\times 10^4$ cells. Data are representative of at least two independent experiments.