Supplementary Table 6. Summary of TRB overlap between circulating and tumor-resident CD8^{+} lymphocyte subsets

			PBMC																						
			3903			3926			3998				3992				3713			3759			3784		
			CD8+	CD8+PD-1-	CD8+PD-1+	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+PD-1hi	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+PD-1hi	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+	CD8+PD-1-	CD8+PD-1+	CD8+	CD8+PD-1-	CD8+PD-1+
Fresh Tumor	3903	CD8+	0.227	0.262	0.597																				
		CD8+PD-1-	0.396	0.382	0.203																				
		CD8+PD-1+	0.097	0.133	0.630																				
	3926	CD8+				0.134	0.119	0.190																	
		CD8+PD-1-				0.134	0.118	0.099																	
		CD8+PD-1+				0.094	0.072	0.316																	
	3998	CD8+							0.123	0.081	0.445	0.307													
		CD8+PD-1-							0.114	0.101	0.140	0.045													
		CD8+PD-1+							0.098	0.060	0.484	0.363													
	3992	CD8+											0.420	0.261	0.525	0.371									
		CD8+PD-1-											0.449	0.307	0.468	0.245									
		CD8+PD-1+											0.211	0.035	0.576	0.710									
	3713	CD8+															0.414	0.352	0.388						
		CD8+PD-1-															0.465	0.438	0.271						
		CD8+PD-1+															0.067	0.041	0.290						
	3759	CD8+																		0.157	0.104	0.467			
		CD8+PD-1-																		0.264	0.256	0.134			
		CD8+PD-1+																		0.055	0.010	0.482			
	3784	CD8+																					0.215	0.200	0.228
		CD8+PD-1-																					0.209	0.206	0.081
		CD8+PD-1+																					0.096	0.083	0.256

Analysis of TRB overlap of nucleotide sequences encoding for the variable V-D-J region of the TRB gene was performed using immunoSEQ (Adaptive Biotechnologies) using the following formula (Sample TCRB overlap between population A and B = [shared sequence reads in A + shared sequence reads in B]/∑sequence reads in A + B). A TRB overlap of 1 represents 100% overlap between two populations. The cells were color coded based on lower (yellow) to greater (blue) TRB overlap

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