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Basic

Research Article

Nurse shark T-cell receptors employ somatic hypermutation preferentially to alter alpha/delta variable segments associated with alpha constant region

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In addition to canonical TCR and BCR, cartilaginous fish assemble noncanonical TCR that employ various B-cell components. For example, shark T cells associate alpha (TCR-α) or delta (TCR-δ) constant (C) regions with Ig heavy chain (H) variable (V) segments or TCR-associated Ig-like V (TAILV) segments to form chimeric IgV-TCR, and combine TCRδC with both Ig-like and TCR-like V segments to form the doubly rearranging NAR-TCR. Activation-induced (cytidine) deaminase-catalyzed somatic hypermutation (SHM), typically used for B-cell affinity maturation, also is used by TCR-α during selection in the shark thymus presumably to salvage failing receptors. Here, we found that the use of SHM by nurse shark TCR varies depending on the particular V segment or C region used. First, SHM significantly alters alpha/delta V (TCRαδV) segments using TCR αC but not δC. Second, mutation to IgHV segments associated with TCR δC was reduced compared to mutation to TCR αδV associated with TCR αC. Mutation was present but limited in V segments of all other TCR chains including NAR-TCR. Unexpectedly, we found preferential rearrangement of the noncanonical IgHV-TCRδC over canonical TCR αδV-TCRδC receptors. The differential use of SHM may reveal how activation-induced (cytidine) deaminase targets V regions.

Keywords: Shark · Somatic hypermutation · T-cell receptor · TCRα/TCRδ locus · Thymus

Additional supporting information may be found online in the Supporting Information section at the end of the article.

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Introduction

Jawed vertebrates evolved a sophisticated Ig superfamily (IgSF)-based adaptive immune system composed of B and T cells, a polymorphic and polygenic MHC, RAG-mediated somatic recombination, and activation-induced (cytidine) deaminase (AID)-mediated SHM [1–3]. This system relies on the rearrangement of variable (V), diversity (D), and joining (J) gene segments to generate the Ig heavy and light chains of BCR and the four canonical TCR chains during lymphocyte development [4–6]. Loci encoding each chain contain numerous V, (D), and J gene segments, and the resulting combinatorial potential results in a highly diverse immune repertoire (see Fig. 1) [7]. Each chain is encoded on separate loci (except TCR-δ, which is embedded within TCR-α) and loci are organized either as clusters of V, (D), and J segments followed by constant (C) region exons $(V\text{-}D\text{-}J\text{-}C)_n$ or as a contiguous translocon containing numerous V segments, (D segments), and J segments followed by C-region exons $(V_nD_nJ_nC)$ [8, 9]. Lymphocytes further diversify antigen receptors during recombination by adding and subtracting nucleotides at gene segment joins, creating a unique third CDR3 that is highly variable in sequence and length. Traditionally, after gene recombination, Ig heavy chains (IgH) dimerize with Ig light chains (IgL) to form BCR expressed on the B-cell surface or antibodies secreted into the body humors, and TCR alpha (α) and beta (β) or gamma (γ) and delta (δ) chains dimerize to form canonical TCR expressed on the surface of T cells (see Fig. 1) [6, 10]. Together these mechanisms construct the efficient and effective adaptive immune repertoire necessary to respond to infection.

In B cells, receptor gene recombination occurs during lymphocyte development and cells exit bone marrow (or analogous primary lymphoid tissues, such as epigonal organ, in sharks) as naïve lymphocytes with functional receptors. Exposure to antigen in the follicles of peripheral lymphoid tissue activates naïve mature B cells, stimulating BCR to undergo affinity maturation. During this process, AID catalyzes SHM of V regions followed by selection of the B cell, ultimately creating highly honed receptors for particular antigens [11]. Receptor gene recombination in T cells occurs similarly during thymic development. However, αβ TCR must undergo both positive and negative selection to ensure suitable binding to self-MHC but not to self-antigen; in this way, self-MHC referential yet self-tolerant T cells emerge from the thymus as mature cells [12, 13]. Research in mice and humans demonstrates that unsuccessful receptors can be rescued by further locus rearrangement (receptor editing), but ultimately most cells undergo apoptosis and are removed from the potential repertoire [14–17].

Recent studies in nurse sharks (*Ginglymostoma cirratum*) and other nonmodel vertebrates suggest that the boundaries between B- and T-cell components and repertoire diversification mechanisms are blurred in comparison to mouse and human. For example, marsupials and monotremes (e.g., *Monodelphis domesticus*, *Ornithorhyncus anatinus*) contain a unique TCRμ locus (TCRμ) that contains V, D, and J gene segments that somatically recombine, or are prejoined within germline DNA [18, 19], to form a receptor chain with two variable domains, the membrane-distal of which resembles IgH. Further, IgHV or Ig-like TCR-δ V segments (VHδ) are found in TCR-α/δ loci of all gnathostome groups except teleosts and placental mammals [20–26]. While many TCR-associating IgHV or VHδ genes are housed within the conventional αδ TCR locus, VHδ segments in Galliform birds are found in a second distinct TCR locus [22]. Nurse shark T cells assemble TCR using components traditionally considered BCR components, rearranging IgM or IgW (analogous to IgD) V segments to TCR alpha or delta constant (C) regions (see Fig. 1), though it remains unclear whether sharks are using IgHV only from within the conventional TCR-α/δ locus (cis-rearrangements) or are recombining Ig and TCR from separate loci (trans-rearrangements) as well [25, 26]. Doubly rearranging NAR-TCR, composed of a membrane-distal Ig-like NAR V domain and a proximal, supporting TCR δV domain, also marries unique Ig and TCR components into a single receptor (see Fig. 1) [27, 28]. Our lab recently discovered Ig-like V segments in nurse sharks that associate with TCR-α or -delta C regions (TCR-associated Ig-like V, TAIL V, see Fig. 1) [25]. Additionally, T cells can exploit BCR diversification mechanisms like AID-catalyzed SHM to generate additional thymic diversity. Chen et al. [29] presented definitive evidence that sandbar sharks utilize SHM to diversify gamma chain of γδ T cells, and camels employ SHM to diversify both TCR gamma and delta chains [29–33]. Additionally, nurse sharks utilize SHM for AID-catalyzed receptor salvaging to assist thymocytes through selection during thymic development [34]. Thus, gnathostome adaptive immunity displays remarkable elasticity in T-cell diversification mechanisms.

We examined a large dataset of TCR sequences to assess whether nurse sharks utilize SHM specifically for alpha-chain receptor salvaging or if SHM affects other canonical TCR chains and noncanonical receptors (IgH-TCRC rearrangements, NAR-TCR, and TAIL V-TCR C) alike. Additionally, this dataset compelled us to revise the current nomenclature for V gene segments within the alpha/delta (TCR-αδ) locus. Finally, we examine the use of SHM in light of the immunogenetic elasticity observed within the nurse shark TCR-αδ locus.

Results

Canonical nurse shark T cell receptor chains suggest few V segment families with many subfamilies

Our TCR data set contained 229 TCR-beta (TCR βV), 158 TCR-gamma (TCR γV), and 761 TCR-α/δ (TCR αδV) newly cloned or previously published V gene sequences (1149 total clones, see Supporting information Table 1 and 2). Using a refined approach to grouping V segments, we reduced the putative number of published TCR βV families to four, with TCR βV1 and TCR βV2 containing four and two subfamilies each, respectively (Fig. 2A; Supporting information Fig. S1A and S5). We reclassified TCR γV clones into four families (TCR γV1-TCR γV4) with multiple

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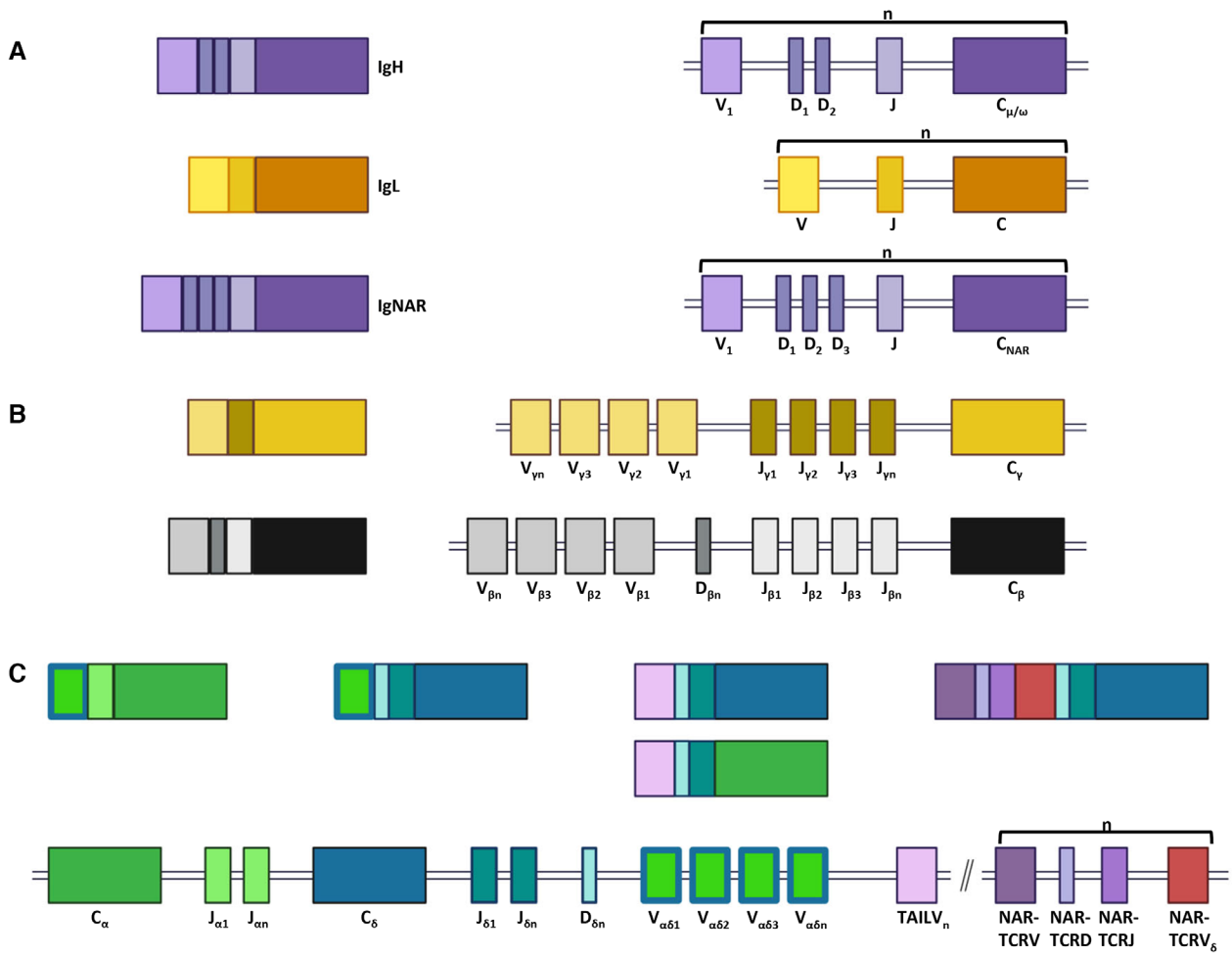

Figure 1. Nurse sharks generate complex B- and T-cell receptors. (A) Immunoglobulin (Ig) heavy (H, top) and light (L, middle) chains, and new (or nurse shark) antigen receptor (IgNAR, bottom) form from traditional B-cell components. B-cell (Ig) loci are organized in clusters of variable (V), (diversifying, D), and joining (J) gene segments followed by a constant region (VDJ-C or VJ-C, shown as a single cluster for each chain). (B) T-cell receptor (TCR) gamma (γ, top) and beta (β, bottom) chains form from traditional T-cell components located within individual translocons. (C) TCR delta (δ) chain is embedded within the TCR alpha (α) translocon and shares a common pool of V gene segments. Additionally, TCR-associated Ig-like V (TAILV) and both domains of NAR-TCR are found within this same locus. NAR-TCR gene segments occur in clusters of NARTCR V, NARTCR D, NARTCR J, and NAR-TCR Vδ (shown as a single cluster). Rearranged gene segments create traditional TCRα and TCRδ chains as well as unique, untraditional receptors (TAILVα or TAILVδ, and both domains of NAR-TCR). Further, IgHV-TCRδ rearrangements integrate components of IgH and TCR loci. VDJ gene segments and constant regions are color coded to correspond to the receptor chain they encode [Figure created with BioRender.com].

subfamilies in all but TCR γV4 (Fig. 2B; Supporting information Fig. S1B and S5). We did not identify any alleles for either chain. The 761 TCR-αδ clones sorted into 11 putative TCR αδV families and 24 subfamilies (Fig. 2C; Supporting information Fig. S2 and S5). Five of the 11 TCR αδV families spliced only to TCRα constant (C) region (TCR αδV 1, 4, 5, 7, and 9), two utilized only TCRδ C (TCR αδV 3 and 10), and four spliced interchangeably with TCR αC and TCR δC (TCR αδV 2, 6, 8, and 11). Five TCR αδV subfamilies included at least two alleles. For all canonical TCR chains, complete V gene segments contained the conserved tryptophan and two cysteine residues common to the IgSF domain (see Fig. 2) except TCR αδV11 (which includes only the conserved cysteine at position 104). This finding contrasts previous results indicating that TCR δV16 (TCR αδV8.2) lacks the first cysteine residue [26].

Noncanonical T cell receptor variable gene segments are highly conserved

In addition to the canonical αβ and γδ TCR, we previously identified three "chimeric" nurse shark TCR containing Ig or Ig-like components: (1) IgHV can be associated with δC (or rarely, TCR-αC), rearranging an IgM or IgW (analogous to IgD) V segment to a TCRδC (or TCRαC) C region [26]; (2) doubly rearranging NAR-TCRs are composed of membrane-distal Ig-like V (NTCR V) and membrane-proximal or "supporting" TCR δV (STCR δV) [28]; and (3) TAIL V segments recombine Ig-like V and D segments to TCR J segments and can associate with either TCR αC or TCR δC regions (see Fig. 1) [25]. We sequenced 195 IgMV-TCR δC, 77 IgWV-TCR δC, 69 NAR-TCR (51 NTCR V and 62 STCR δV complete domains), and nine TAIL V clones (Supporting information Table S1 and S2).

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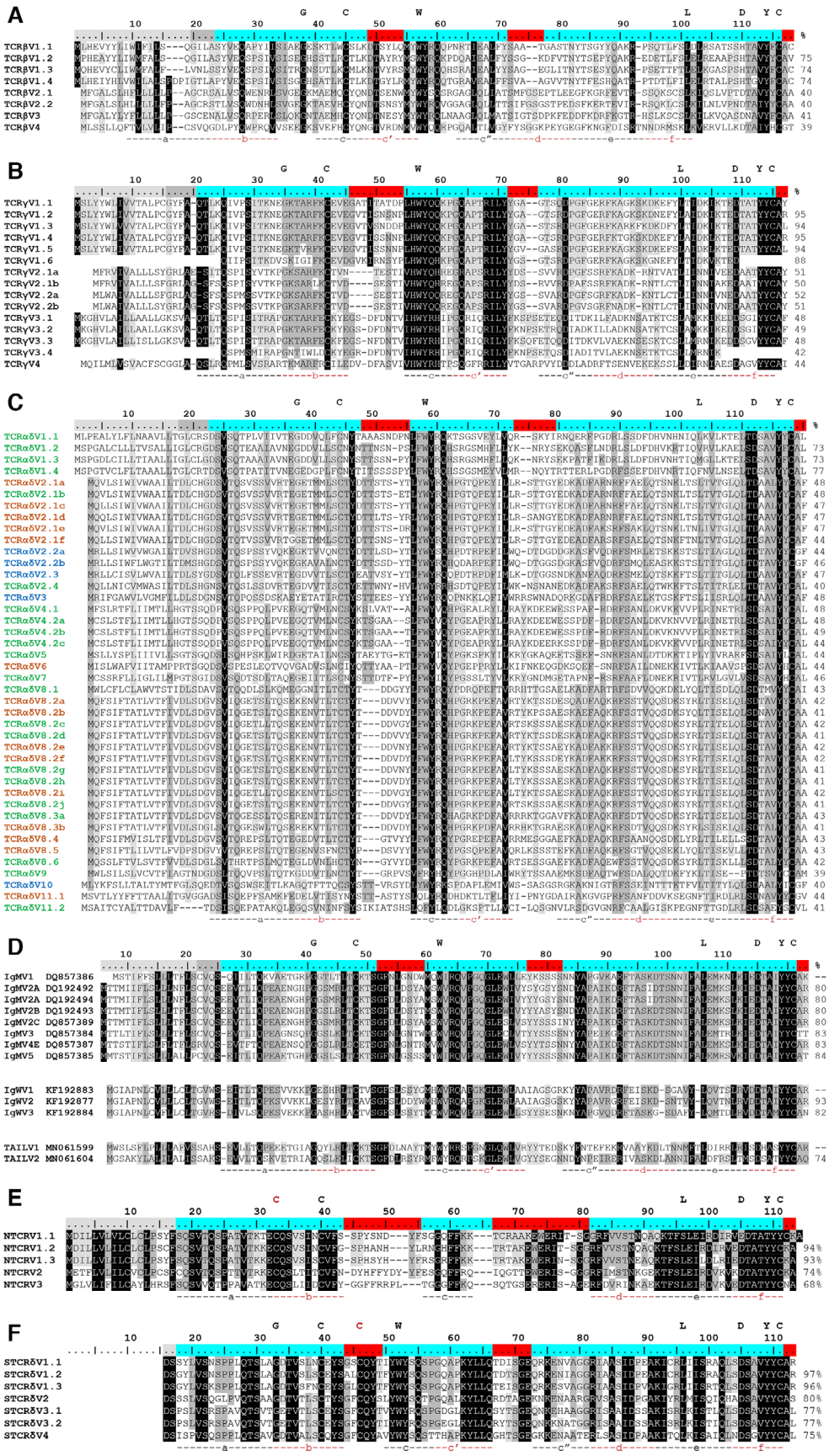

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IgHV-TCR δC clones aligned with five of the six canonical IgM germline groups (IgM V1-V5) and three of the six canonical IgW groups (IgW V1-V3) [35]. We identified three IgM V2 subfamilies and two IgW V1 subfamilies in our dataset (Fig. 2D; Supporting information Fig. S3 and S5). IgM V2C is an Ig pseudogene (due to defective Ig constant region exons), but we observed functional transcripts associated with TCR δC. Interestingly, our 5' RACE libraries primed with TCR δC-specific primers generated more clones associated with IgM/IgW V segments (58%) than to canonical TCR αδV segments. These libraries comprised data from two "young" sharks (Tom Thumb, a neonate and Florence Nightingale, 3' in length) and two "old" sharks (White and Grumpy, both greater than 8' in length). Libraries from younger sharks generated more canonical TCR αδV-TCR δC arrangements (69 of 115 clones, 60%) and those from older sharks generated more noncanonical IgHV-TCR δC arrangements (75 of 126 clones, 60%). However, further study characterizing IgHV-TCR δC rearrangements is required to verify these observations.

Based on our conservative naming strategy, all NTCR V gene segments belonged to a single family containing three subfamilies, and subfamily NTCR V1 included four different alleles (Fig. 2E; Supporting information Fig. S4 and S5). All "supporting" V gene segments (STCR δV) comprised a single gene family composed of four subfamilies. Both STCR δV1 and STCR δV3 contained multiple alleles. However, we retained subfamily names in V segment identities for consistency with published data. We observed multiple combinations between NTCR V and STCR δV domains, but in general NTCR V1 associated with STCR δV1 (NTCR V1.1- STCR δV1.1a, NTCR V1-STCR δV1.1b; NTCR V1.2-STCR δV1.1b; NTCR V1.3-STCR δV1.2; NTCR V1.4-STCR δV1.3), NTCR V2 associated with both STCR δV2 and STCR δV4, and NTCR V3 associated with STCR δV3 (V3.1 and V3.2). In addition to the conserved tryptophan and two cysteine residues found in other TCR, all functional NAR-TCR sequences contained the noncanonical interdomain cysteine in FR1 of NTCR V (and CDR1 of STCR δV) required for domain stability [36].

Hotspot motifs in nurse shark T cell receptor variable segments do not necessarily predict mutation

AID preferentially alters C and G residues of WRCH/DGYW motifs of antigen receptors [37]. The number of WRCH/DGYW AID hotspot motifs in CDR did not differ from FR motifs in any of the canonical TCR V segments (see Fig. 3, Table 1). However, FR2 of TCR βV contained more WRCH/DGYW motifs than other FR. As expected, both CDR of IgHV contained more motifs than FR domains. NAR-TCR domains (NTCR V and STCR δV) contained the fewest WRCH/DGYW motifs in any region of all V segment types and within NTCR V, most WRCH motifs overlapped DGYW motifs, a pattern not observed in other V gene segments. Motif patterns did not vary by region. Thus, motif patterns alone do not predict mutation.

Mutation occurs in TCR αδV associated with TCR αC but not with TCR δC or other canonical TCR chains

SHM within TCR was first identified in TCRγ chain of sandbar sharks [29, 30]. However, although mutation appeared to target nucleotide motifs preferred by AID (WRCH/DGYW), mutation tended not to result in aa replacement within CDR, a requisite for paratope changes during affinity maturation. Rather, sandbar sharks appeared to use SHM to generate a more diverse repertoire [29, 30]. We previously confirmed that SHM occurred within TCRγ and TCR δV segments of nurse shark, but we found that SHM altered TCR αV far more than it did gamma or delta, with replacement mutation targeting AID-preferred motifs of CDR within the thymus. This suggested that TCR-α likely uses SHM to salvage failing receptors during thymic selection [34]. In both BCRs and TCRs of sharks, SHM can occur as single point mutations or tandem mutations of two or more contiguous nucleotides, indicating at least two different cellular mechanisms generate mutations [38–40].

We first attempted to corroborate earlier findings of SHM in canonical TCR of nurse sharks. However, despite having unique CDR3 regions, TCRβ and TCRγ showed very little variation within V segment nucleotide sequences (see Supporting information Table S1), with about 0.002 substitutions per nucleotide (S/N) for both chains (see Fig. 3 and 4, Supporting information Fig. S6A). While we observed contiguous mutations within both chains, the majority of mutation occurred as single base changes and most base changes resulted in aa replacement (R) rather than silent (S) mutation (TCR βV: R/S = 2.7; TCR γV: R/S = 2.1; Supporting information Fig. S6A). As previously observed, TCR γV segments contained substantially more mutation than TCR βV segments.

Figure 2. Consensus sequence alignments for T-cell receptor V segments indicate substantial conservation between segments. V gene segments are grouped by identity for (A) beta (TCRβV) (B) gamma (TCRγV), (C) alpha/delta (TCRαδV), (D) immunoglobulin (Ig, IgMV and IgWV) and TCR-associated Ig-like V (TAILV), (E) NAR-TCR distal V domain (NTCRV), and (F) NAR-TCR proximal Vδ domain (STCRδV). V segment families share >70% nucleotide identity (e.g., TCRαδV2) and subfamilies have >80% nucleotide identity (e.g., TCRαδV2.1). Alleles share >90% nucleotide identity and common differences appear in more than one shark (e.g., TCRαδV2.1a). Letters above the scale denote conserved residues of antigen receptor domains. Regions below the alignment designate predicted beta strand location and direction. Shading within an alignment indicates amino acid conservation (Blosum62 score matrix [Threshold = 1]: black = 100% similar; dark grey = 80-100%; light grey = 60-80%). Values to the right of the alignments show the percent nucleotide identity to the first sequence. Highlighting within the scale indicates leader peptides (gray), framework regions (blue), and complementarity-determining regions (CDR, red). Coloring within the TCRαδV consensus sequence names identify the constant region used (green = TCR αC; blue = TCR δC; orange = both TCR αV and TCR δC). IgM or IgW germline sequence accession numbers are in sequence titles. IgM V2C is an Ig pseudogene due to defective Ig constant region exons but can form functional transcripts when associated with TCRα or TCRδ C. Each NAR-TCR V domain is encoded by V gene segments from a single gene family, but we employed original names to indicate the NARTCR cluster used. Gaps within a sequence are for alignment purposes only. Data from a single experiment, where each PCR tube represents a single replicate for each chain, shark, and tissue sample (see Supporting information Table 1 and 2).

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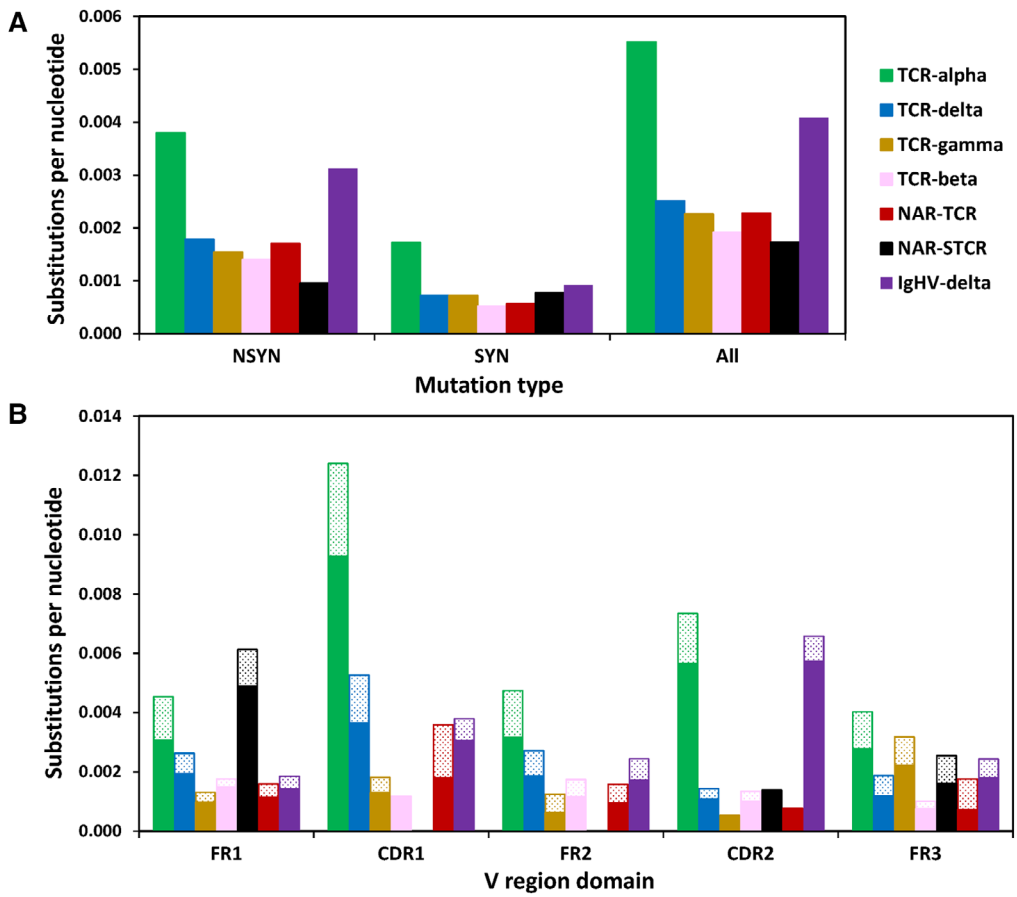

Figure 3. SHM targets complementarity-determining regions (CDR) of TCR-α associated with alpha constant regions. (A) TCR-α accumulates significantly more nonsynonymous (NSYN, solid) mutations than all other TCR chains except IgHV-δ sequences and significantly more synonymous (SYN, stippled) mutations than all other chains. (B) TCR-α/δ V gene segments associated with TCR-α constant (C) regions accumulate significantly more mutations in both framework (FR) and CDR than when associated with TCR-δ C, and in general, accumulate significantly more mutation than all other TCR chains except CDR2 domains of IgHV-δ (Student's one-way, unpaired *t*-test, $p < 0.01$). We counted the number of mutations within 422 TCR-α/δ V-TCR-α C (green), 137 TCR-α/δ V-TCR-δ C (blue), 158 TCR-γ V (gold), 237 TCR-beta V (pink), 51 NARTCR V (red), 62 supporting NARTCR-δ V (NAR-STCR, black), and 275 IgHV-TCR-δ C (purple) sequences (Student's one-way, unpaired *t*-test, $^{*}p < 0.05$; $^{**}p < 0.01$). Data from a single experiment, where each PCR tube represents a single replicate for each chain, shark, and tissue sample (see Supporting information Tables 1 and 2).

While TCR βV sequences accumulated more mutations to FR1 (0.0018 S/N) and fewer to CDR1 (0.0012 S/N; Fig. 3 and 4), TCR γV mutation was highest in FR3 (0.0032) and lowest in CDR2 (0.0005; Fig. 3 and 4). Most mutations in TCR βV (61%) and TCR γV (67%) were to C and G nucleotides, though only 35% of C/G mutations in TCR βV and 30% in TCR γV actually occurred within WRCH/DGYW motifs (Fig. 3 and 4; Table 2). Both TCR βV and TCR γV mutations were biased toward transitions (TCR βV FR: 49%, CDR: 44%; TCR γV FR:56%, CDR:63%; Table 2). TCR βV4 sequences exhibited the most mutation, with 64% of sequences (23 of 36) containing at least one nucleotide change (Supporting information Fig. S1). Again, we observed no mutation within any TCR γV4 segment (except a single base change in a leader region), suggesting this V segment may be useful as a partner chain with noncanonical receptors or with receptors highly specific for particular antigen.

We analyzed mutation data for V segments within the TCRαδ locus only if we could identify with certainty the constant region associated with the V segment. Thus, we included 422 TCR αδV associated with TCR αC and 140 TCR αδV associated with TCR δC in our analyses. We first confirmed previous results that CDRs of TCR αδV-TCR αC mutated significantly more than FRs (Fig. 3 and 4), with CDR1 accumulating the most mutation [34]. Within the TCRαδ locus, TCR αδV-TCR αC accrued more than twice as many mutations (0.0055 S/N) as TCR αδV-TCR δC (0.0025; $p = 0.002$; Fig. 3 and 4, Supporting information Fig. S6B). As expected, WRCH/DGYW motifs within V segments used by TCR αC strongly correlate with those used by TCR δC (Pearson correlation, $r = 0.94$; $p < 0.001$). However, TCR αδV-TCR αC mutated significantly more than other canonical TCR chains (beta: $p = 0.0006$; gamma: $p = 0.007$). Mutation in TCR αδV-TCR αC was biased toward C/G mutations (57%) and slightly biased toward transitions (45%) (Table 2). Most C/G mutations occurred within WRCH/DGYW motifs, especially in CDR (FR: 58%, CDR: 71%; 57% overall). TCR αδV-TCR δC mutation also was biased toward C and G nucleotides (63%) within WRCH/DGYW motifs

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Table 1. Target nucleotide mutation frequency in DGYW/WRCH mutation hotspots within framework regions (FR) and complementarity-determining regions (CDR) of T cell receptor (TCR) variable region (V) segments

V segment	Hotspot motif	Region	# G/C Bases	% G/C	S/N	Observed G/C mutations	Expected G/C mutations	MI[a)]	χ^2 p[b)]
TCRαδV-TCRαC	DGYW/WRCH	FR	11008	1.9	1.27	140	5.9	23.62	0.0000
		CDR	2997	0.5	1.94	58	2.6	22.73	
		All	14005	2.4	1.41	198	8.3	23.96	0.0000
	Outside motif		568931		0.03	146	335.7	0.43	
TCRαδV-TCRδC	DGYW/WRCH	FR	4012	4.2	0.65	26	2.3	11.15	0.0000
		CDR	714	0.7	0.84	6	0.5	11.15	
		All	4726	4.9	0.68	32	2.9	11.15	0.0000
	Outside motif		90762		0.03	26	55.1	0.47	
TCRβV	DGYW/WRCH	FR	5476	9.8	0.29	16	5.5	2.92	0.0000
		CDR	925	1.7	0.32	3	0.7	4.28	
		All	6401	11.5	0.30	19	6.2	3.07	0.0000
	Outside motif		49435		0.07	35	47.8	0.73	
TCRγV	DGYW/WRCH	FR	3099	5.6	0.42	13	3.4	3.78	0.0000
		CDR	581	1.0	0.69	4	0.4	11.27	
		All	3680	6.6	0.46	17	3.7	4.58	0.0000
	Outside motif		51898		0.08	39	52.3	0.75	
IgHV-TCRδC	DGYW/WRCH	FR	4604	6.2	0.56	26	6.0	4.37	0.0000
		CDR	1995	2.7	1.10	22	3.5	6.33	
		All	6599	8.9	0.73	48	9.4	5.12	0.0000
	Outside motif		67254		0.08	57	95.6	0.60	
NTCRV	DGYW/WRCH	FR	644	14.6	0.47	3	1.7	1.80	0.2240
		CDR	102	2.3	2.94	3	2.1	1.44	
		All	746	16.9	0.80	6	3.6	1.69	0.1542
	Outside motif		3664		0.41	15	17.4	0.86	
STCRδV	DGYW/WRCH	FR	1019	11.3	0.20	2	1.4	1.40	0.5413
		CDR	279	3.1	0.00	0	0.1	0.00	
		All	1298	14.3	0.15	2	1.6	1.27	0.7161
	Outside motif		7754		0.12	9	9.4	0.96	

DGYW/WRCH (G/C is the mutable position; D = A/G/T, Y = C/T, W = A/T, R = A/G, and H = T/C/A); "ALL" refers to G and C nucleotides found within hotspot motifs along the entire V segment (FR and CDR); "Outside motif" refers to G and C nucleotides outside a hotspot motif; S/N = substitutions per nucleotide; MI = mutability index[a)]; %G/C = proportion of all nucleotides in that category that are G or C. TCRαδV-TCRαC, alpha; TCRαδV-TCRδC, delta; TCRβV, beta; TCRγV, gamma; IgHV-TCRδC, trans-rearrangements between immunoglobulin heavy chain (IgH) and delta TCR constant regions; NTCRV and STCRδV, components of NARTCR.

[a)] Mutability index is the observed number of mutations of a specific nucleotide divided by the expected number of mutations of that nucleotide, with a value of 1.00 indicating random mutation.

[b)] χ^2 analysis was used to compare observed and expected numbers of mutations between (a) FR and CDR regions and (b) all mutations inside and outside hotspot motifs for each V segment type.

(55%) and toward transition mutations, despite having a much lower rate of mutation (53%; Fig. 3 and 4; Table 2). Replacement mutations occurred significantly more often than silent mutation regardless of constant region utilized (alpha: R/S = 2.2; delta: R/S = 2.48). Generally, TCR αδV gene segments incurred more tandem base mutations than all other chains except perhaps IgHV.

Our previous data suggested that mutation to TCRα may be higher in thymus than in peripheral lymphoid tissues (spleen, spiral valve, and blood), but the limited data set constrained our ability to find a significant difference between tissue types [34]. Thus, we attempted to evaluate any difference in mutation between primary and secondary lymphoid tissues here. We compared frequency of mutation in clones originating from thymus tissue to those originating from peripheral lymphoid tissues. Unfortunately, even our larger dataset constrained analysis. We identified four groups of sequences with identical CDR3 that contained clones from both the thymus and the periphery. Unfortunately, we observed no mutation to any of these sequence groups, so we were unable to compare tissues directly. Using our entire dataset, we analyzed mutation separately for sequences derived from thymus and from peripheral lymphoid tissues. For TCRα, TCRαδ, TCRβ, and TCRγ, results suggested that peripheral lymphoid tissues have a higher frequency of mutation (Supporting information Table S4). However, because we are unable to directly assess mutation in clones derived from common

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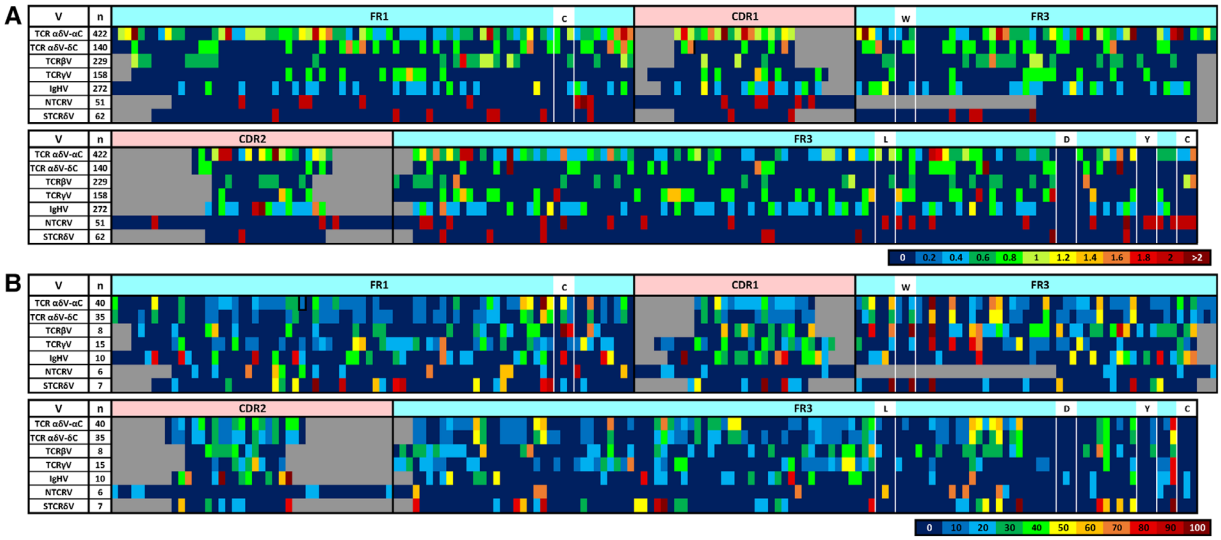

Figure 4. Heatmap coloring indicates (A) the proportion of sequences (n = number of sequences represented) within each segment type that contain a mutation or the (B) proportion of Vs within each segment type (n = number of V family groups) that contain a G/C target (within a DGYW/WRCH motif) at any single position along the sequence length (5' to 3'). White boxes indicate the locations of conserved antigen receptor domain residues. Putative locations of framework regions (FR, light blue) and complementarity-determining regions (CDR, pink) are indicated above the heatmaps. Gaps (grey space) within the sequences are for alignment purposes only (segments are aligned by domain and conserved residue placement only). Numbers within each color scale represent the greatest value for that color. TCR, T-cell receptor, V, V segment, TCR αδV, TCR-α/δ V; TCR βV, TCR-beta V, TCR γV, TCR-gamma V; IgHV, immunoglobulin heavy chain V; NTCR V, NAR-TCR V; STCR δV, supporting TCR-δ V (NTCR V-STCR δV for doubly rearranged NAR-TCR). Data from a single experiment, where each PCR tube represents a single replicate for each chain, shark, and tissue sample (see Supporting information Table 1 and 2).

progenitors found in both thymus and peripheral tissues, we hesitate to definitively claim that additional mutation occurs after T cells arrive in the periphery. Further experiments are necessary to ascertain whether mutation frequencies of non-alpha Vs differ between thymus and periphery. Specifically, we need germline genomic Vs and a much deeper CDR3 family clone analysis, but unfortunately no nurse shark genome exists at this time.

