

Table S1. Nucleotide sequence and frequency of ten most abundant TCR clones of tumor-infiltrating and splenic  $\alpha\beta$ T cells, CD4 T cells, and CD8 T cells<sup>a,b</sup>.

$\alpha\beta$ T	Frequency of Clone	Amino Acid Sequence	Productive Rearrangement	V Chain Resolved	D Chain Resolved	J Chain Resolved
Tumor Clone 1	4.255%	CASSSQGADEQYF	AGGACTCAGCTGTGTATCTGTGT GCCAGCAGTTCGCAGGGGGAGAT GAACAGTAC	TCRBV15 -01*01	TCRBD01 -01*01	TCRBJ02 -07*01
Tumor Clone 2	3.546%	CASSPTGGSYEQYF	ACTCGGCCACATACTTCTGTGCCA GCAGCCCGACTGGGGGCTCCTAT GAACAGTAC	TCRBV02 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Tumor Clone 3	2.837%	CASSSGQGNEQYF	AGGACTCAGCTGTGTA CTCTGTG CCAGCAGCTCGGGACAGGGCAA TGAACAGTAC	TCRBV03 -01*01	TCRBD01 -01*01	TCRBJ02 -07*01
Tumor Clone 4	2.837%	CASGDEQYF	TGGCTACCCCTCTCAGACATCAG TGTACTTCTGTGCCAGCGGTGAT GAACAGTAC	TCRBV13 -02*01	Unknown	TCRBJ02 -07*01
Tumor Clone 5	2.837%	CASSGRDWGYEQYF	AGACAGCTGTATATTTCTGTGCCA GCAGTGGCCGGGACTGGGGCTAT GAACAGTAC	TCRBV13 -03*01	TCRBD02 -01*01	TCRBJ02 -07*01
Tumor Clone 6	2.837%	CASSETGEQYF	CTCCCTCTCAGACATCTTTGTA CT TCTGTGCCAGTGAGACAGGTGAA CAGTAC	TCRBV13 -01*02	TCRBD01 -01*01	TCRBJ02 -07*01
Tumor Clone 7	2.837%	CASSLAANSDYTF	AGGACTCTGCTATGTA CTCTGTG CCAGCTCTCTCGCAGCAA ACTCC GACTACACC	TCRBV12 -01*01	TCRBD01 -01*01	TCRBJ01 -02*01
Tumor Clone 8	2.837%	CASSQDLGDSYEQYF	CGGCCACATATCTGTGCCAGCA GCCAAGATCTGGGGGACTCCTAT GAACAGTAC	TCRBV12 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Tumor Clone 9	2.127%	CASSLSSYEQYF	CCCAGGACTCAGCGGRGTATCTT TGTGCAAGCAGCTTGAGCTCCTAT GAACAGTAC	TCRBV16 -01*01	Unknown	TCRBJ02 -07*01
Tumor Clone 10	2.127%	CASSRGQSGNTLYF	ACTCGGCCACATACTTCTGTGCCA GCAGAGGGACAATCTGGAAATAC GCTCTAT	TCRBV02 -01*01	TCRBD01 -01*01	TCRBJ01 -03*01

