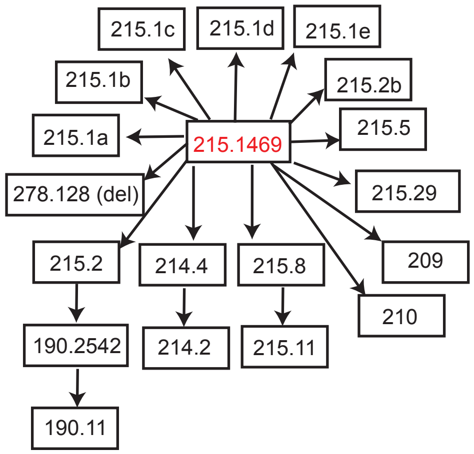
Supplemental Figure 3

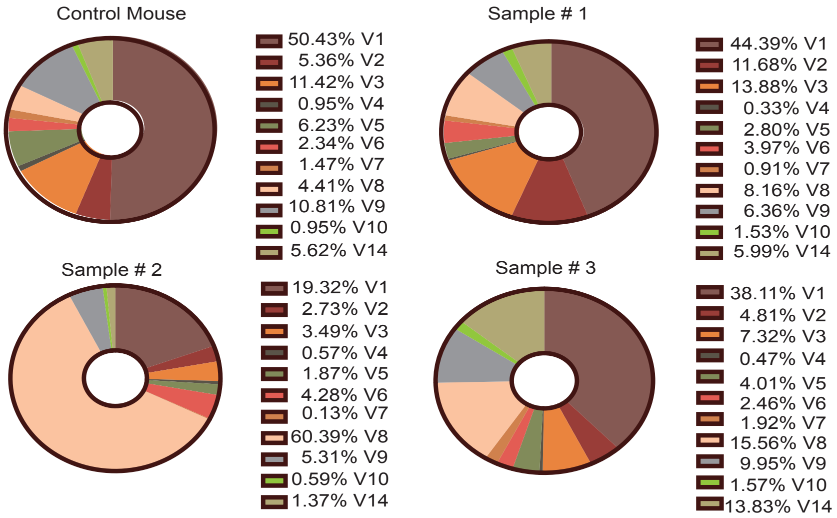
A

Sample	Sequences assigned to clonotypes	Independent clonotypes Identified	Clonotypes above 1% of total samples	Clonal Size of major clonotypes	VDJ Clonal Association	CDR3 Sequence	SMH in the V region	Homogeneity (size of clonotypes)	Number of Variants
# 1	6517	3015	3	1.69%	[V2-5/D1-1/JH1]	AKNRAIYYGSTYGYFDV	1.5%	44.55%	13
				1.10%	[V8-8/D1-1/JH1]	ARIYYYGSYWYFDV	1.23%	93.06%	4
				1.00%	[V8-12/D4-1/JH1]	ARRGVGRKGYFDV	1.38%	100%	1
# 2	7962	1617	6	52.21%	[V8-12/D2-4/JH1]	ARRRGLRWYFDV	0.57%	60%	18
				2.20%	[V1-78/D1-1/JH2]	ARYGPYYFDY	1.25%	96.57%	5
				1.58%	[V8-12/D/JH1]	ARYFDV	0.59%	95.24%	2
				1.41%	[V9-3/D2-4/JH1]	ARSSASLIYYDYEGYCDV	1.60%	88.39%	6
				1.34%	[V6-3/D4-1/JH2]	TEANWAFYFDY	0.55%	95.33%	3
				1.13%	[V1-9/D3-1/JH2]	ARSWLGLYFDY	2.01%	96.67%	3
# 3	9973	3895	8	7.09%	[V14-4/D2-14/JH2]	TTRYQ	1.39%	93.58%	6
				4.84%	[V8-8/D1-1/JH2]	ARIAPLFITTVVAPFDY	0.8%	53.62%	20
				3.30%	[V1-53/D2-1/JH2]	ARLLGDY	1.74%	93.01%	6
				3.08%	[V9-1/D2-5/JH4]	VMKGDYSNYVRGYYAMDY	0.83%	82.41%	10
				2.11%	[V1-53/D2-14/JH2]	ARLIGDY	1.54%	51.43%	2
				1.74%	[V3-6/D2-13/JH2]	ARDGDWGYFDY	0.6%	98.28%	3
				1.65%	[V8-8/D2-14/JH2]	AQIDWYYFDY	0.8%	36.26%	10
				1.32%	[V1-80/D2-13/JH2]	ARDWRRFDY	1.83%	100%	1

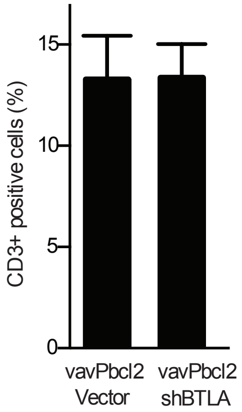
B



C



D



E