Mutation only minimally affects NAR-TCR and IgHV-TCR δC rearrangements

We observed significantly less mutation in both variable domains of NAR-TCR (NTCR V and STCR δV) compared to alpha chain V (NTCR V: $p = 0.02$; STCR δV: $p = 0.01$). This lack of mutation confirms earlier reports that NAR-TCR does not utilize SHM [28]. We also found that silent mutation occurred nearly as often as replacement mutation (NTCR V: $p = 0.13$; STCR δV: $p = 0.22$; Fig. 3 and 4, Supporting information Fig. S6C). Interestingly, mutations in FR tended to be transversions (NTCR V: 47%; STCR δV: 55%), while those in CDR were biased toward transitions (NTCR V: 63%; STCR δV: 67%; Table 2). Rearrangements between IgHV and TCR constant regions (IgHV-TCR δC) contained more mutation in CDR2 (0.0066) than other regions, and mutation frequency was greater in IgHV-TCR δC than all other TCR V segment types except alpha (TCR αδV-TCR αC; Fig. 3 and 4, Supporting information Fig. S6D). However, mutation in IgHV was substantially lower than would be expected during an antigen-specific response in B cells as they affinity mature in spleen [39, 41, 42]. Mutations to CDR were biased toward G and C nucleotides (71%) within WRCH/DGYW motifs (59%) and tended to be transitions (51%). However, G and C mutation within FR was much lower (49%) and only occurred in motifs 38% of the time (Table 2). Mutations to IgHV-TCR δC typically caused aa replacement at that position (R/S = 3.4, $p = 0.02$).

Discussion

We previously published the novel use of SHM in TCRα chain of αβ T cells within the thymus of nurse sharks [34]. The frequency of mutation at α was similar to that seen in BCR loci in sharks and mammals. As in B cells, SHM in shark T cells appeared catalyzed by AID and resulted in both point and tandem mutations that accumulated nonconservative aa replacements within antigen-binding regions (CDR) of receptors. However, unlike B cells that use SHM for affinity maturation after exposure to antigen, shark T cells instead use SHM for repertoire diversification during T-cell development within the thymus, implying that SHM contributes to receptor modifications that enhance selection. Here, we extend these findings with an analysis of SHM in other canonical TCR chains, including TCRβ chain of αβ T cells and TCRγ and TCRδ chains of γδ T cells, as well as in noncanonical TCR that associate Ig or Ig-like variable (V) segments with TCR constant (C) regions.

In our previous report, we described an overall mutation frequency of 0.0225 S/N in TCRα chain, with 66% of all mutations to G and C nucleotides [34]. Here, we observed an overall mutation rate of 0.0055 S/N in TCR αδV associated with TCR αC. While these

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Table 2. Mutation bias within T-cell receptor variable (TCRV) segments differed by V segment type

V segment	Region	% Transition mutations	% Transversion mutations	% All mutations to G or C nucleotides	% G and C mutations inside motifs
TCRαδV-TCRαC	FR	45.58	43.54	59.41	53.44
	CDR	43.40	43.40	51.57	70.73
	All	45.00	43.50	57.33	57.56
TCRαδV-TCRδC	FR	53.33	34.67	62.67	55.32
	CDR	52.94	47.06	64.71	54.55
	All	53.26	36.96	63.04	55.17
TCRβV	FR	48.75	36.25	60.00	33.33
	CDR	44.44	44.44	66.67	50.00
	All	48.31	37.08	60.67	35.19
TCRγV	FR	56.00	34.67	65.33	26.53
	CDR	62.50	25.00	87.50	57.14
	All	56.63	33.73	67.47	30.36
IgHV-TCRδC	FR	50.72	37.68	49.28	38.24
	CDR	51.92	46.15	71.15	59.46
	All	51.05	40.00	55.26	45.71
NTCRV	FR	42.86	47.62	42.86	30.00
	CDR	62.50	25.00	37.50	27.27
	All	48.28	41.38	41.38	28.57
STCRδV	FR	40.91	54.55	45.45	20.00
	CDR	66.67	33.33	33.33	0.00
	All	44.00	52.00	44.00	18.18

FR, framework region; CDR, complementarity-determining region; TCRαδV-TCRαC, alpha; TCRαδV-TCRδC, delta; TCRβV, beta; TCRγV, gamma; IgHV-TCRδC, trans-rearrangements between immunoglobulin heavy chain (IgH) and TCRδ constant regions; NTCRV and STCRδV, distal and proximal (supporting) components of NAR-TCR.

frequencies are considerably lower than those we found before, they reflect the much larger data set used in the current study and likely are more representative of actual substitution rates within TCRα chain. Again, we observed that mutation within TCR αδV-TCR αC affected C and G nucleotides 57% of the time, and 70% of these mutations occurred within CDR and targeted WRCH/DGYW motifs. Mutation was 2.3 times more likely within CDR than framework regions (FR), similar to the 1.87 times we reported before, and mutation was biased toward transitions. Although some V segments accumulated mutation at higher rates than others (i.e., TCR αδV2.4 contained no mutation while TCR αδV5 mutated at a rate of 0.026 S/N), it is clear that AID-catalyzed SHM alters TCR alpha chain in nurse shark.

We then assessed whether SHM is used by the other canonical T-cell chains (beta, gamma, and delta) or by the noncanonical receptor chains that associate IgV segments with TCR C regions (e.g., IgHV-TCR δC rearrangements, doubly rearranging NAR-TCR, and Ig-like TAIL V; see, Fig. 1). To fairly assess mutation patterns between TCRα and TCRδ (since they share a locus), we reclassified and renumbered all new and previously published alpha and delta V segments and identified the constant region associated with each V segment for all sequences within our dataset (see Fig. 2C and Supporting information Fig. S2). We then analyzed mutation data separately for sequences associated with alpha constant regions (TCR αδV-TCR αC) and those associated with delta constant regions (TCR αδV-TCR δC). We found that SHM in nurse sharks significantly alters TCR αδV segments bound to TCR αC but not to TCR δC ($p < 0.001$). Mutation was found twice as often in TCRα (TCR αδV-TCR αC, 0.0051 S/N) than TCRδ (TCR αδV-TCR δC, 0.0021 S/N) overall, and CDR of TCRα (0.0098 S/N) accumulate more than three times as many mutations as TCRδ CDR (0.0032 S/N). Further, 71% of all G/C mutations to TCR αδV-TCR αC were located within AID-preferred WRCH/DGYW hotspot motifs, compared to 52% in TCR αδV-TCR δC. Mutation in TCR βV and TCR γV reflected similar patterns as TCRδ, with relatively low mutation (TCR βV: 0.0014 S/N; TCR γV: 0.0021 S/N) that is not directed at hotspot motifs (TCR βV: 35%; TCR γV: 30%). The differential use of SHM by TCRα compared to other TCR chains suggests a regulatory control mechanism modulates AID access to the locus during transcription. In mice and humans, V(D)J recombination in Ig heavy chain (IgH: IgM/IgW) V regions is controlled by regulatory elements upstream of the IgH constant (C) region exons (between the V and D clusters) [43, 44]. However, AID accessibility to the IgHC locus is controlled by transcriptional enhancers located in the 3' regulatory region (RR) downstream of the IgHC exons [43, 45, 46], and SHM requires both the transcription of IgH V regions and the upregulation of AID expression [46]. It is likely that these same transcriptional enhancers regulate SHM of nurse shark TCR, allowing AID access to TCRα chain but limiting access in other TCR chains, evidenced by the greater use of SHM by TCR αδV segments associated with TCRα than with TCRδ constant regions. Since SHM appears to

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occur in thymus tissue, this differential use of SHM also suggests that AID may be targeting hotspot motifs of TCRα chain to salvage receptors during selection. Roughly half of all beta, gamma, and delta transcripts in our sequence library originated from thymus tissue, and we observed mutation within transcripts from thymus in all TCR chains. Thus, is seems likely that mutation to TCRδ, TCRβ, and TCRγ chain occurs inadvertently as T cells migrate through the thymic cortex during development.

Mutation was low in both V domains — NAR-TCR V and supporting TCR δV — of doubly rearranging NAR-TCR (NTCR V: 0.0023 S/N and STCR δV: 0.0017 S/N). We observed more replacement mutation in NTCR V FR, but replacements did not occur significantly more than silent mutation in either domain (NTCR V: p = 0.13; STCR δV: $p = 0.22$). Mutation also did not differ between FR and CDR (NTCR V: $p = 0.10$; STCR δV: $p = 0.99$) and did not appear to target G and C nucleotides (NTCR V: 41%; STCR δV: 44%) or WRCH/DGYW motifs (NTCR V: 29%; STCR δV: 18%). Mutation in NTCR V and STCR δV mirrors patterns observed in IgH new antigen receptor (IgNAR) transmembrane (Tm) transcripts (0.007 S/N), where mutation has been shown to not target CDR or display bias towards replacements. Though secreted IgNAR forms use SHM for antigen-driven immune responses following antigen stimulation, Tm IgNAR is not used to generate the primary IgNAR repertoire [42, 47]. Diaz et al. suggested the reduced mutation within Tm IgNAR may result from downregulating mutation mechanisms to avoid the risk of creating nonfunctional receptors after four gene rearrangement events [47]. Unusually, mutation in NTCR V and STCR δV favored transversions within FR (NTCR V: 48%; STCR δV: 55%) but transitions within CDR (NTCR V: 63%; STCR δV: 67%). While it is possible that NAR-TCR mutations result unintentionally during thymocyte migration as above, the disparate bias toward transitions and transversions in both domains suggests an alternate or additional process besides AID-catalyzed SHM [48, 49]. Our observations of more limited mutation in TCR γV4 also may indicate that NAR-TCR preferentially pairs with TCR γV4, though no data currently exist to confirm this prediction.

Mutation to V segments of IgHV-TCR δC rearrangements significantly altered nucleotides of CDR2 ($p < 0.0001$) but not of other regions. Similar to IgHV in B cells, mutation in CDR appeared targeted to G and C nucleotides (71%) within DGWY/WRCH hotspot motifs (59%) and were biased toward transitions (52%). IgHV segments used by TCRs are identical to germline IgHV segments used by B cells, so the similarity in mutation patterns makes sense. Although mutation to IgHV is substantially reduced when associated with a TCR constant region versus a B cell one [39], the significantly greater mutation in CDR2 that is targeted to AID-favored G and C nucleotides suggests that SHM is altering IgHV segments in T cells as well as B cells. The antigen ligands that IgHV-TCR δC receptors bind is not known, nor is the developmental pathway of these cells within the thymus. Nurse shark T cells may simply be using these additional V segments to improve thymic diversity by increasing the pool of Vs available during recombination [34]. Successful rearrangements between an IgHV pseudogene and TCR constant regions support this idea. The motif-rich V domains may be mutated inadvertently as the cells travel through thymic cortical areas where AID is being expressed. However, it also is plausible that these IgHV-T cells are actively modified for simple diversification for free antigen or to salvage receptors during selection that are unable to receive adequate survival signals, though it is unclear whether or not selection is required by this cell type to exit the thymus. Additional studies that assess the anatomical location of developing double-negative thymocytes in addition to functional studies of receptors are necessary to discern further why these V domains are altered.

Recent studies in nonmouse/human organisms confirm the versatility of the TCRαδ locus in the vertebrate immune system. Besides IgHV-TCR δC, TAIL V and NAR-TCR rearrangements in shark, TCRμ of monotremes and marsupials is a hybrid receptor derived from Ig and TCR components [21]. Isoform TCRμ2.0 requires the rearrangement (and in platypus, recombination) of two V domains and is structurally analogous to the doubly rearranging NAR-TCR in nurse sharks [18, 28]. While the C regions of TCRμ resemble traditional TCR δC, the V regions are more similar to IgH V genes, and the TCRμ locus itself reflects the tandem cluster arrangement of Ig rather than the translocon arrangement of TCR [19]. In fact, antibody-like TCR δV segments (VHδ) occur in nearly all gnathostome groups: elasmobranchs (nurse sharks), bony fish (*coelacanth*), amphibians (*Xenopus*), birds (chickens), and mammals (platypus, *Florida manatee*) [20–26]. The passerine zebra finch contains VHδ within a conventional TCR-α/δ locus, while Galliform birds house VHδ gene segments within a second nonsyntenic TCR-δ locus [22]. Thus, the sharing of antigen receptor gene segments seems to be a primordial condition, where the basic immune system started as a "big soup" of receptor parts that, in some lineages, became more and more divergent (and arguably, constrained) as vertebrates moved to land and evolved warm-blooded systems.

Other examples exist to suggest that not only are Ig and TCR gene components interchangeable, but mechanisms of receptor diversification also are shared between B and T cells. In camelids, both gamma- and delta-V gene segments employ SHM to improve structural stability of receptors rather than antigen selection [31]. Analyses included only sequences from peripheral lymphoid tissues, but mutation patterns are parallel to those of TCR γV and TCR αδV-TCR δC in our study. While overall mutation was fairly low (and did not favor G/C nucleotides), replacement mutation was biased toward AID hotspot motifs and resulted in greater length and diversity of CDR3 [31, 32]. Crystalline structures of γδ TCR bound to nonclassical MHC demonstrate that MHC recognition occurs through direct contact by CDR3 of TCR delta [50], suggesting that cells with longer or more diverse CDR3 may be selected for survival. We have evidence that IgHV-TCR δC rearrangements also create longer CDR3 by incorporating one or two diversifying (D) segments from Ig in addition to the single D and J segments from TCR delta (IgV-IgD1-(IgD2)-TCR δD-TCR δJ) during recombination (data not shown). While MHC presentation is not obligatory for γδ T cells, receptors may require stimulation by cell-to-cell contact [51]. Thus, SHM may provide a tool to fine tune receptors to recognize particular antigens, and since both

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gamma and delta chains are preloaded with numerous hotspot motifs, opportunistic mutation along the V segment is likely.

As we learn more about the immune systems of nonmodel vertebrates, it becomes clearer that ancient lymphocytes likely did not follow the unambiguous rules of B- and T-cell biology found in modern textbooks, and we only just are beginning to understand the myriad schema different vertebrate groups evolved to diversify Ig and TCR repertoires. For example, lymphocyte rearrangement and diversification mechanisms predate the primordial "big bang" of IgSF-based adaptive immunity, as AID-like APOBEC mutators (i.e., CDA1 and CDA2) exist in agnathan vertebrates (hagfish and lamprey) to diversify the variable lymphocyte receptors (VLR) of this more ancient lymphocyte adaptive antigen receptor system [16, 52]. The data presented here offer additional clues to the possible evolutionary relationship between the immune systems of agnathan and jawed vertebrates, suggesting a sustained bipartite use of APOBEC family enzymes to diversify humoral and cellular antigen receptor repertoires, with CDA acting upon variable lymphocyte receptors and AID upon Ig and TCR loci.

Materials and methods

Study animals

TCR sequence data used in this study came from six nurse sharks (*G. cirratum*) collected off the Florida Keys. We harvested peripheral blood and immune tissues (thymus, spleen, spiral valve) after MS-222 (Argent, Redmond, WA) overdose from five sharks ("Joannie," "Mary Junior," "White," "Grumpy," "Tom Thumb") at the University of Maryland's Center of Marine Biotechnology and one shark ("Florence Nightingale") at Texas A&M University's College of Veterinary Medicine. We immediately purified RNA with TRIzol reagent (Life Technologies, Carlsbad, CA). We conducted all research under the Florida Fish and Wildlife Commission Special Activity License SAL-18-2013-SR.

Additionally, we incorporated T-cell sequences from published datasets [25, 26, 28, 35, 53–55] and transcripts from an unpublished multitissue Illumina transcriptome to improve analysis of V segment alignments. We reference published sequences by their GenBank accession number in all relevant Figures.

5' RACE library generation, cloning, and Sanger sequencing

We used 5 μg total RNA to generate a 5' RACE (Rapid Amplification of cDNA Ends) library using the GeneRacer Kit (Life Technologies) and a 50:50 mix of oligo-dT and random hexamer primers for cDNA synthesis (Superscript III First Strand Synthesis System, Thermo Fisher Scientific, Inc., Waltham, MA, USA). We estimated cDNA concentration using a Nanodrop 2000 Spectrophotometer (Thermo Fisher Scientific, Inc.).

We used the GeneRacer 5' forward primer (Life Technologies) and reverse primers designed to TCR beta (TCRβ), gamma (TCRγ), or delta (TCRδ) constant (C) regions to amplify RACE products for Sanger sequencing (Supporting information Table S4). We followed protocols outlined in [34] for PCR conditions, product visualization, and cloning. We submitted either plasmids or purified PCR products for Sanger sequencing to the DNA Technologies Core Lab on the Texas A&M University campus (College Station, TX, USA) or to GENEWIZ (South Plainfield, NJ, USA). We deposited annotated sequences into the National Center for Biotechnology Information's (NCBI) GenBank sequence database with the following accession numbers: MN748005-MN748891 and MN788155-MN788287.

Sequence alignment

We used Geneious (version 9.1.8, Biomatters Inc., Auckland, NZ) bioinformatics software to manage DNA sequence data following the same methods as Ott et al. [34]. Sequence alignments and region annotations followed IMGT guidelines [56]. We predicted the location of signal peptide cleavage sites between leader and V segment sequences using SignalP (version 5.0) [57]. A V segment included all bases from the first predicted nucleotide of the V segment to the conserved cysteine (C) residue (YxC motif) at position 104 ("V only"). A V region included all bases between the first predicted nucleotide of the V segment to the last predicted nucleotide of the J segment (V and J). The CDR3 included all bases after the conserved cysteine of the V segment and before the conserved phenylalanine (F) residue (FGxG motif) of the J segment.

We grouped sequences into unique V families based on 70% nucleotide sequence identity and further refined groups into subfamilies based on 80% nucleotide identity [55, 58]. For beta and gamma Vs, we revised the V-segment numbering scheme used by Criscitiello et al. [26] to reflect these parameters. However, we integrated alpha- and delta-V segments into a single group of "αδ Vs" (TCR αδV) to more clearly characterize the locus and avoid confusing name replication within the data. We then numbered the segments according to their position on a phylogenetic tree, from the most divergent branch (TCR αδV1) to the most recent branch (TCR αδV11). For NAR-TCR V segments, we reassigned numbers using this same strategy and renamed the supporting TCR δV segments "STCR δV" to distinguish them from the canonical TCR αδV segments in alignments. We used the same locus-informed numbering system for IgH V identity [53] for all IgHV-TCR δC and IgHV-TCR αC rearrangements. We retained constant region identity (TCR αC/TCR δC) for use in mutation analyses. This system allowed us to clarify V segment usage and analyze differences in mutation patterns for the entire locus. Sequence names followed IMGT unique numbering standards for TCRs [56, 59, 60]. Sequence clone names signify the individual shark (letter following V segment [e.g., TCR γV1X] J = Joannie, M = Mary Junior, G = Grumpy, F = Florence Nightingale, T = Tom Thumb, or W = White] and the tissue type (letter preceding clone

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number [e.g., T19]: T = thymus, S = spleen, B = peripheral blood leukocytes, and V = spiral valve [intestine]) from which the clone came. For previously published sequences, we use the accession numbers as clone names.

Our preliminary dataset contained 761 TCR αδV, 229 TCR βV, 158 TCR γV, 195 IgMV, 77 IgWV, 11 TAIL V, and 113 NAR-TCR V sequences. For individual Vs within a group (subfamily or allele), we generated a consensus sequence by evaluating sequences found in multiple tissue types and/or sharks, assuming if the exact V nucleotide sequence appeared in more than one tissue or individual that it did not result from the same clone. We equated this consensus sequence to the germline sequence. For all "trans"-rearrangements, we compared mutation in IgHV segments to published germline IgHV sequences [53]. We considered only mutations to IgHV segments associated with TCR δC (not resulting from affinity maturation of B cells). Finally, we compared the incidence of AID hotspot motifs (WRCH/DGYW) between V segments that exhibited mutation and those that lacked mutation to determine the likelihood that AID might catalyze these changes.

Mutation analysis

We analyzed mutation data in beta, gamma, and alpha/delta variable (V) gene segments using methods described by Ott et al. [34] for alpha chain. Mutation frequency was the number of nucleotide changes divided by the total number of nucleotides within a region (e.g., FR, CDR, J, and C), based on differences to a consensus sequence, and recorded disagreements to the consensus as synonymous (S, aa unaltered) or nonsynonymous (N, aa altered). Although insertions and deletions (indels) likely result from similar DNA repair mechanisms as single and tandem mutations, we did not include indels in our mutation data and removed them from nucleotide alignments. However, we indicated the location of each indel in nucleotide alignments by highlighting the nucleotides to either side of the indel (Supporting information Fig. S1–S4). Further, individual sequences that shared less than 70% identity to any group were excluded from mutational analyses. We indicate these sequences using an asterisk next to the clone name within the alignment. We used one-tailed, unpaired Student's *t*-test to compare mutation rates between alpha V (TCR αδV-TCR αC) and other V segment types.

To assess whether mutation was AID mediated, we examined V segment consensus sequences for the AID-favored ProSite motifs WRCH/DGYW (G:C mutable target) (International Union of Pure and Applied Chemistry, Zürich, Switzerland; see Sigrist et al. [61]). These motifs serve as common "hotspots" for SHM, where AID favors the G/C bases within WRCH/DGYW motifs [29, 37, 62]. We counted motifs present in consensus sequences (rather than those created by mutation) and compared mutations within clone sequences to target nucleotides within the motif. We defined the frequency of hotspot mutation as the number of mutations to target nucleotides within hotspots for a region (FR or CDR) divided by the total number of mutations in that region and compared FR and CDR regions using χ^2 analysis.

We calculated a mutability index for each nucleotide as the observed number of mutations of a specific nucleotide divided by the expected number of mutations of that nucleotide, with a value of 1.00 indicating random mutation [29]. We derived the expected number of mutations by multiplying the frequency of a particular nucleotide within a family of sequences by the total number of observed mutations within that family. We used χ^2 analysis to compare mutability indices between FR and CDR regions.

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Abbreviations: **AID**: activation-induced (cytidine) deaminase · **C**: constant region · **FR**: framework region · **IgH V**: immunoglobulin heavy chain V (IgM/IgW) · **IgNAR**: immunoglobulin heavy chain new (or nurse shark) antigen receptor · **IgSF**: immunoglobulin superfamily · **TAIL V**: TCR associated immunoglobulin-like V · **NTCR V**: NAR T cell receptor distal V domain · **R**: replacement (nonsynonymous) mutation · **S**: silent (synonymous) mutation · **SHM**: somatic hypermutation · **S/N**: substitutions per nucleotide · **STCR δV**: NAR T cell receptor supporting (proximal) δV domain · **TCRδC**: TCR delta constant region · **TCRαC**: TCR alpha constant region · **TCRαδV**: TCR alpha/delta variable segment · **TCRβV**: TCR beta variable segment · **TCRγV**: TCR gamma variable segment · **V**: variable segment · **VHδ**: Ig-like TCR-δ V segments

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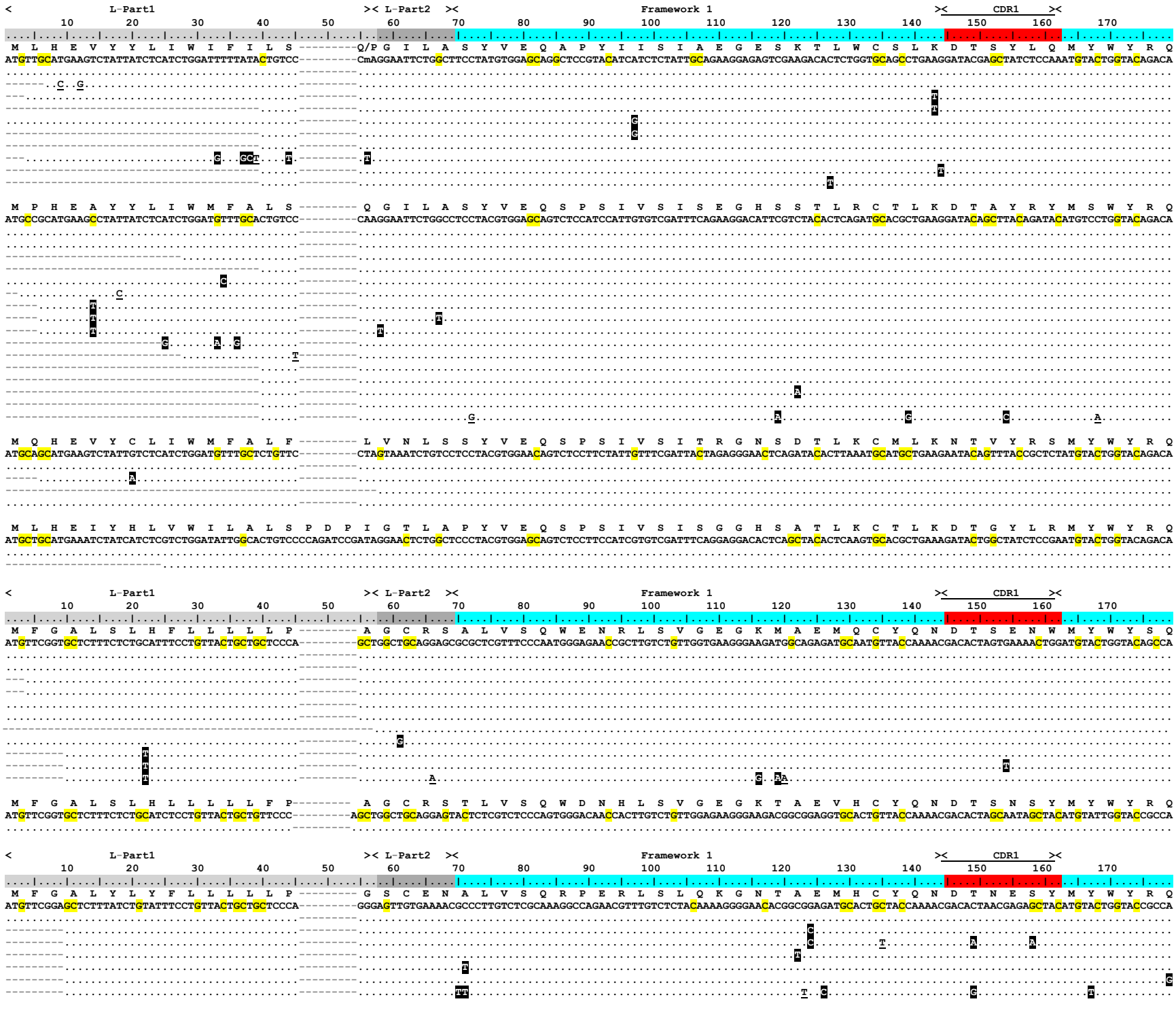
Supplemental Figure 1. Alignments of variable segments from canonical (A) beta (TCRβ V) and (B) gamma (TCRγ V) T cell chains suggest minimal somatic hypermutation. We include amino acids above the nucleotide consensus sequence; dots signify identity to this sequence. Nucleotides highlighted in black indicate non-synonymous changes to the consensus sequence and underlined nucleotides indicate synonymous changes. We denote leader [L-Part1 (light gray) is exon 1; L-Part2 (dark gray) is exon 2], framework (blue), and complementarity-determining regions (CDRs, red) below the scale. Each alignment contains only unique nucleotide sequences, with corroborating clones for lines containing identical bases referenced in Supplemental Figure 5. We used degenerate symbols (lower case) to indicate nucleotide differences likely due to allelic polymorphisms rather than mutation (see text for explanation). Highlighted nucleotides within the consensus sequence represent G or C target nucleotides within AID hotspot motifs (DGYW/WRCH). Highlighted nucleotides (pink) within a transcript mark the location of introns or indels present within a sequence but removed from the alignment (see text for details). Dashes at the 5' or 3' end indicate shortened sequences. Gaps within a sequence are for alignment purposes only. Clone numbers that contain "T" are from thymus, "S" from spleen, "B" from peripheral blood leukocytes, and "V" from spiral valve (intestine). We deposited all sequences into GenBank under accession numbers MN748625-MN748891.