$\alpha\beta$ T	Frequency of Clone	Amino Acid Sequence	Productive Rearrangement	V Chain Resolved	D Chain Resolved	J Chain Resolved
Splenic Clone 1	1.761%	CASTPLGGYDEQYF	CAGCCACCTATCTCTGTGCCAGCAC CCCGCTGGGGGGGTATGGGGATGA ACAGTAC	TCRBV14 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Splenic Clone 2	1.408%	CASRGLVFEQYF	TTTCTCAGACAGCTGTATATTTCTCT GTGCCAGCAAGGACTGGTCTTTGAA CAGTAC	TCRBV13 -03*01	TCRBD02 -01*01	TCRBJ02 -07*01
Splenic Clone 3	1.056%	CASSPDWGDYEQYF	ATTCTGCCATGTACCTCTGTGCTAG CAGTCCCAGCTGGGGACTATGAAC AGTAC	TCRBV17 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Splenic Clone 4	1.056%	CAWLGPYEQYF	TCAGCCACTCTGGCTTCTACCTCTG TGCTGGAGACTGGGCCCTTATGA ACAGTAC	TCRBV31 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Splenic Clone 5	1.056%	CASSPGNQAPLF	CAGGAGACTCAGCACTGTACCTCTG TGCCAGCAGTCCGGCAACCAGGCT CCGCTT	TCRBV26 -01*01	Unknown	TCRBJ01 -05*01
Splenic Clone 6	1.056%	CASGDEGTGAYEQYF	AGACATCAGTGTACTTCTGTGCCAG CGGCGACTGGGGGGCTCCTATGA AGAGTAC	TCRBV13 -02*01	TCRBD02 -01*01	TCRBJ02 -07*01
Splenic Clone 7	1.056%	CASGDEGTGAYEQYF	CATCAGTGTACTTCTGTGCCAGCGG TGATGAGGGACAGGGGCCTATGA ACAGTAC	TCRBV13 -02*01	TCRBD01 -01*01	TCRBJ02 -07*01
Splenic Clone 8	1.056%	CASSLQYEQYF	AACTGGAGGACTCTGCTATGTACTT CTGTGCCAGCTCTCTCCAGTATGAA CAGTAC	TCRBV12 -01*01	TCRBD01 -01*01	TCRBJ02 -07*01
Splenic Clone 9	1.056%	CASSLAGQGVGNSDYTF	TGTATCTGTGTGCCAGCAGTTGGC AGGACAGGGGGTTGGAACTCCGA CTACACC	TCRBV15 -01*01	TCRBD01 -01*01	TCRBJ01 -02*01
Splenic Clone 10	1.056%	CASTPGEDNQAPLF	AGACATCTGTGTACTTCTGTGCTAG CACCAGGGGAAGACAACCAGGCT CCGCTT	TCRBV29 -01*01	TCRBD01 -01*01	TCRBJ01 -05*01

CD4	Frequency of Clone	Amino Acid Sequence	Productive Rearrangement	V Chain Resolved	D Chain Resolved	J Chain Resolved
Tumor Clone 1	8.793%	CASRGTGTDERLFF	AGATGGCCGTTTTTCTCTGTGCCA GCAGAGGGACAGGGACCGACGAA AGATTATTT	TCRBV19 -01*01	TCRBD01 -01*01	TCRBJ01 -04*01
Tumor Clone 2	4.499%	CASIKLGS AETLYF	AGATGGCCGTTTTTCTCTGTGCCA GCATAAACTGGGTAGTGCAGAA ACGCTGTAT	TCRBV19 -01*01	TCRBD02 -01*01	TCRBJ02 -03*01
Tumor Clone 3	1.636%	CTCSADPQGEYTF	GCCAGGGCAGAACCTGTACTGC ACCCGCAGTGCAGATCCCAGGG AGAGTACACC	TCRBV01 -01*01	TCRBD01 -01*01	TCRBJ01 -02*01
Tumor Clone 4	1.636%	CASSQDNSGNTLYF	ACTCGGCCACATACTTCTGTGCCA GCAGCCAAGACAATTCTGGAAAT ACGCTCTAT	TCRBV02 -01*01	TCRBD01 -01*01	TCRBJ01 -03*01
Tumor Clone 5	1.431%	CASSQGRAGAEQFF	ACTCGGCCACATACTTCTGTGCCA GCAGCCAAGGGAGGGCGGGCCT GCTGAGCAGTTC	TCRBV02 -01*01	Unknown	TCRBJ02 -01*01
Tumor Clone 6	1.227%	CASSQDLGSSYEQYF	CGGCCACATACTTCTGTGCCAGC AGCCAAGACCTGGGGAGCCCCTA TGAACAGTAC	TCRBV19 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Tumor Clone 7	1.227%	CASRVTGS AETLYF	AGATGGCCGTTTTTCTCTGTGCCA GCAGAGTGACTGGGAGTGCAGAA ACGCTGTAT	TCRBV02 -01*01	TCRBD02 -01*01	TCRBJ02 -03*01
Tumor Clone 8	1.022%	CASSQDYISNERLFF	CGGCCACATACTTCTGTGCCAGC AGCCAAGATTACATATCCAACGAA AGATTATTT	TCRBV16 -01*01	TCRBD01 -01*01	TCRBJ01 -04*01
Tumor Clone 9	1.022%	CASSLAGQSGNTLYF	CAGCGGTGTATCTTTGTGCAAGC AGCTTAGCGGGACAATCTGGAAA TACGCTCTAT	TCRBV16 -01*01	TCRBD01 -01*01	TCRBJ01 -03*01
Tumor Clone 10	1.022%	CASSLQGTGQLYF	ACTCAGCTGTGTA CTCTGTGCCA GCAGCTTGAGGGACCACGGG CAGCTCTAC	TCRBV03 -01*01	TCRBD02 -01*01	TCRBJ02 -02*01

