

PerC B-1a (n=310 total sequences)			PerC B-1b (n=340 total sequences)			Spleen B-1a (n=214 total sequences)			Spleen B-1b (n=155 total sequences)		
CDR-H3 Sequence	V-D-J	Number of CDR-H3 specific replicates (%)	CDR-H3 Sequence	V-D-J	Number of CDR-H3 specific replicates (%)	CDR-H3 Sequence	V-D-J	Number of CDR-H3 specific replicates (%)	CDR-H3 Sequence	V-D-J	Number of CDR-H3 specific replicates (%)
AGDYDGYWYFDV	VH12 - DH2 - JH1	217 (70 %)	AGDRDGYWYFDV	VH12 - DH2 - JH1	91 (26.8 %)	AREVTTMYYFDY	VH1 - DH2 - JH2	30 (14 %)	AREDYYGSSYYFDY	VH1 - DH1 - JH2	15 (9.7 %)
ARSYYYGSSYYFDY	VH1 - DH1-1 - JH2	13 (4.2 %)	AREDYYGSSYYFDY	VH1 - DH2 - JH2	52 (15.3 %)	AGDYDGYWYFDV	VH12 - DH2 - JH1	20 (9.3 %)	TYYGNYENYTDY	VH14 - DH2 - JH4	14 (9.0 %)
AGDRWGYWYFDV	VH12 - DH4 - JH1	13 (4.2 %)	AREVTTMYYFDY	VH1 - DH2 - JH2	18 (5.3 %)	MRYGDYWYFDV	VH11 - DH2 - JH1	8 (3.7 %)	ARAYGSSPYWYFDV	VH1 - DH1 - JH1	6 (3.9 %)
ARYYGNYWYFDV	VH1 - DH2 - JH1	6 (1.9 %)	AGDLLGYWYFDV	VH12 - DH2 - JH1	11 (3.2 %)	MRYSNYWYFDV	VH11 - DH2 - JH1	8 (3.7 %)	ARDDGYHGDWYFDV	VH1 - DH2 - JH1	4 (2.6 %)
AGDLLGYWYFDV	VH12 - DH2 - JH1	5 (1.6 %)	AREATTLDDFFDY	VH1 - DH1 - JH2	5 (1.5 %)	AGSDSGYWYFDV	VH12 - DH2 - JH1	6 (2.8 %)	ATGSSFDY	VH1 - DH1 - JH2	3 (1.9 %)
ARDYYWYFDV	VH1 - DH2 - JH1	4 (1.3 %)	ARWDYDYPYRAMDY	VH1 - DH1- JH4	5 (1.5 %)	TRYYGSSAMDY	VH6 - DH1 - JH4	6 (2.8 %)	ASITTVVATPYYFDY	VH1 - DH1 - JH2	3 (1.9 %)
AGSDSGYWYFDV	VH12 - DH2 - JH1	4 (1.3 %)	ATGSSFDY	VH1 - DH1 - JH2	3 (0.9 %)	ASYYGNYWYFDV	VH1 - DH2 - JH1	4 (1.9 %)	MRYGDYWYFDV	VH11 - DH2 - JH1	3 (1.9 %)
AGDYGYWYFDV	VH12 - DH1-1 - JH1	3 (1.0 %)	AGDTTGYWYFDV	VH12 - DH2 - JH1	3 (0.9 %)	ARSYYYGSSYYFDY	VH1 - DH1 - JH2	4 (1.9 %)	MRYSNYWYFDV	VH11 - DH2 - JH1	3 (1.9 %)
ASYYGNYWYFDV	VH1 - DH2 - JH1	2 (0.6 %)	TYYGNYENYTDY	VH14 - DH1 - JH4	3 (0.9 %)	AGDYGYWYFDV	VH12 - DH1 - JH1	4 (1.9 %)	AGSDSGYWYFDV	VH12 - DH2 - JH1	2 (1.3 %)