[A] Beta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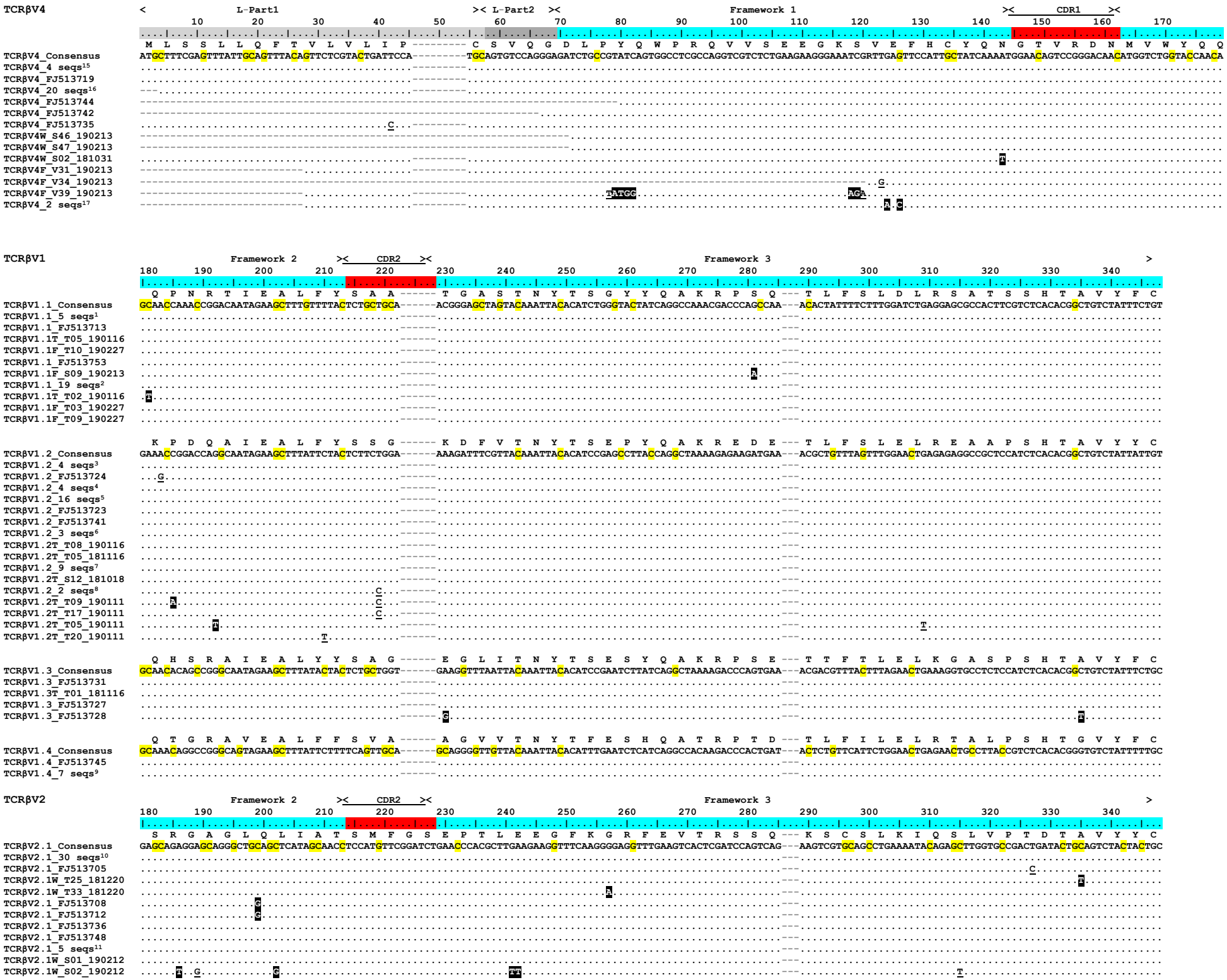
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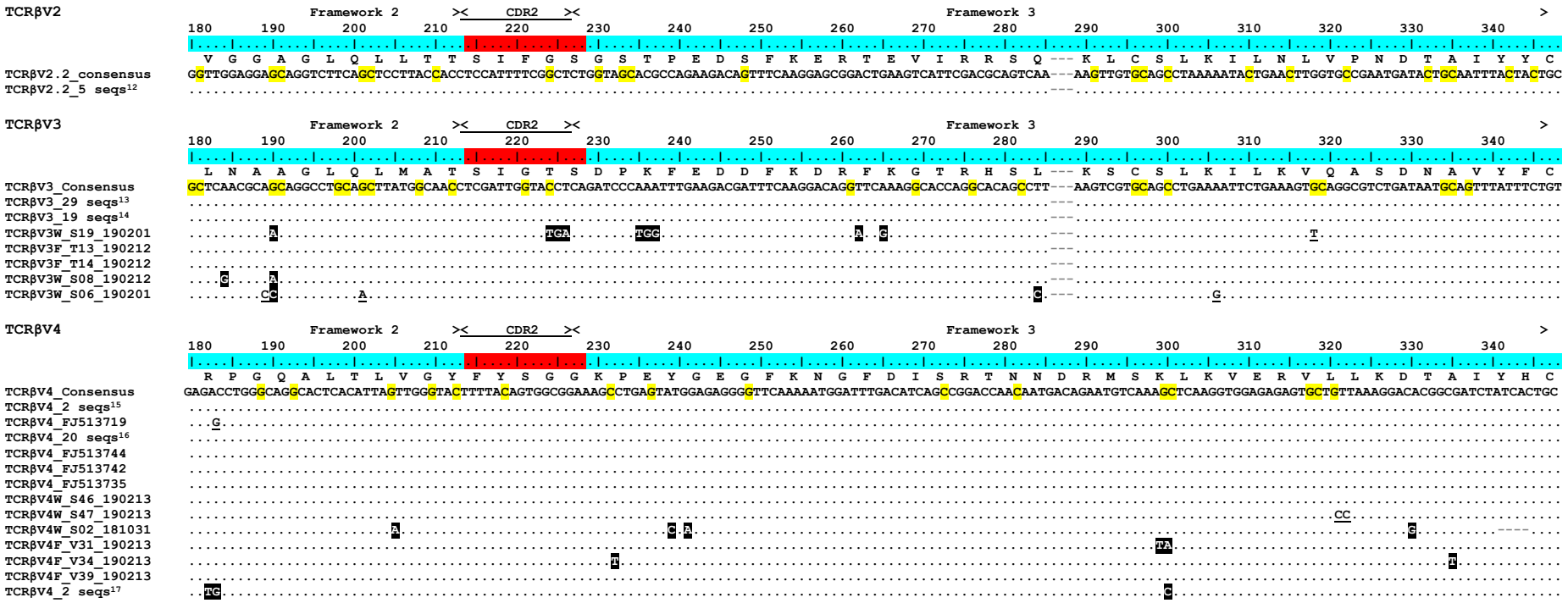
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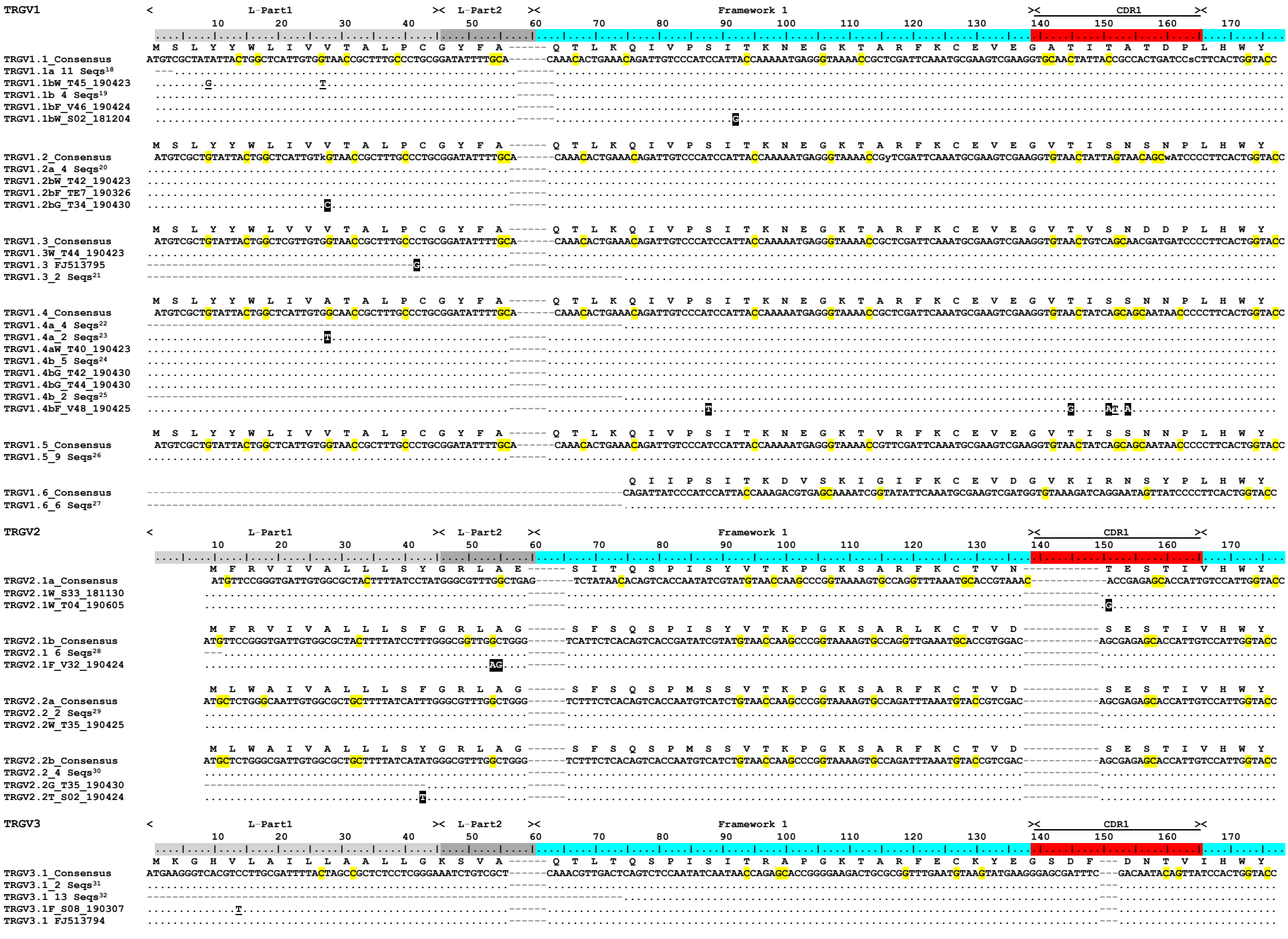
[B] Gamma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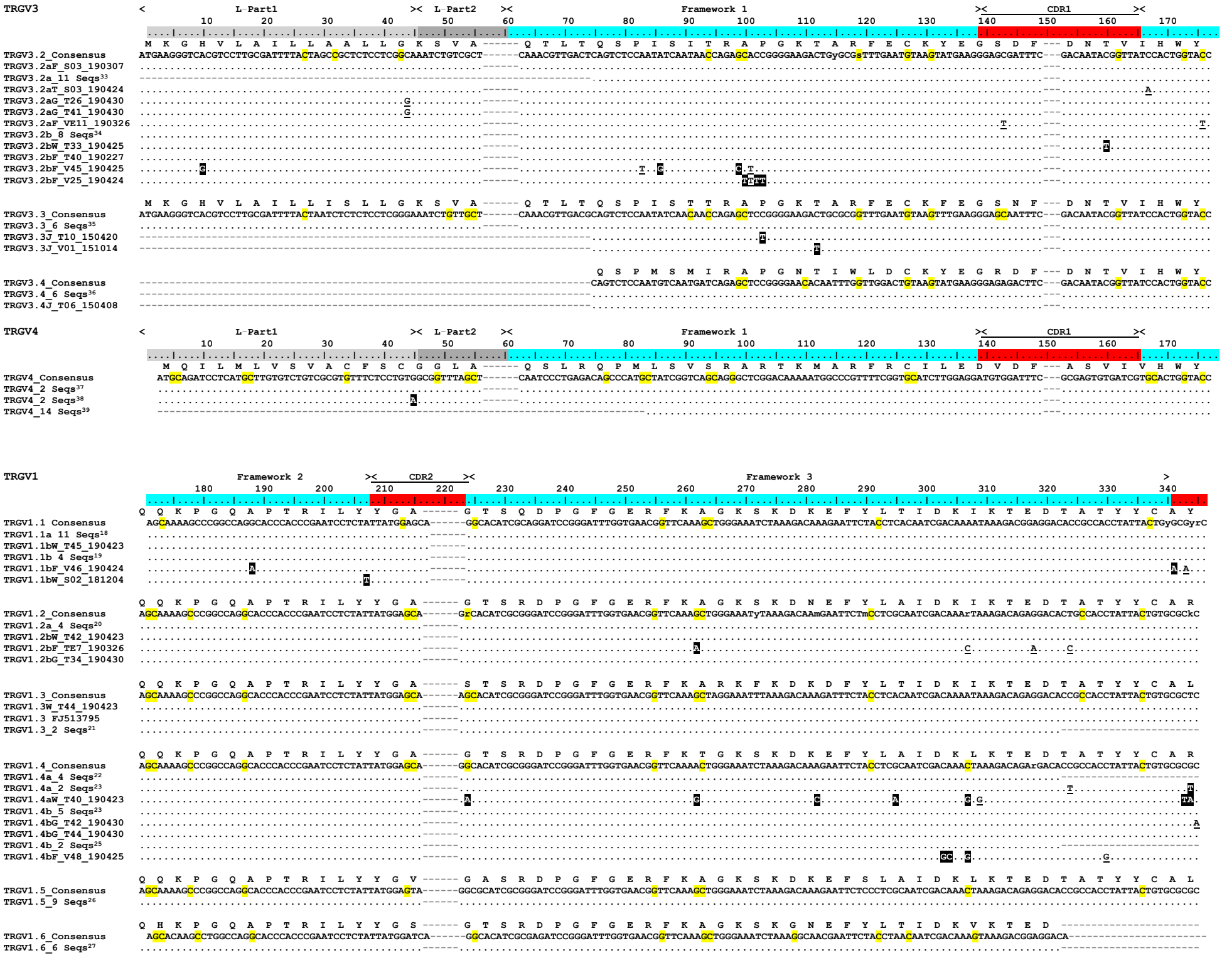
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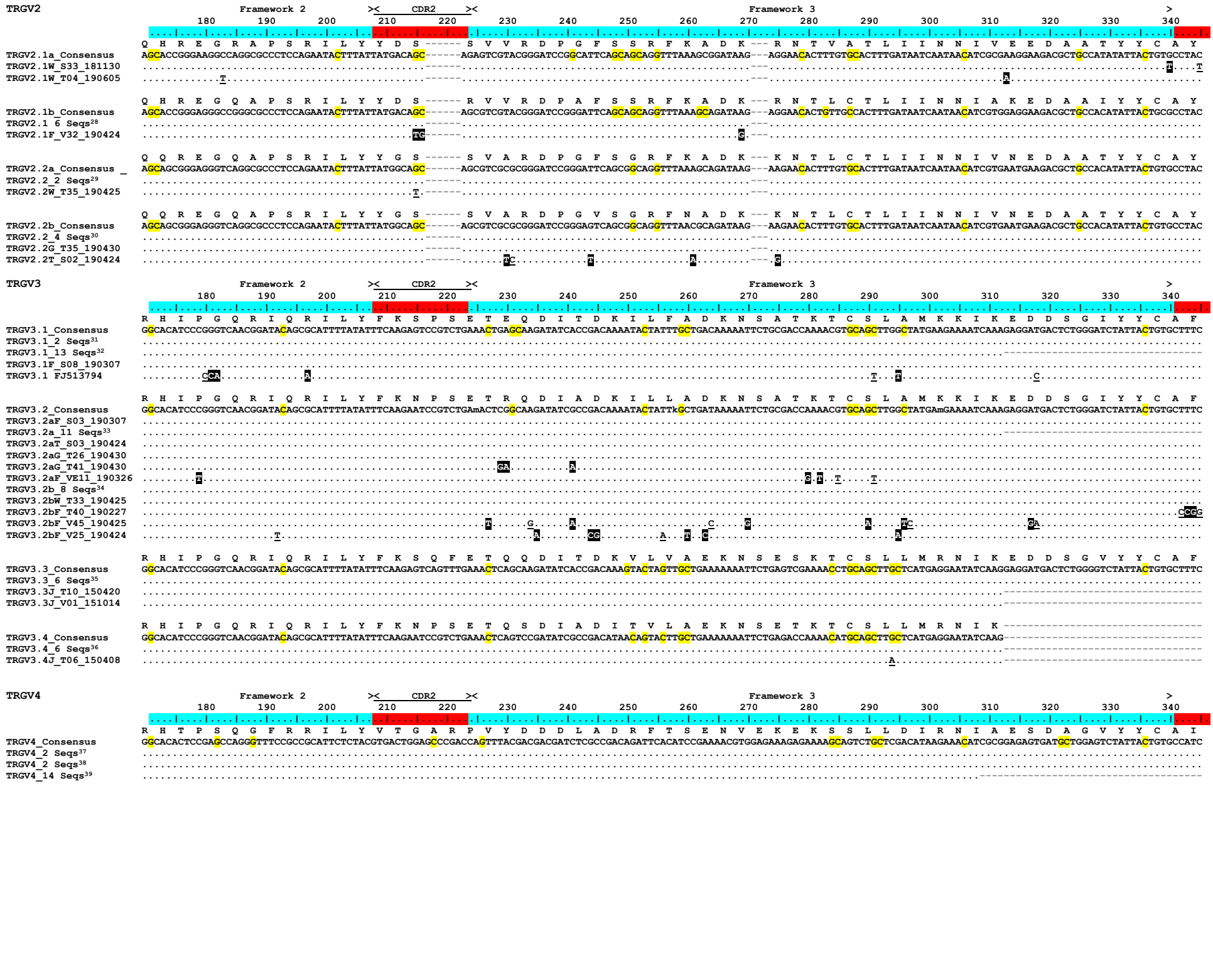
TRGV2
Framework 2
CDR2
Framework 3
TRGV2.1a_Consensus
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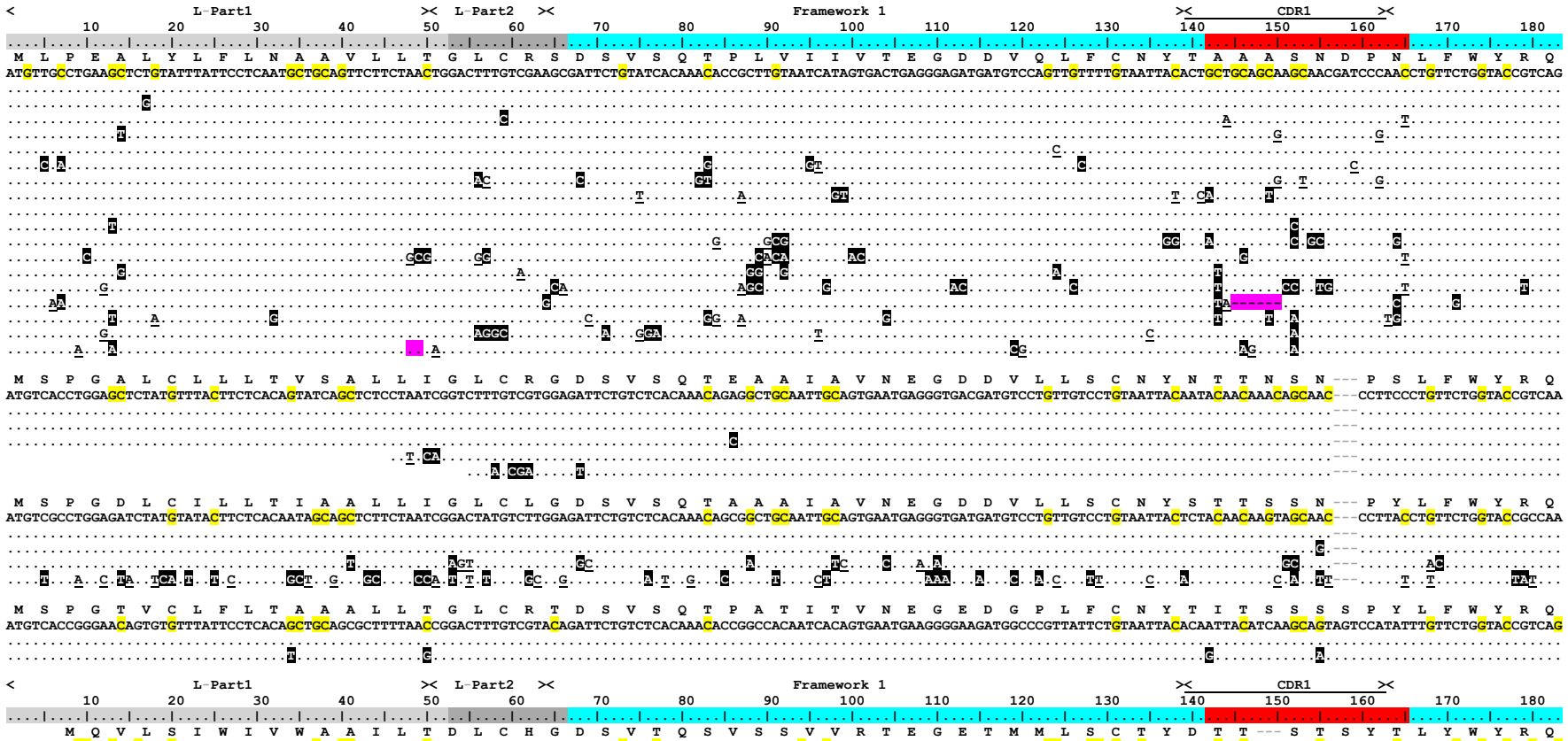
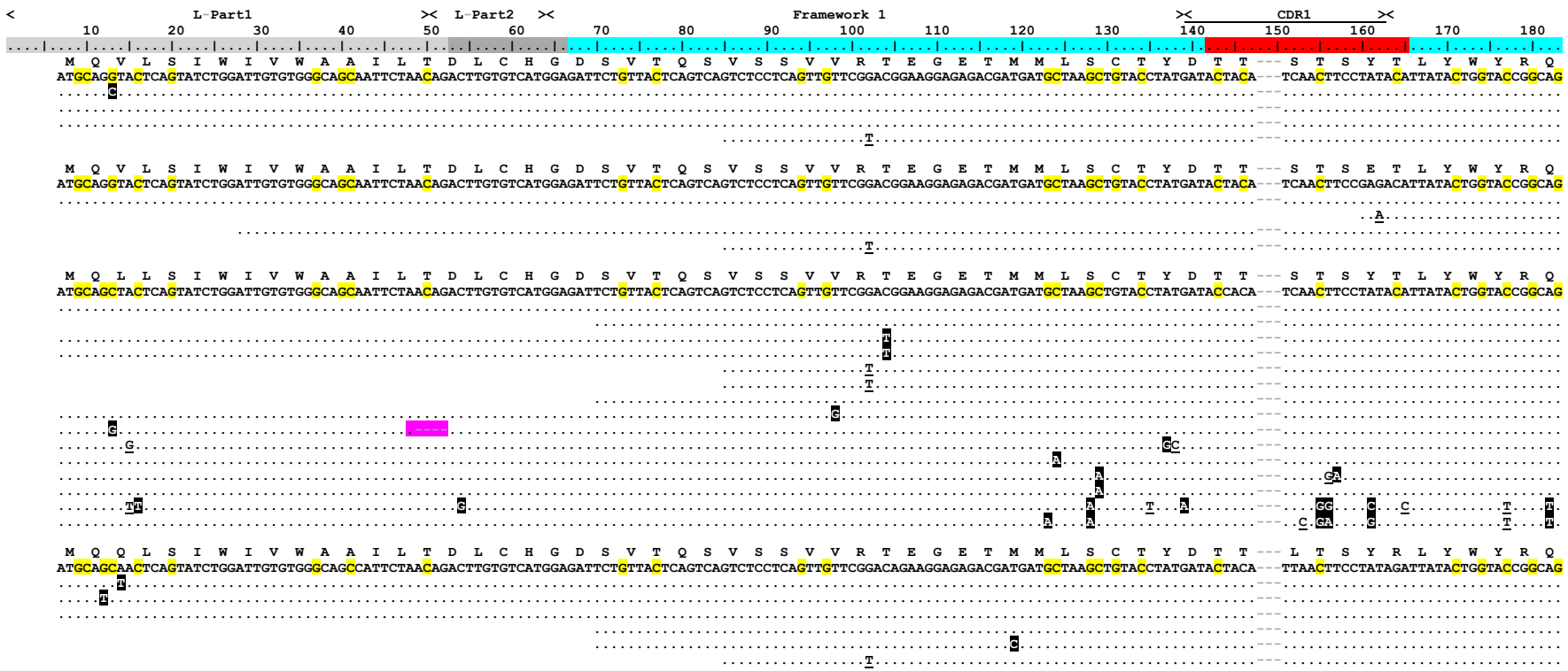
TRGV2.1W_T04_190605
TRGV2.1b_Consensus
TRGV2.1 6 Seqs28
TRGV2.1F_V32_190424
TRGV2.2a_Consensus _
TRGV2.2_2 Seqs29
TRGV2.2W_T35_190425
TRGV2.2b_Consensus
TRGV2.2_4 Seqs30
TRGV2.2G_T35_190430
TRGV2.2T_S02_190424
TRGV3
Framework 2
CDR2
Framework 3
TRGV3.1_Consensus
TRGV3.1_2 Seqs31
TRGV3.1_13 Seqs32
TRGV3.1F_S08_190307
TRGV3.1 FJ513794
TRGV3.2_Consensus
TRGV3.2aF_S03_190307
TRGV3.2a_11 Seqs33
TRGV3.2aT_S03_190424
TRGV3.2aG_T26_190430
TRGV3.2aG_T41_190430
TRGV3.2aF_VE11_190326
TRGV3.2b_8 Seqs34
TRGV3.2bW_T33_190425
TRGV3.2bF_T40_190227
TRGV3.2bF_V45_190425
TRGV3.2bF_V25_190424
TRGV3.3_Consensus
TRGV3.3_6 Seqs35
TRGV3.3J_T10_150420
TRGV3.3J_V01_151014
TRGV3.4_Consensus
TRGV3.4_6 Seqs36
TRGV3.4J_T06_150408
TRGV4
Framework 2
CDR2
Framework 3
TRGV4_Consensus
TRGV4_2 Seqs37
TRGV4_2 Seqs38
TRGV4_14 Seqs39

<u>Supplemental Figure 2</u>. Alignment of variable (V) segments from canonical alpha/delta (TCRαδ V) T cell receptor chains suggest somatic hypermutation preferentially impacts Vs associated with alpha constant regions. We include amino acids above the nucleotide consensus sequence; dots signify identity to this sequence. Nucleotides highlighted in black indicate non-synonymous changes to the consensus sequence and underlined nucleotides indicate synonymous changes. We denote leader [L-Part1 (light grey) is exon 1; L-Part2 (dark grey) is exon 2], framework (blue), and complementarity-determining regions (CDRs, red) below the scale. Each alignment contains only unique nucleotide sequences, with corroborating clones for lines containing identical bases referenced in Supplemental Figure 5. To assess mutation rather than changes due to allelic polymorphism, we divided sequences representing each putative allele (see text for details) into separate groups. Highlighted nucleotides within the consensus sequence represent G or C target nucleotides within AID hotspot motifs (D<u>G</u>YW/WR<u>C</u>H). Highlighted nucleotides (pink) mark the location of introns or indels present within a transcript but removed from the alignment (see text for details). Dashes at the 5' or 3' end indicate shortened sequences. Gaps within a sequence are for alignment purposes only. Clone numbers that contain "T" are from thymus, "S" from spleen, "B" from peripheral blood leukocytes, and "V" from spiral valve (intestine). Clones with an asterisk in front of the name are sequences that share less than 70% identity to their group and were not analyzed for mutation. We deposited all sequences into GenBank under accession numbers MN748048-MN748624.

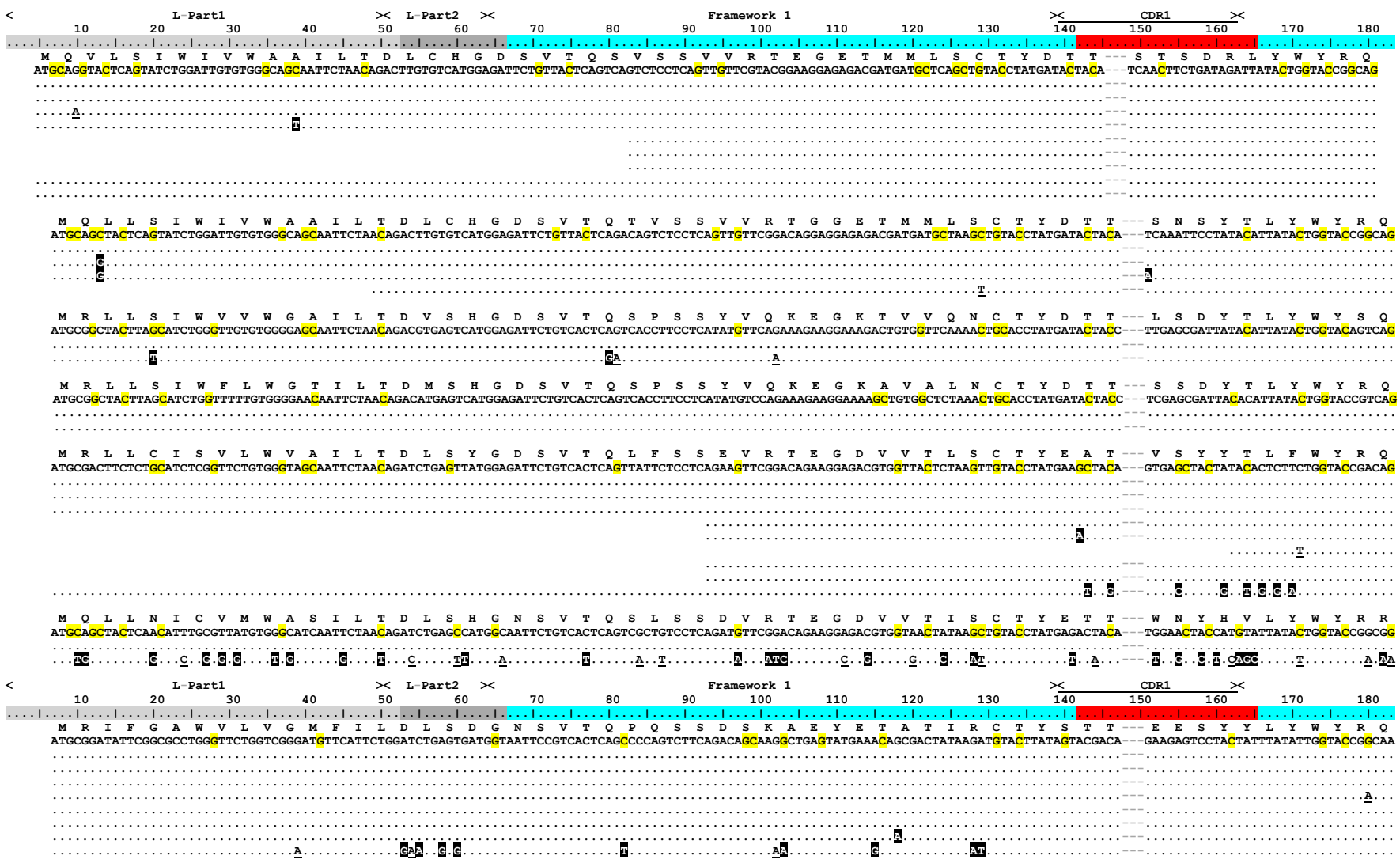
TCRαδV1



TCRαδV2



TCRαδV2



TCRαδV3

TCRαδV4

TCRαδV4

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TCRαδV4.2_2 sequences[31]
TCRαδV4.2_7 sequences[32]
TCRαδV4M_T11A_060712
TCRαδV4M_T04A_060712
TCRαδV4_KY346767
TCRαδV4J_T29_020210

M C S L S T F L I I M T L L H G T S S Q D P V S Q S P P Q L P V E E G Q T V M L N C S Y K T S --- G A A --- T L F W Y V Q

TCRαδV4.2b ATGTGTTCCCTGAGCACATTCCTGATAATCATGACTCTTCTGCATGGAACGAGTAGTCAAGATCCAGTTTCCCAGAGCCCACCTCAGTTACCGGTTGAGGAAGGACAAACTGTAATGTTGAACTGTAGTTACAAAACGTCG---GGTGCTGCT---ACTCTCTTCTGGTACGTCCAA

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TCRαδV4.2_4 sequences[33]
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TCRαδV4B_A_419.29
TCRαδV4M_T30_051410
TCRαδV4B_A_419.11
TCRαδV4J_T02_031210

M C S L S T F L I I M T L L H G T S S Q D P V S Q S P P Q L P V E E G Q T V M L N C S Y K T S --- G A A --- T L F W Y V Q

TCRαδV4.2c ATGTGTTCCCTGAGCACATTCCTGATAATCATGATTCTTCTGCATGGAACGAGTAGTCAAGATCCAGTTTCCCAGAGCCCACCTCAGTTACCGGTTGAGGAAGGACAAACTGTAATGTTGAACTGTAGTTACAAAACGTCG---GGTGCTGCT---ACTCTCTTCTGGTACGTCCAA

TCRαδV4.2_4 sequences[34]
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TCRαδV4.2_3 sequences[35]
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TCRαδV4.2_2 sequences[36]
TCRαδV4J_V22_102810
TCRαδV4.2_4 sequences[37]
TCRαδV4.2_2 sequences[38]
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TCRαδV4M_KY346752

TCRαδV5

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TCRαδV5J_T05_100410
TCRαδV5_KY189338
TCRαδV5_KY189337

TCRαδV6

< L-Part1 >< L-Part2 >< Framework 1 >< CDR1 ><

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TCRαδV6 ATGATTTCCCTGTGGGCTTTTGTAATAATAACGGCCATGCCACCGAGAACGAGCGGCCAAGATTCAGTTTCCCCGGAATCACTTGAGCAAACGGTTCAGGTAGGAGCTGATGTAAGCCTGAACTGCATTTACCAAACAACG---TATGCTGCTCCGACTCTCTTCTGGTACGTCCAG

TCRαδV6 FJ513824
TCRαδV6_21 sequences[39]
TCRαδV6 FJ513804
TCRαδV6_3 sequences[40]

TCRαδV7

< L-Part1 >< L-Part2 >< Framework 1 >< CDR1 ><

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M C S S R F L L I G L I L M P G T S G I D S V S Q D T S D L T A Q E G E I I T L S C N Y S T T D T F --- P Y L F W Y I Q

TCRαδV7 ATGTGTTCTTCACGTTTCTTGCTGATAGGACTGATCTTGATGCCTGGTACGAGTGGCATAGATTCAGTATCTCAGGATACGTCTGATTTAACAGCTCAGGAAGGAGAGATTATCACACTGAGCTGCAATTATTCCACGACTGATACTTTT---CCTTACCTCTTCTGGTATATTCAA

TCRαδV7_4 sequences[41]
TCRαδV7J_T04_022010
TCRαδV7B_A_419.1
TCRαδV7B_A_419.36
TCRαδV7J_V02_090110

TCRαδV8

< L-Part1 >< L-Part2 >< Framework 1 >< CDR1 ><

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TCRαδV8.1 ATGTGGCTGTGCTTTCTCTGTCTGGCCTGGGTGACTTCTACTATT---GATTTGAGTGATGCCGTTTCTGTTACTCAGCAGGATCTTTCGCTAAAGCAGATGGAGGGAGGCAATATCACGTTAACCTGTACCTACACTGACGATGGT------TATTACTTGTTCTGGTATCGTCAG

TCRαδV8.1_3 sequences[42]
TCRαδV8.1J_V11_090110
TCRαδV8.1_2 sequences[42]
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TCRαδV8.1M_T11B_060712

M Q F S I F T A T L V T F I V --- D L S D G V S V I Q G E T S L T Q S E K E N V T L T C T Y T D D V ------ V Y L F W Y R Q

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TCRαδV8.2_KY189341
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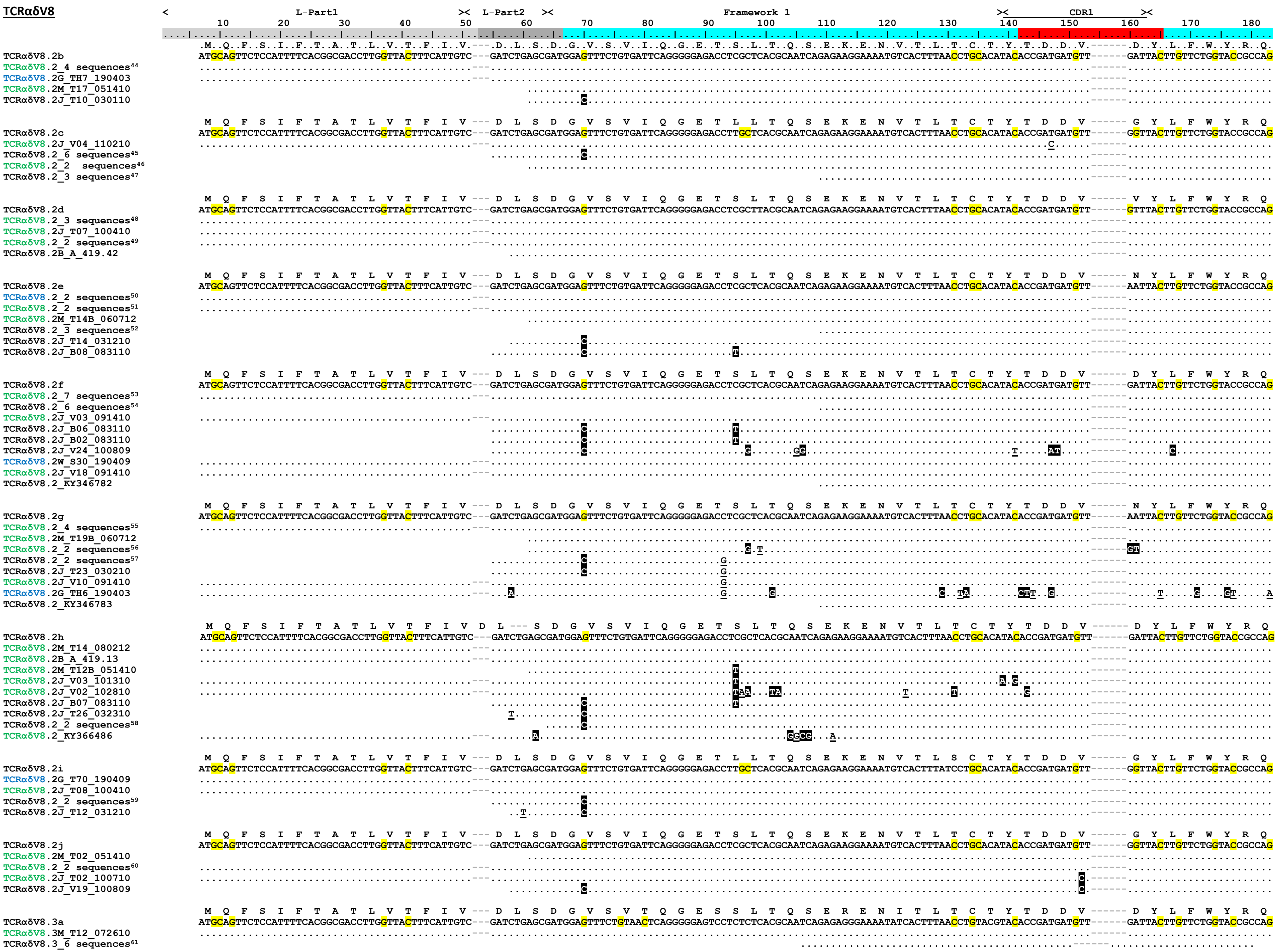
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L-Part1
L-Part2
Framework 1
CDR1
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TCRαδV8.2J_T10_030110
TCRαδV8.2c
TCRαδV8.2J_V04_110210
TCRαδV8.2_6 sequences[45]
TCRαδV8.2_2 sequences[46]
TCRαδV8.2_3 sequences[47]
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TCRαδV8.2_2 sequences[49]
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TCRαδV8.2_3 sequences[52]
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TCRαδV8.2_7 sequences[53]
TCRαδV8.2_6 sequences[54]
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TCRαδV8.2J_B02_083110
TCRαδV8.2J_V24_100809
TCRαδV8.2W_S30_190409
TCRαδV8.2J_V18_091410
TCRαδV8.2_KY346782
TCRαδV8.2g
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TCRαδV8.2_2 sequences[57]
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TCRαδV8.2_KY346783
TCRαδV8.2h
TCRαδV8.2M_T14_080212
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TCRαδV8.2j
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TCRαδV8.3M_T12_072610
TCRαδV8.3_6 sequences[61]

TCRαδV8

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                                 L-Part1                   L-Part2                                Framework 1                                  CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                 10        20        30        40        50        60        70        80        90        100       110       120       130       140       150       160       170       180
                                 M  Q  F  S  I  F  T  A  T  L  V  T  F  I  V  ---  D  L  S  D  G  L  S  V  T  Q  G  E  S  W  L  T  Q  S  E  R  E  K  V  T  L  T  C  T  Y  T  D  D  V  ------  D  Y  L  F  W  Y  R  Q
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TCRαδV8.3_FJ513801
TCRαδV8.3_4 sequences[63]

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TCRαδV8.4                        ATGCAGTTCTCAATTTTCATGGTGATCTCGTTGACTTTCATTGTC---GATCTAAGTGATGGAGTTTCTGTTACCCAGCGGGAGCCCTCACTCACACAAACAGAGGGAGAAGACGTCACTTTAACCTGCACATACACCGGGACTGTT------TATTACTTGTTTTGGTACCGCCAA
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*TCRαδV8.4_KY366487
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TCRαδV9

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                                 M  W  L  S  I  L  S  L  V  C  V  T  F  I  A  G  ---  T  N  D  G  D  S  L  T  Q  Q  V  P  S  L  T  Q  T  K  G  D  D  V  T  L  N  C  T  Y  T  G  R  P  ------  V  S  V  F  R  Y  H  Q
TCRαδV9                          ATGTGGCTCTCCATCCTCTCTCTGGTGTGTGTGACATTCATTGCAGGC---ACGAACGATGGAGATTCTCTCACTCAGCAGGTGCCCTCACTCACACAGACGAAGGGCGACGATGTCACTCTAAACTGTACTTACACTGGTCGTCCT------GTTTCCGTGTTCCGGTACCATCAG
TCRαδV9_3 sequences[68]
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TCRαδV10

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                                 L-Part1                   L-Part2                                Framework 1                                  CDR1
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                                 M  L  Y  K  F  S  L  L  T  A  L  T  Y  M  T  F  G  L  S  Q  E  D  T  V  S  Q  S  W  S  E  I  T  L  K  A  G  Q  T  F  T  T  Q  C  S  Y  S  T  T  V  ---  R  S  Y  D  L  Y  W  Y  R  K
TCRαδV10                         ATGCTTTACAAATTCAGCCTTTTAACTGCTCTCACCTACATGACATTCGGTTTGTCTCAGGAAGATACCGTGTCTCAGTCTTGGTCAGAAATAACCTTGAAAGCAGGTCAAACTTTCACAACGCAATGCAGCTATTCAACAACAGTA---AGATCGTATGATCTGTACTGGTACCGAAAG
TCRαδV10_9 sequences[69]
TCRαδV10_23 sequences[70]
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TCRαδV10_KY346803
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TCRαδV11

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                                 L-Part1                   L-Part2                                Framework 1                                  CDR1
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                                 M  S  ---  V  T  L  Y  Y  F  F  T  T  A  A  L  I  T  G  V  G  G  A  D  S  I  S  Q  E  P  F  S  A  M  K  F  E  D  E  L  V  T  I  S  Y  N  Y  S  T  T  A  ---  S  T  Y  S  L  Q  L  Y  R  Q
TCRαδV11.1                       ATGTCG---GTTACTCTATACTATTTCTTCACTACCGCAGCTCTCATAACTGGTGTTGGTGGTGCAGACTCGATCTCCCAGGAGCCGTTTTCAGCGATGAAATTTGAAGATGAATTGGTGACCATTAGTTACAATTATTCGACCACTGCT---AGTACATATTCTTTGCAACTATATCGTCAG
TCRαδV11_16 sequences[71]
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TCRαδV11M_T14_062012
TCRαδV11_3 sequences[72]
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TCRαδV11_KY189354
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TCRαδV11_KY189347
TCRαδV11_2 sequences[73]
TCRαδV11_14 sequences[74]