CD8	Frequency of Clone	Amino Acid Sequence	Productive Rearrangement	V Chain Resolved	D Chain Resolved	J Chain Resolved
Tumor Clone 1	9.722%	CASSLELGGREQYF	ACTCAGCGGTGTATCTTTGTGCAA GCAGCTTAGAACTGGGGGGCGC GAACAGTAC	TCRBV16 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Tumor Clone 2	8.796%	CGASGQGPERLFF	AAGACAGAGGCTTATATCTCTGTG GTGCTAGCGGACAGGGGCCCGAA AGATTATT	TCRBV20 -01*01	TCRBD01 -01*01	TCRBJ01 -04*01
Tumor Clone 3	7.407%	CASSQEGDNQAPLF	ACTCGGCCACATACTTCTGTGCCA GCAGCCAAGAGGGGGACAACCAG GCTCCGCTT	TCRBV02 -01*01	Unknwon	TCRBJ01 -05*01
Tumor Clone 4	3.241%	CASSQDWLGGLSYEQYF	TCTATTTTTGTGCCAGCAGCCAAG ATTGGCTGGGGGGCTCTCCTAT GAACAGTAC	TCRBV05 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Tumor Clone 5	2.778%	CASSKAGASAETLYF	CTGCTGTGTATCTCTGTGCCAGCA GCAAGGCAGGAGCTAGTGCAGAA ACGCTGTAT	TCRBV04 -02*01	TCRBD01 -01*01	TCRBJ02 -03*01
Tumor Clone 6	2.778%	CASSLMGYEQYF	CCAAGGACTCAGCTGTCTATCTGT GTGCCAGCAGTTAACTGGGTGC TGAGCAGTTC	TCRBV15 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Tumor Clone 7	2.315%	CASSRDRVAEQFF	ACGAGATGGCCGTTTTTCTCTGTG CCAGCAGTCGGGACAGGGTTGCT GAGCAGTTC	TCRBV19 -01*01	TCRBD01 -01*01	TCRBJ02 -01*01
Tumor Clone 8	1.389%	CASSMGLDEQYF	ACGAGATGGCCGTTTTTCTCTGTG CCAGCAGTATGGGGGGCTGGAT GAACAGTAC	TCRBV19 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Tumor Clone 9	1.389%	CARAGASYEQYF	AAGACGACTCAGCACTGTAGCTC TGTGCCAGGGCTGGGCCTCCTAT GAACAGTAC	TCRBV24 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01
Tumor Clone 10	1.389%	CASSRDWGDGEQYF	ACTCAGCTGTGTACTTCTGTGCCA GCAGAGGGACTGGGGGGATGGC TGAACAGTAC	TCRBV03 -01*01	TCRBD02 -01*01	TCRBJ02 -07*01

<sup>a</sup>The frequency of each clone within the T cell population is shown as well as the cysteine to phenylalanine amino acid sequence of the TCR. The full productive rearrangement for each clone including the V-gene, CDR3 region, N1 junction, D-gene, N2 Junction, and J-Gene is indicated. The resolved V, D, and J-Chains, if known, are listed for each clone.

<sup>b</sup> Grey = V-Gene

Green = Start of CDR3 Region in V-Gene

Purple = N1 Junction

Blue = D-Gene

Red = N2 Junction

Orange = J-Gene