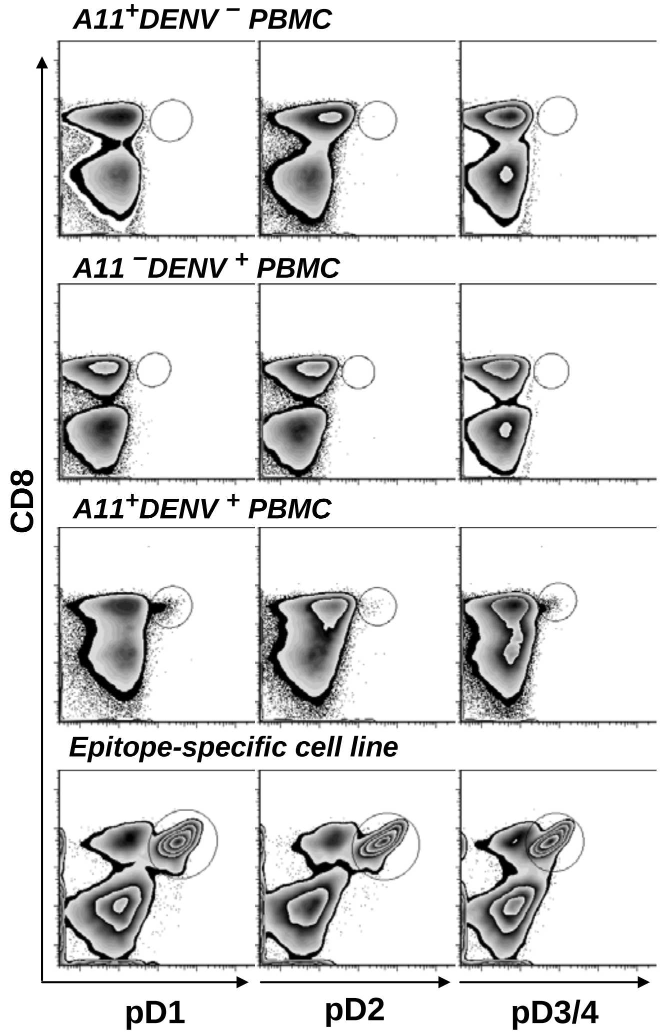
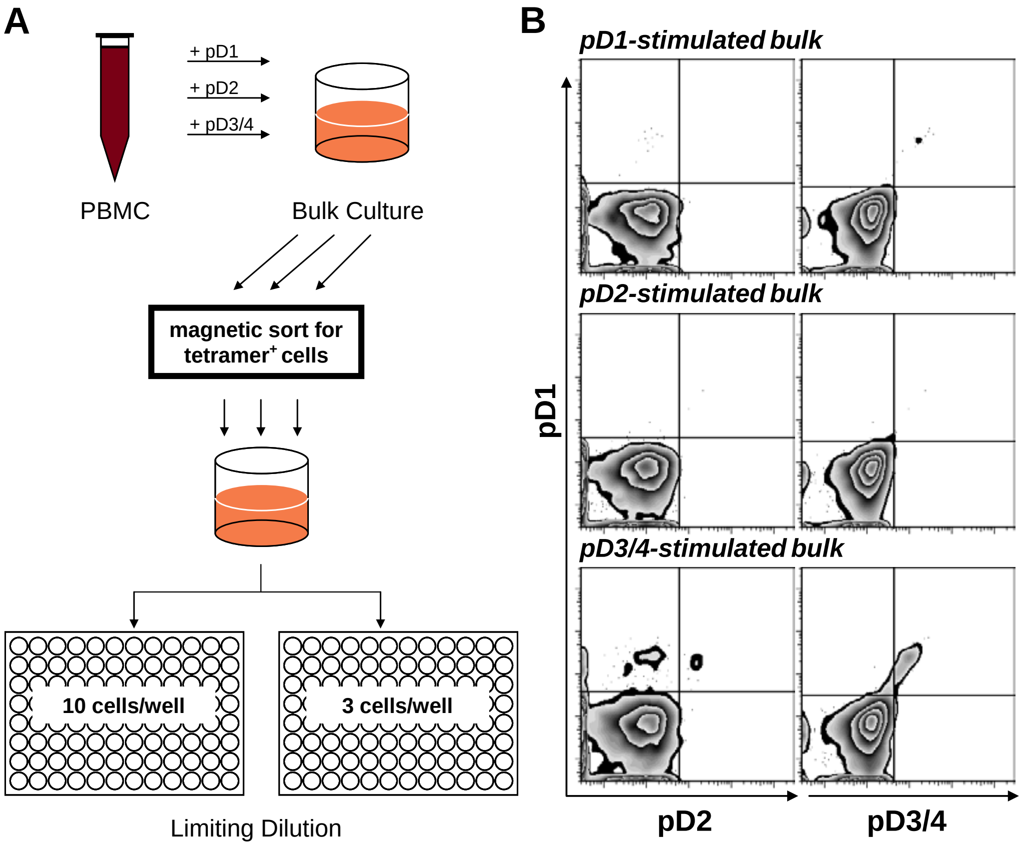
SUPPLEMENTARY FIGURE 1



SUPPLEMENTARY FIGURE 2



SUPPLEMENTARY TABLE 1

Supplementary Table 1: Peptide-MHC binding predictions of epitope variants

Peptide variant	MHC-I Binding Prediction (nM)[1]		
	ann[2]	smm	arb
pD1	87.5	102.1	52.0
pD2	185.2	222.5	136.3
pD3/4	52.8	71.1	37.4

[1] *Determined by the Immune Epitope Database and Analysis Resource T cell epitope prediction tool for peptide binding to HLA-A*1101*

[2] *MHC class I binding prediction methods: ann=Artificial neural network, smm=Stabilized matrix method, arb=Average relative binding*