                                 M  S  A  I  T  C  Y  A  L  T  T  D  A  V  L  F  T  ---------------  D  S  I  S  Q  E  P  A  T  A  K  Q  L  E  G  Q  S  V  N  I  N  F  S  Y  S  I  K  I  A  T  S  H  S  L  Q  F  Y  L  Q
TCRαδV11.2                       ATGTCAGCTATTACATGTTATGCATTAACCACAGATGCAGTTCTCTTCACT---------------GATTCGATCTCACAGGAGCCAGCTACAGCAAAACAGCTTGAAGGACAGTCGGTGAACATTAACTTTAGCTATTCGATCAAAATAGCTACTTCACATTCCTTACAATTCTACCTGCAA
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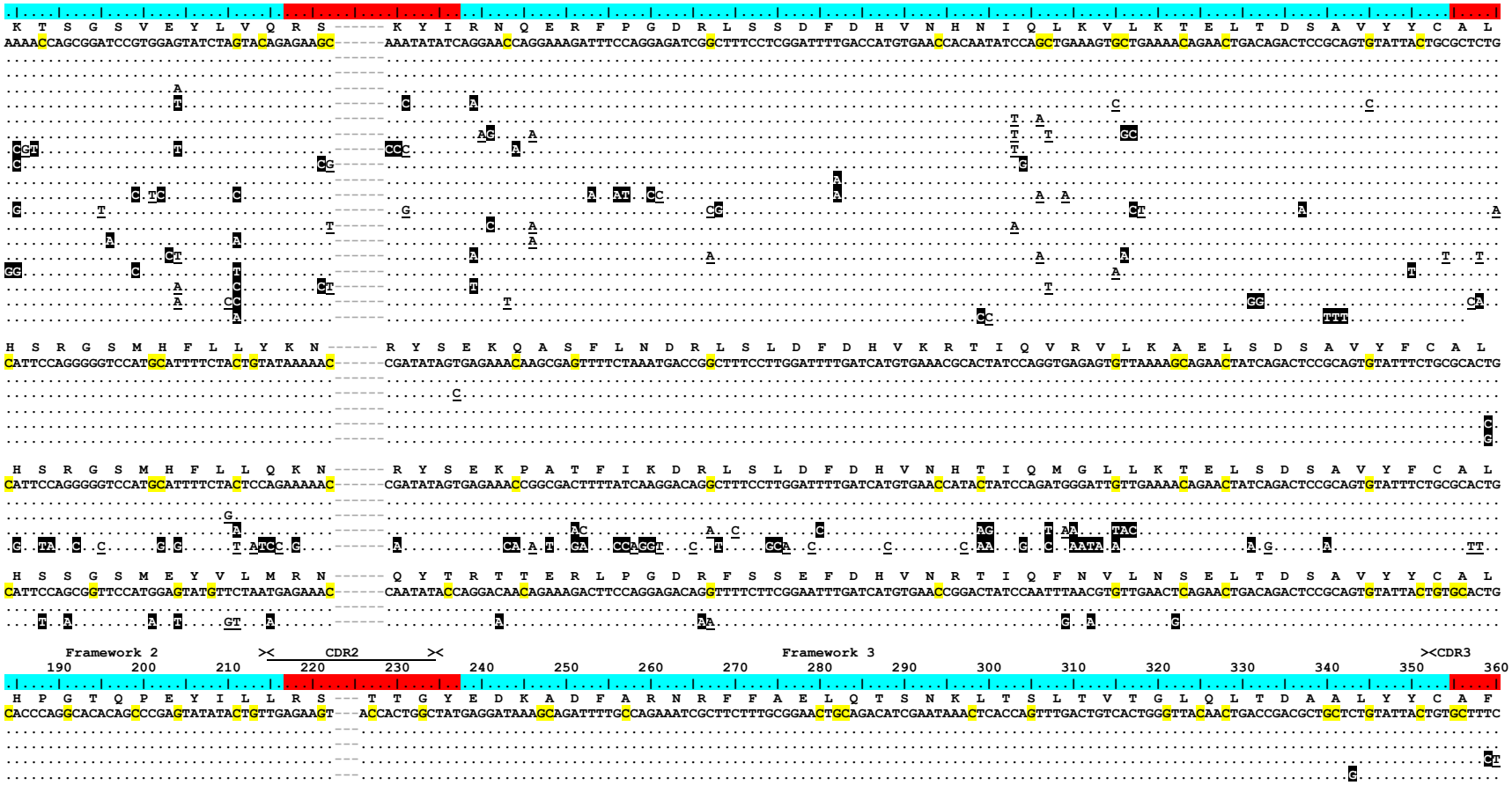
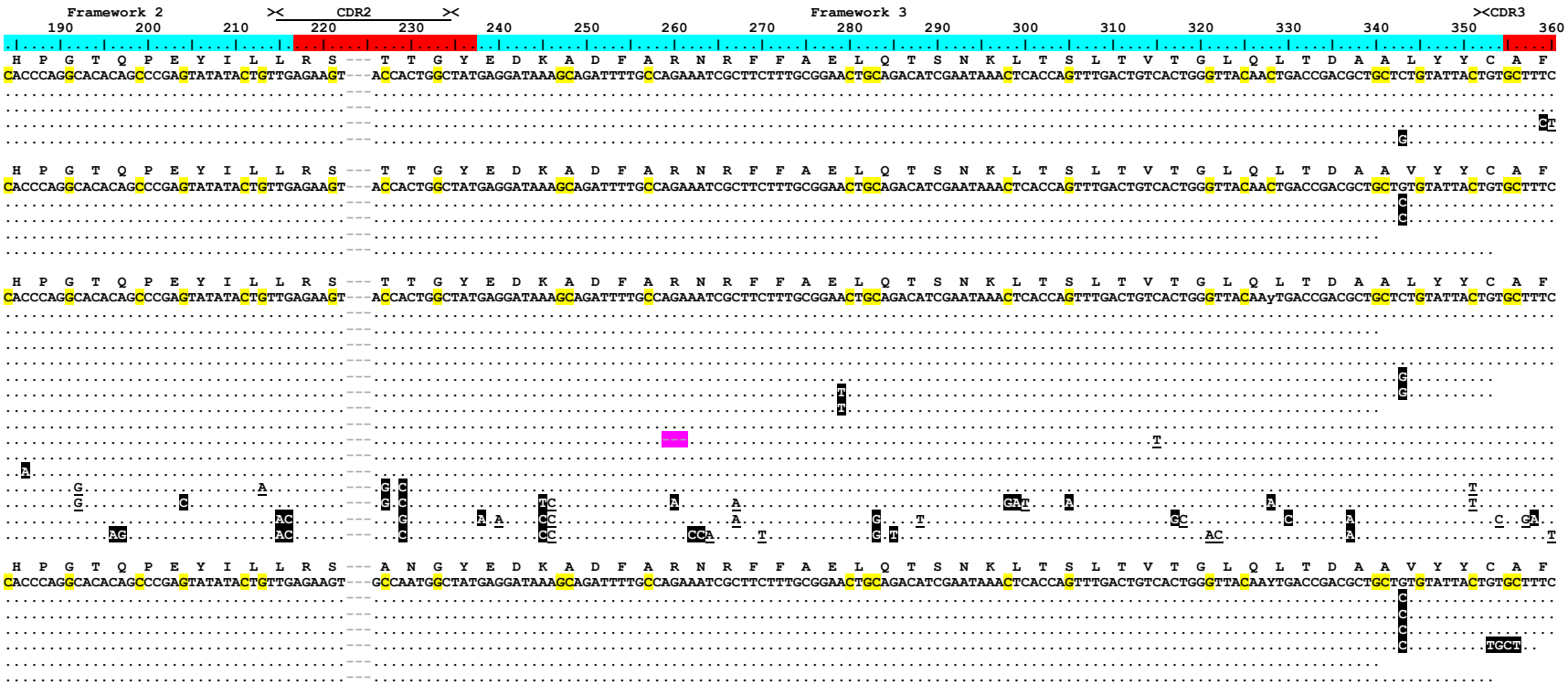
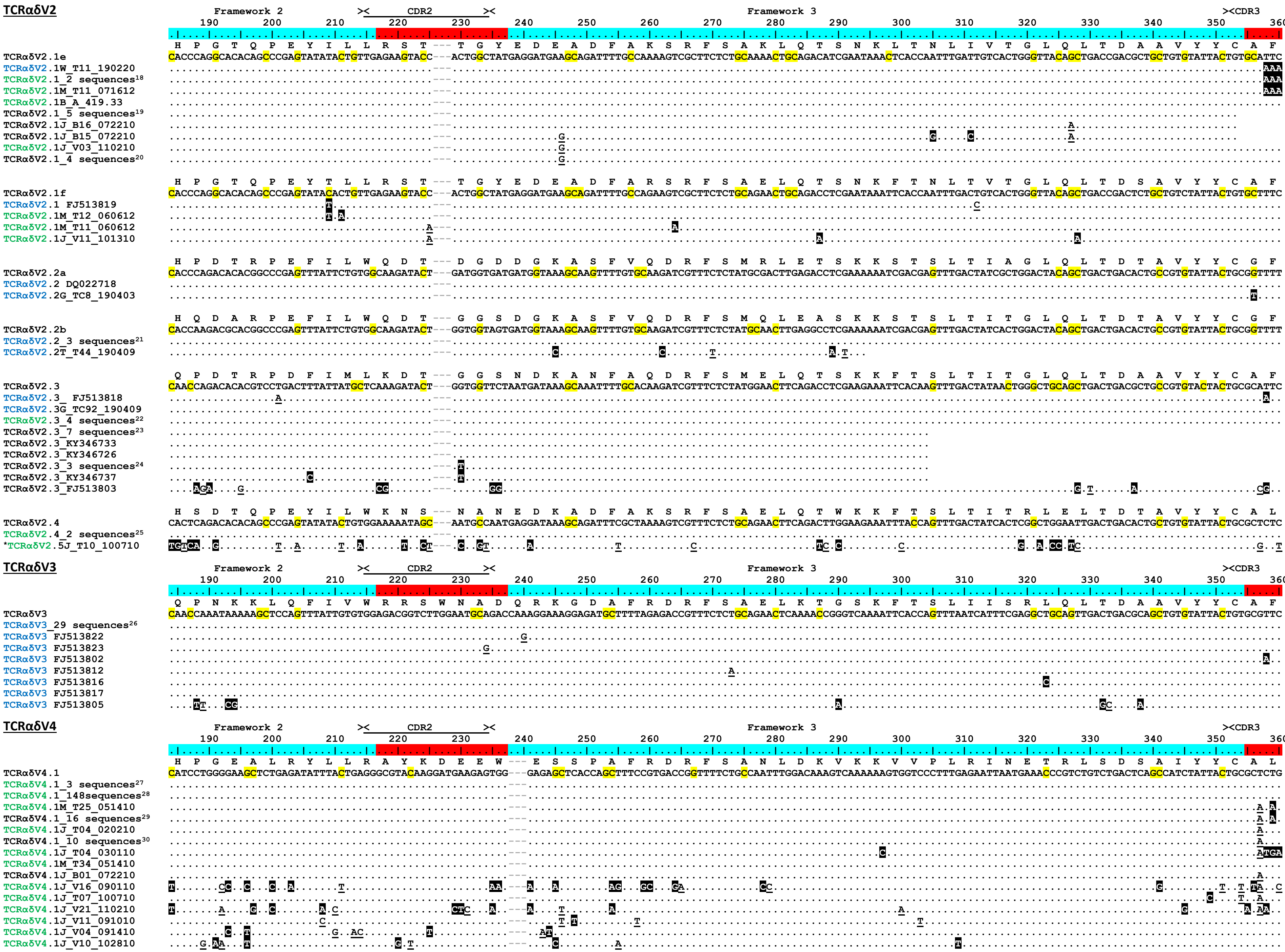
TCRαδV1



TCRαδV2





TCRαδV2
Framework 2
CDR2
Framework 3
CDR3
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TCRαδV2.1_5 sequences19
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TCRαδV2.1 FJ513819
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TCRαδV2.2G_TC8_190403
TCRαδV2.2b
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TCRαδV2.3G_TC92_190409
TCRαδV2.3_4 sequences22
TCRαδV2.3_7 sequences23
TCRαδV2.3_KY346733
TCRαδV2.3_KY346726
TCRαδV2.3_3 sequences24
TCRαδV2.3_KY346737
TCRαδV2.3_FJ513803
TCRαδV2.4
TCRαδV2.4_2 sequences25
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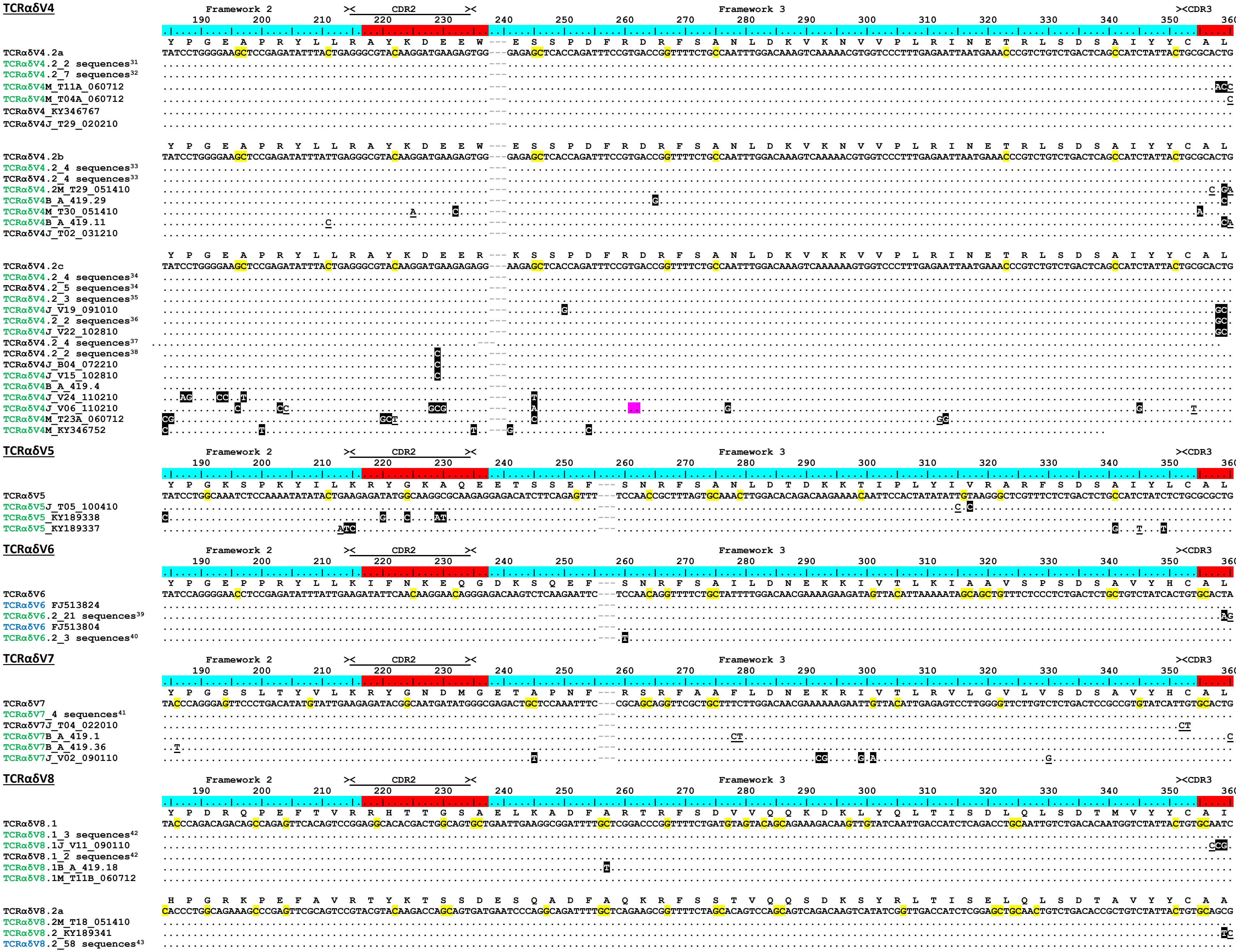
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CDR2
Framework 3
CDR3
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TCRαδV4.2b TATCCTGGGGAAGCTCCGAGATATTTATTGAGGGCGTACAAGGATGAAGAGTGG---GAGAGCTCACCAGATTTCCGTGACCGGTTTTCTGCCAATTTGGACAAAGTCAAAAACGTGGTCCCTTTGAGAATTAATGAAACCCGTCTGTCTGACTCAGCCATCTATTACTGCGCACTG
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TCRαδV4J_T02_031210
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TCRαδV4J_V06_110210
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TCRαδV5
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TCRαδV7_4 sequences[41]
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TCRαδV8
Y P D R Q P E F T V R R H T T G S A E L K A D F A R T R F S D V V Q Q K D K L Y Q L T I S D L Q L S D T M V Y Y C A I
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TCRαδV8.1_3 sequences[42]
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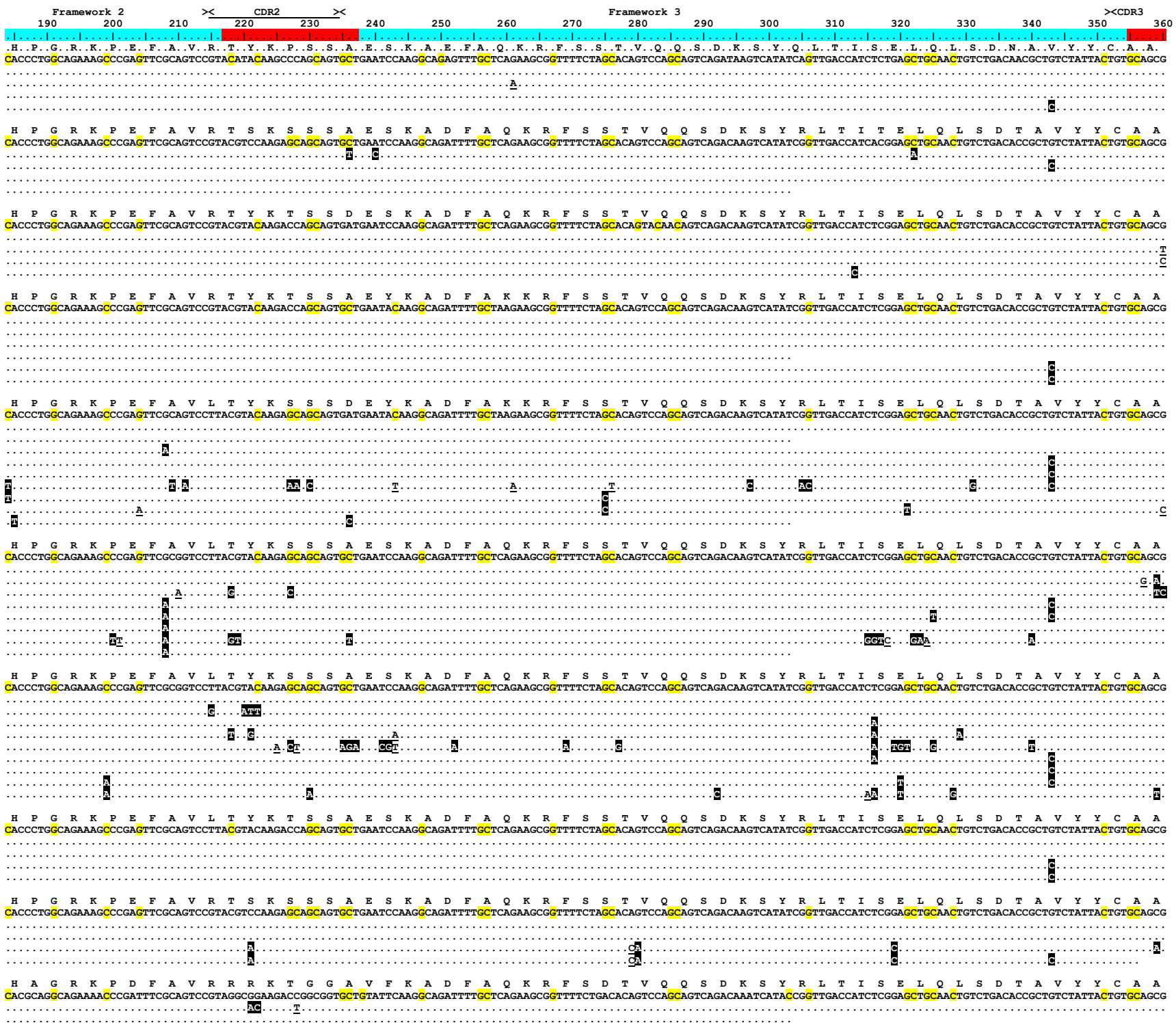
TCRαδV8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Framework 3
CDR3
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TCRαδV8.2_3 sequences47
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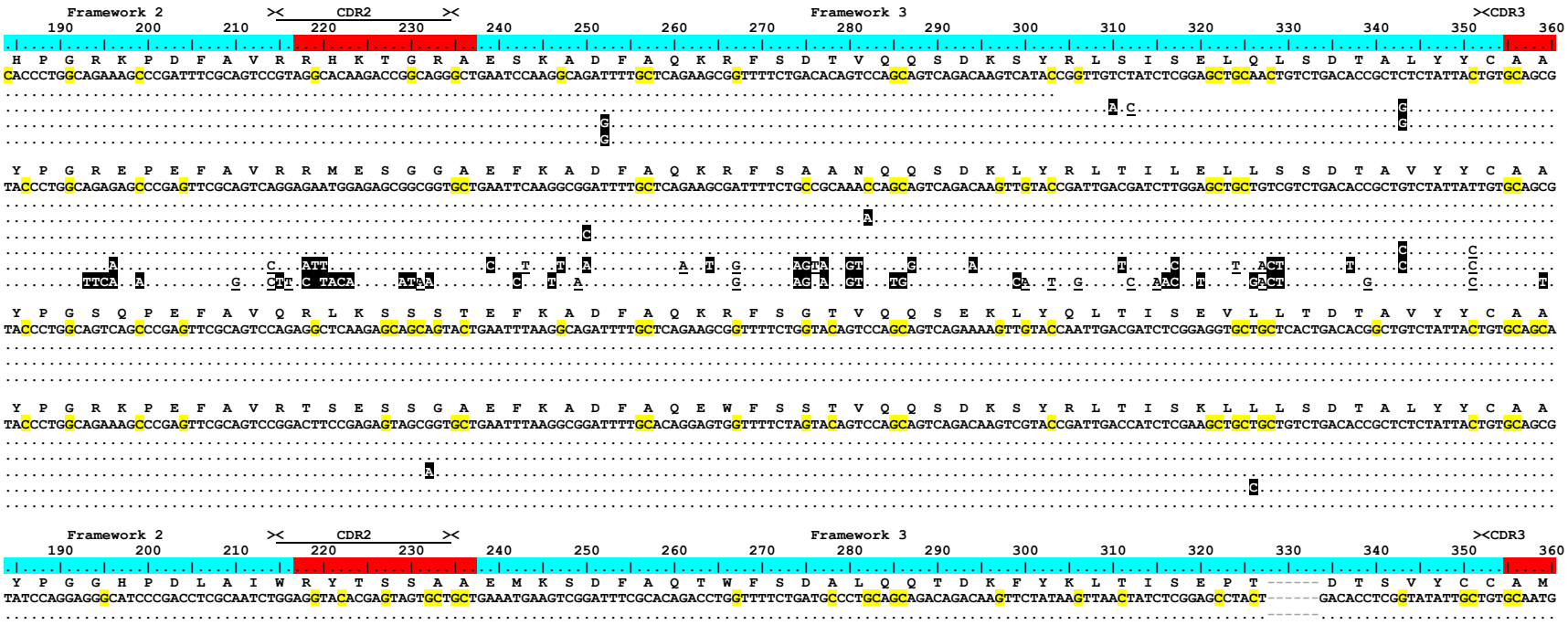
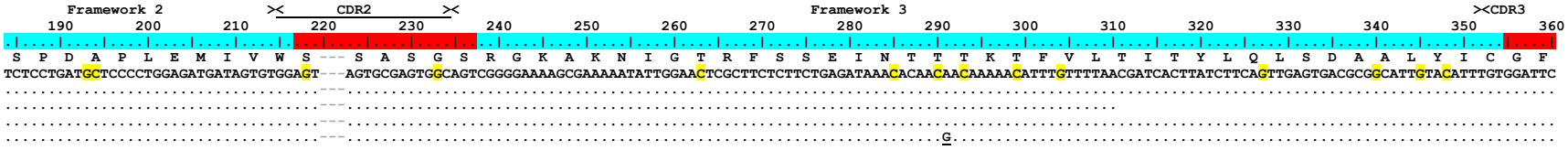
TCRαδV8.3_6 sequences61

TCRαδV8

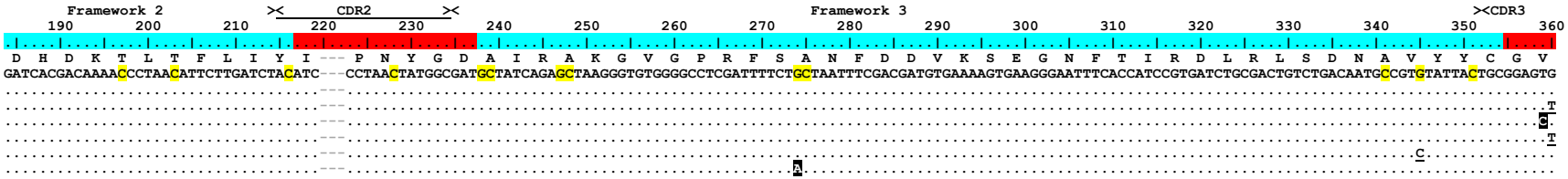


TCRαδV9

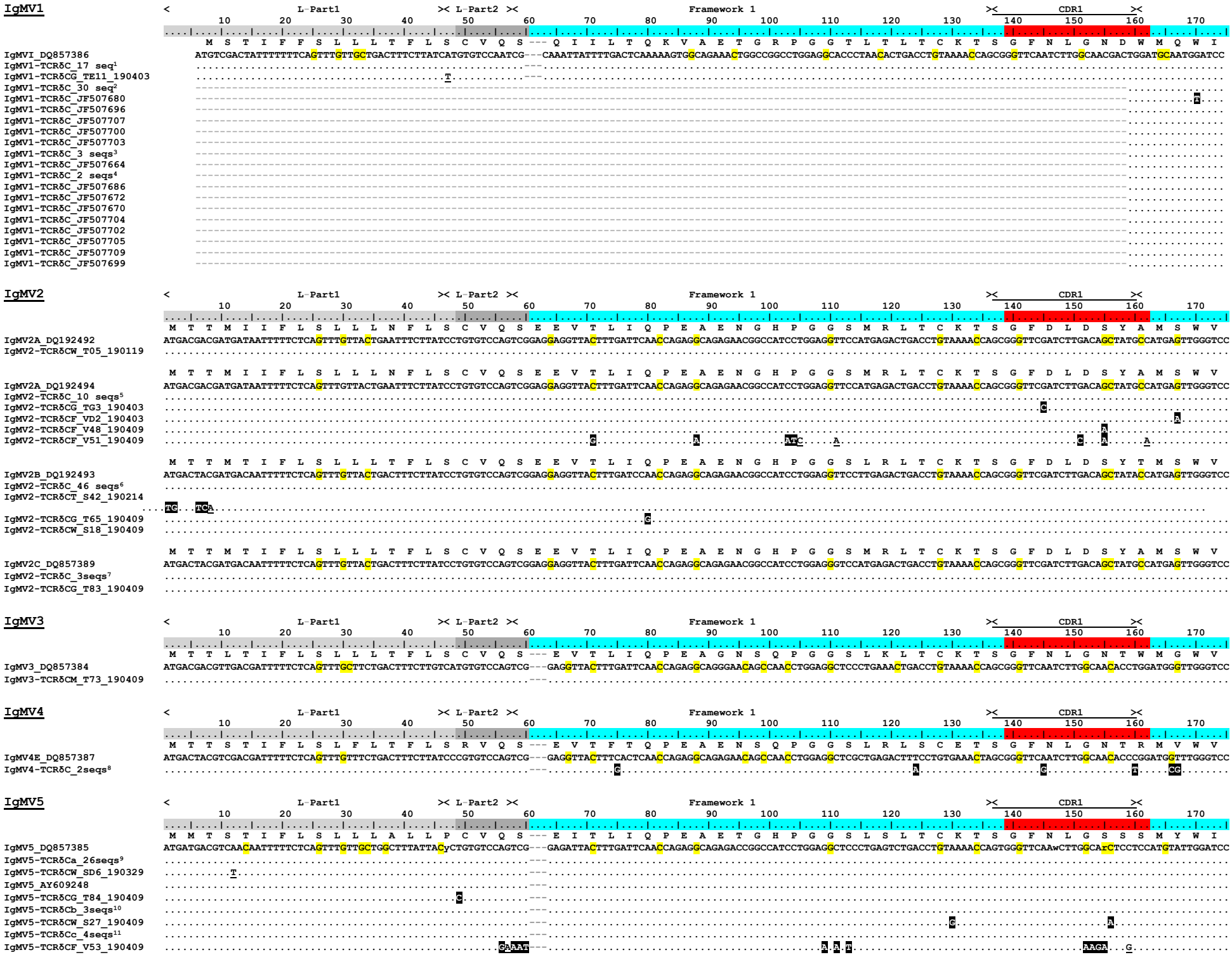
TCRαδV10



TCRαδV11



Supplemental Figure 3. Alignments of variable segments from "trans" rearrangements between (A) IgM V or (B) IgW V and T cell receptor delta constant (TCRδ C) regions suggest minimal somatic hypermutation. We include amino acids above the germline nucleotide sequence; dots signify identity to this sequence. Nucleotides highlighted in black indicate non-synonymous changes to the germline sequence and underlined nucleotides indicate synonymous changes. We denote leader [L-Part1 (light gray) is exon 1; L-Part2 (dark gray) is exon 2], framework (blue), and complementarity-determining regions (CDRs, red) below the scale. Each alignment contains only unique nucleotide sequences, with corroborating clones for lines containing identical bases referenced in Supplemental Figure 5. We used degenerate symbols (lower case) to indicate nucleotide differences likely due to allelic polymorphisms rather than mutation (see text for explanation). Highlighted nucleotides within the germline sequence represent G or C target nucleotides within AID hotspot motifs (DGYW/WRCH). Highlighted nucleotides (pink) within a transcript mark the location of introns or indels present within a sequence but removed from the alignment (see text for details). Dashes at the 5' or 3' end indicate shortened sequences. Gaps within a sequence are for alignment purposes only. Clone numbers that contain "T" are from thymus, "S" from spleen, "B" from peripheral blood leukocytes, and "V" from spiral valve (intestine). We deposited all sequences into GenBank under accession numbers MN748038-MN748047 (TAILV) and MN788155 - MN788287 (IgHV).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IgMV3
IgMV4
IgMV5
L-Part1
L-Part2
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IgMV1-TCRδCG_TE11_190403
IgMV1-TCRδC_30 seq2
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IgMV1-TCRδC_JF507696
IgMV1-TCRδC_JF507707
IgMV1-TCRδC_JF507700
IgMV1-TCRδC_JF507703
IgMV1-TCRδC_3 seqs3
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IgMV1-TCRδC_2 seqs4
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IgMV1-TCRδC_JF507672
IgMV1-TCRδC_JF507670
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IgMV1-TCRδC_JF507705
IgMV1-TCRδC_JF507709
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IgMV2-TCRδCF_VD2_190403
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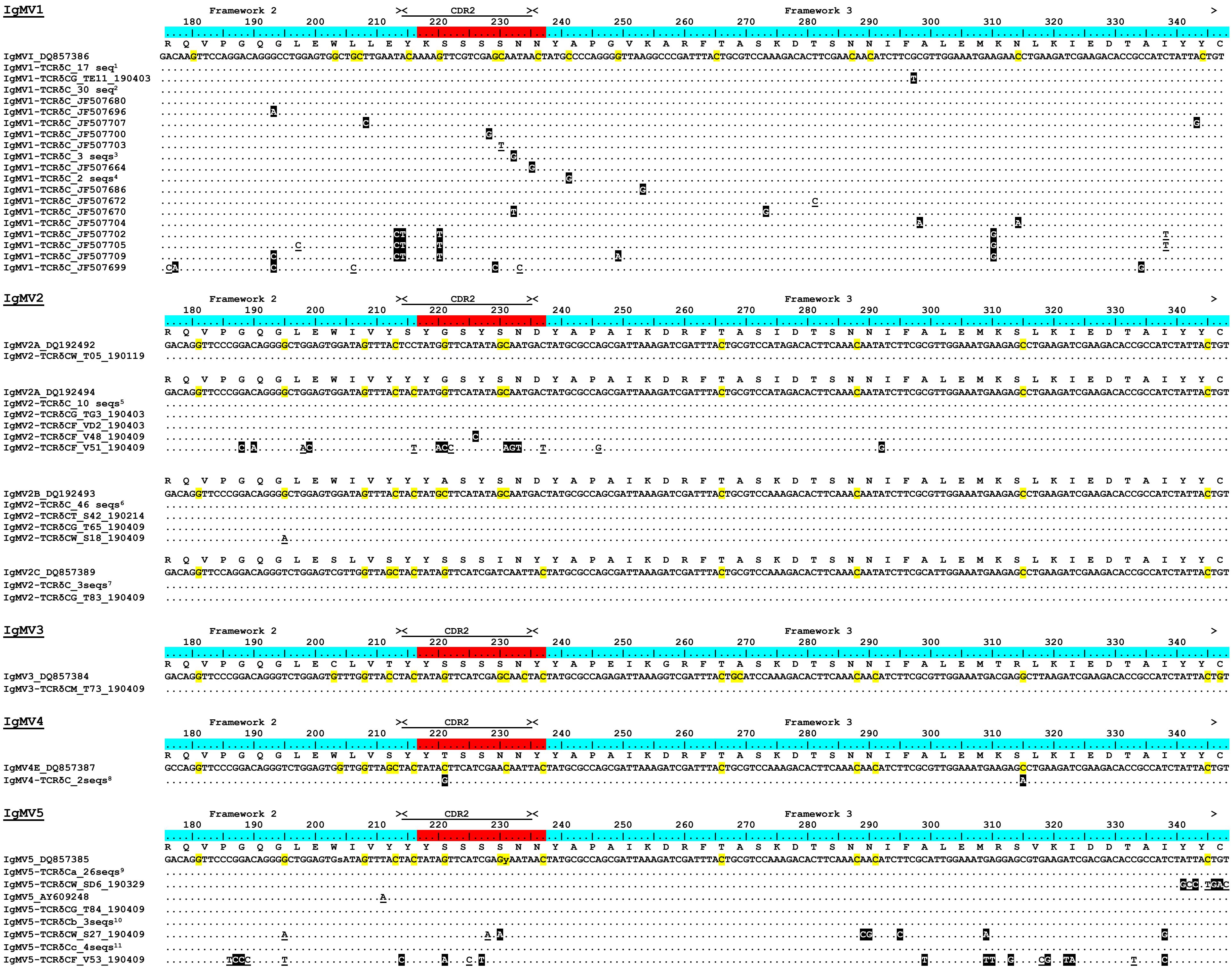
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CDR2
Framework 3
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IgMV1-TCRδC_JF507696
IgMV1-TCRδC_JF507707
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IgMV1-TCRδC_JF507664
IgMV1-TCRδC_2 seqs⁴
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IgMV1-TCRδC_JF507672
IgMV1-TCRδC_JF507670
IgMV1-TCRδC_JF507704
IgMV1-TCRδC_JF507702
IgMV1-TCRδC_JF507705
IgMV1-TCRδC_JF507709
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IgMV2-TCRδCF_V48_190409
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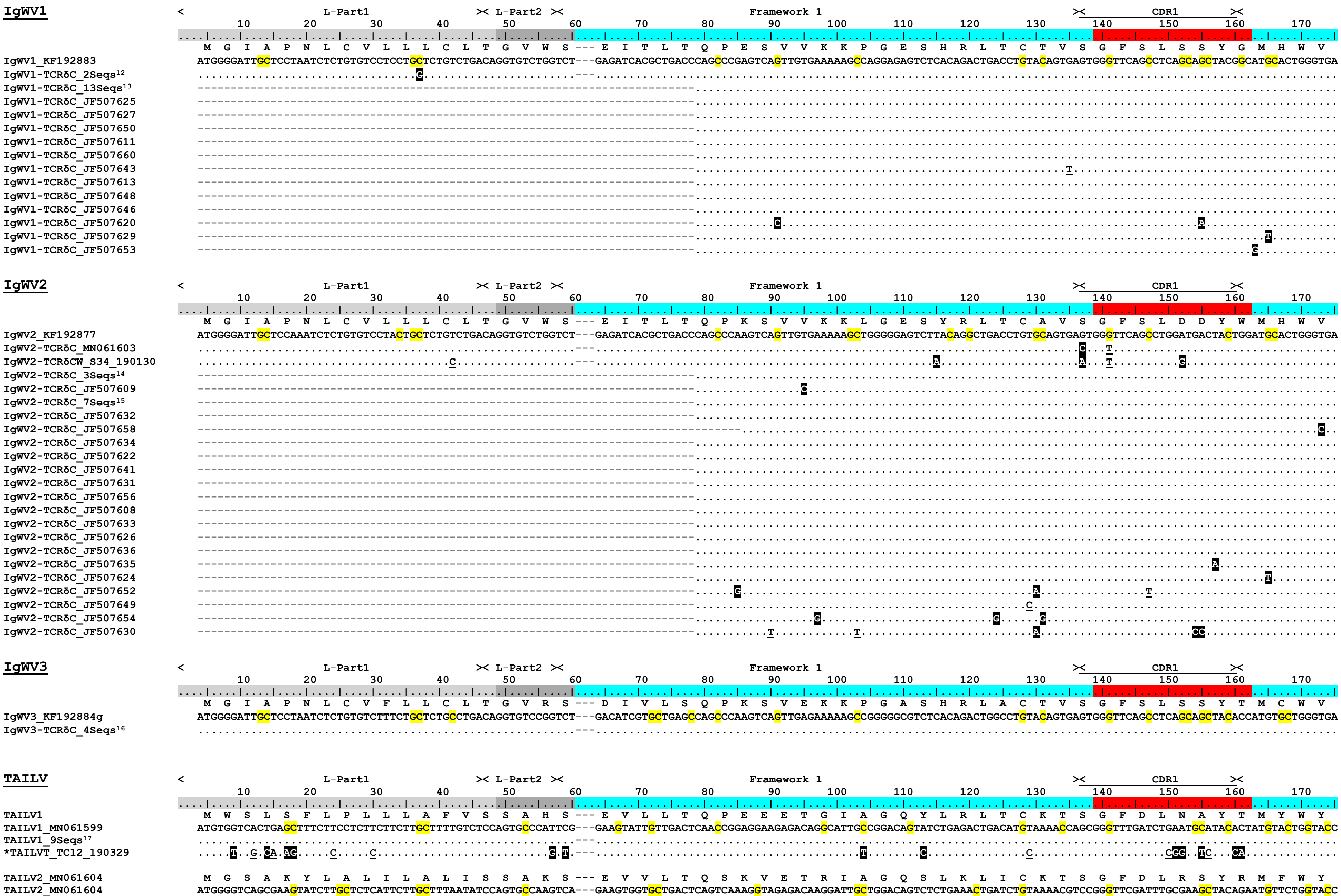
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L-Part2
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CDR1
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IgWV2
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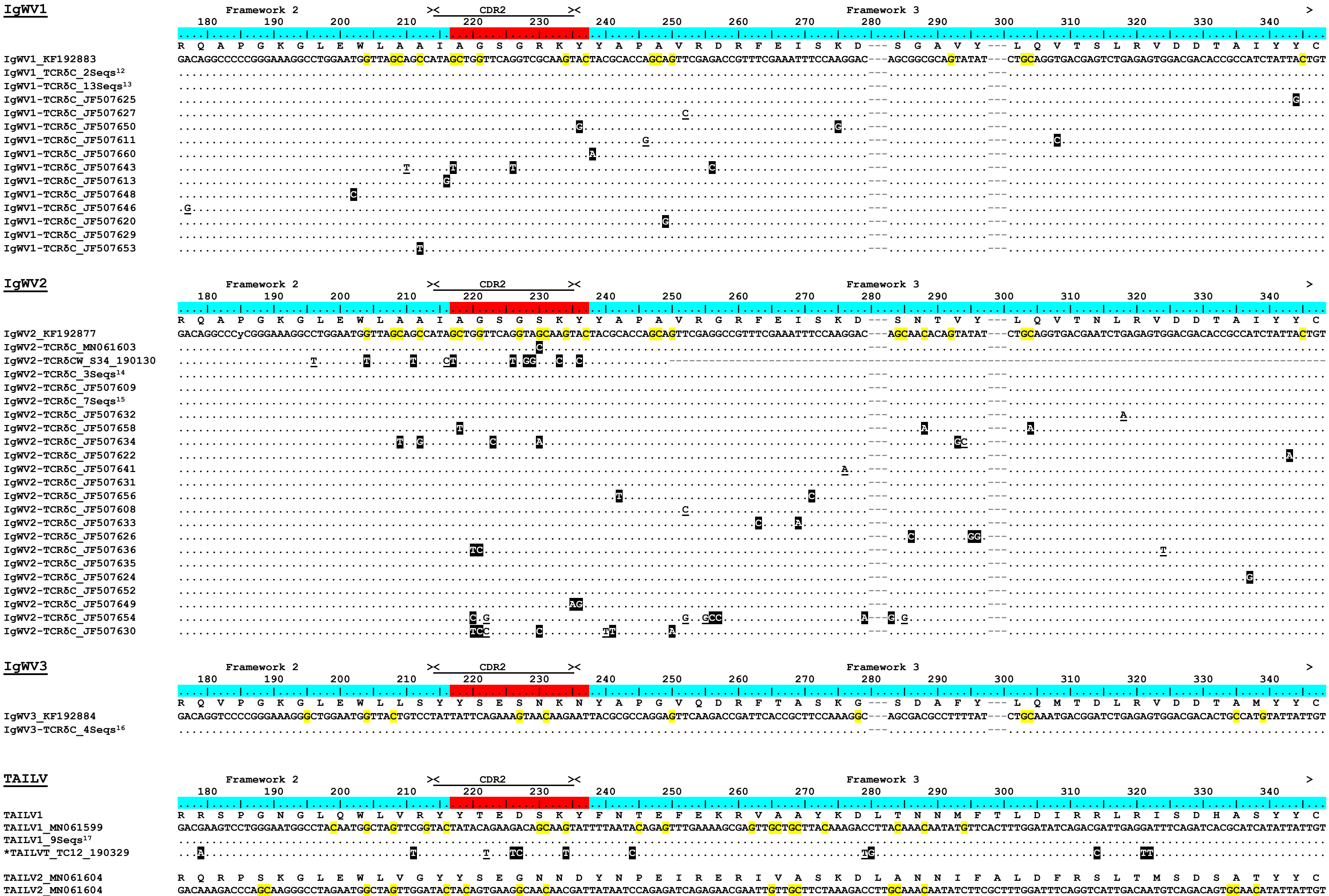
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IgWV1-TCRδC_JF507653
IgWV2
Framework 2
CDR2
Framework 3
IgWV2_KF192877
IgWV2-TCRδC_MN061603
IgWV2-TCRδCW_S34_190130
IgWV2-TCRδC_3Seqs14
IgWV2-TCRδC_JF507609
IgWV2-TCRδC_7Seqs15
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IgWV2-TCRδC_JF507622
IgWV2-TCRδC_JF507641
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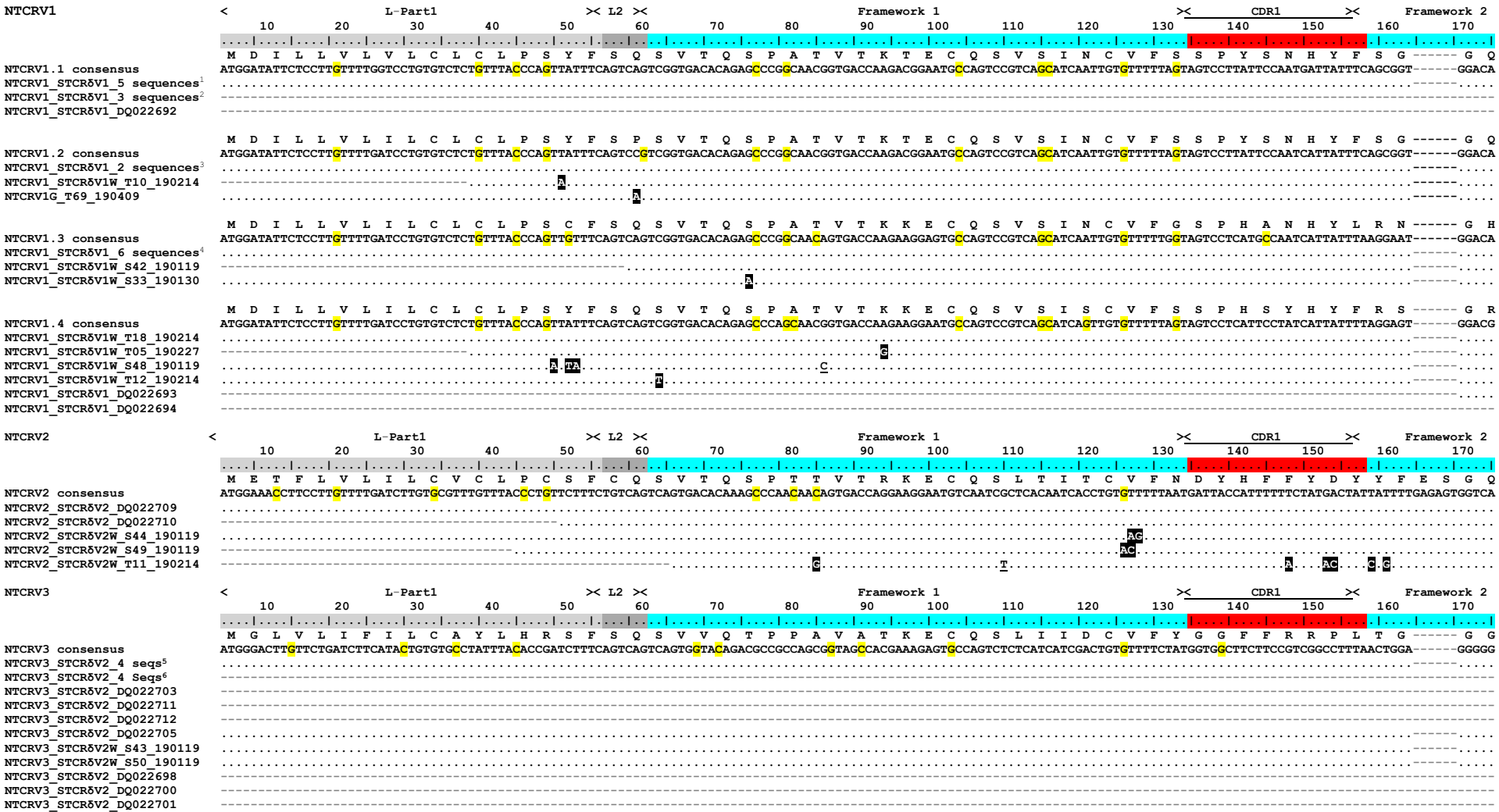
IgWV2-TCRδC_JF507630
IgWV3
Framework 2
CDR2
Framework 3
IgWV3_KF192884
IgWV3-TCRδC_4Seqs16
TAILV
Framework 2
CDR2
Framework 3
TAILV1
TAILV1_MN061599
TAILV1_9Seqs17
*TAILVT_TC12_190329
TAILV2_MN061604
TAILV2_MN061604

Supplemental Figure 4. Alignments of variable segments from NAR-TCR V (NTCRV) and supporting T cell receptor delta V (STCRδV) suggest minimal mutation. We include amino acids above the nucleotide consensus sequence; dots signify identity to this sequence. Nucleotides highlighted in black indicate non-synonymous changes to the consensus sequence and underlined nucleotides indicate synonymous changes. We denote leader [L-Part1 (light gray) is exon 1; L-Part2 (dark gray) is exon 2], framework (blue), and complementarity-determining regions (CDRs, red) below the scale. Each alignment contains only unique nucleotide sequences, with corroborating clones for lines containing identical bases referenced in Supplemental Figure 5. We used degenerate symbols (lower case) to indicate nucleotide differences likely due to allelic polymorphisms rather than mutation (see text for explanation). Highlighted nucleotides within the consensus sequence represent G or C target nucleotides within AID hotspot motifs (DGYW/WRCH). Dashes at the 5' or 3' end indicate shortened sequences. Gaps within a sequence are for alignment purposes only. Clone numbers that contain "T" are from thymus, "S" from spleen, "B" from peripheral blood leukocytes, and "V" from spiral valve (intestine). We deposited all sequences into GenBank under accession numbers MN748005-MN748037.


