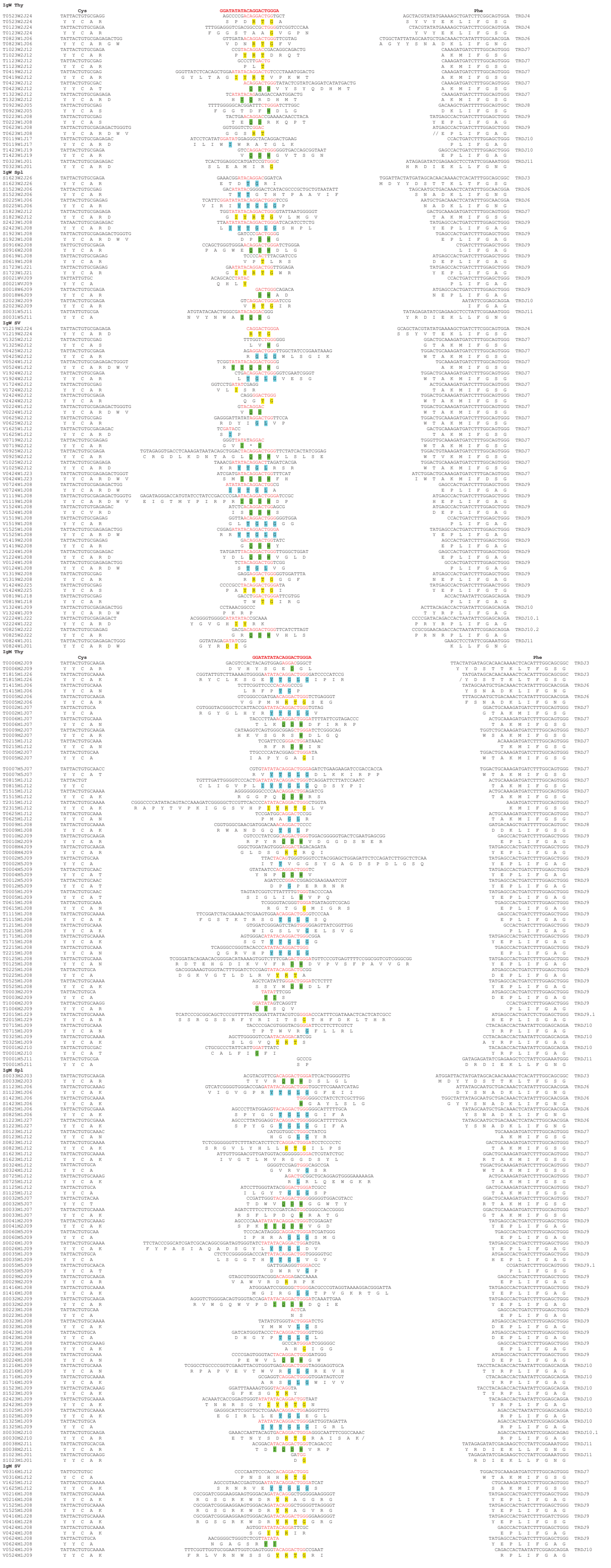
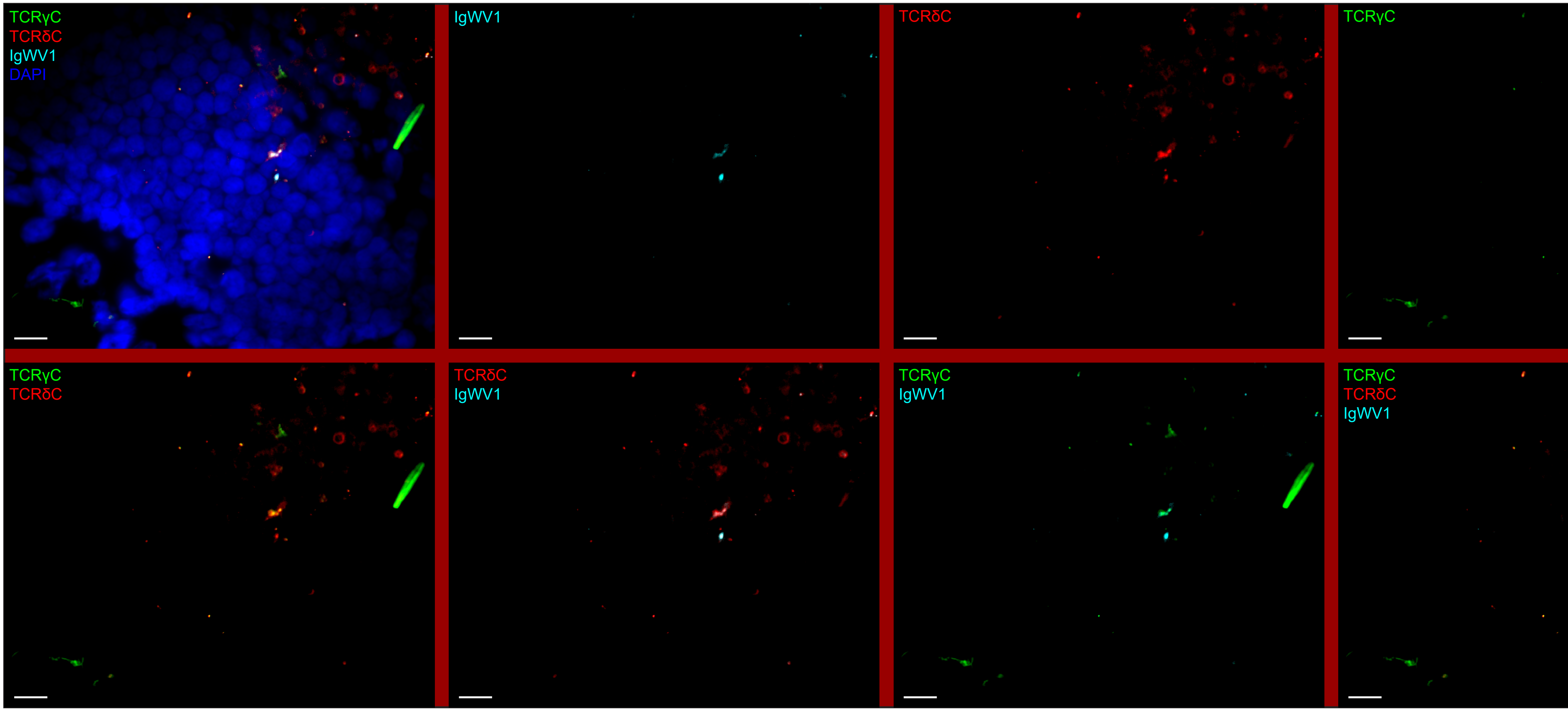
Supplemental Table 1: Primers

Primer Name	For/Rev	Domain	Sequence	Priming Site
FLAJ1701	F	IgM1 V region	5’-TTCAATCTTGGCAACGAC-3’	FNLGND
FLAJ1703	F	IgM1 V region	5’-GTTCGATCTTGACAGCTATG-3’	FDLDSY
FLAJ1699	F	IgW1 V region	5’-TCTGAGATCACGCTGACC-3’	SEITLT
MFC185	F	IgW2 V region	5’-TATAATGGAAGGATTTCAGAGATCGTCCTGAGACAGCCCGAG-3’	EIVLRQPE
MFC239	F	IgMV1 FR3	5’-AACCTGAAGATCGAAGACACC-3’	NLKIEDT
MFC214	F	IgMV2 FR3	5’-CTGCGTCCAAAGACACTTCA-3’	ASKDTS
MFC215	F	IgWV1 FR3	5’-CCAAGGACAGCGACACAGTA-3’	KDSDTV
FLAJ861	F	TCRδV1	5'-ATCATTTCGAGGCTGCAGTTGACT-3'	IISRLQLT
FLAJ862	F	TCRδV2	5'-ACTGTCACTGGGTTACAACTGACC-3'	TVTGLQLT
FLAJ863	F	TCRδV3	5'-ACTATCAATGGGCTAGAACTCACT-3'	TINGLELT
FLAJ864	F	TCRδV4	5'-ACTATAACTGGGCTGCAGCTGACT-3'	TITGLQLT
FLAJ865	F	TCRδV5	5'-ACTATCGCTGGACTACAGCTGACT-3'	TIAGLQLT