ATYYSNYWYFDV	VH1 - DH2 - JH1	2 (0.6 %)	ARRGNSYGNTFWYFDV	VH3 - DH1 - JH1	3 (0.9 %)	AKNDYGIYYAMDY	VH2 - DH1 - JH4	4 (1.9 %)	AGDRNGYYHFDV	VH12 - DH2 - JH1	2 (1.3 %)
AREGDYYYGSSYWFA	VH1 - DH1-1 - JH3	2 (0.6 %)	ARSYGYAMDY	VH1 - DH2 - JH4	2 (0.6 %)	AKNEWLLERYAMDY	VH2 - DH2 - JH4	3 (1.4 %)	AGDRDGYWYFDV	VH12 - DH2 - JH1	2 (1.3 %)
MRYSNYWYFDV	VH11 - DH2 - JH1	2 (0.6 %)	ARGGFAY	VH1 - DH1 - JH3	2 (0.6 %)	ARSYGYAMDY	VH1 - DH3 - JH4	2 (0.9 %)	TYYANSENYTDY	VH14 - DH2 - JH4	2 (1.3 %)
AGDTTGYWYFDV	VH12 - DH4 - JH1	2 (0.6 %)	ASGLGVYWYFDV	VH1 - DH1 - JH1	2 (0.6 %)	ARYDYDEGDY	VH1 - DH2 - JH2	2 (0.9 %)	ARRGDYFDY	VH2 - DH1 - JH2	2 (1.3 %)
AGDRTGYWYFDV	VH12 - DH4 - JH1	2 (0.6 %)	ARSNYAMDY	VH1 - DH2 - JH4	2 (0.6 %)	ARMGNYGSRYFDV	VH1 - DH1 - JH1	2 (0.9 %)			
AGDPYDGYYGFA	VH12 - DH2 - JH3	2 (0.6 %)	AREDYYGSNYFDY	VH1 - DH1 - JH2	2 (0.6 %)	ARGWLLRYYYAMDY	VH1 - DH2 - JH4	2 (0.9 %)			
AGDRDGYWYFDV	VH12 - DH2 - JH1	2 (0.6 %)	AGDNDGYYGFA	VH12 - DH1 - JH3	2 (0.6 %)	ARRDGYGGFA	VH1 - DH2 - JH3	2 (0.9 %)			
AKLR*XLL*L	VH2 - DH1-1 - JH2	2 (0.6 %)	AGDRDGYYSFDV	VH12 - DH1 - JH3	2 (0.6 %)	ANWAY	VH1 - DH4 - JH3	2 (0.9 %)			
ARYYYGSSYAMDY	VH7 - DH1-1 - JH4	2 (0.6 %)	AGSDGYWYFDV	VH12 - DH2 - JH1	2 (0.6 %)	AREDYYGSSYYFDY	VH1 - DH1 - JH2	2 (0.9 %)			
			TTPSPNSNSFDY	VH14 - DH1 - JH2	2 (0.6 %)	VRDGITTVVAWDYAMDY	VH10 - DH1 - JH4	2 (0.9 %)			
			TPHYYGSPWFA	VH14 - DH2 - JH3	2 (0.6 %)	AGDPDGYDFDV	VH12 - DH2 - JH1	2 (0.9 %)			
			TYYGNYESVMDY	VH14 - DH1 - JH4	2 (0.6 %)	AGDKTGWYFDV	VH12 - DH4 - JH1	2 (0.9 %)			
			ARNGGGLWSYYAMDY	VH2 - DH1 - JH4	2 (0.6 %)	AGDRTGYWYFDV	VH12 - DH4 - JH1	2 (0.9 %)			
			TRYYGSSAMDY	VH6 - DH2 - JH4	2 (0.6 %)	ARRDYYYGSSYDYWYFDV	VH2 - DH1 - JH1	2 (0.9 %)			
			TYDYDWYFDV	VH6 - DH2 - JH1	2 (0.6 %)						
Frequency of replicate sequences:		91.5 %	65.6 %			54.2 %			39.3 %		