NTCRV1
L-Part1
L2
Framework 1
CDR1
Framework 2
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NTCRV1_STCRδV1_5 sequences[1]
NTCRV1_STCRδV1_3 sequences[2]
NTCRV1_STCRδV1_DQ022692
NTCRV1.2 consensus
NTCRV1_STCRδV1_2 sequences[3]
NTCRV1_STCRδV1W_T10_190214
NTCRV1G_T69_190409
NTCRV1.3 consensus
NTCRV1_STCRδV1_6 sequences[4]
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NTCRV2_STCRδV2W_T11_190214
NTCRV3
NTCRV3 consensus
NTCRV3_STCRδV2_4 seqs[5]
NTCRV3_STCRδV2_4 Seqs[6]
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NTCRV3_STCRδV2W_S50_190119
NTCRV3_STCRδV2_DQ022698
NTCRV3_STCRδV2_DQ022700
NTCRV3_STCRδV2_DQ022701

```
NTCRV1                                  ><                      CDR2          ><                                    Framework 3                                  >
                                         180       190       200       210       220       230       240       250       260       270       280       290       300       310       320
                                         |....|....|..|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                          F  F  K  K  T  R  A  A  K  E  W  E  R  I  T  S  G  G  R  F  V  V  S  T  N  Q  A  Q  K  T  F  S  L  E  I  R  D  I  R  V  E  D  T  A  T  Y  Y  C  K  A
NTCRV1.1 consensus                      GTTCTTCAAAAAAACGCGTGCAGCGAAGGAGTGGGAGCGGATCACCAGCGGCGGGAGATTTGTTGTGTCCACGAATCAAGCACAAAAGACATTTTCGTTGGAAATTCGGGATATCAGAGTTGAAGACACTGCCACTTATTACTGTAAGGCT
NTCRV1_STCRδV1_5 sequences[1]           ..........................................................................................................................................
NTCRV1_STCRδV1_3 sequences[2]           ------------..........................................................................................................................
NTCRV1_STCRδV1_DQ022692                 ------------------..................................................................................................................A..

                                          F  F  K  K  T  R  A  A  K  E  W  E  R  I  T  S  G  G  R  F  V  V  S  T  N  Q  A  Q  K  T  F  S  L  E  I  R  D  I  R  V  E  D  T  A  T  Y  Y  C  K  A
NTCRV1.2 consensus                      GTTCTTCAAAAAAACGCGTGCAGCGAAGGAGTGGGAGCGGATCACCAGCGGCGGGAGATTTGTTGTGTCCACGAATCAAGCACAAAAGACATTTTCGTTGGAAATTCGGGATATCAGAGTTGAAGACACTGCCACTTATTACTGTAAGGCT
NTCRV1_STCRδV1_2 sequences[3]           ..........................................................................................................................................
NTCRV1_STCRδV1W_T10_190214              ..........................................................................................................................................
NTCRV1G_T69_190409                      ..........................................................................................................................................

                                          F  F  K  K  T  R  T  A  K  E  W  E  R  I  T  S  G  G  R  F  V  V  S  T  N  Q  A  Q  K  T  F  S  L  E  I  R  D  I  R  V  E  D  T  A  T  Y  Y  C  K  A
NTCRV1.3 consensus                      TTTCTTCAAAAAAACGCGGACAGCGAAGGAGTGGGAGCGGATCACCAGCGGCGGGAGATTTGTTGTGTCCACGAATCAAGCACAAAAGACATTTTCGTTGGAAATTCGAGATATCAGAGTTGAAGACACTGCCACCTATTACTGTAAGGCT
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NTCRV1_STCRδV1W_S33_190130              ..........................................................................................................................C.............

                                          F  F  K  K  T  R  T  A  K  E  W  E  R  I  N  S  G  G  R  F  V  V  S  T  N  E  A  Q  K  T  F  S  L  E  I  L  D  L  R  I  E  D  T  A  T  Y  Y  C  K  A
NTCRV1.4 consensus                      TTTCTTCAAAAAAACGCGGACAGCGAAGGAATGGGAGCGAATCAACAGCGGCGGGAGATTTGTTGTGTCCACGAATGAAGCACAAAAGACATTTTCGTTGGAAATTCTGGATCTCAGAATTGAAGACACTGCCACCTATTACTGTAAGGCT
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NTCRV1_STCRδV1_DQ022693                 ..........................................................................................................................................
NTCRV1_STCRδV1_DQ022694                 ----------................................................................................................................................

NTCRV2                                  ><                      CDR2          ><                                    Framework 3                                  >
                                         180       190       200       210       220       230       240       250       260       270       280       290       300       310       320
                                         |....|....|..|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                          F  F  R  Q  I  Q  G  T  T  E  W  E  R  I  S  G  G  G  R  F  I  M  S  T  N  K  G  E  K  T  F  S  L  E  I  R  D  V  K  V  K  D  T  A  T  Y  Y  C  K  A
NTCRV2 consensus                        ATTCTTCAGACAAATACAGGGAACGACGGAATGGGAGCGGATCTCTGGCGGTGGGAGATTTATTATGTCCACAAATAAAGGGGAAAAGACATTTTCGTTGGAAATTCGTGACGTCAAAGTTAAAGACACCGCGACCTATTACTGTAAGGCT
NTCRV2_STCRδV2_DQ022709                 ..........................................................................................................................................
NTCRV2_STCRδV2_DQ022710                 ..........................................................................................................................................
NTCRV2_STCRδV2W_S44_190119              ..........................................................................................................................................A..
NTCRV2_STCRδV2W_S49_190119              ..........................................................................................................................................
NTCRV2_STCRδV2W_T11_190214              .......................G..........................A..............................C..............................G.............

NTCRV3                                  ><                      CDR2          ><                                    Framework 3                                  >
                                         180       190       200       210       220       230       240       250       260       270       280       290       300       310       320
                                         |....|....|..|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                          F  F  K  Q  S  Q  T  G  S  E  R  E  R  I  S  A  G  E  R  F  D  V  R  I  N  K  A  E  K  T  F  S  L  E  I  R  D  V  K  V  E  D  T  A  T  Y  Y  C  N  A
NTCRV3 consensus                        TTTCTTCAAACAAAGCCAGACAGGATCAGAGCGGGAGCGGATCTCGGCAGGGGAGAGGTTTGATGTGAGGATAAATAAAGCAGAAAAGACATTTTCGCTGGAAATTCGGGATGTGAAAGTTGAAGACACCGCCACCTATTATTGTAACGCA
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NTCRV3_STCRδV2_DQ022711                 ----------................................................................................................................
NTCRV3_STCRδV2_DQ022712                 ------------..............................................................................................................
NTCRV3_STCRδV2_DQ022705                 ..........................................................................................................................G.................
NTCRV3_STCRδV2W_S43_190119              ..........................................................................................................................A...T.............
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NTCRV3_STCRδV2_DQ022698                 ------------..............................G...........................................................................
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NTCRV3_STCRδV2_DQ022701                 ----......................G.....................CT....G.....................................................T.T.
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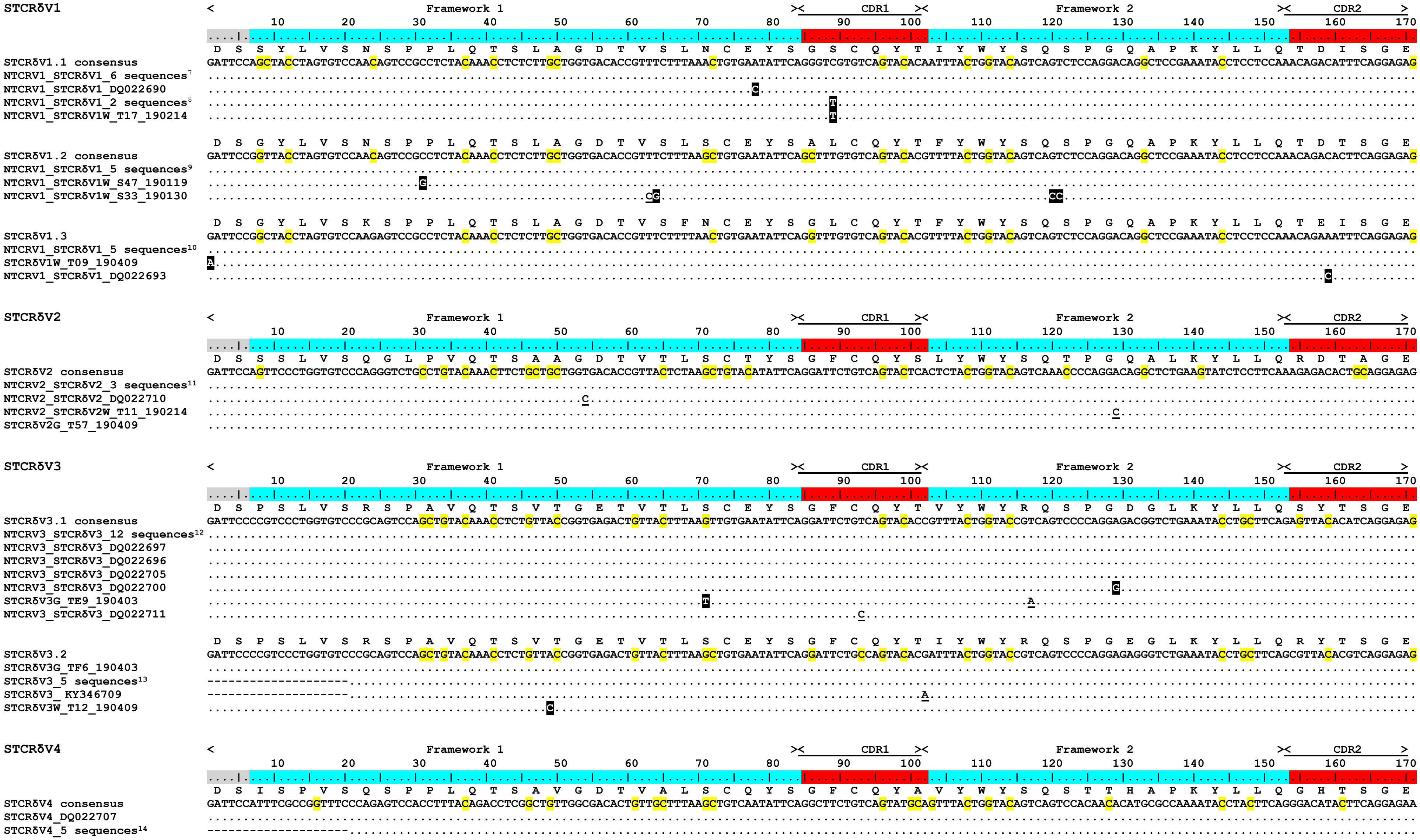
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Framework 1
CDR1
Framework 2
CDR2
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NTCRV1_STCRδV1_2 sequences[8]
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STCRδV1.2 consensus
NTCRV1_STCRδV1_5 sequences[9]
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STCRδV1.3
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STCRδV2
STCRδV2 consensus
NTCRV2_STCRδV2_3 sequences[11]
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STCRδV3G_TE9_190403
NTCRV3_STCRδV3_DQ022711
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STCRδV3G_TF6_190403
STCRδV3_5 sequences[13]
STCRδV3_ KY346709
STCRδV3W_T12_190409
STCRδV4
STCRδV4 consensus
STCRδV4_DQ022707
STCRδV4_5 sequences[14]

```
STCRδV1                    <                                   Framework 3                                                                  >
                                     190       200       210       220       230       240       250       260       270       280       290
                           ...|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....
                            Q  R  K  E  N  V  A  G  G  R  I  A  A  S  I  D  P  E  A  K  I  C  R  L  I  I  S  R  A  Q  L  S  D  S  A  V  Y  Y  C  A  R
STCRδV1.1 consensus        CAGAGAAAAGAAAATGTTGCCGGAGGAAGAATTGCTGCTTCCATTGATCCTGAGGCGAAAATCTGTCGGTTAATAATCTCTCGAGCACAACTGAGTGATTCTGCTGTTTATTACTGTGCACGG
NTCRV1_STCRδV1_6 sequences[7]  ..........................................................................................................................
NTCRV1_STCRδV1_DQ022690    ..........................................................................................................................
NTCRV1_STCRδV1_2 seqs[8]   ...............A..........................................................................................................
NTCRV1_STCRδV1W_T17_190214 ....A..........A..........................................................................................................

                            Q  R  K  E  N  I  A  G  G  R  I  A  A  S  I  D  P  E  A  K  I  C  R  L  I  I  S  R  A  Q  L  S  D  S  A  V  Y  Y  C  A  R
STCRδV1.2 consensus        CAGAGAAAAGAAAATATTGCCGGAGGAAGAATTGCTGCTTCCATTGATCCTGAGGCGAAAATCTGTCGGTTAATAATCTCTCGAGCACAACTGAGTGATTCTGCTGTTTATTACTGTGCACGG
NTCRV1_STCRδV1_5 sequences[9]  ......................................--------------------------------------------------------------------------
NTCRV1_STCRδV1W_S47_190119 ..........................................................................................................................
NTCRV1_STCRδV1W_S33_190130 ..........................................................................................................................-

                            Q  R  K  E  S  V  A  G  G  R  I  A  A  S  I  D  P  V  A  K  I  G  R  L  I  I  S  R  T  Q  L  S  D  S  A  V  Y  Y  C  A  R
STCRδV1.3 consensus        CAGAGAAAAGAAAGTGTTGCCGGAGGAAGAATTGCTGCTTCCATTGATCCTGTGGCGAAAATCGGTCGGTTAATAATCTCTCGAACACAACTGAGTGATTCGGCTGTTTATTACTGTGCACGG
NTCRV1_STCRδV1_5 sequences[10] ..........................................................................................................................
STCRδV1W_T09_190409        ..........................................................................................................................
NTCRV1_STCRδV1_DQ022693    ..........................................................................................................................

STCRδV2                    <                                   Framework 3                                                                  >
                                     190       200       210       220       230       240       250       260       270       280       290
                           ...|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....
                            K  N  K  E  N  A  A  R  G  R  V  S  A  S  I  D  P  G  A  K  I  Y  R  L  M  I  S  Q  I  Q  H  A  D  S  A  V  Y  Y  C  A  S
STCRδV2 consensus          AAGAATAAAGAAAATGCTGCGAGGGGACGGGTGTCTGCATCTATTGATCCTGGGGCGAAAATCTATCGGTTAATGATCTCTCAAATTCAACACGCTGATTCTGCTGTTTATTACTGCGCAAGT
NTCRV2_STCRδV2_3 sequences[11] ..........................................................................................................................
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NTCRV2_STCRδV2W_T11_190214 ..............................................................A...........................................................
STCRδV2G_T57_190409        ..............................................................A...........................................................

STCRδV3                    <                                   Framework 3                                                                  >
                                     190       200       210       220       230       240       250       260       270       280       290
                           ...|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....
                            Q  N  K  E  H  A  A  G  G  R  I  S  A  A  I  D  S  S  A  K  I  S  R  L  K  I  S  T  L  Q  L  S  D  S  A  V  Y  Y  C  A  L
STCRδV3.1 consensus        CAGAATAAAGAACATGCAGCTGGAGGCAGAATTTCTGCTGCTATTGACTCCTCGGCAAAAATCAGTCGACTAAAGATCTCCACATTACAACTGAGTGACTCTGCGGTGTATTACTGCGCACTG
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NTCRV3_STCRδV3_DQ022696    ...................G......................................................................................
NTCRV3_STCRδV3_DQ022705    ..........................................................................................G.......................
NTCRV3_STCRδV3_DQ022700    ..........................................................................................................................
STCRδV3G_TE9_190403        ..........................................................................................................................
NTCRV3_STCRδV3_DQ022711    ..........................................................................................................................

                            Q  N  K  K  N  A  T  G  G  R  I  S  A  A  I  D  S  S  A  K  I  S  R  L  K  I  S  T  I  Q  L  S  D  S  A  V  Y  Y  C  A  L
STCRδV3.2 consensus        CAGAATAAAAAAAATGCAACTGGAGGCAGAATTTCTGCTGCTATTGACTCCTCAGCAAAAATCAGTCGATTAAAGATCTCCACAATACAACTGAGCGACTCTGCTGTGTATTACTGTGCACTG
STCRδV3G_TF6_190403        ..........................................................................................................................
STCRδV3_5 sequences[13]    ..........................................................................................--------------------
STCRδV3_ KY346709          ...........G..........................................G.......................................T......--------------------
STCRδV3W_T12_190409        ..........................................................................................T.........................