FLAJ866	F	TCRδV6	5’-ATAATCTCTCGAACACAACTGAGT-3’	IISRTQLS
FLAJ867	F	TCRδV7	5’-AAGATCTCCACATTACAACTGAGT-3’	KISTLQLS
FLAJ868	F	TCRδV8	5'-AAGATCTCTGCAATACAACTGAAT-3'	KISAIQLN
FLAJ869	F	TCRδV9	5'-ATAATCTCTCGAGCACAACTGAGT-3'	IISRAQLS
FLAJ870	F	TCRδV10	5'-TCTATCTCGGAGCTGCAACTGTCT-3'	SISELQLS
FLAJ871	F	TCRδV11	5'-AAAATAGCAGCTGTTTCTCCCTCT-3'	KIAAVSPS
FLAJ872	F	TCRδV12	5'-ACGATCTCGGAGGTGCTGCTCACT-3'	TISEVLLT
FLAJ873	F	TCRδV13	5'-ACCATCCGTGATCTGCGACTGTCT-3'	TIRDLRLS
FLAJ874	F	TCRδV14	5'-AGAATTAATGAAACCCGTCTGTCT-3'	RINETRLS
FLAJ710	R	TCRδ cyto. tail	5’-AGAAATCCAGACTCGGGCAG-3’	ARVWIS
FLAJ767	R	TCRδ C	5’-CTGAACGCCACATAGCTGCCA-3’	GSYVAFS
MFC132	R	IgM C1	5’-TGACAGGAGGAGACGAGACC-3’	GLVSSCQ
MFC242	R	TCRδ C	5’-TCTTTGCTTGAGGATTTTGGTG-3’	PKSSSKD
MFC243	R	TCRδ C	5’-CAGACAGACTGCAGCTTGG-3’	QAAVCL
MFC133	R	IgM C1	5’-ATCGCCAAACAACCAAAAAT-3’	IFGCLAM
MFC225	R	IgW C1	5’-TCACACGAAGGATTAGAGATG-3’	ISNPSCD