STCRδV4                    <                                   Framework 3                                                                  >
                                     190       200       210       220       230       240       250       260       270       280       290
                           ...|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....
                            G  K  K  E  N  A  A  T  E  R  L  S  A  S  I  D  P  A  A  K  I  T  Q  L  K  I  S  A  I  Q  L  N  D  S  G  V  Y  Y  C  A  L
STCRδV4 consensus          GGGAAGAAAGAAAATGCTGCCACGGAAAGACTTTCTGCCTCCATCGATCCTGCAGCGAAAATCACCCAGTTAAAGATCTCTGCAATACAACTGAATGATTCTGGTGTGTATTACTGTGCACTC
STCRδV4_DQ022707           ..........................................................................................................................
STCRδV4_5 sequences[14]    ..........................................................................................--------------------
```

<u>Supplemental Figure 5</u>. Clone sequences contained within footnotes of Supplemental Figures 1 through 4. Clones listed in a single footnote contain identical nucleotide sequences for T cell receptor (TCR) variable segments (V) of **[A]** Beta (TCRβ V) and **[B]** Gamma (TCRγ V) [Supplemental Figure 1], **[C]** Alpha/Delta (TCRαδ V) [Supplemental Figure 2], **[D]** NAR-TCR (NTCRV-STCRδV) [Supplemental Figure 3], or **[E]** IgHV-TCRδC "trans"-rearrangements (IgM-TCRδC) and TAILV [Supplemental Figure 4]. For TCRαδ V sequences, sequence colors indicate the constant (C) regions utilized by the segment (green=alpha C; blue=delta C; black=incomplete/no C).

[A] Beta Alignment (Supplemental Figure 1A)

1.	TCRβV1.1T_FJ513739	TCRβV1.1T_T02_181116	TCRβV1.1T_T09_190116	TCRβV1.1T_T04_181116	TCRβV1.1T_T10_190116
2.	TCRβV1.1F_SPL02_190213	TCRβV1.1T_T15_190111	TCRβV1.1F_T17_190213	TCRβV1.1T_T06_190111	TCRβV1.1T_T07_190111
	TCRβV1.1T_T03_190111	TCRβV1.1F_T18_190213	TCRβV1.1T_T22_190111	TCRβV1.1F_T02_190227	TCRβV1.1F_T13_190213
	TCRβV1.1T_T24_190111	TCRβV1.1T_T14_190111	TCRβV1.1T_T08_190111	TCRβV1.1F_T14_190213	TCRβV1.1T_T16_190111
	TCRβV1.1T_T21_190111	TCRβV1.1T_T19_190111	TCRβV1.1T_T10_190111	TCRβV1.1F_T19_190213	
3.	TCRβV1.1T_FJ513725	TCRβV1.1T_FJ513766	TCRβV1.1T_FJ513768	TCRβV1.1T_FJ513722	
4.	TCRβV1.2T_SPL10_181018	TCRβV1.2F_SPL29_190320	TCRβV1.2F_SPL24_190320	TCRβV1.2F_SPL28_190320	
5.	TCRβV1.2F_T11_190213	TCRβV1.2T_T06_181116	TCRβV1.2F_T20_190213	TCRβV1.2F_T08_190227	TCRβV1.2F_T12_190213
	TCRβV1.2F_SPL08_190213	TCRβV1.2F_T01_190227	TCRβV1.2F_T05_190227	TCRβV1.2F_T15_190213	TCRβV1.2T_T18_190111
	TCRβV1.2T_T11_190111	TCRβV1.2T_T12_190111	TCRβV1.2F_SPL10_190213	TCRβV1.2F_T04_190227	TCRβV1.2F_SPL03_190213
	TCRβV1.2F_T07_190227				
6.	TCRβV1.2T_T04_190116	TCRβV1.2T_SPL02_181018	TCRβV1.2T_T06_190116		
7.	TCRβV1.2W_T21_190213	TCRβV1.2W_T12_190227	TCRβV1.2W_T17_190227	TCRβV1.2W_T28_190213	TCRβV1.2W_T25_190213
	TCRβV1.2W_T14_190227	TCRβV1.2W_T16_190227	TCRβV1.2F_V33_190213	TCRβV1.2W_T19_19022	TCRβV1.2T_T07_190723
	TCRβV1.2T_T10_190723	TCRβV1.2T_T18_190723	TCRβV1.2T_T21_190723		
8.	TCRβV1.2T_T02_190111	TCRβV1.2T_SPL24_181018			
9.	TCRβV1.4W_T15_190227	TCRβV1.4W_T27_190213	TCRβV1.4W_T18_190227	TCRβV1.4W_T20_190227	TCRβV1.4W_T23_190213
	TCRβV1.4W_T22_190213	TCRβV1.4F_T11_190227	TCRβ4T_T05_190723	TCRβV1.4T_T23_190723	
10.	TCRβV5W_T01_181220	TCRβV2.1W_T04_181220	TCRβV2.1W_T15_181220	TCRβV2.1W_T28_181220	TCRβV2.1W_T31_181220
	TCRβV2.1W_T20_181220	TCRβV2.1W_T14_181220	TCRβV2.1W_T11_181220	TCRβV2.1W_T18_181220	TCRβV2.1W_T17_181220
	TCRβV2.1W_T08_181220	TCRβV2.1W_T36_181220	TCRβV2.1W_T34_181220	TCRβV2.1W_T29_181220	TCRβV2.1W_T21_181220
	TCRβV2.1W_T19_181220	TCRβV2.1W_T30_181220	TCRβV2.1W_T16_181220	TCRβV2.1W_T13_181220	TCRβV2.1W_T26_181220
	TCRβV2.1W_T35_181220	TCRβV2.1W_T23_181220	TCRβV2.1W_T27_181220	TCRβV2.1W_T06_181220	TCRβV2.1W_T10_181220
	TCRβV2.1W_T05_181220	TCRβV2.1W_T03_181220	TCRβV2.1_FJ513752	TCRβV2.1_FJ513711	TCRβV2.1_FJ513704
	TCRβV2.1G_T22_190719				
11.	TCRβV2.1F_T10_190212	TCRβV2.1W_SPL35_190212	TCRβV2.1W_SPL24_190201	TCRβV2.1W_T16_181214	TCRβV2.1W_T19_190212
12.	TCRβV2.2_FJ513707	TCRβV2.2W_T07_181220	TCRβV2.2W_T24_181220	TCRβV2.2W_T32_181220	TCRβV2.2W_T12_181220
13.	TCRβV3_FJ513710	TCRβV3_FJ513759	TCRβV3_FJ513759	TCRβV3_FJ513740	TCRβV3W_T17_181214
	TCRβV3W_T20_181214	TCRβV3W_T13_181214	TCRβV3F_T12_190201	TCRβV3W_T12_181214	TCRβV3W_SPL36_190212
	TCRβV3F_T16_190212	TCRβV3F_T07_190201	TCRβV3F_SPL39_190212	TCRβV3W_SPL03_190212	TCRβV3W_T05_181214
	TCRβV3F_T10_190201	TCRβV3W_T08_181214	TCRβV3F_T15_190212	TCRβV3F_T11_190212	TCRβV3W_T21_190212
	TCRβV3F_SPL44_190212	TCRβV3F_T12_190212	TCRβV3F_T17_190212	TCRβV3W_T18_181214	TCRβV3T_T11_190207
	TCRβV3T_T04_190207	TCRβV3F_T08_190201	TCRβV3F_SPL29_190201	TCRβV3F_T09_190201	TCRβV3G_T36_190719
14.	TCRβV3W_T26_190212	TCRβV3T_T02_190207	TCRβV3T_T05_190207	TCRβV3T_T07_190207	TCRβV3T_T08_190207
	TCRβV3T_T09_190207	TCRβV3T_T10_190207	TCRβV3W_SPL23_190201	TCRβV3W_T13_190201	TCRβV3W_SPL34_190212
	TCRβV3W_T21_181214	TCRβV3W_T22_181214	TCRβV3W_T41_190201	TCRβV3W_T09_181214	TCRβV3W_T18_190201
	TCRβV3W_T25_190212	TCRβV3W_T11_181214	TCRβV3W_SPL22_190201	TCRβV3W_T10_181214	
15.	TCRβV4_FJ513737	TCRβV4_FJ513732	TCRβV4G_T47_190710	TCRβV4G_T36_190710	
16.	TCRβV4T_T31_190111	TCRβV4W_SPL12_181031	TCRβV4T_T37_190111	TCRβV4T_T41_190111	TCRβV4T_T38_190111
	TCRβV4T_T40_190111	TCRβV4T_T12_181116	TCRβV4T_T35_190111	TCRβV4T_T43_190111	TCRβV4T_T42_190111
	TCRβV4T_T44_190111	TCRβV4T_T36_190111	TCRβV4F_V36_190213	TCRβV4F_V21_190227	TCRβV4F_V28_190227
	TCRβV4F_V24_190227	TCRβV4W_SPL41_190213	TCRβV4F_V27_190227	TCRβV4W_SPL44_190213	TCRβV4F_V22_190227
17.	TCRβV4F_V23_190227	TCRβV4F_V32_190213			

[B] Gamma Alignment (Supplemental Figure 1B)

18.	TCRγV1.1a FJ513776	TCRγV1.1a FJ513777	TCRγV1.1a FJ513781	TCRγV1.1a FJ513783	TCRγV1.1a FJ513782
	TCRγV1.1aF_S36_190227	TCRγV1.1aF_S30_190227	TCRγV1.1aJ_T01_150408	TCRγV1.1aF_S04_190307	TCRγV1.1bG_T32_190430
	TCRγV1.1bW_S05_181210				
19.	TCRγV1.1b FJ513789	TCRγV1.1bG_T30_190430	TCRγV1.1b FJ513790	TCRγV1.1b_KY351639	
20.	TCRγV1.2a_FJ513775	TCRγV1.2a_FJ513774	TCRγV1.2aG_T33_190430	TCRγV1.2aW_T47_190423	
21.	TCRγV1.3J_B05_150824	TCRγV1.3J_T12_150415			
22.	TCRγV1.4aJ_B06_150824	TCRγV1.4aJ_B08_150824	TCRγV1.4aJ_T02_150420	TCRγV1.4aJ_T11_150415	
23.	TCRγV1.4aG_T43_190430	TCRγV1.4aG_T46_190430			
24.	TCRγV1.4bW_T43_190423	TCRγV1.4bF_S35_190227	TCRγV1.4bW_T46_190423	TCRγV1.4b FJ513786	TCRγV1.4b FJ513787
25.	TCRγV1.4bJ_B10_150824	TCRγV1.4bJ_T09_150415			
26.	TCRγV1.5T_S10_190424	TCRγV1.5G_T39_190430	TCRγV1.5F_S33_190227	TCRγV1.5F_S39_190227	TCRγV1.5W_S32_181130
	TCRγV1.5F_S38_190227	TCRγV1.5 FJ513791	TCRγV1.5 FJ513779	TCRγV1.5 FJ513784	
27.	TCRγV1.6J_B07_150824	TCRγV1.6J_B09_150824	TCRγV1.6J_B09_150831	TCRγV1.6J_B11_150831	TCRγV1.6J_B13_150831
	TCRγV1.6J_B15_150831				

[B] Gamma Alignment (Supplemental Figure 1B) [*continued*]

28.	TCRγV2.1 FJ513778	TCRγV2.1T_S15_190424	TCRγV2.1T_S14_190424	TCRγV2.1T_S18_190424	TCRγV2.1W_S12_181130
	TCRγV2.1W_S08_181130				
29.	TCRγV2.2G_T25_190430	TCRγV2.2W_T31_190425			
30.	TCRγV2.2W_T34_190425	TCRγV2.2G_T29_190430	TCRγV2.2T_S16_190424	TCRγV2.2F_V46_190425	
31.	TCRγV3.1W_T32_190307	TCRγV3.1G_T48_190430			
32.	TCRγV3.1J_T12_150415	TCRγV3.1J_T14_150415	TCRγV3.1J_T15_150415	TCRγV3.1J_V02_151014	TCRγV3.1J_V06_151014
	TCRγV3.1J_T05_150408	TCRγV3.1J_B13_150625	TCRγV3.1J_B18_150722	TCRγV3.1J_B22_150722	TCRγV3.1J_T01_150514
	TCRγV3.1J_T02_150514	TCRγV3.1J_T03_150520	TCRγV3.1J_T04_150520		
33.	TCRγV3.2aJ_V04_151014	TCRγV3.2aJ_T08_150408	TCRγV3.2aJ_B19_150722	TCRγV3.2aJ_B20_150625	TCRγV3.2aJ_B21_150722
	TCRγV3.2aJ_T04_150514	TCRγV3.2aJ_B23_150722	TCRγV3.2aJ_B17_150625	TCRγV3.2aJ_B16_150625	TCRγV3.2aJ_B14_150625
	TCRγV3.2aJ_B15_150625				
34.	TCRγV3.2bT_T28_190604	TCRγV3.2bT_S37_190425	TCRγV3.2bT_S38_190425	TCRγV3.2bT_S42_190425	TCRγV3.2bF_T44_190227
	TCRγV3.2bF_T42_190227	TCRγV3.2b FJ513792	TCRγV3.2b FJ513793		
35.	TCRγV3.3F_S31_190227	TCRγV3.3J_V03_151014	TCRγV3.3J_T07_150408	TCRγV3.3J_T11_150420	TCRγV3.3J_B17_150722
	TCRγV3.3J_B19_150625				
36.	TCRγV3.4J_V05_151014	TCRγV3.4J_V07_151014	TCRγV3.4J_V08_151014	TCRγV3.4J_T09_150420	TCRγV3.4J_T16_150415
	TCRγV3.4J_T01_150520				
37.	TCRγV4W_T41_190423	TCRγV4W_T39_190423			
38.	TCRγV4T_S23_190424	TCRγ V4 FJ513785			
39.	TCRγV4J_B11_150824	TCRγV4J_B17_150831	TCRγV4J_B18_150831	TCRγV4J_B19_150831	TCRγV4J_B20_150831
	TCRγV4J_B22_150831	TCRγV4J_B23_150831	TCRγV4J_B24_150831	TCRγV4J_T02_150621	TCRγV4J_T05_150621
	TCRγV4J_T06_150621	TCRγV4J_T08_150621	TCRγV4J_T10_150621	TCRγV4J_T04_150621	

[C] Alpha/Delta Alignment (Supplemental Figure 2)

1.	TCRαδV1J_V13_101310	TCRαδV1M_T08_060512	TCRαδV1J_V02_110210	TCRαδV1M_T13_072610	TCRαδV1J_V08_102810
	TCRαδV1J_T17_100710	TCRαδV1J_V09_110210	TCRαδV1M_T02_060512	TCRαδV1M_T18_072610	TCRαδV1M_T17_072610
	TCRαδV1M_T14_080912	TCRαδV1M_T13_060512	TCRαδV1J_V07_091410	TCRαδV1J_V18_090110	TCRαδV1M_T14_060512
	TCRαδV1M_T23_071212	TCRαδV1M_T21_072012	TCRαδV1J_V19_110210	TCRαδV1J_V05_101310	TCRαδV1M_T17_071212
2.	TCRαδV1J_V14_101310	TCRαδV1J_V16_101310			
3.	TCRαδV1_KY366476	TCRαδV1_KY366469			
4.	TCRαδV1_KY366470	TCRαδV1_KY366477			
5.	TCRαδV1M_T24_080212	TCRαδV1M_T11_070612			
6.	TCRαδV1B_A419.3	TCRαδV1J_T43_100410	TCRαδV1_KY189333	TCRαδV1_KY189334	TCRαδV1_KY189335
	TCRαδV1_KY189336				
7.	TCRαδV1M_T04_071212	TCRαδV1M_T11_072012			
8.	TCRαδV2M_T07_061812	TCRαδV2M_T09_061812			
9.	TCRαδV2J_B07_062512	TCRαδV2J_B13_072210			
10.	TCRαδV2M_T04_062512	TCRαδV2M_T09_062512			
11.	TCRαδV2J_T05_031210	TCRαδV2J_T08_032310			
12.	TCRαδV2_KY346724	TCRαδV2_KY346719	TCRαδV2_KY346720		
13.	TCRαδV2_KY346716	TCRαδV2_KY346717			
14.	TCRαδV2J_T07_030110	TCRαδV2J_B09_062512	TCRαδV2J_B14_072210	TCRαδV2J_T08_022510	
15.	TCRαδV2J_B10_062512	TCRαδV2J_B12_072210	TCRαδV2J_B12_062512		
16.	TCRαδV2_KY346715	TCRαδV2_KY346712	TCRαδV2_KY346718	TCRαδV2_KY346721	TCRαδV2_KY346723
17.	TCRαδV2J_T08_030110	TCRαδV2J_B06_062512	TCRαδV2J_B11_062512	TCRαδV2J_T05_022010	
18.	TCRαδV2M_T09_080212	TCRαδV2M_T02_070612			
19.	TCRαδV2J_T06_030110	TCRαδV2J_B11_072210	TCRαδV2J_B10_072210	TCRαδV2J_T06_031210	TCRαδV2J_B05_062512
20.	TCRαδV2J_B08_062512	TCRαδV2J_T05_022510	TCRαδV2J_B09_072210	TCRαδV2J_T07_022510	
21.	TCRαδV2T_T37_190409	TCRαδV2G_T78_190409	TCRαδV2W_S26_190409		
22.	TCRαδV2J_V12_091410	TCRαδV2M_T06_071212	TCRαδV2M_T24_071612	TCRαδV2M_T02_072612	
23.	TCRαδV2_KY346728	TCRαδV2_KY346729	TCRαδV2_KY346730	TCRαδV2_KY346731	TCRαδV2_KY346734
	TCRαδV2_KY346735	TCRαδV2_KY346736			
24.	TCRαδV2_KY346725	TCRαδV2_KY346727	TCRαδV2_KY346732		
25.	TCRαδV2M_T24_080912	TCRαδV2J_T14_100710			
26.	TCRαδV3F_V72_190308	TCRαδV3T_S34_190220	TCRαδV3W_T22_190220	TCRαδV3W_T18_190220	TCRαδV3W_S31_190119
	TCRαδV3T_S46_190214	TCRαδV3T_S48_190214	TCRαδV3T_S49_190214	TCRαδV3T_S50_190214	TCRαδV3T_S51_190214
	TCRαδV3T_S52_190214	TCRαδV3T_S54_190214	TCRαδV3T_S38_190214	TCRαδV3T_S39_190214	TCRαδV3T_S45_190214
	TCRαδV3T_S61_190214	TCRαδV3T_S68_190214	TCRαδV3T_S70_190214	TCRαδV3W_T19_190214	TCRαδV3W_T21_190214
	TCRαδV3W_T25_190214	TCRαδV3W_T26_190214	TCRαδV3G_TC91_190409	TCRαδV3W_T13_190409	TCRαδV3T_T43_190409
	TCRαδV3T_S34_190214	TCRαδV3W_S31_190409	TCRαδV3W_S29_190119	TCRαδV3 FJ513808	
27.	TCRαδV4B_A_419.12	TCRαδV4J_T11_100710	TCRαδV4J_T14_100410		

[C] Alpha/Delta Alignment (Supplemental Figure 2) [*continued*]

28.	TCRαδV4M_T33_051410	TCRαδV4M_T15A_060712	TCRαδV4M_T02A_060712	TCRαδV4M_T22_051410	TCRαδV4M_T10A_060712
	TCRαδV4M_T18A_060712	TCRαδV4M_T12_071712	TCRαδV4M_T11_071712	TCRαδV4M_T07_062012	TCRαδV4M_T21_062012
	TCRαδV4M_T13_062512	TCRαδV4M_T17_062512	TCRαδV4M_T22_071712	TCRαδV4M_T18_062012	TCRαδV4M_T06_062612
	TCRαδV4M_T11_060512	TCRαδV4M_T24_052410	TCRαδV4M_T14_070912	TCRαδV4M_T03_052410	TCRαδV4M_T15_071712
	TCRαδV4M_T21_062512	TCRαδV4M_T21_071712	TCRαδV4M_T03_062612	TCRαδV4M_T15_062012	TCRαδV4M_T02_071712
	TCRαδV4M_T03_071712	TCRαδV4M_T21_061812	TCRαδV4M_T16_071712	TCRαδV4M_T22B_060712	TCRαδV4M_T11_062012
	TCRαδV4M_T05_062612	TCRαδV4M_T21_052410	TCRαδV4M_T28_052410	TCRαδV4M_T22A_060712	TCRαδV4M_T16_062612
	TCRαδV4M_T08_061812	TCRαδV4M_T19_062612	TCRαδV4M_T24A_060712	TCRαδV4M_T08_062012	TCRαδV4M_T11_052410
	TCRαδV4M_T20_052410	TCRαδV4M_T13_062012	TCRαδV4M_T14_062612	TCRαδV4M_T04_070912	TCRαδV4M_T15_061812
	TCRαδV4M_T15_062512	TCRαδV4M_T06_071712	TCRαδV4M_T04_071712	TCRαδV4M_T18_071712	TCRαδV4M_T05_052410
	TCRαδV4M_T03_062512	TCRαδV4M_T09_071712	TCRαδV4M_T01_061812	TCRαδV4M_T01_062012	TCRαδV4M_T16_061812
	TCRαδV4M_T10_062612	TCRαδV4M_T12_062612	TCRαδV4M_T18_061812	TCRαδV4M_T21_060512	TCRαδV4M_T04_062012
	TCRαδV4M_T06_061812	TCRαδV4M_T09_052410	TCRαδV4M_T15_060512	TCRαδV4M_T03_060512	TCRαδV4M_T15_052410
	TCRαδV4M_T10_060612	TCRαδV4M_T14_061812	TCRαδV4M_T21A_060712	TCRαδV4M_T14_052410	TCRαδV4M_T17_071712
	TCRαδV4M_T26_052410	TCRαδV4M_T16_060612	TCRαδV4M_T01_071712	TCRαδV4M_T19_062012	TCRαδV4M_T19_071712
	TCRαδV4M_T07_071712	TCRαδV4M_T09_070912	TCRαδV4M_T07_062612	TCRαδV4M_T05_061812	TCRαδV4M_T14_071712
	TCRαδV4M_T08_062512	TCRαδV4M_T19_061812	TCRαδV4M_T23_062612	TCRαδV4M_T07_052410	TCRαδV4M_T02_062612
	TCRαδV4M_T21B_060712	TCRαδV4M_T03_060612	TCRαδV4M_T10_062512	TCRαδV4M_T22_062012	TCRαδV4M_T11_062612
	TCRαδV4M_T23_062012	TCRαδV4M_T16_052410	TCRαδV4M_T29_052410	TCRαδV4M_T17_062012	TCRαδV4M_T30_052410
	TCRαδV4M_T20_062612	TCRαδV4M_T24_061812	TCRαδV4M_T23_062512	TCRαδV4M_T19_060512	TCRαδV4M_T22_062512
	TCRαδV4M_T09_060612	TCRαδV4M_T10_061812	TCRαδV4M_T23_061812	TCRαδV4M_T20_061812	TCRαδV4M_T10_070912
	TCRαδV4M_T22_052410	TCRαδV4M_T06_062012	TCRαδV4M_T24_062512	TCRαδV4M_T20_060512	TCRαδV4M_T09_062012
	TCRαδV4M_T22_062612	TCRαδV4M_T23B_060712	TCRαδV4M_T01_062612	TCRαδV4M_T23_052410	TCRαδV4M_T25_052410
	TCRαδV4M_T08_071712	TCRαδV4M_T16_062012	TCRαδV4M_T01_060612	TCRαδV4M_T08_070912	TCRαδV4M_T13_052410
	TCRαδV4M_T24_062612	TCRαδV4M_T22_061812	TCRαδV4M_T15_062612	TCRαδV4M_T07_062512	TCRαδV4M_T27_052410
	TCRαδV4M_T06_060612	TCRαδV4M_T05_071712	TCRαδV4M_T05_062512	TCRαδV4M_T17_061812	TCRαδV4M_T13_061812
	TCRαδV4M_T18_062612	TCRαδV4M_T02_061812	TCRαδV4M_T11_062512	TCRαδV4M_T17_062612	TCRαδV4M_T01_060512
	TCRαδV4M_T01_062512	TCRαδV4M_T24_071712	TCRαδV4M_T24B_060712	TCRαδV4M_T10_062012	TCRαδV4M_T09_062612
	TCRαδV4M_T04_060512	TCRαδV4M_T19_052410	TCRαδV4M_T13_060612	TCRαδV4M_T02_062512	TCRαδV4M_T14_062512
	TCRαδV4M_T24_062012	TCRαδV4M_T12_052410	TCRαδV4M_T17_052410		
29.	TCRαδV4_KY346745	TCRαδV4_KY346751	TCRαδV4_KY346755	TCRαδV4_KY346753	TCRαδV4_KY346748
	TCRαδV4_KY346750	TCRαδV4_KY346744	TCRαδV4_KY346746	TCRαδV4_KY346757	TCRαδV4_KY346749
	TCRαδV4_KY346756	TCRαδV4_KY346758	TCRαδV4_KY346747	TCRαδV4_KY346754	TCRαδV4_KY346743
	TCRαδV4_KY346759				
30.	TCRαδV4J_T01_030110	TCRαδV4J_T04_032310	TCRαδV4J_T04_031210	TCRαδV4J_B03_072210	TCRαδV4J_T04_022510
	TCRαδV4J_T28_020210	TCRαδV4J_T12_020110	TCRαδV4J_T03_032310	TCRαδV4J_T03_030110	TCRαδV4J_T01_032310
31.	TCRαδV4J_T21_100710	TCRαδV4J_V24_102810			
32.	TCRαδV4M_T21_051410	TCRαδV4M_T24_051410	TCRαδV4M_T26_051410	TCRαδV4M_T35_051410	TCRαδV4M_T13A_060712
	TCRαδV4M_T27_051410	TCRαδV4M_T32_051410			
33.	TCRαδV4M_T28_051410	TCRαδV4M_T23_051410 T	RADV4M_T10_052410	TCRαδV4M_T17A_060712	TCRαδV4J_T02_020210
	TCRαδV4_KY346760	TCRαδV4_KY346768	TCRαδV4_KY346766		
34.	TCRαδV4M_T20A_060712	TCRαδV4M_T31_051410	TCRαδV4M_T16A_060712	TCRαδV4M_T08A_060712	TCRαδV4_KY346762
	TCRαδV4_KY346764	TCRαδV4_KY346765	TCRαδV4_KY346761		
35.	TCRαδV4J_V06_102810	TCRαδV4J_T18_100710	TCRαδV4J_T21_100410		
36.	TCRαδV4J_V19_101310	TCRαδV4J_V18_091010			
37.	TCRαδV4J_T02_032310	TCRαδV4J_T03_031210	TCRαδV4J_T01_031210	TCRαδV4J_T26_020210	
38.	TCRαδV4J_B02_072210	TCRαδV4J_T02_022510			
39.	TCRαδV6M_T08_072712	TCRαδV6M_T06_072712	TCRαδV6M_T15_072712	TCRαδV6M_T20_072712	TCRαδV6M_T02_072712
	TCRαδV6M_T11_072712	TCRαδV6M_T04_072712	TCRαδV6M_T23_072712	TCRαδV6M_T05_072712	TCRαδV6M_T14_072712
	TCRαδV6M_T17_072712	TCRαδV6M_T03_072712	TCRαδV6M_T13_072712	TCRαδV6M_T24_072712	TCRαδV6M_T10_072712
	TCRαδV6M_T19_072712	TCRαδV6M_T21_072712	TCRαδV6M_T07_072712	TCRαδV6M_T18_072712	TCRαδV6M_T16_080912
	TCRαδV6M_T03_080212				
40.	TCRαδV6J_T06_100410	TCRαδV6M_T07_071212	TCRαδV6M_T20_080912		
41.	TCRαδV7J_T39_100410	TCRαδV7J_T05_100710	TCRαδV7J_V08_091410	TCRαδV7J_T03_100410	
42.	TCRαδV8B_A_419.23	TCRαδV8M_T05_070912	TCRαδV8B_A_419.32	TCRαδV8W_T15_190409	TCRαδV8W_S34_190409
43.	TCRαδV8T_S11_190308	TCRαδV8T_S06_190308	TCRαδV8T_S04_190308	TCRαδV8T_S05_190308	TCRαδV8T_S03_190308
	TCRαδV8T_S10_190308	TCRαδV8T_S14_190308	TCRαδV8T_S15_190308	TCRαδV8T_S12_190308	TCRαδV8T_S08_190308
	TCRαδV8T_S09_190308	TCRαδV8T_S16_190308	TCRαδV8F_T40_190308	TCRαδV8T_S07_190308	TCRαδV8T_S13_190308
	TCRαδV8T_S02_190308	TCRαδV8T_S01_190308	TCRαδV8T_T61_190308	TCRαδV8T_T63_190308	TCRαδV8T_T60_190308
	TCRαδV8T_T58_190308	TCRαδV8F_T39_190308	TCRαδV8T_T57_190308	TCRαδV8T_T53_190308	TCRαδV8T_T51_190308
	TCRαδV8T_T49_190308	TCRαδV8T_T62_190308	TCRαδV8F_T38_190308	TCRαδV8T_T56_190308	TCRαδV8F_T34_190308
	TCRαδV8T_T55_190308	TCRαδV8F_T24_190308	TCRαδV8F_T36_190308	TCRαδV8T_T59_190308	TCRαδV8T_T50_190308
	TCRαδV8T_T54_190308	TCRαδV8W_T47_190308	TCRαδV8F_T35_190308	TCRαδV8W_T29_190308	TCRαδV8W_T48_190308
	TCRαδV8F_T33_190308	TCRαδV8F_T22_190308	TCRαδV8F_T20_190308	TCRαδV8F_T19_190308	TCRαδV8W_T44_190308
	TCRαδV8W_T31_190308	TCRαδV8W_T42_190308	TCRαδV8W_T28_190308	TCRαδV8W_T45_190308	TCRαδV8W_T41_190308
	TCRαδV8F_T17_190308	TCRαδV8F_V68_190308	TCRαδV8F_V67_190308	TCRαδV8F_V66_190308	TCRαδV8F_V64_190308
	TCRαδV8W_T46_190308	TCRαδV8W_T25_190308	TCRαδV8F_T18_190308		
44.	TCRαδV8M_T17_071612	TCRαδV8M_T21_072610	TCRαδV8J_T16_100710	TCRαδV8J_V21_090110	
45.	TCRαδV8J_V20_100809	TCRαδV8J_V22_100809	TCRαδV8J_T16_031210	TCRαδV8J_T11_030110	TCRαδV8J_T14_022510
	TCRαδV8J_B03_082410				
46.	TCRαδV8M_T04_051410	TCRαδV8M_T03_051410			
47.	TCRαδV8_KY346773	TCRαδV8_KY346774	TCRαδV8_KY346775		

[C] Alpha/Delta Alignment (Supplemental Figure 2) [*continued*]

48.	TCRαδV8J_T20_100410	TCRαδV8J_T04_100710	TCRαδV8M_T06_051410		
49.	TCRαδV8M_T17_080212	TCRαδV8M_T10_071212			
50.	TCRαδV8W_S24_190119	TCRαδV8F_V65_190308			
51.	TCRαδV8M_T21_080912	TCRαδV8M_T05_072610			
52.	TCRαδV8_KY346777	TCRαδV8_KY346781	TCRαδV8_KY346780		
53.	TCRαδV8M_T10_072012	TCRαδV8M_T18_071612	TCRαδV8J_T22_100410	TCRαδV8M_T12_072712	TCRαδV8M_T16_072712
	TCRαδV8M_T09_072712	TCRαδV8M_T22_072712			
54.	TCRαδV8_KY346779	TCRαδV8_KY346784	TCRαδV8_KY346786	TCRαδV8_KY346776	TCRαδV8_KY346778
	TCRαδV8_KY346785				
55.	TCRαδV8M_T11_080212	TCRαδV8M_T03_080912	TCRαδV8M_T17_080912	TCRαδV8M_T20_051410	
56.	TCRαδV8M_T13B_060712	TCRαδV8M_T20B_060712			
57.	TCRαδV8J_T13_031210	TCRαδV8J_T25_032310			
58.	TCRαδV8J_T13_022510	TCRαδV8J_T15_022510			
59.	TCRαδV8J_T01_082410	TCRαδV8J_T09_030110			
60.	TCRαδV8J_V09_090110	TCRαδV8J_T01_100710			
61.	TCRαδV8_KY346787	TCRαδV8_KY346792	TCRαδV8_KY346788	TCRαδV8_KY346789	TCRαδV8_KY346791
	TCRαδV8_KY346790				
62.	TCRαδV8_KY346772	TCRαδV8_KY346769	TCRαδV8_KY346770	TCRαδV8_KY346771	
63.	TCRαδV8J_T16_022510	TCRαδV8J_B01_082410	TCRαδV8J_T09_031210	TCRαδV8J_B04_082410	
64.	TCRαδV8J_T15_100710	TCRαδV8J_V11_110210			
65.	TCRαδV8J_B05_083110	TCRαδV8J_B02_082410	TCRαδV8J_B01_083110	TCRαδV8J_T24_030210	
66.	TCRαδV8J_V23_100809	TCRαδV8J_B04_083110	TCRαδV8J_T21_030210		
67.	TCRαδV8_KY189339	TCRαδV8_KY189340			
68.	TCRαδV9M_T11_080912	TCRαδV9M_T17_072012	TCRαδV9M_T01_080912		
69.	TCRαδV10F_V50_190409	TCRαδV10G_TH3_190403	TCRαδV10W_T08_190214	TCRαδV10W_T02_190220	TCRαδV10F_T23_190308
	TCRαδV10G_T66_190409	TCRαδV10W_S28_190130	TCRαδV10G_T72_190409	TCRαδV10G_TC96_190409	
70.	TCRαδV10_KY346800	TCRαδV10_KY346806	TCRαδV10_KY346798	TCRαδV10_KY346794	TCRαδV10_KY346812
	TCRαδV10_KY346813	TCRαδV10_KY346807	TCRαδV10_KY346795	TCRαδV10_KY346802	TCRαδV10_KY346809
	TCRαδV10_KY346816	TCRαδV10_KY346814	TCRαδV10_KY346811	TCRαδV10_KY346793	TCRαδV10_KY346808
	TCRαδV10_KY346801	TCRαδV10_KY346810	TCRαδV10_KY346815	TCRαδV10_KY346796	TCRαδV10_KY346804
	TCRαδV10_KY346799	TCRαδV10_KY346805	TCRαδV10_KY346797		
71.	TCRαδV11M_T23_080212	TCRαδV11M_T21_071212	TCRαδV11M_T15_080912	TCRαδV11M_T06_070612	TCRαδV11M_T02_080212
	TCRαδV11M_T12_070912	TCRαδV11J_T01_100410	TCRαδV11J_T46_100410	TCRαδV11M_T20_071212	TCRαδV11M_T15_072612
	TCRαδV11M_T14_072612	TCRαδV11M_T09_072612	TCRαδV11J_V18_102810	TCRαδV11_KY189343	TCRαδV11_KY189353
	TCRαδV11_KY189351				
72.	TCRαδV11_KY189342	TCRαδV11_KY189348	TCRαδV11_KY189345		
73.	TCRαδV11W_T01_190220	TCRαδV11W_T05_190214			
74.	TCRαδV11M_T01_071212	TCRαδV11M_T08_071612	TCRαδV11M_T09_080912	TCRαδV11M_T18_080212	TCRαδV11M_T19_080212
	TCRαδV11M_T17_070612	TCRαδV11M_T18_072012	TCRαδV11M_T13_071212	TCRαδV11M_T16_071212	TCRαδV11M_T23_072612
	TCRαδV11M_T20_062512	TCRαδV11M_T07_060612	TCRαδV11M_T03_062012	TCRαδV11M_T05_060612	

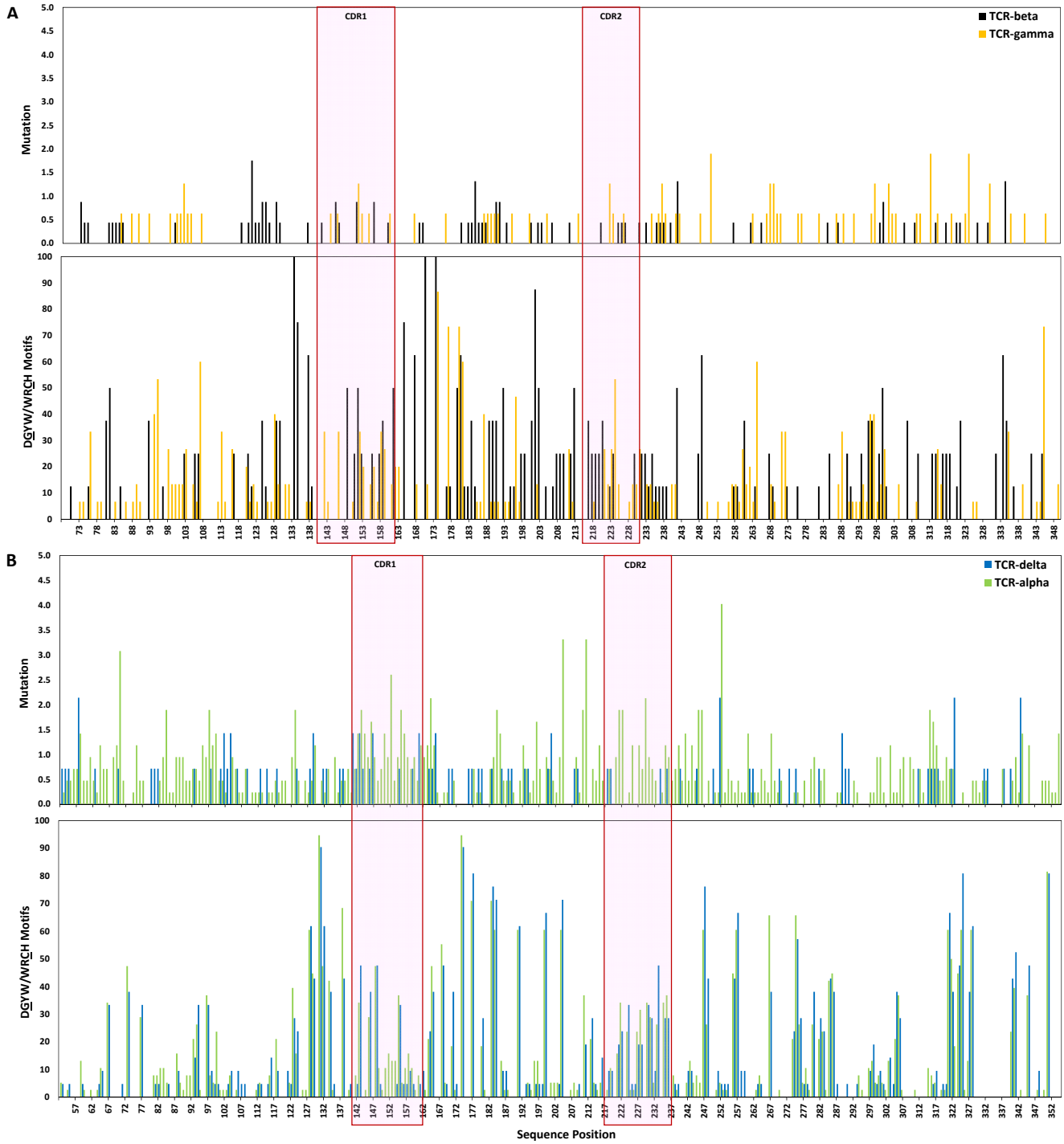
[D] NTCRV-STCRδV (NAR-TCR) sequences (Supplemental Figure 3)

1.	NTCRV1_STCRδV1_DQ022688	NTCRV1_STCRδV1W_T17_190214	NTCRV1G_T88_190409	NTCRV1T_T39_190409	
	NTCRV1W_T27_190308	NTCRV1_STCRδV1_DQ022689	NTCRV1_STCRδV1_DQ022690	NTCRV1_STCRδV1_DQ022691	
2.	NTCRV1_STCRδV1W_S41_190119	NTCRV1_STCRδV1W_T13_190214	NTCRV1_STCRδV1W_S35_190130	NTCRV1_STCRδV1W_S47_190119	
	NTCRV1_STCRδV1W_T01_190227	NTCRV1_STCRδV1W_T03_190227	NTCRV1_STCRδV1W_T16_190214	NTCRV1T_S36_190214	
3.	NTCRV3_STCRδV2_DQ022704	NTCRV3_STCRδV2_DQ022706	NTCRV3_STCRδV2W_S45_190119	NTCRV3_STCRδV2W_S46_190119	
4.	NTCRV3_STCRδV2_DQ022702	NTCRV3_STCRδV2_DQ022696	NTCRV3_STCRδV2_DQ022697	NTCRV3_STCRδV2_DQ022699	
5.	NTCRV1_STCRδV1_DQ022692	NTCRV1_STCRδV1_DQ022691	NTCRV1_STCRδV1W_T10_190214	NTCRV1_STCRδV1W_T13_190214	
	STCRδV1W_T30_190308	NTCRV1_STCRδV1W_S41_190119			
6.	NTCRV1_STCRδV1_DQ022689	NTCRV1_STCRδV1_DQ022688			
7.	NTCRV1_STCRδV1W_S35_190130	NTCRV1_STCRδV1W_T01_190227	NTCRV1_STCRδV1W_T03_190227	NTCRV1_STCRδV1W_T16_190214	
	NTCRV1_STCRδV1W_S42_190119				
8.	NTCRV1_STCRδV1_DQ022694	NTCRV1_STCRδV1W_S48_190119	NTCRV1_STCRδV1W_T05_190227	NTCRV1_STCRδV1W_T12_190214	
	NTCRV1_STCRδV1W_T18_190214				
9.	NTCRV2_STCRδV2W_S44_190119	NTCRV2_STCRδV2_DQ022709	NTCRV2_STCRδV2W_S49_190119		
10.	NTCRV3_STCRδV3W_S45_190119	NTCRV3_STCRδV3W_S43_190119	NTCRV3_STCRδV3W_S46_190119	NTCRV3_STCRδV3W_S50_190119	
	NTCRV3_STCRδV3_DQ022704	NTCRV3_STCRδV3_DQ022706	NTCRV3_STCRδV3_DQ022702	NTCRV3_STCRδV3_DQ022699	
	NTCRV3_STCRδV3_DQ022701	NTCRV3_STCRδV3_DQ022712	NTCRV3_STCRδV3_DQ022698	NTCRV3_STCRδV3_DQ022703	
11.	STCRδV3_KY346705	STCRδV3_ KY346706	STCRδV3_KY346707	STCRδV3_ KY346708	STCRδV3_
	KY346710				
12.	STCRδV4_KY346738	STCRδV4 _KY346739	STCRδV4_KY346740	STCRδV4_KY346741	
	STCRδV4_ KY346742				

[E] IgHC Sequences (Supplemental Figure 4)

1.	IgMV1-TCRδCG_TC94_190409	IgMV1-TCRδCW_T02_190130	IgMV1-TCRδCG_T55_190409	IgMV1-TCRδCT_T41_190409	IgMV1-TCRδCF_VE1_190403
	IgMV1-TCRδCW_T05_190130	IgMV1-TCRδCW_T09_190214	IgMV1-TCRδCW_S26_190130	IgMV1-TCRδCG_TF11_190403	IgMV1-TCRδCT_S35_190214
	IgMV1-TCRδCW_T04_190220	IgMV1-TCRδCW_T06_190130	IgMV1-TCRδCG_T58_190409	IgMV1-TCRδCT_S33_190214	IgMV1-TCRδCF_T21_190308
	IgMV1-TCRδCW_T11_190409	IgMV1-TCRδCT_S31_190214			
2.	IgMV1-TCRδC_JF507668	IgMV1-TCRδC_JF507677	IgMV1-TCRδC_JF507669	IgMV1-TCRδC_JF507661	IgMV1-TCRδC_JF507673
	IgMV1-TCRδC_JF507665	IgMV1-TCRδC_JF507685	IgMV1-TCRδC_JF507692	IgMV1-TCRδC_JF507663	IgMV1-TCRδC_JF507697
	IgMV1-TCRδC_JF507708	IgMV1-TCRδC_JF507683	IgMV1-TCRδC_JF507695	IgMV1-TCRδC_JF507662	IgMV1-TCRδC_JF507675
	IgMV1-TCRδC_JF507684	IgMV1-TCRδC_JF507698	IgMV1-TCRδC_JF507671	IgMV1-TCRδC_JF507682	IgMV1-TCRδC_JF507681
	IgMV1-TCRδC_JF507676	IgMV1-TCRδC_JF507693	IgMV1-TCRδC_JF507688	IgMV1-TCRδC_JF507678	IgMV1-TCRδC_JF507689
	IgMV1-TCRδC_JF507701	IgMV1-TCRδC_JF507666	IgMV1-TCRδC_JF507694	IgMV1-TCRδC_JF507679	IgMV1-TCRδC_JF507674
3.	IgMV1-TCRδC_JF507687	IgMV1-TCRδC_JF507706	IgMV1-TCRδC_JF507690		
4.	IgMV1-TCRδC_JF507691	IgMV1-TCRδC_JF507667			
5.	IgMV2-TCRδCW_T01_190214	IgMV2-TCRδCW_S28_190409	IgMV2-TCRδCG_T61_190409	IgMV2-TCRδCW_T06_190220	IgMV2-TCRδCF_VH1_190403
	IgMV2-TCRδCW_S21_190409	IgMV2-TCRδCT_T52_190308	IgMV2-TCRδCG_T75_190409	IgMV2-TCRδCT_S30_190214	IgMV2-TCRδCW_T05_190220
6.	IgMV2-TCRδCT_S29_190220	IgMV2-TCRδCT_S41_190220	IgMV2-TCRδCT_S71_190214	IgMV2-TCRδCT_S42_190220	IgMV2-TCRδCT_S57_190214
	IgMV2-TCRδCT_T42_190409	IgMV2-TCRδCT_S43_190220	IgMV2-TCRδCG_T81_190409	IgMV2-TCRδCG_T60_190409	IgMV2-TCRδCW_SD7_190329
	IgMV2-TCRδCW_S29_190409	IgMV2-TCRδCT_S44_190214	IgMV2-TCRδCT_S26_190220	IgMV2-TCRδCW_S32_190119	IgMV2-TCRδCT_S29_190214
	IgMV2-TCRδCT_S66_190214	IgMV2-TCRδCT_S43_190214	IgMV2-TCRδCT_S58_190214	IgMV2-TCRδCT_S46_190220	IgMV2-TCRδCT_S45_190220
	IgMV2-TCRδCF_V71_190308	IgMV2-TCRδCG_TG9_190403	IgMV2-TCRδCT_S38_190220	IgMV2-TCRδCT_S28_190220	IgMV2-TCRδCF_V70_190308
	IgMV2-TCRδCT_S31_190220	IgMV2-TCRδCW_S39_190119	IgMV2-TCRδCT_S39_190220	IgMV2-TCRδCT_S40_190220	IgMV2-TCRδCW_S25_190409
	IgMV2-TCRδCG_T56_190409	IgMV2-TCRδCT_S41_190214	IgMV2-TCRδCT_S25_190220	IgMV2-TCRδCW_S23_190409	IgMV2-TCRδCT_S59_190214
	IgMV2-TCRδCT_S63_190214	IgMV2-TCRδCT_S33_190220	IgMV2-TCRδCT_S67_190214	IgMV2-TCRδCT_S36_190220	IgMV2-TCRδCT_S62_190214
	IgMV2-TCRδCT_S47_190220	IgMV2-TCRδCT_S35_190220	IgMV2-TCRδCG_T62_190409	IgMV2-TCRδCT_S40_190214	IgMV2-TCRδCW_S38_190119
	IgMV2-TCRδCW_S33_190119				
7.	IgMV2-TCRδCG_T82_190409	IgMV2-TCRδCW_T06_190119	IgMV2-TCRδCW_T09_190119		
8.	IgMV4-TCRδCW_T43_190308	IgMV4-TCRδCW_T08_190119			
9.	IgMV5-TCRδCW_T07_190220	IgMV5-TCRδCF_V47_190409	IgMV5-TCRδCT_S72_190214	IgMV5-TCRδCG_T85_190409	IgMV5-TCRδCT_S27_190220
	IgMV5-TCRδCW_S17_190409	IgMV5-TCRδCW_S40_190119	IgMV5-TCRδCG_T80_190409	IgMV5-TCRδCF_V52_190409	IgMV5-TCRδCG_TH5_190403
	IgMV5-TCRδCF_V69_190308	IgMV5-TCRδCG_T59_190409	IgMV5-TCRδCG_T64_190409	IgMV5-TCRδCW_T12_190220	IgMV5-TCRδCW_T16_190409
	IgMV5-TCRδCW_TD4_190329	IgMV5-TCRδCW_TC4_190329	IgMV5-TCRδCG_T54_190409	IgMV5-TCRδCW_S33_190409	IgMV5-TCRδCW_S24_190409
	IgMV5-TCRδCW_T10_190409	IgMV5-TCRδCW_T01_190119	IgMV5-TCRδCW_T02_190119	IgMV5-TCRδCW_T03_190220	IgMV5-TCRδCT_S55_190214
	IgMV5-TCRδCW_T04_190214				
10.	IgMV5-TCRδCT_S60_190214	IgMV5-TCRδCT_S53_190214	IgMV5-TCRδCW_S36_190119		
11.	IgMV5-TCRδCT_S37_190214	IgMV5-TCRδCW_S32_190130	IgMV5-TCRδCT_S37_190220	IgMV5-TCRδCW_S35_190119	
12.	IgWV1-TCRδCG_T63_190409	IgWV1-TCRδCF_V46_190409			
13.	IgWV1-TCRδC_JF507628	IgWV1-TCRδC_JF507659	IgWV1-TCRδC_JF507616	IgWV1-TCRδC_JF507651	IgWV1-TCRδC_JF507617
	IgWV1-TCRδC_JF507612	IgWV1-TCRδC_JF507647	IgWV1-TCRδC_JF507615	IgWV1-TCRδC_JF507614	IgWV1-TCRδC_JF507607
	IgWV1-TCRδC_JF507640	IgWV1-TCRδC_JF507657	IgWV1-TCRδC_JF507637		
14.	IgWV2-TCRδC_JF507655	IgWV2-TCRδC_JF507606	IgWV2-TCRδC_JF507618		
15.	IgWV2-TCRδC_JF507621	IgWV2-TCRδC_JF507645	IgWV2-TCRδC_JF507623	IgWV2-TCRδC_JF507638	IgWV2-TCRδC_JF507610
	IgWV2-TCRδC_JF507619	IgWV2-TCRδC_JF507639			
16.	IgWV3-TCRδCG_T79_190409	IgWV3-TCRδCG_TH12_190403	IgWV3-TCRδCG_TH4_190403	IgWV3-TCRδCW_S31_190130	
17.	TAILV1J_T19_100410	TAILV1m_T10_080212	TAILV1m_T20_072012	TAILV1m_T05_080212	TAILV1m_T16_072612
	TAILV1J_V10_090110	TAILV1m_T16_071612	TAILV1m_T15_080212	TAILV1m_T09_071612	

<u>Supplemental Figure 6</u>. Despite the presence of AID-preferred hotspot motifs (DGYW/WRCH) in all V segments used by T cell receptors, only alpha/delta V (TCRαδ V) segments associated with alpha constant regions incorporate significant mutation. Proportion of mutations (both single and tandem) [A-D, top panels] and DGYW/WRCH motifs [A-D, bottom panels] observed at each position along the sequence length of [A] TCRβ V (black, 89 mutations; 228 sequences; 8 V gene segment groups) and TCRγ V (gold, 82 mutations; 158 sequences; 15 V gene segment groups), [B] TCRαδ V associated with TCRδ constant region (blue, 102 mutations; 140 sequences; 21 V gene segment groups) and TCRα constant region (green, 769 mutations; 422 sequences; 38 V gene segment groups), [C] NARTCR distal V domains (red, 37 mutations; 51 sequences; 6 V gene segment groups) and proximal supporting V domains (black, 25 mutations; 62 sequences; 7 V gene segment groups), and [D] IgHV associated with TCRδ constant region (purple, 100 mutations; 237 sequences; 14 V gene segment groups) and TCR-associated Ig-like V (TAILV, no mutations; 11 sequences; 2 V gene segment groups) associated with TCRδ or TCRα constant regions. Position indicates the forward (3' to 5') location of the mutable base within a Geneious-derived consensus sequence for each group. We counted mutations and motifs by sequence domain [framework region (FR) and complementarity-determining region (CDR)]. Red (and black) boxes indicate the locations of CDR [TCRβ CDR1: 145-162, CDR2: 214-231; TCRγ CDR1: 139-165, CDR2: 217-231; TCRαδ CDR1: 139-162, CDR2: 217-237; distal NARTCR V domain (red) CDR1: 130-152, CDR2: 184-226; supporting NARTCRδ V domain (black) CDR1: 133-147, CDR2: 202-219; IgHV CDR1: 139-162, CDR2: 217-237; TAILV CDR1: 133-147, CDR2: 202-219]. DGYW/WRCH: G:C is the mutable position; W = A/T, D = A/G/T, Y = C/T, R = A/G, and H = T/C/A. Data from a single experiment, where each PCR tube represents a single replicate for each chain, shark, and tissue sample (see Supplemental Tables 1 and 2).


A
CDR1
CDR2
TCR-beta
TCR-gamma
Mutation
DGYW/WRCH Motifs
B
CDR1
CDR2
TCR-delta
TCR-alpha
Mutation
DGYW/WRCH Motifs
Sequence Position

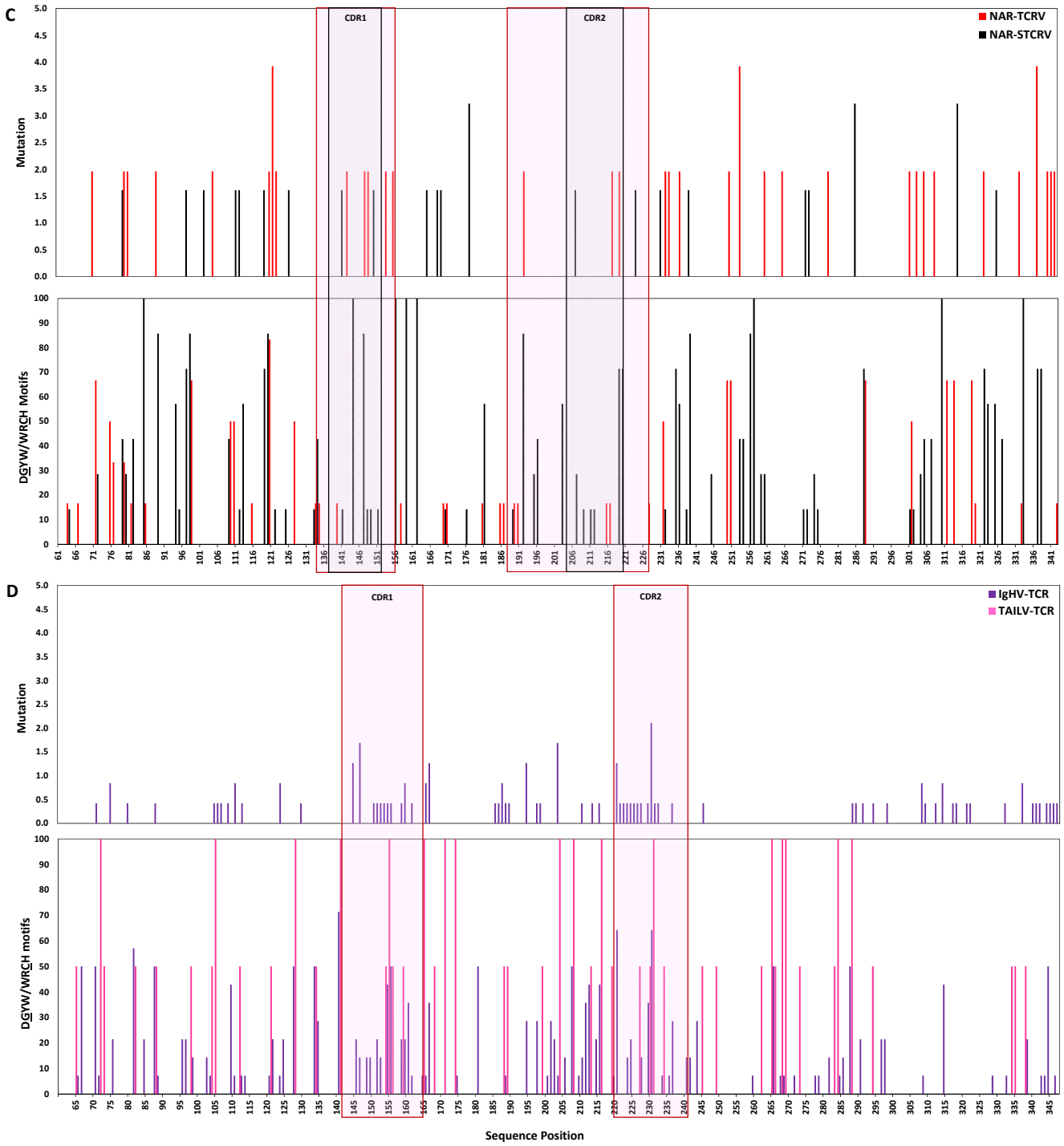

C
CDR1
CDR2
NAR-TCRV
NAR-STCRV
Mutation
DGYW/WRCH Motifs
D
CDR1
CDR2
IgHV-TCR
TAILV-TCR
Mutation
DGYW/WRCH motifs
Sequence Position

Figure 3 – Source Data. Frequency of mutation within FR and CDR of T cell receptor variable regions. Mutation frequency is the total number of nucleotide (nuc) changes to a Geneious-derived consensus sequence divided by the total number of nucleotides within a region. We counted nonsynymous (N) and synonymous (S) mutations separately for each FR and CDR within [A] 422 TRADV-TRAC, [B] 137 TRADV-TRDC, [C] 158 TRGV, [D] 237 TRBV, [E] 51 NTRV, [F] 62 STRDV, and 275 IgHV-TRDC sequences.

[A] Alpha: TRADV-TRAC

Total nucleotides

Region	FR1	CDR1	FR2	CDR2	FR3	Total
	31556	7982	21522	8313	48669	121359

Number mutations

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	97	74	68	47	135	461
S	46	25	34	14	61	209
All	143	99	102	61	196	670

Mutation Frequency

Type	FR1	FR2	FR3	CDR1	CDR2	Total
N	0.31	0.93	0.32	0.57	0.28	0.38
S	0.15	0.31	0.16	0.17	0.13	0.17
All	0.45	1.24	0.47	0.73	0.40	0.55

[B] Delta: TRADV-TRDC

Total nucleotides

Region	FR1	CDR1	FR2	CDR2	FR3	Total
	10275	2469	6987	2784	16023	40221

Number mutations

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	20	9	13	3	19	72
S	7	4	6	1	11	29
All	27	13	19	4	30	101

Mutation Frequency

Type	FR1	FR2	FR3	CDR1	CDR2	Total
N	0.19	0.36	0.19	0.11	0.12	0.18
S	0.07	0.16	0.09	0.04	0.07	0.07
All	0.26	0.53	0.27	0.14	0.19	0.25

[C] Gamma

Total nucleotides

Region	FR1	CDR1	FR2	CDR2	FR3	Total
	9198	3856	8057	1890	16681	42841

Number mutations

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	9	5	5	1	37	66
S	3	2	5	0	16	31
All	12	7	10	1	53	97

Mutation Frequency

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	0.10	0.13	0.06	0.05	0.22	0.15
S	0.03	0.05	0.06	0.00	0.10	0.07
All	0.13	0.18	0.12	0.05	0.32	0.23

[D] Beta

Total nucleotides

Region	FR1	CDR1	FR2	CDR2	FR3	Total
	17568	4248	12069	2979	27823	65544

Number mutations

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	26	5	14	3	21	92
S	5	0	7	1	7	34
All	31	5	21	4	28	126

Mutation Frequency

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	0.15	0.12	0.12	0.10	0.08	0.14
S	0.03	0.00	0.06	0.03	0.03	0.05
All	0.18	0.12	0.17	0.13	0.10	0.19

[E] NTRV

Total nucleotides

Region	FR1	CDR1	FR2	CDR2	FR3	Total
	1632	1530	915	2154	4317	10548

Number mutations

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	8	0	0	3	7	18
S	2	0	0	0	4	6
All	10	0	0	3	11	24

Mutation Frequency

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	0.49	0.00	0.00	0.14	0.16	0.17
S	0.12	0.00	0.00	0.00	0.09	0.06
All	0.61	0.00	0.00	0.14	0.25	0.23

[F] STRDV

Total nucleotides

Region	FR1	CDR1	FR2	CDR2	FR3	Total
	4376	1116	3162	1302	6825	16781

Number mutations

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	5	2	3	1	5	16
S	2	2	2	0	7	13
All	7	4	5	1	12	29

Mutation Frequency

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	0.11	0.18	0.09	0.08	0.07	0.10
S	0.05	0.18	0.06	0.00	0.10	0.08
All	0.16	0.36	0.16	0.08	0.18	0.17

[G] IgHV-TRDC

Total nucleotides

Region	FR1	CDR1	FR2	CDR2	FR3	Total
	16226	5545	13963	4712	31691	68540

Number mutations

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	23	17	24	27	57	214
S	7	4	10	4	17	63
All	30	21	34	31	77	280

Mutation Frequency

Type	FR1	CDR1	FR2	CDR2	FR3	Total
N	0.14	0.31	0.17	0.57	0.18	0.31
S	0.04	0.07	0.07	0.08	0.05	0.09
All	0.18	0.38	0.24	0.66	0.24	0.41

Figure 4A Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
67	0.00	67	0.00	70	0.87	61	0.00	61	0.00	13	0.00	61	0.00
68	0.95	68	0.00	71	0.44	62	0.00	62	0.00	14	0.00	62	0.00
69	1.18	69	0.00	72	0.44	63	0.00	63	0.00	15	0.00	63	0.00
70	3.08	70	0.71	73	0.00	64	0.00	64	0.00	16	0.00	64	0.00
71	0.47	71	0.00	74	0.00	65	0.00	65	0.00	17	0.00	65	0.00
72	0.00	72	0.00	75	0.00	66	0.00	66	0.00	18	0.00	66	0.00
73	0.00	73	0.00	76	0.00	67	0.00	67	0.00	19	0.00	67	0.00
74	0.24	74	0.00	77	0.00	68	0.00	68	0.00	20	0.00	68	0.00
75	1.18	75	0.00	78	0.44	69	0.00	69	0.00	21	0.00	69	0.00
76	0.47	76	0.00	79	0.44			70	0.00	22	0.00	70	0.00
77	0.47	77	0.00	80	0.44			71	1.96	23	0.00	71	0.37
78	0.00	78	0.00	81	0.44			72	0.00	24	0.00	72	0.00
79	0.00	79	0.00	82	0.44	70	0.00	73	0.00	25	0.00	73	0.00
80	0.00	80	0.71	83	0.00	71	0.00	74	0.00	26	0.00	74	0.00
81	0.00	81	0.71	84	0.00	72	0.00	75	0.00	27	0.00	75	0.74
82	0.47	82	0.71	85	0.00	73	0.00	76	0.00	28	0.00	76	0.00
83	0.95	83	0.00	86	0.00	74	0.00	77	0.00	29	0.00	77	0.00
84	1.90	84	0.00	87	0.00	75	0.00	78	0.00	30	0.00	78	0.00
85	0.24	85	0.00	88	0.00	76	0.00	79	0.00	31	1.61	79	0.00
86	0.24	86	0.00	89	0.00	77	0.00	80	1.96	32	0.00	80	0.37
87	0.95	87	0.00	90	0.00	78	0.00	81	1.96	33	0.00	81	0.00
88	0.95	88	0.00	91	0.00	79	0.00	82	0.00	34	0.00	82	0.00
89	0.95	89	0.00	92	0.00	80	0.00	83	0.00	35	0.00	83	0.00
90	0.47	90	0.00	93	0.00	81	0.00	84	0.00	36	0.00	84	0.00
91	0.47	91	0.00	94	0.00	82	0.00	85	0.00	37	0.00	85	0.37
92	0.71	92	0.00	95	0.00	83	0.00	86	0.00	38	0.00	86	0.00
93	0.71	93	0.71	96	0.00	84	0.63	87	0.00	39	0.00	87	0.00
94	0.47	94	0.00	97	0.44	85	0.00	88	0.00	40	0.00	88	0.37
95	1.18	95	0.00	98	0.00	86	0.00	89	1.96	41	0.00	89	0.00
96	0.95	96	0.00	99	0.00	87	0.63	90	0.00	42	0.00	90	0.37
97	1.90	97	0.00	100	0.00	88	0.00	91	0.00	43	0.00	91	0.37
98	1.18	98	0.71	101	0.00	89	0.63	92	0.00	44	0.00	92	0.00
99	1.42	99	0.00	102	0.00	90	0.00	93	0.00	45	0.00	93	0.00
100	0.47	100	0.00	103	0.00	91	0.00	94	0.00	46	0.00	94	0.00
101	0.47	101	0.71	104	0.00	92	0.63	95	0.00	47	0.00	95	0.37
102	0.24	102	1.43	105	0.00	93	0.00	96	0.00	48	0.00	96	0.00
103	0.00	103	0.71	106	0.00	94	0.00	97	0.00	49	1.61	97	0.37
104	0.95	104	1.43	107	0.00	95	0.00	98	0.00	50	0.00	98	0.00
105	0.71	105	0.00	108	0.00	96	0.00	99	0.00	51	0.00	99	0.00
106	0.24	106	0.71	109	0.00	97	0.00	100	0.00	52	0.00	100	0.00
107	0.24	107	0.00	110	0.00	98	0.63	101	0.00	53	0.00	101	0.00
108	0.71	108	0.00	111	0.00	99	0.00	102	0.00	54	1.61	102	0.00
109	0.00	109	0.71	112	0.00	100	0.63	103	0.00	55	0.00	103	0.37
110	0.24	110	0.00	113	0.00	101	0.63	104	0.00	56	0.00	104	0.00
111	0.24	111	0.00	114	0.00	102	1.27	105	1.96	57	0.00	105	0.37
112	0.24	112	0.00	115	0.00	103	0.63	106	0.00	58	0.00	106	0.37
113	0.24	113	0.71	116	0.44	104	0.63	107	0.00	59	0.00	107	0.37
114	0.00	114	0.00	117	0.00	105	0.00	108	0.00	60	0.00	108	0.00
115	0.24	115	0.71	118	0.44	106	0.00	109	0.00	61	0.00	109	0.37
116	0.24	116	0.00	119	1.75	107	0.63	110	0.00	62	0.00	110	0.00
117	0.47	117	0.00	120	0.44	108	0.00	111	0.00	63	1.61	111	0.74
118	0.24	118	0.71	121	0.44	109	0.00	112	0.00	64	1.61	112	0.00
119	0.47	119	0.00	122	0.87	110	0.00	113	0.00	65	0.00	113	0.37
120	0.47	120	0.00	123	0.87	111	0.00	114	0.00	66	0.00	114	0.00
121	0.00	121	0.00	124	0.44	112	0.00	115	0.00	67	0.00	115	0.37
122	0.95	122	0.00	125	0.00	113	0.00	116	0.00	68	0.00	116	0.00
123	1.90	123	0.00	126	0.87	114	0.00	117	0.00	69	0.00	117	0.00
124	0.47	124	0.71	127	0.44	115	0.00	118	0.00	70	0.00	118	0.00
125	0.00	125	0.00	128	0.00	116	0.00	119	0.00	71	1.61	119	0.00
126	0.47	126	0.00	129	0.00	117	0.00	120	0.00	72	0.00	120	0.00
127	0.24	127	0.00	130	0.00	118	0.00	121	1.96	73	0.00	121	0.00

Figure 4A Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
128	0.47	128	0.71	131	0.00	119	0.00	122	3.92	74	0.00	122	0.00
129	1.18	129	1.43	132	0.00	120	0.00	123	1.96	75	0.00	123	0.00
130	0.00	130	0.00	133	0.00	121	0.00	124	0.00	76	0.00	124	1.10
131	0.47	131	0.00	134	0.00	122	0.00	125	0.00	77	0.00	125	0.00
132	0.24	132	0.71	135	0.44	123	0.00	126	0.00	78	1.61	126	0.00
133	0.71	133	0.71	136	0.00	124	0.00	127	0.00	79	0.00	127	0.00
134	0.00	134	0.00	137	0.00	125	0.00	128	0.00	80	0.00	128	0.00
135	0.95	135	0.00	138	0.00	126	0.00	129	0.00	81	0.00	129	0.37
136	0.24	136	0.00	139	0.44	127	0.00			82	0.00	130	0.74
137	0.47	137	0.71	140	0.00	128	0.00			83	0.00	131	0.37
138	0.47	138	0.71	141	0.00	129	0.00			84	0.00	132	0.00
139	0.71	139	0.00	142	0.00	130	0.00					133	0.00
140	0.24	140	0.00	143	0.87	131	0.00					134	0.00
141	0.71	141	1.43	144	0.44	132	0.00					135	0.37
142	1.42	142	0.71			133	0.00					136	0.00
143	1.90	143	1.43			134	0.00					137	0.74
144	1.42	144	0.71			135	0.00					138	0.00
145	0.95	145	0.00	145	0.00	136	0.00	130	0.00	85	0.00	139	0.00
146	1.66	146	0.71	146	0.00	137	0.00	131	0.00	86	0.00	140	0.00
147	0.95	147	1.43	147	0.00	138	0.00	132	0.00	87	0.00	141	0.37
148	0.47	148	0.00	148	0.00	139	0.00	133	0.00	88	0.00	142	0.00
149	0.71	149	0.00	149	0.87	140	0.00	134	0.00	89	0.00	143	0.00
150	1.42	150	0.00	150	0.00	141	0.00	135	0.00	90	0.00	144	0.00
151	0.95	151	0.00	151	0.00	142	0.00	136	0.00	91	0.00	145	1.10
152	2.61	152	0.00	152	0.00	143	0.00	137	0.00	92	0.00	146	0.00
153	0.47	153	0.00	153	0.00	144	0.63	138	0.00	93	1.61	147	0.37
154	0.95	154	0.00	154	0.87	145	0.00	139	0.00	94	0.00	148	0.00
155	1.90	155	0.71	155	0.00	146	0.63	140	0.00	95	0.00	149	0.00
156	1.42	156	0.00	156	0.00	147	0.00	141	0.00	96	0.00	150	0.00
157	0.95	157	0.00	157	0.00	148	0.00	142	0.00	97	0.00	151	0.37
158	0.71	158	0.00	158	0.44	149	0.00	143	1.96	98	0.00	152	0.74
159	0.95	159	0.71	159	0.00	150	0.00	144	0.00	99	0.00	153	0.37
160	0.47	160	0.00	160	0.00	151	0.00	145	0.00	100	0.00	154	0.37
161	1.18	161	1.43	161	0.00	152	1.27	146	0.00	101	0.00	155	1.84
162	0.95	162	0.00	162	0.00	153	0.63	147	0.00	102	1.61	156	0.37
						154	0.00	148	1.96			157	0.37
						155	0.63	149	1.96			158	0.00
						156	0.00	150	0.00			159	0.37
						157	0.00	151	0.00			160	0.74
						158	0.00	152	0.00			161	0.00
						159	0.00	153	0.00			162	0.37
						160	0.00	154	1.96				
						161	0.63	155	0.00				
						162	0.00	156	1.96				
								157	0.00				
								158	0.00				
								159	0.00				
								160	0.00				
								161	0.00				
								162	0.00				
163	1.18	163	0.00	163	0.00	163	0.00	163	0.00	103	0.00	163	0.37
164	2.13	164	0.71	164	0.00	164	0.00	164	0.00	104	0.00	164	0.00
165	1.18	165	0.71	165	0.00	165	0.00	165	0.00	105	0.00	165	0.74
166	0.24	166	1.43	166	0.00	166	0.00	166	0.00	106	0.00	166	0.74
167	0.00	167	0.00	167	0.44	167	0.00	167	0.00	107	0.00	167	1.10
168	0.24	168	0.00	168	0.44	168	0.63	168	0.00	108	0.00	168	0.00
169	0.24	169	0.00	169	0.00	169	0.00	169	0.00	109	0.00	169	0.00
170	0.00	170	0.71	170	0.00	170	0.00	170	0.00	110	0.00	170	0.00
171	0.47	171	0.71	171	0.00	171	0.00	171	0.00	111	0.00	171	0.37
172	0.00	172	0.00	172	0.00	172	0.00	172	0.00	112	0.00	172	0.00

Figure 4A Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
173	0.00	173	0.00	173	0.00	173	0.00	173	0.00	113	0.00	173	0.37
174	0.00	174	0.00	174	0.00	174	0.00	174	0.00	114	0.00	174	0.00
175	0.00	175	0.00	175	0.00	175	0.00	175	0.00	115	0.00	175	0.00
176	0.00	176	0.71	176	0.00	176	0.00	176	0.00	116	0.00	176	0.00
177	0.71	177	0.71	177	0.00	177	0.63	177	0.00	117	1.61	177	0.74
178	0.24	178	0.00	178	0.00	178	0.00	178	0.00	118	0.00	178	0.37
179	0.24	179	0.71	179	0.44	179	0.00	179	0.00	119	0.00	179	0.00
180	0.00	180	0.71	180	0.00	180	0.00	180	0.00	120	1.61	180	0.00
181	0.00	181	0.00	181	0.44	181	0.00	181	0.00	121	1.61	181	0.00
182	0.71	182	0.00	182	0.44	182	0.00	182	0.00	122	0.00	182	0.00
183	0.95	183	0.71	183	1.31	183	0.00	183	0.00	123	0.00	183	0.00
184	1.90	184	0.00	184	0.44	184	0.00	184	0.00	124	0.00	184	0.00
185	1.42	185	0.00	185	0.44	185	0.00	185	0.00	125	0.00	185	0.00
186	0.47	186	0.71	186	0.44	186	0.00	186	0.00	126	0.00	186	0.37
187	0.47	187	0.00	187	0.00	187	0.00			127	0.00	187	0.37
188	0.47	188	0.71	188	0.00	188	0.63			128	0.00	188	0.74
189	0.24	189	0.71	189	0.87	189	0.63			129	3.23	189	0.37
190	0.00	190	0.00	190	0.87	190	0.63			130	0.00	190	0.37
191	0.47	191	0.00	191	0.00	191	0.63			131	0.00	191	0.00
192	1.18	192	0.00	192	0.44	192	0.63			132	0.00	192	0.00
193	0.71	193	0.71	193	0.00	193	0.00			133	0.00	193	0.00
194	0.24	194	0.71	194	0.00	194	0.00			134	0.00	194	0.37
195	0.47	195	0.00	195	0.00	195	0.00			135	0.00	195	1.10
196	1.66	196	0.00	196	0.00	196	0.63			136	0.00	196	0.37
197	0.71	197	0.00	197	0.00	197	0.00			137	0.00	197	0.00
198	0.00	198	0.00	198	0.00	198	0.00			138	0.00	198	0.74
199	0.95	199	0.00	199	0.44	199	0.00			139	0.00	199	0.37
200	0.71	200	0.71	200	0.00	200	0.00			140	0.00	200	0.00
201	0.47	201	1.43	201	0.44	201	0.63			141	0.00	201	0.00
202	0.24	202	0.00	202	0.44	202	0.00			142	0.00	202	0.37
203	0.95	203	0.00	203	0.00	203	0.00			143	0.00	203	0.00
204	3.32	204	0.00	204	0.00	204	0.00			144	0.00	204	0.00
205	0.00	205	0.00	205	0.44	205	0.00			145	0.00	205	0.00
206	0.00	206	0.00	206	0.00	206	0.63			146	0.00	206	0.00
207	0.00	207	0.00	207	0.00	207	0.00			147	0.00	207	0.37
208	0.95	208	0.71	208	0.00	208	0.00			148	0.00	208	0.00
209	0.24	209	0.71	209	0.00	209	0.00			149	0.00	209	0.74
210	1.90	210	0.00	210	0.44	210	0.00			150	0.00	210	0.37
211	3.32	211	0.00	211	0.00	211	0.00			151	0.00	211	0.37
212	0.00	212	0.00	212	0.00	212	0.00			152	0.00	212	0.74
213	0.71	213	0.00	213	0.00	213	0.00			153	0.00	213	0.00
214	0.47	214	0.00										
215	1.18	215	0.00										
216	0.47	216	0.00										
217	0.00	217	0.00	214	0.00	214	0.00	187	0.00	154	0.00	214	0.37
218	0.71	218	0.71	215	0.00	215	0.63	188	0.00	155	0.00	215	0.00
219	0.00	219	0.71	216	0.00	216	0.00	189	0.00	156	0.00	216	0.74
220	0.95	220	0.00	217	0.00	217	0.00	190	0.00	157	0.00	217	0.37
221	1.90	221	0.00	218	0.00	218	0.00	191	0.00	158	0.00	218	0.37
222	1.90	222	0.00	219	0.44	219	0.00	192	0.00	159	1.61	219	0.00
223	0.00	223	0.00	220	0.00	220	0.00	193	1.96	160	0.00	220	0.00
224	0.24	224	0.00	221	0.00	221	0.00	194	0.00	161	0.00	221	1.84
225	1.18	225	0.00	222	0.00	222	0.00	195	0.00	162	0.00	222	2.21
226	0.00	226	0.00	223	0.00	223	0.00	196	0.00	163	0.00	223	0.74
227	1.18	227	0.00	224	0.44	224	1.27	197	0.00	164	0.00	224	0.37
228	0.71	228	0.00	225	0.44	225	0.63	198	0.00	165	0.00	225	0.37
229	2.13	229	0.00	226	0.44	226	0.00	199	0.00	166	0.00	226	0.74
230	0.95	230	0.00	227	0.00	227	0.00	200	0.00	167	0.00	227	0.37
231	0.71	231	0.00	228	0.00	228	0.63	201	0.00	168	0.00	228	0.37
232	0.47	232	0.00					202	0.00	169	0.00	229	0.37

Figure 4A Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
233	0.00	233	0.00					203	0.00	170	0.00	230	1.47
234	0.24	234	0.71					204	0.00	171	0.00	231	0.74
235	1.18	235	0.00					205	0.00				
236	0.95	236	0.71					206	0.00				
237	0.47	237	0.00					207	0.00				
								208	0.00				
								209	0.00				
								210	0.00				
								211	0.00				
								212	0.00				
								213	0.00				
								214	0.00				
								215	0.00				
								216	0.00				
								217	0.00				
								218	1.96				
								219	0.00				
								220	1.96				
								221	0.00				
								222	0.00				
								223	0.00				
								224	0.00				
								225	0.00				
								226	0.00				
								227	0.00				
								228	0.00				
238	0.71	238	0.00	229	0.00	229	0.00	229	0.00	172	0.00	232	0.37
239	1.18	239	0.00	230	0.44	230	0.00	230	0.00	173	0.00	233	0.74
240	0.47	240	0.71	231	0.00	231	0.00	231	0.00	174	0.00	234	0.37
241	1.42	241	0.00	232	0.44	232	0.00	232	0.00	175	0.00	235	0.00
242	0.47	242	0.00	233	0.00	233	0.00	233	1.96	176	1.61	236	1.47
243	1.18	243	0.00	234	0.00	234	0.00	234	1.96	177	0.00	237	0.37
244	0.47	244	0.00	235	0.44	235	0.00	235	0.00	178	0.00	238	0.37
245	1.90	245	0.71	236	0.44	236	0.63	236	0.00	179	0.00	239	0.00
246	1.90	246	0.00	237	0.44	237	0.00	237	1.96	180	0.00	240	0.37
247	0.00	247	0.00	238	0.00	238	0.63	238	0.00	181	0.00	241	0.37
248	0.47	248	0.00	239	0.44	239	1.27	239	0.00	182	0.00	242	0.37
249	0.00	249	0.00	240	0.00	240	0.63	240	0.00	183	1.61	243	0.00
250	0.24	250	0.71	241	1.31	241	0.00	241	0.00	184	0.00	244	0.00
251	0.24	251	0.00	242	0.00	242	0.00	242	0.00	185	0.00	245	0.00
252	4.03	252	2.14	243	0.00	243	0.63	243	0.00	186	0.00	246	0.74
253	0.24	253	0.00	244	0.00	244	0.63	244	0.00	187	0.00	247	0.00
254	0.71	254	0.00	245	0.00	245	0.00	245	0.00	188	0.00	248	0.00
255	0.47	255	0.00	246	0.00	246	0.00	246	0.00	189	0.00	249	0.37
256	0.24	256	0.00	247	0.00	247	0.00	247	0.00	190	0.00	250	0.74
257	0.47	257	0.00	248	0.00	248	0.00	248	0.00	191	1.61	251	0.00
258	0.24	258	0.00	249	0.00	249	0.00	249	0.00	192	0.00	252	1.10
259	0.24	259	0.00	250	0.00	250	0.63	250	0.00	193	0.00	253	0.00
260	1.42	260	0.00	251	0.00	251	0.00	251	1.96	194	0.00	254	0.37
261	0.24	261	0.71	252	0.00	252	0.00	252	0.00	195	0.00	255	0.37
262	0.24	262	0.71	253	0.00	253	1.90	253	0.00	196	0.00	256	0.37
263	0.24	263	0.00	254	0.00	254	0.00	254	3.92	197	0.00	257	0.74
264	0.71	264	0.00	255	0.00	255	0.00	255	0.00	198	0.00	258	0.00
265	0.47	265	0.00	256	0.00	256	0.00	256	0.00	199	0.00	259	0.00
266	0.24	266	0.00	257	0.44	257	0.00	257	0.00	200	0.00	260	0.00
267	1.42	267	0.00	258	0.00	258	0.00	258	0.00	201	0.00	261	0.00
268	0.47	268	0.00	259	0.00	259	0.00	259	0.00	202	0.00	262	0.00
269	0.24	269	0.00	260	0.00	260	0.00	260	0.00	203	0.00	263	0.37
270	0.47	270	0.71	261	0.00	261	0.00	261	1.96	204	0.00	264	0.00
271	0.00	271	0.00	262	0.44	262	0.00	262	0.00	205	0.00	265	0.00

Figure 4A Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
272	0.00	272	0.00	263	0.00	263	0.00	263	0.00	206	0.00	266	0.00
273	0.00	273	0.71	264	0.00	264	0.00	264	0.00	207	0.00	267	0.00
274	0.24	274	0.00	265	0.44	265	0.63	265	0.00	208	0.00	268	0.00
275	0.24	275	0.71	266	0.00	266	0.00	266	1.96	209	0.00	269	0.37
276	0.00	276	0.00	267	0.00	267	0.00	267	0.00	210	0.00	270	0.00
277	0.47	277	0.00	268	0.00	268	0.00	268	0.00	211	0.00	271	0.74
278	0.00	278	0.00	269	0.00	269	0.63	269	0.00	212	0.00	272	0.00
279	0.71	279	0.00	270	0.00	270	1.27	270	0.00	213	0.00	273	0.00
280	0.95	280	0.00	271	0.00	271	1.27	271	0.00	214	0.00	274	0.37
281	0.00	281	0.00	272	0.00	272	0.63	272	0.00	215	0.00	275	0.37
282	0.47	282	0.71	273	0.00	273	0.63	273	0.00	216	0.00	276	0.37
283	0.71	283	0.00	274	0.00	274	0.00	274	0.00	217	0.00	277	0.00
284	0.00	284	0.00	275	0.00	275	0.00	275	0.00	218	0.00	278	0.00
285	0.00	285	0.00	276	0.00	276	0.00	276	0.00	219	0.00	279	0.37
286	0.00	286	0.00	277	0.00	277	0.00	277	0.00	220	0.00	280	0.00
287	0.24	287	0.00	278	0.00	278	0.63	278	0.00	221	0.00	281	0.00
288	0.24	288	0.00	279	0.00	279	0.63	279	1.96	222	0.00	282	0.37
289	0.00	289	1.43	280	0.00	280	0.00	280	0.00	223	0.00	283	0.00
290	0.00	290	0.71	281	0.00	281	0.00	281	0.00	224	1.61	284	0.00
291	0.00	291	0.71	282	0.00	282	0.00	282	0.00	225	1.61	285	0.74
292	0.47	292	0.00	283	0.00	283	0.00	283	0.00	226	0.00	286	0.37
293	0.24	293	0.00	284	0.44	284	0.63	284	0.00	227	0.00	287	0.00
294	0.00	294	0.00	285	0.00	285	0.00	285	0.00	228	0.00	288	0.37
295	0.00	295	0.00	286	0.00	286	0.00	286	0.00	229	0.00	289	0.37
296	0.00	296	0.00	287	0.44	287	0.00	287	0.00	230	0.00	290	0.37
297	0.24	297	0.00	288	0.00	288	0.00	288	0.00	231	0.00	291	0.00
298	0.24	298	0.00	289	0.00	289	0.63	289	0.00	232	0.00	292	0.37
299	0.95	299	0.00	290	0.00	290	0.00	290	0.00	233	0.00	293	0.00
300	0.95	300	0.00	291	0.00	291	0.63	291	0.00	234	0.00	294	0.74
301	0.24	301	0.00	292	0.00	292	0.00	292	0.00	235	0.00	295	0.37
302	0.00	302	0.00	293	0.00	293	0.00	293	0.00	236	0.00	296	0.74
303	1.18	303	0.00	294	0.00	294	0.63	294	0.00	237	0.00	297	0.00
304	0.24	304	0.00	295	0.00	295	0.00	295	0.00	238	3.23	298	0.37
305	0.24	305	0.00	296	0.00	296	0.00	296	0.00	239	0.00	299	0.74
306	0.71	306	0.00	297	0.00	297	0.00	297	0.00	240	0.00	300	0.00
307	0.95	307	0.00	298	0.00	298	0.00	298	0.00	241	0.00	301	0.00
308	0.00	308	0.00	299	0.44	299	0.63	299	0.00	242	0.00	302	0.00
309	0.95	309	0.00	300	0.87	300	1.27	300	0.00	243	0.00	303	0.00
310	0.71	310	0.00	301	0.00	301	0.00	301	0.00	244	0.00	304	0.37
311	0.00	311	0.00	302	0.00	302	0.00	302	1.96	245	0.00	305	0.00
312	0.71	312	0.71	303	0.00	303	0.00	303	0.00	246	0.00	306	0.00
313	0.24	313	0.00	304	0.00	304	1.27	304	1.96	247	0.00	307	0.00
314	0.00	314	0.00	305	0.00	305	0.63	305	0.00	248	0.00	308	0.37
315	1.90	315	0.71	306	0.44	306	0.63	306	1.96	249	0.00	309	0.74
316	1.66	316	0.71	307	0.00	307	0.00	307	0.00	250	0.00	310	0.37
317	1.18	317	0.71	308	0.00	308	0.00	308	0.00	251	0.00	311	0.00
318	0.47	318	0.71	309	0.44	309	0.00	309	1.96	252	0.00	312	0.00
319	0.47	319	0.00	310	0.00	310	0.00	310	0.00	253	0.00	313	0.37
320	0.95	320	0.00	311	0.00	311	0.00	311	0.00	254	0.00	314	0.00
321	0.71	321	0.00	312	0.00	312	0.63	312	0.00	255	0.00	315	1.10
322	0.71	322	0.71	313	0.00	313	0.63	313	0.00	256	0.00	316	0.00
323	0.00	323	2.14	314	0.00	314	0.00	314	0.00	257	0.00	317	0.00
324	0.00	324	0.00	315	0.44	315	0.00	315	0.00	258	0.00	318	0.74
325	0.24	325	0.00	316	0.00	316	1.90	316	0.00	259	0.00	319	0.37
326	0.00	326	0.00	317	0.00	317	0.00	317	0.00	260	0.00	320	0.00
327	0.00	327	0.00	318	0.44	318	0.63	318	0.00	261	0.00	321	0.00
328	0.47	328	0.00	319	0.00	319	0.00	319	0.00	262	0.00	322	0.37
329	0.47	329	0.00	320	0.00	320	0.00	320	0.00	263	0.00	323	0.37
330	0.24	330	0.00	321	0.44	321	0.00	321	0.00	264	0.00	324	0.37
331	0.47	331	0.00	322	0.44	322	0.63	322	0.00	265	0.00	325	0.00
332	0.47	332	0.71	323	0.00	323	0.00	323	1.96	266	0.00	326	0.00

Figure 4A Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
333	0.00	333	0.71	324	0.00	324	0.00	324	0.00	267	3.23	327	0.00
334	0.00	334	0.00	325	0.00	325	0.00	325	0.00	268	0.00	328	0.00
335	0.00	335	0.00	326	0.00	326	0.63	326	0.00	269	0.00	329	0.00
336	0.00	336	0.00	327	0.44	327	1.90	327	0.00	270	0.00	330	0.00
337	0.71	337	0.00	328	0.00	328	0.00	328	0.00	271	0.00	331	0.00
338	0.00	338	0.71	329	0.00	329	0.00	329	0.00	272	0.00	332	0.00
339	0.00	339	0.00	330	0.44	330	0.00	330	0.00	273	0.00	333	0.37
340	0.47	340	0.71	331	0.00	331	0.00	331	0.00	274	0.00	334	0.00
341	0.95	341	0.00	332	0.00	332	0.00	332	0.00	275	0.00	335	0.37
342	0.24	342	0.00	333	0.00	333	1.27	333	1.96	276	0.00	336	0.00
343	1.42	343	2.14	334	0.00	334	0.00	334	0.00	277	0.00	337	0.37
344	0.00	344	0.00	335	1.31	335	0.00	335	0.00	278	1.61	338	0.74
345	1.18	345	0.00	336	0.00	336	0.00	336	0.00	279	0.00	339	0.37
346	0.00	346	0.00	337	0.00	337	0.00	337	0.00	280	0.00	340	0.00
347	0.00	347	0.00	338	0.00	338	0.00	338	3.92	281	0.00	341	0.00
348	0.00	348	0.00	339	0.00	339	0.63	339	0.00	282	0.00	342	0.00
349	0.47	349	0.00	340	0.00	340	0.00	340	0.00	283	0.00	343	0.37
350	0.47	350	0.00	341	0.00	341	0.00	341	1.96	284	0.00	344	0.74
351	0.47	351	0.00	342	0.00	342	0.00	342	1.96	285	0.00	345	0.00
352	0.24	352	0.00	343	0.00	343	0.63	343	1.96	286	0.00	346	0.00
353	0.24	353	0.00	344	0.00	344	0.00	344	0.00	287	0.00	347	0.00
354	1.42	354	0.00	345	0.00	345	0.00	345	1.96	288	0.00	348	0.00
				346	0.00	346	0.00	346	1.96				
				347	0.00	347	0.00	347	1.96				
				348	0.00	348	0.00	348	1.96				
355	0.71	355	0.00	349	0.00	349	0.63	349	3.92	289	0.00	349	0.74
356	3.79	356	2.14	350	0.87	350	0.00	350	3.92	290	0.00	350	0.74
357	2.84	357	0.00	351	1.31	351	0.63	351	19.61	291	0.00	351	2.21
358	9.24	358	3.57	352	3.49	352	1.27	352	17.65	292	0.00	352	3.31
359	12.09	359	0.71	353	5.68	353	1.90	353	49.02	293	0.00	353	10.29
360	12.32	360	0.71	354	4.80	354	2.53	354	74.51	294	0.00	354	14.34

Figure 4B Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
				1	0.00								
				2	0.00								
				3	37.50								
1	0.00	1	0.00	4	25.00								
2	0.00	2	0.00	5	0.00								
3	0.00	3	0.00	6	87.50								
4	0.00	4	0.00	7	50.00								
5	0.00	5	0.00	8	0.00								
6	0.00	6	2.86	9	0.00								
7	5.00	7	5.71	10	0.00	1	0.00	1	0.00			1	0.00
8	2.50	8	0.00	11	0.00	2	0.00	2	0.00			2	0.00
9	57.50	9	37.14	12	0.00	3	0.00	3	0.00			3	0.00
10	55.00	10	37.14	13	37.50	4	0.00	4	0.00			4	0.00
11	12.50	11	0.00	14	50.00	5	0.00	5	0.00			5	0.00
12	50.00	12	40.00	15	0.00	6	6.67	6	0.00			6	0.00
13	20.00	13	14.29	16	0.00	7	6.67	7	0.00			7	0.00
14	12.50	14	2.86	17	0.00	8	0.00	8	16.67			8	0.00
15	0.00	15	0.00	18	0.00	9	26.67	9	0.00			9	0.00
16	17.50	16	20.00	19	0.00	10	0.00	10	16.67			10	30.00
17	5.00	17	0.00	20	0.00	11	0.00	11	0.00			11	30.00
18	7.50	18	0.00	21	12.50	12	26.67	12	0.00			12	0.00
19	0.00	19	0.00	22	12.50	13	13.33	13	0.00			13	0.00
20	32.50	20	22.86	23	0.00	14	0.00	14	0.00			14	10.00
21	15.00	21	14.29	24	37.50	15	33.33	15	0.00			15	0.00
22	5.00	22	2.86	25	12.50	16	0.00	16	66.67			16	0.00
23	5.00	23	0.00	26	0.00	17	0.00	17	0.00			17	0.00
24	0.00	24	0.00	27	0.00	18	40.00	18	0.00			18	0.00
25	5.00	25	0.00	28	0.00	19	6.67	19	0.00			19	0.00
26	0.00	26	0.00	29	12.50	20	6.67	20	0.00			20	10.00
27	2.50	27	2.86	30	0.00	21	0.00	21	0.00			21	0.00
28	7.50	28	11.43	31	12.50	22	0.00	22	0.00			22	0.00
29	2.50	29	2.86	32	0.00	23	0.00	23	0.00			23	0.00
30	2.50	30	0.00	33	50.00	24	0.00	24	0.00			24	10.00
31	2.50	31	2.86	34	0.00	25	6.67	25	16.67			25	0.00
32	0.00	32	2.86	35	0.00	26	6.67	26	0.00			26	70.00
33	0.00	33	0.00	36	0.00	27	0.00	27	0.00			27	10.00
34	7.50	34	0.00	37	62.50	28	40.00	28	0.00			28	10.00
35	7.50	35	2.86	38	12.50	29	0.00	29	0.00			29	0.00
36	0.00	36	0.00	39	37.50	30	0.00	30	0.00			30	70.00
37	62.50	37	34.29	40	50.00	31	0.00	31	0.00			31	20.00
38	10.00	38	0.00	41	0.00	32	53.33	32	16.67			32	0.00
39	0.00	39	0.00	42	50.00	33	20.00	33	0.00			33	40.00
40	27.50	40	20.00	43	25.00	34	26.67	34	0.00			34	80.00
41	57.50	41	42.86	44	0.00	35	6.67	35	66.67			35	0.00
42	0.00	42	5.71	45	0.00	36	6.67	36	0.00			36	0.00
43	0.00	43	0.00	46	0.00	37	0.00	37	0.00			37	10.00
44	0.00	44	0.00	47	0.00	38	0.00	38	0.00			38	0.00
45	2.50	45	0.00	48	0.00	39	0.00	39	0.00			39	10.00
46	5.00	46	2.86	49	25.00	40	33.33	40	83.33			40	0.00
47	2.50	47	0.00	50	0.00	41	6.67	41	0.00			41	0.00
48	10.00	48	0.00	51	0.00	42	0.00	42	0.00			42	0.00
49	15.00	49	0.00	52	0.00	43	0.00	43	0.00			43	0.00
50	30.00	50	25.71	53	0.00	44	6.67	44	66.67			44	0.00
51	0.00	51	0.00	54	0.00	45	6.67	45	0.00			45	0.00
52	0.00	52	0.00	55	0.00	46	0.00	46	0.00			46	10.00
53	5.00	53	2.86	56	37.50	47	0.00	47	16.67			47	0.00

Figure 4B Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
54	0.00	54	0.00	57	12.50	48	0.00	48	0.00			48	0.00
55	2.50	55	2.86	58	12.50	49	0.00	49	0.00	1	0.00	49	0.00
56	0.00	56	0.00	59	37.50	50	6.67	50	0.00	2	0.00	50	0.00
57	0.00	57	0.00	60	0.00	51	6.67	51	0.00	3	0.00	51	0.00
58	0.00	58	0.00	61	0.00	52	6.67	52	0.00	4	0.00	52	0.00
59	12.50	59	2.86	62	37.50	53	6.67	53	0.00	5	0.00	53	0.00
60	2.50	60	0.00	63	25.00	54	0.00	54	0.00	6	0.00	54	0.00
61	0.00	61	0.00	64	0.00	55	73.33	55	0.00	7	0.00	55	0.00
62	2.50	62	0.00	65	0.00	56	46.67	56	0.00	8	57.14	56	0.00
63	0.00	63	0.00	66	0.00	57	6.67	57	0.00	9	14.29	57	0.00
64	2.50	64	2.86	67	25.00	58	0.00	58	0.00	10	0.00	58	0.00