MFC180	F	IgMV FR1	5’-TATGATGGAAGGATTTCACAAATTATTTTGACTCAAAAAGTGGCAGAA-3’	QIILTQKVAE
MFC181	R	IgMV1 J	5’- TATTATAAGCTTTCAAGTCACGGTCACCATGGTCCCTTG-3’	QGTMVTVT
MFC182	F	IgWV1 FR1	5’-TATAATGGAAGGATTTCAGAGATCACGCTGACCCAGCCCGAG-3’	EITLTQPE
MFC183	R	IgWV J	5’-TATTACAAGCTTGTCATGAAGTCACTTCCAGAAAGGTTCCGCT-3’	SGTFLEVTS
MFC184	F	IgW2 FR1	5’- TATAATGGAAGGATTTCAGAGATCACGCTGACCCAGCCCAAG-3’	EITLTQPK



Supplemental Figure 1. Nucelotide alignment of Ig-TCRδ CDR3 region. Nucleotide alignments of Ig-TCRδ transcripts from thymus (Thy), spleen (Spl), and spiral valve (SV) are displayed with accompanying amino acid residues. The contributing IgHV class and group are denoted in the second column preceding the nucleotide alignment. The TCRδJ used in the rearrangements are labelled immediately following the nucleotide alignment. The TRDD1 originating nucleotides are highlighted in red with the accompanying amino acid residues highlighted according to the frame the D-segment is read in (frame1-green, frame 2-yellow, frame 3-cyan). The Cys and Phe residues highlighted above the nucleotide indicate the 5' and 3' CDR3 boundaries respectively.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IgWV1
DAPI
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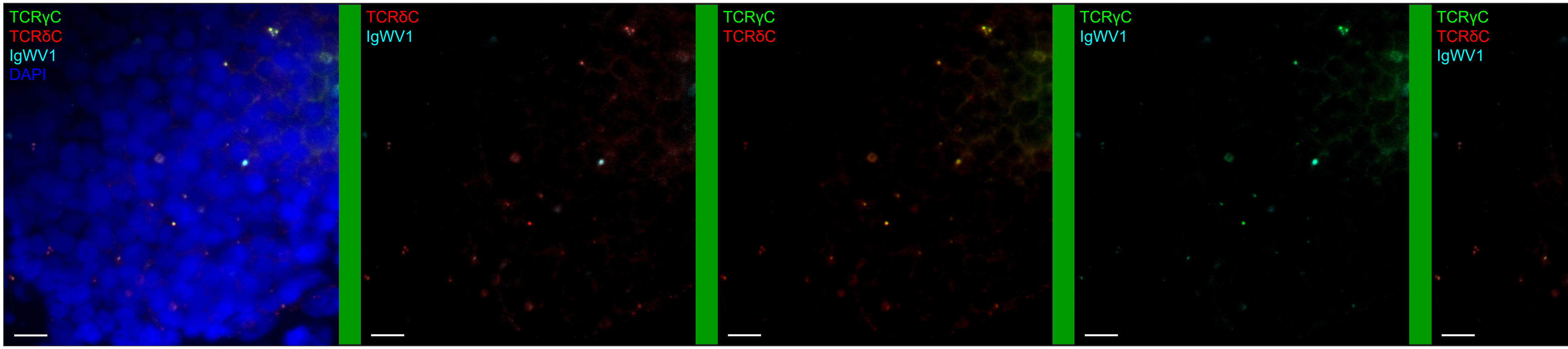
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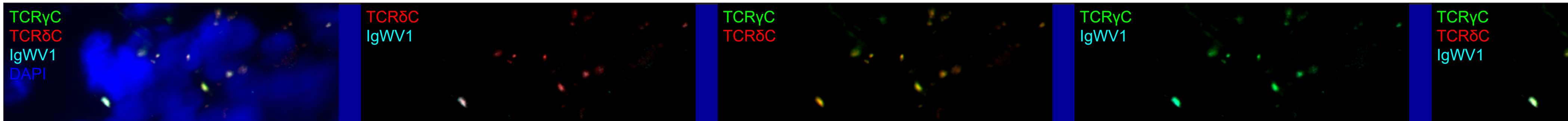
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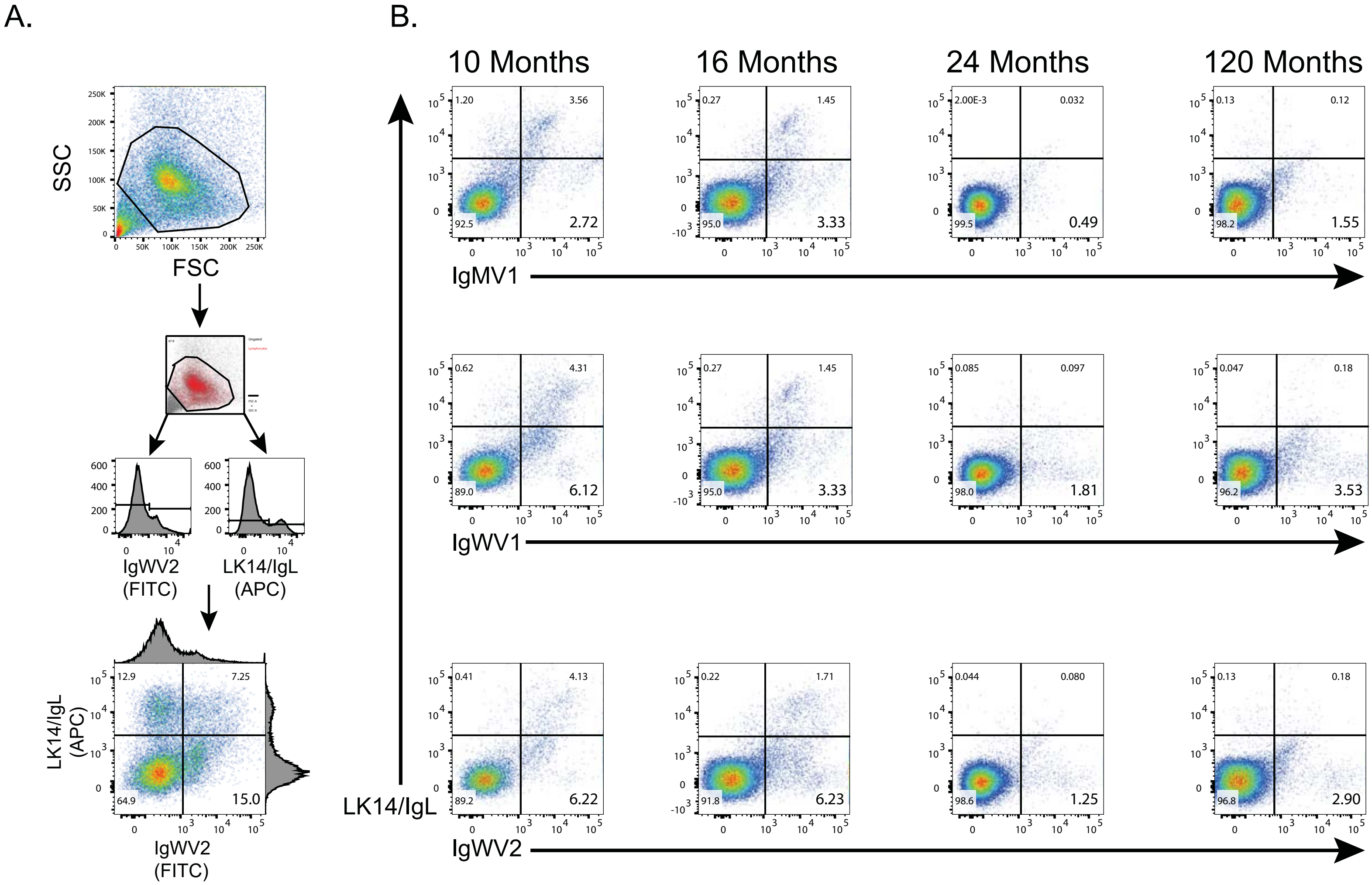

Supplemental Figure 3. Flow cytometric analysis with Ig specific polyclonal antibodies evince IgHV-TCRδ as a cell surface receptor. (A) Gating and signal threshold workflow using splenic lymphocytes. Lymphocyte populations were isolated using forward and side scatter (top, selected cells red in middle). Thresholds for quadrant gating was determined via histogram analysis of the FITC (IgHV polyclonal) and APC (LK14) channels (middle and bottom). All samples were analyzed with identical threshold parameters except the 120-month sample, which had lower overall fluorescent intensity. (B) Quadrant plots and population percentages for sorted thymic lymphocytes. Anti-IgHV polyclonal fluorescent intensity is plotted on the x-axis, while anti-LK14/IgL intensity is plotted on the y-axis. Quadrants were all determined using splenic controls that did not diverge amongst groups except the aforementioned 120-month sample. The bottom left quadrant houses T cells (percentages in enlarged text), while the top right houses B cell populations. The bottom right quadrant, housing cells that were IgHV+/IgL- are the prospective IgHV-TCRδ chimeric receptor bearing cells.