65	10.00	65	5.71	68	12.50	59	0.00	59	0.00	11	0.00	59	0.00
66	0.00	66	0.00	69	0.00	60	0.00	60	0.00	12	42.86	60	0.00
67	32.50	67	20.00			61	0.00	61	0.00	13	0.00	61	0.00
68	0.00	68	0.00			62	0.00	62	0.00	14	0.00	62	0.00
69	0.00	69	0.00			63	0.00	63	0.00	15	0.00	63	0.00
70	0.00	70	0.00	70	0.00	64	0.00	64	16.67	16	14.29	64	0.00
71	0.00	71	2.86	71	12.50	65	0.00	65	0.00	17	0.00	65	0.00
72	0.00	72	0.00	72	0.00	66	0.00	66	0.00	18	0.00	66	10.00
73	45.00	73	22.86	73	0.00	67	6.67	67	16.67	19	0.00	67	70.00
74	0.00	74	0.00	74	0.00	68	33.33	68	0.00	20	0.00	68	0.00
75	0.00	75	0.00	75	0.00	69	0.00	69	0.00	21	0.00	69	0.00
76	0.00	76	0.00	76	12.50	70	0.00	70	0.00	22	0.00	70	0.00
77	27.50	77	20.00	77	0.00	71	0.00	71	0.00	23	0.00	71	70.00
78	0.00	78	0.00	78	0.00	72	0.00	72	66.67	24	28.57	72	10.00
79	0.00	79	0.00	79	0.00	73	6.67	73	0.00	25	0.00	73	0.00
80	0.00	80	0.00	80	0.00	74	6.67	74	0.00	26	0.00	74	0.00
81	7.50	81	2.86	81	37.50	75	0.00	75	0.00	27	0.00	75	0.00
82	7.50	82	2.86	82	50.00	76	33.33	76	50.00	28	0.00	76	30.00
83	10.00	83	0.00	83	0.00	77	0.00	77	33.33	29	0.00	77	0.00
84	10.00	84	0.00	84	0.00	78	6.67	78	0.00	30	0.00	78	0.00
85	5.00	85	2.86	85	12.50	79	6.67	79	0.00	31	42.86	79	0.00
86	0.00	86	0.00	86	0.00	80	0.00	80	33.33	32	28.57	80	0.00
87	0.00	87	0.00	87	0.00	81	0.00	81	0.00	33	0.00	81	0.00
88	15.00	88	5.71	88	0.00	82	0.00	82	16.67	34	42.86	82	80.00
89	5.00	89	0.00	89	0.00	83	6.67	83	0.00	35	0.00	83	0.00
90	2.50	90	0.00	90	0.00	84	0.00	84	0.00	36	0.00	84	0.00
91	7.50	91	0.00	91	0.00	85	0.00	85	0.00	37	100.00	85	30.00
92	7.50	92	0.00	92	0.00	86	6.67	86	16.67	38	0.00	86	0.00
93	20.00	93	8.57	93	37.50	87	0.00	87	0.00	39	0.00	87	0.00
94	25.00	94	20.00	94	0.00	88	6.67	88	0.00	40	0.00	88	70.00
95	2.50	95	0.00	95	0.00	89	13.33	89	0.00	41	85.71	89	10.00
96	0.00	96	0.00	96	0.00	90	6.67	90	0.00	42	0.00	90	0.00
97	35.00	97	20.00	97	12.50	91	0.00	91	0.00	43	0.00	91	0.00
98	7.50	98	5.71	98	0.00	92	0.00	92	0.00	44	0.00	92	0.00
99	5.00	99	2.86	99	0.00	93	0.00	93	0.00	45	0.00	93	0.00
100	22.50	100	2.86	100	0.00	94	40.00	94	0.00	46	57.14	94	0.00
101	2.50	101	0.00	101	0.00	95	53.33	95	0.00	47	14.29	95	0.00
102	2.50	102	0.00	102	0.00	96	0.00	96	0.00	48	0.00	96	30.00
103	2.50	103	2.86	103	25.00	97	0.00	97	0.00	49	71.43	97	30.00
104	7.50	104	5.71	104	0.00	98	26.67	98	0.00	50	85.71	98	0.00
105	0.00	105	0.00	105	0.00	99	13.33	99	66.67	51	0.00	99	20.00
106	2.50	106	5.71	106	25.00	100	13.33	100	0.00	52	0.00	100	0.00
107	0.00	107	2.86	107	25.00	101	13.33	101	0.00	53	0.00	101	0.00
108	0.00	108	2.86	108	0.00	102	13.33	102	0.00	54	0.00	102	0.00
109	0.00	109	0.00	109	0.00	103	26.67	103	0.00	55	0.00	103	20.00

Figure 4B Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
110	0.00	110	0.00	110	0.00	104	0.00	104	0.00	56	0.00	104	10.00
111	0.00	111	0.00	111	0.00	105	13.33	105	0.00	57	0.00	105	0.00
112	2.50	112	2.86	112	0.00	106	6.67	106	0.00	58	0.00	106	0.00
113	5.00	113	2.86	113	0.00	107	60.00	107	0.00	59	0.00	107	0.00
114	0.00	114	0.00	114	0.00	108	0.00	108	0.00	60	0.00	108	0.00
115	0.00	115	2.86	115	0.00	109	0.00	109	0.00	61	42.86	109	0.00
116	7.50	116	8.57	116	0.00	110	0.00	110	50.00	62	0.00	110	60.00
117	0.00	117	0.00	117	25.00	111	0.00	111	50.00	63	0.00	111	10.00
118	20.00	118	5.71	118	0.00	112	6.67	112	0.00	64	14.29	112	0.00
119	0.00	119	0.00	119	0.00	113	33.33	113	0.00	65	57.14	113	10.00
120	0.00	120	0.00	120	0.00	114	6.67	114	0.00	66	0.00	114	10.00
121	0.00	121	5.71	121	25.00	115	0.00	115	0.00	67	0.00	115	0.00
122	5.00	122	2.86	122	12.50	116	26.67	116	16.67	68	0.00	116	0.00
123	37.50	123	17.14	123	0.00	117	0.00	117	0.00	69	0.00	117	0.00
124	15.00	124	14.29	124	0.00	118	0.00	118	0.00	70	0.00	118	0.00
125	0.00	125	0.00	125	37.50	119	0.00	119	0.00	71	71.43	119	0.00
126	2.50	126	0.00	126	12.50	120	20.00	120	0.00	72	85.71	120	0.00
127	2.50	127	0.00	127	0.00	121	6.67	121	83.33	73	0.00	121	10.00
128	57.50	128	37.14	128	0.00	122	13.33	122	0.00	74	14.29	122	30.00
129	42.50	129	25.71	129	37.50	123	6.67	123	0.00	75	0.00	123	0.00
130	0.00	130	0.00	130	37.50	124	0.00	124	0.00	76	0.00	124	10.00
131	90.00	131	54.29	131	0.00	125	0.00	125	0.00	77	14.29	125	30.00
132	45.00	132	37.14	132	0.00	126	6.67	126	0.00	78	0.00	126	0.00
133	0.00	133	0.00	133	0.00	127	6.67	127	0.00	79	0.00	127	0.00
134	40.00	134	22.86	134	100.00	128	40.00	128	50.00	80	0.00	128	70.00
135	2.50	135	2.86	135	75.00	129	13.33	129	0.00	81	0.00	129	0.00
136	0.00	136	0.00	136	0.00	130	0.00	130	0.00	82	0.00	130	0.00
137	0.00	137	0.00	137	0.00	131	13.33	131	0.00	83	0.00	131	0.00
138	65.00	138	25.71	138	62.50	132	13.33	132	0.00	84	0.00	132	0.00
139	0.00	139	0.00	139	12.50	133	0.00	133	0.00			133	0.00
140	2.50	140	2.86	140	0.00	134	0.00	134	16.67			134	70.00
141	0.00	141	0.00	141	0.00	135	0.00	135	16.67			135	40.00
142	7.50	142	2.86	142	0.00	136	0.00	136	0.00			136	0.00
143	32.50	143	28.57	143	0.00	137	6.67	137	0.00			137	0.00
144	0.00	144	0.00	144	0.00	138	6.67	138	0.00			138	0.00
145	2.50	145	0.00	145	0.00	139	0.00	139	0.00	85	14.29	139	0.00
146	27.50	146	22.86	146	0.00	140	0.00	140	16.67	86	42.86	140	0.00
147	0.00	147	0.00	147	0.00	141	0.00	141	0.00	87	0.00	141	100.00
148	45.00	148	28.57	148	0.00	142	33.33	142	0.00	88	0.00	142	0.00
149	10.00	149	2.86	149	50.00	143	6.67	143	0.00	89	0.00	143	0.00
150	2.50	150	0.00	150	0.00	144	0.00	144	0.00	90	0.00	144	0.00
151	10.00	151	0.00	151	25.00	145	0.00	145	0.00	91	0.00	145	0.00
152	15.00	152	0.00	152	50.00	146	33.33	146	0.00	92	0.00	146	30.00
153	12.50	153	0.00	153	25.00	147	0.00	147	0.00	93	14.29	147	20.00
154	12.50	154	2.86	154	0.00	148	0.00	148	0.00	94	0.00	148	0.00
155	35.00	155	20.00	155	0.00	149	0.00	149	0.00	95	0.00	149	20.00
156	5.00	156	2.86	156	25.00	150	6.67	150	0.00	96	100.00	150	20.00
157	10.00	157	2.86	157	0.00	151	0.00	151	0.00	97	0.00	151	0.00
158	15.00	158	5.71	158	25.00	152	33.33	152	0.00	98	0.00	152	30.00
159	10.00	159	2.86	159	37.50	153	20.00	153	0.00	99	85.71	153	20.00
160	2.50	160	0.00	160	0.00	154	0.00	154	0.00	100	14.29	154	0.00
161	7.50	161	2.86	161	0.00	155	13.33	155	0.00	101	14.29	155	60.00
162	0.00	162	5.71	162	50.00	156	20.00	156	0.00	102	0.00	156	70.00
						157	6.67	157	0.00			157	0.00
						158	33.33	158	16.67			158	0.00
						159	26.67	159	0.00			159	30.00

Figure 4B Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
						160	0.00	160	0.00			160	30.00
						161	13.33	161	0.00			161	50.00
						162	20.00	162	0.00			162	10.00
163	2.50	163	0.00	163	0.00	163	20.00	163	0.00	103	14.29	163	0.00
164	20.00	164	14.29	164	0.00	164	0.00	164	0.00	104	0.00	164	0.00
165	45.00	165	22.86	165	75.00	165	0.00	165	0.00	105	0.00	165	10.00
166	0.00	166	0.00	166	0.00	166	0.00	166	0.00	106	0.00	166	10.00
167	0.00	167	0.00	167	0.00	167	0.00	167	0.00	107	0.00	167	50.00
168	52.50	168	28.57	168	62.50	168	13.33	168	0.00	108	100.00	168	0.00
169	5.00	169	2.86	169	0.00	169	0.00	169	0.00	109	0.00	169	0.00
170	0.00	170	0.00	170	0.00	170	0.00	170	16.67	110	0.00	170	0.00
171	17.50	171	22.86	171	100.00	171	13.33	171	16.67	111	100.00	171	0.00
172	2.50	172	2.86	172	0.00	172	0.00	172	0.00	112	0.00	172	0.00
173	0.00	173	0.00	173	0.00	173	0.00	173	0.00	113	0.00	173	0.00
174	90.00	174	54.29	174	100.00	174	86.67	174	0.00	114	100.00	174	0.00
175	0.00	175	0.00	175	0.00	175	0.00	175	0.00	115	0.00	175	10.00
176	0.00	176	0.00	176	0.00	176	0.00	176	0.00	116	0.00	176	0.00
177	67.50	177	48.57	177	12.50	177	73.33	177	0.00	117	0.00	177	0.00
178	0.00	178	0.00	178	12.50	178	0.00	178	0.00	118	0.00	178	0.00
179	0.00	179	0.00	179	0.00	179	0.00	179	0.00	119	0.00	179	0.00
180	17.50	180	17.14	180	50.00	180	73.33	180	0.00	120	0.00	180	0.00
181	2.50	181	0.00	181	62.50	181	60.00	181	16.67	121	0.00	181	70.00
182	0.00	182	0.00	182	12.50	182	0.00	182	0.00	122	14.29	182	0.00
183	67.50	183	45.71	183	12.50	183	0.00	183	0.00	123	0.00	183	0.00
184	57.50	184	42.86	184	37.50	184	0.00	184	0.00	124	0.00	184	0.00
185	0.00	185	0.00	185	12.50	185	6.67	185	0.00	125	0.00	185	0.00
186	12.50	186	5.71	186	0.00	186	6.67	186	16.67	126	0.00	186	0.00
187	2.50	187	5.71	187	0.00	187	40.00			127	0.00	187	0.00
188	2.50	188	0.00	188	0.00	188	0.00			128	14.29	188	0.00
189	0.00	189	0.00	189	37.50	189	6.67			129	0.00	189	10.00
190	0.00	190	0.00	190	37.50	190	6.67			130	0.00	190	0.00
191	57.50	191	37.14	191	37.50	191	6.67			131	0.00	191	0.00
192	0.00	192	0.00	192	0.00	192	0.00			132	0.00	192	0.00
193	0.00	193	2.86	193	50.00	193	6.67			133	57.14	193	0.00
194	5.00	194	2.86	194	0.00	194	6.67			134	0.00	194	0.00
195	2.50	195	0.00	195	12.50	195	0.00			135	0.00	195	40.00
196	12.50	196	2.86	196	12.50	196	46.67	187	16.67	136	0.00	196	0.00
197	12.50	197	2.86	197	0.00	197	6.67	188	0.00	137	0.00	197	0.00
198	0.00	198	2.86	198	25.00	198	0.00	189	0.00	138	0.00	198	40.00
199	57.50	199	40.00	199	25.00	199	0.00	190	16.67	139	0.00	199	0.00
200	0.00	200	0.00	200	0.00	200	0.00	191	16.67	140	0.00	200	0.00
201	5.00	201	0.00	201	37.50	201	0.00	192	0.00	141	14.29	201	10.00
202	5.00	202	0.00	202	87.50	202	13.33	193	0.00	142	0.00	202	40.00
203	5.00	203	2.86	203	50.00	203	0.00	194	0.00	143	0.00	203	30.00
204	57.50	204	42.86	204	0.00	204	0.00	195	0.00	144	85.71	204	10.00
205	0.00	205	0.00	205	12.50	205	0.00	196	0.00	145	0.00	205	0.00
206	0.00	206	0.00	206	0.00	206	0.00	197	0.00	146	0.00	206	20.00
207	2.50	207	0.00	207	12.50	207	0.00	198	0.00	147	28.57	207	0.00
208	5.00	208	0.00	208	25.00	208	0.00	199	0.00	148	42.86	208	70.00
209	2.50	209	2.86	209	25.00	209	0.00	200	0.00	149	0.00	209	0.00
210	0.00	210	0.00	210	25.00	210	0.00	201	0.00	150	0.00	210	10.00
211	35.00	211	11.43	211	0.00	211	26.67	202	0.00	151	0.00	211	20.00
212	0.00	212	0.00	212	25.00	212	6.67	203	0.00	152	0.00	212	50.00
213	20.00	213	17.14	213	50.00	213	0.00	204	0.00	153	0.00	213	60.00
214	5.00	214	2.86					205	0.00				
215	2.50	215	0.00					206	0.00				

Figure 4B Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
216	5.00	216	8.57					207	0.00				
217	0.00	217	0.00					208	0.00				
218	2.50	218	5.71					209	0.00				
219	10.00	219	5.71					210	0.00				
220	0.00	220	0.00					211	0.00	154	0.00	214	0.00
221	15.00	221	11.43					212	0.00	155	57.14	215	30.00
222	32.50	222	14.29					213	0.00	156	0.00	216	60.00
223	0.00	223	0.00	214	0.00	214	0.00	214	0.00	157	0.00	217	0.00
224	22.50	224	20.00	215	0.00	215	0.00	215	0.00	158	0.00	218	0.00
225	2.50	225	2.86	216	0.00	216	0.00	216	16.67	159	28.57	219	0.00
226	2.50	226	2.86	217	37.50	217	0.00	217	16.67	160	0.00	220	10.00
227	22.50	227	11.43	218	25.00	218	6.67	218	0.00	161	14.29	221	90.00
228	30.00	228	11.43	219	25.00	219	0.00	219	0.00	162	0.00	222	0.00
229	0.00	229	0.00	220	25.00	220	0.00	220	0.00	163	14.29	223	0.00
230	32.50	230	20.00	221	37.50	221	26.67	221	0.00	164	14.29	224	20.00
231	27.50	231	17.14	222	0.00	222	13.33	222	0.00	165	0.00	225	30.00
232	5.00	232	5.71	223	12.50	223	26.67	223	0.00	166	0.00	226	0.00
233	25.00	233	28.57	224	25.00	224	53.33	224	0.00	167	0.00	227	0.00
234	0.00	234	0.00	225	0.00	225	13.33	225	0.00	168	0.00	228	20.00
235	32.50	235	17.14	226	0.00	226	0.00	226	0.00	169	0.00	229	0.00
236	35.00	236	17.14	227	0.00	227	0.00	227	0.00	170	0.00	230	50.00
237	0.00	237	0.00	228	0.00	228	6.67	228	16.67	171	71.43	231	90.00
238	7.50	238	2.86	229	0.00	229	13.33	229	0.00	172	71.43	232	0.00
239	2.50	239	2.86	230	25.00	230	13.33	230	0.00	173	0.00	233	0.00
240	0.00	240	0.00	231	0.00	231	26.67	231	0.00	174	0.00	234	10.00
241	0.00	241	0.00	232	25.00	232	0.00	232	50.00	175	0.00	235	0.00
242	5.00	242	5.71	233	25.00	233	13.33	233	0.00	176	0.00	236	10.00
243	12.50	243	5.71	234	12.50	234	13.33	234	0.00	177	0.00	237	40.00
244	5.00	244	0.00	235	25.00	235	6.67	235	0.00	178	0.00	238	0.00
245	7.50	245	0.00	236	12.50	236	6.67	236	0.00	179	0.00	239	0.00
246	5.00	246	0.00	237	12.50	237	0.00	237	0.00	180	0.00	240	0.00
247	57.50	247	45.71	238	12.50	238	0.00	238	0.00	181	0.00	241	20.00
248	25.00	248	25.71	239	12.50	239	0.00	239	0.00	182	0.00	242	20.00
249	0.00	249	0.00	240	0.00	240	13.33	240	0.00	183	0.00	243	0.00
250	0.00	250	0.00	241	0.00	241	13.33	241	0.00	184	14.29	244	40.00
251	2.50	251	5.71	242	50.00	242	0.00	242	0.00	185	0.00	245	0.00
252	5.00	252	2.86	243	0.00	243	0.00	243	0.00	186	0.00	246	0.00
253	2.50	253	2.86	244	0.00	244	0.00	244	0.00	187	71.43	247	0.00
254	2.50	254	2.86	245	0.00	245	0.00	245	0.00	188	57.14	248	0.00
255	0.00	255	0.00	246	0.00	246	0.00	246	0.00	189	0.00	249	0.00
256	42.50	256	25.71	247	0.00	247	0.00	247	0.00	190	14.29	250	0.00
257	57.50	257	40.00	248	25.00	248	0.00	248	0.00	191	85.71	251	0.00
258	0.00	258	5.71	249	62.50	249	0.00	249	0.00	192	0.00	252	0.00
259	0.00	259	5.71	250	0.00	250	6.67	250	66.67	193	0.00	253	0.00
260	0.00	260	0.00	251	0.00	251	0.00	251	66.67	194	0.00	254	0.00
261	0.00	261	0.00	252	0.00	252	0.00	252	0.00	195	0.00	255	0.00
262	0.00	262	0.00	253	0.00	253	6.67	253	0.00	196	0.00	256	0.00
263	2.50	263	2.86	254	0.00	254	0.00	254	0.00	197	28.57	257	0.00
264	7.50	264	2.86	255	0.00	255	0.00	255	0.00	198	0.00	258	0.00
265	0.00	265	0.00	256	0.00	256	6.67	256	0.00	199	0.00	259	0.00
266	0.00	266	0.00	257	0.00	257	13.33	257	0.00	200	0.00	260	10.00
267	62.50	267	22.86	258	12.50	258	13.33	258	0.00	201	0.00	261	0.00
268	0.00	268	0.00	259	12.50	259	6.67	259	0.00	202	0.00	262	0.00
269	0.00	269	0.00	260	0.00	260	26.67	260	0.00	203	0.00	263	0.00
270	2.50	270	0.00	261	37.50	261	13.33	261	0.00	204	0.00	264	0.00
271	0.00	271	0.00	262	0.00	262	20.00	262	0.00	205	42.86	265	0.00

Figure 4B Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
272	0.00	272	0.00	263	0.00	263	6.67	263	0.00	206	42.86	266	70.00
273	0.00	273	0.00	264	12.50	264	60.00	264	0.00	207	0.00	267	0.00
274	20.00	274	14.29	265	0.00	265	0.00	265	0.00	208	85.71	268	10.00
275	62.50	275	34.29	266	0.00	266	0.00	266	0.00	209	100.00	269	10.00
276	25.00	276	17.14	267	0.00	267	0.00	267	0.00	210	0.00	270	0.00
277	5.00	277	2.86	268	25.00	268	13.33	268	0.00	211	28.57	271	0.00
278	10.00	278	2.86	269	12.50	269	6.67	269	0.00	212	28.57	272	10.00
279	2.50	279	0.00	270	0.00	270	0.00	270	0.00	213	0.00	273	0.00
280	25.00	280	22.86	271	0.00	271	33.33	271	0.00	214	0.00	274	0.00
281	0.00	281	0.00	272	0.00	272	33.33	272	0.00	215	0.00	275	0.00
282	20.00	282	17.14	273	12.50	273	0.00	273	0.00	216	0.00	276	0.00
283	22.50	283	14.29	274	0.00	274	0.00	274	0.00	217	0.00	277	0.00
284	2.50	284	0.00	275	0.00	275	0.00	275	0.00	218	0.00	278	10.00
285	40.00	285	25.71	276	12.50	276	0.00	276	0.00	219	0.00	279	10.00
286	42.50	286	22.86	277	0.00	277	0.00	277	0.00	220	0.00	280	0.00
287	0.00	287	2.86	278	0.00	278	0.00	278	0.00	221	0.00	281	0.00
288	0.00	288	0.00	279	0.00	279	0.00	279	0.00	222	0.00	282	20.00
289	0.00	289	0.00	280	0.00	280	0.00	280	0.00	223	14.29	283	0.00
290	0.00	290	2.86	281	0.00	281	0.00	281	0.00	224	14.29	284	0.00
291	0.00	291	0.00	282	12.50	282	0.00	282	0.00	225	0.00	285	10.00
292	0.00	292	0.00	283	0.00	283	0.00	283	0.00	226	28.57	286	20.00
293	0.00	293	2.86	284	0.00	284	0.00	284	0.00	227	14.29	287	0.00
294	7.50	294	0.00	285	25.00	285	0.00	285	0.00	228	0.00	288	70.00
295	2.50	295	0.00	286	0.00	286	0.00	286	0.00	229	0.00	289	0.00
296	0.00	296	0.00	287	0.00	287	13.33	287	0.00	230	0.00	290	0.00
297	10.00	297	5.71	288	0.00	288	33.33	288	0.00	231	0.00	291	30.00
298	12.50	298	11.43	289	0.00	289	0.00	289	66.67	232	0.00	292	0.00
299	5.00	299	2.86	290	25.00	290	6.67	290	0.00	233	0.00	293	0.00
300	7.50	300	5.71	291	12.50	291	6.67	291	0.00	234	0.00	294	0.00
301	5.00	301	2.86	292	0.00	292	6.67	292	0.00	235	0.00	295	0.00
302	2.50	302	0.00	293	0.00	293	6.67	293	0.00	236	0.00	296	0.00
303	12.50	303	8.57	294	25.00	294	13.33	294	0.00	237	0.00	297	30.00
304	0.00	304	2.86	295	0.00	295	6.67	295	0.00	238	0.00	298	30.00
305	20.00	305	22.86	296	37.50	296	40.00	296	0.00	239	0.00	299	0.00
306	35.00	306	17.14	297	37.50	297	40.00	297	0.00	240	71.43	300	0.00
307	2.50	307	0.00	298	0.00	298	6.67	298	0.00	241	0.00	301	0.00
308	0.00	308	0.00	299	25.00	299	13.33	299	0.00	242	0.00	302	0.00
309	0.00	309	0.00	300	50.00	300	26.67	300	0.00	243	0.00	303	0.00
310	0.00	310	0.00	301	12.50	301	0.00	301	0.00	244	0.00	304	0.00
311	2.50	311	0.00	302	0.00	302	0.00	302	50.00	245	0.00	305	0.00
312	0.00	312	0.00	303	0.00	303	0.00	303	0.00	246	0.00	306	0.00
313	0.00	313	0.00	304	0.00	304	13.33	304	0.00	247	0.00	307	0.00
314	0.00	314	0.00	305	0.00	305	0.00	305	0.00	248	0.00	308	0.00
315	10.00	315	0.00	306	0.00	306	0.00	306	0.00	249	0.00	309	10.00
316	7.50	316	2.86	307	37.50	307	0.00	307	0.00	250	0.00	310	0.00
317	5.00	317	5.71	308	0.00	308	0.00	308	0.00	251	0.00	311	0.00
318	0.00	318	0.00	309	0.00	309	6.67	309	0.00	252	0.00	312	0.00
319	2.50	319	2.86	310	25.00	310	0.00	310	0.00	253	14.29	313	0.00
320	2.50	320	2.86	311	0.00	311	0.00	311	0.00	254	14.29	314	0.00
321	57.50	321	40.00	312	0.00	312	0.00	312	66.67	255	0.00	315	60.00
322	47.50	322	22.86	313	0.00	313	0.00	313	0.00	256	28.57	316	0.00
323	17.50	323	0.00	314	25.00	314	0.00	314	66.67	257	42.86	317	0.00
324	42.50	324	28.57	315	25.00	315	26.67	315	0.00	258	0.00	318	0.00
325	57.50	325	48.57	316	0.00	316	13.33	316	0.00	259	42.86	319	0.00
326	2.50	326	0.00	317	25.00	317	0.00	317	0.00	260	0.00	320	0.00
327	12.50	327	22.86	318	25.00	318	0.00	318	0.00	261	0.00	321	0.00

Figure 4B Source Data. Proportion of mutations at each location along sequence length

TRADV-TRAC Position	TRADV-TRAC Proportion	TRADV-TRDC Position	TRADV-TRDC Proportion	TRBV Position	TRBV Proportion	TRGV Position	TRGV Proportion	NTRV Position	NTRV Proportion	STRDV Position	STRDV Proportion	IgHV Position	IgHV Proportion
328	57.50	328	37.14	319	25.00	319	0.00	319	66.67	262	100.00	322	0.00
329	0.00	329	0.00	320	0.00	320	0.00	320	16.67	263	0.00	323	0.00
330	0.00	330	0.00	321	12.50	321	0.00	321	0.00	264	0.00	324	0.00
331	0.00	331	0.00	322	37.50	322	0.00	322	0.00	265	0.00	325	0.00
332	0.00	332	0.00	323	0.00	323	0.00	323	0.00	266	0.00	326	0.00
333	0.00	333	0.00	324	0.00	324	0.00	324	0.00	267	0.00	327	0.00
334	0.00	334	0.00	325	0.00	325	6.67	325	0.00	268	0.00	328	0.00
335	0.00	335	0.00	326	0.00	326	6.67	326	0.00	269	0.00	329	10.00
336	0.00	336	0.00	327	0.00	327	0.00	327	0.00	270	0.00	330	0.00
337	0.00	337	0.00	328	0.00	328	0.00	328	0.00	271	0.00	331	0.00
338	0.00	338	0.00	329	0.00	329	0.00	329	0.00	272	0.00	332	0.00
339	0.00	339	0.00	330	0.00	330	0.00	330	0.00	273	0.00	333	10.00
340	22.50	340	25.71	331	0.00	331	0.00	331	0.00	274	71.43	334	0.00
341	37.50	341	31.43	332	25.00	332	0.00	332	0.00	275	57.14	335	0.00
342	0.00	342	0.00	333	0.00	333	0.00	333	16.67	276	0.00	336	0.00
343	2.50	343	0.00	334	62.50	334	0.00	334	0.00	277	57.14	337	0.00
344	0.00	344	0.00	335	37.50	335	33.33	335	0.00	278	0.00	338	0.00
345	35.00	345	28.57	336	0.00	336	0.00	336	0.00	279	42.86	339	30.00
346	0.00	346	0.00	337	12.50	337	0.00	337	0.00	280	0.00	340	0.00
347	0.00	347	0.00	338	0.00	338	0.00	338	0.00	281	0.00	341	0.00
348	2.50	348	5.71	339	0.00	339	13.33	339	0.00	282	0.00	342	0.00
349	0.00	349	0.00	340	0.00	340	0.00	340	0.00	283	0.00	343	10.00
350	2.50	350	0.00	341	0.00	341	0.00	341	0.00	284	0.00	344	10.00
351	77.50	351	48.57	342	25.00	342	0.00	342	0.00	285	100.00	345	70.00
352	0.00	352	0.00	343	0.00	343	6.67	343	16.67	286	0.00	346	0.00
353	0.00	353	0.00	344	0.00	344	6.67	344	0.00	287	0.00	347	10.00
354	0.00	354	0.00	345	25.00	345	73.33	345	0.00	288	0.00	348	0.00
				346	0.00	346	0.00	346	0.00				
				347	0.00	347	0.00	347	16.67				
				348	0.00	348	0.00	348	0.00				
355	65.00	355	40.00	349	0.00	349	13.33	349	100.00	289	71.43	349	60.00
356	65.00	356	45.71	350	0.00	350	26.67	350	0.00	290	71.43	350	70.00
357	2.50	357	0.00	351	0.00	351	0.00	351	0.00	291	0.00	351	0.00
358	5.00	358	2.86	352	0.00	352	0.00	352	0.00	292	0.00	352	0.00
359	2.50	359	2.86	353	0.00	353	0.00	353	0.00	293	0.00	353	20.00
360	0.00	360	0.00	354	0.00	354	0.00	354	0.00	294	0.00	354	0.00

Figure 4A Source Data. Proportion of mutations at each location along sequence length

A

V	n	FR1																																																																													
																																																																			C										
TRADV-TRAC	422	0.00	0.95	1.18	3.08	0.47	0.00	0.00	0.24	1.18	0.47	0.47	0.00	0.00	0.00	0.00	0.47	0.95	1.90	0.24	0.24	0.95	0.95	0.95	0.47	0.47	0.71	0.71	0.47	1.18	0.95	1.90	1.18	1.42	0.47	0.47	0.24	0.00	0.95	0.71	0.24	0.24	0.71	0.00	0.24	0.24	0.24	0.24	0.00	0.24	0.24	0.47	0.24	0.47	0.47	0.00	0.95	1.90	0.47	0.00	0.47	0.24	0.47	1.18	0.00	0.47	0.24	0.71	0.00	0.95	0.24	0.47	0.47	0.71	0.24	0.71	1.42	1.90	1.42
TRADV-TRDC	140	0.00	0.00	0.00	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.71	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.71	1.43	0.71	1.43	0.00	0.71	0.00	0.00	0.71	0.00	0.00	0.00	0.71	0.00	0.71	0.00	0.00	0.71	0.00	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.00	0.71	1.43	0.00	0.00	0.71	0.71	0.00	0.00	0.00	0.71	0.71	0.00	0.00	1.43	0.71	1.43	0.71
TRBV	229				0.87	0.44	0.44	0.00	0.00	0.00	0.00	0.00	0.44	0.44	0.44	0.44	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.44	1.75	0.44	0.44	0.87	0.87	0.44	0.00	0.87	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.00	0.44	0.00	0.00	0.00	0.87	0.44
TRGV	158				0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.63	0.00	0.00	0.63	0.00	0.63	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.00	0.63	0.00	0.63	0.63	1.27	0.63	0.63	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IgHV	272	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.37	0.00	0.00	0.00	0.74	0.00	0.00	0.00	0.00	0.37	0.00	0.00	0.00	0.00	0.37	0.00	0.00	0.37	0.00	0.37	0.37	0.00	0.00	0.00	0.37	0.00	0.37	0.00	0.00	0.00	0.00	0.00	0.37	0.00	0.37	0.37	0.37	0.00	0.37	0.00	0.74	0.00	0.37	0.00	0.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10	0.00	0.00	0.00	0.00	0.37	0.74	0.37	0.00	0.00	0.00	0.37	0.00	0.74	0.00
NTRV	51										0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	3.92	1.96	0.00	0.00	0.00	0.00	0.00	0.00
STRDV	62							0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00

V	n	CDR1																															FR2																																																								
																																								W																																														
TRADV-TRAC	422							0.95	1.66	0.95	0.47	0.71	1.42	0.95	2.61	0.47	0.95	1.90	1.42	0.95	0.71	0.95	0.47	1.18	0.95										1.18	2.13	1.18	0.24	0.00	0.24	0.24	0.00	0.47	0.00	0.00	0.00	0.00	0.00	0.71	0.24	0.24	0.00	0.00	0.71	0.95	1.90	1.42	0.47	0.47	0.47	0.24	0.00	0.47	1.18	0.71	0.24	0.47	1.66	0.71	0.00	0.95	0.71	0.47	0.24	0.95	3.32	0.00	0.00	0.00	0.95	0.24	1.90	3.32	0.00	0.71	0.47	1.18	0.47
TRADV-TRDC	140							0.00	0.71	1.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.00	0.71	0.00	1.43	0.00										0.00	0.71	0.71	1.43	0.00	0.00	0.00	0.71	0.71	0.00	0.00	0.00	0.00	0.71	0.71	0.00	0.71	0.71	0.00	0.00	0.71	0.00	0.00	0.71	0.00	0.71	0.71	0.00	0.00	0.00	0.71	0.71	0.00	0.00	0.00	0.00	0.00	0.71	1.43	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00
TRBV	229							0.00	0.00	0.00	0.00	0.87	0.00	0.00	0.00	0.00	0.87	0.00	0.00	0.00	0.44	0.00	0.00	0.00	0.00										0.00	0.00	0.00	0.00	0.44	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.44	0.44	1.31	0.44	0.44	0.44	0.00	0.00	0.87	0.87	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.44	0.44	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.00			
TRGV	158			0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.63	0.00	0.63	0.00	0.00	0.00	0.00	0.00	1.27	0.63	0.00	0.63	0.00	0.00	0.00	0.00	0.00	0.63	0.00					0.00	0.00	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.63	0.63	0.63	0.63	0.63	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00			
IgHV	272					0.00	0.00	0.37	0.00	0.00	0.00	1.10	0.00	0.37	0.00	0.00	0.00	0.37	0.74	0.37	0.37	1.84	0.37	0.37	0.00	0.37	0.74	0.00	0.37						0.37	0.00	0.74	0.74	1.10	0.00	0.00	0.00	0.37	0.00	0.37	0.00	0.00	0.00	0.74	0.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.37	0.37	0.74	0.37	0.37	0.00	0.00	0.00	0.37	1.10	0.37	0.00	0.74	0.37	0.00	0.00	0.37	0.00	0.00	0.00	0.00	0.37	0.00	0.74	0.37	0.37	0.74	0.00			
NTRV	51	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	1.96	1.96	0.00	0.00	0.00	0.00	1.96	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00																													0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00			
STRDV	62							0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61										0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	1.61	1.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00			

V	n	CDR2																																								FR3																																																
TRADV-TRAC	422													0.00	0.71	0.00	0.95	1.90	1.90	0.00	0.24	1.18	0.00	1.18	0.71	2.13	0.95	0.71	0.47	0.00	0.24	1.18	0.95	0.47													0.71	1.18	0.47	1.42	0.47	1.18	0.47	1.90	1.90	0.00	0.47	0.00	0.24	0.24	4.03	0.24	0.71	0.47	0.24	0.47	0.24	0.24	1.42	0.24	0.24	0.24	0.71	0.47	0.24	1.42	0.47	0.24	0.47	0.00	0.00	0.00	0.24	0.24	0.00	0.47	0.00	0.71
TRADV-TRDC	140													0.00	0.71	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.00	0.71	0.00													0.00	0.00	0.71	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.00	0.00	0.71	0.00	2.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.71	0.00	0.71	0.00	0.00	0.00	0.00
TRBV	229																0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.44	0.44	0.44	0.00	0.00	0.00	0.44	0.00													0.44	0.00	0.00	0.44	0.44	0.44	0.00	0.44	0.00	1.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
TRGV	158																0.00	0.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.27	0.63	0.00	0.00	0.63													0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.63	0.00	0.63	1.27	0.63	0.00	0.00	0.63	0.63	0.00	0.00	0.00	0.00	0.00	0.63	0.00	0.00	1.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.63	1.27	1.27	0.63	0.63
IgHV	272															0.37	0.00	0.74	0.37	0.37	0.00	0.00	1.84	2.21	0.74	0.37	0.37	0.74	0.37	0.37	0.37	1.47	0.74														0.37	0.74	0.37	0.00	1.47	0.37	0.37	0.00	0.37	0.37	0.37	0.00	0.00	0.00	0.74	0.00	0.00	0.37	0.74	0.00	1.10	0.00	0.37	0.37	0.37	0.74	0.00	0.00	0.00	0.00	0.00	0.37	0.00	0.00	0.00	0.00	0.00	0.37	0.00	0.74	0.00	0.00
NTRV	51	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	1.96	0.00	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	3.92	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00
STRDV	62															0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00														0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

V	n	FR3																																																																								
																												L																										D												Y						C	
TRADV-TRAC	422	0.95	0.00	0.47	0.71	0.00	0.00	0.00	0.24	0.24	0.00	0.00	0.00	0.47	0.24	0.00	0.00	0.00	0.24	0.24	0.95	0.95	0.24	0.00	1.18	0.24	0.24	0.71	0.95	0.00	0.95	0.71	0.00	0.71	0.24	0.00	1.90	1.66	1.18	0.47	0.47	0.95	0.71	0.71	0.00	0.00	0.24	0.00	0.00	0.47	0.47	0.24	0.47	0.47	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.47	0.95	0.24	1.42	0.00	1.18	0.00	0.00	0.00	0.47	0.47	0.47	0.24	0.24	1.42
TRADV-TRDC	140	0.00	0.00	0.71	0.00	0.00	0.00	0.00	0.00	0.00	1.43	0.71	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.71	0.71	0.71	0.71	0.00	0.00	0.00	0.71	2.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.71	0.00	0.00	0.00	0.00	0.71	0.00	0.71	0.00	0.00	2.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
TRBV	229	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.87	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.44	0.00	0.00	0.44	0.44	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.44	0.00	0.00	0.00	0.00	1.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.87	1.31
TRGV	158	0.00	0.00	0.00	0.00	0.63	0.63	0.00	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.63	0.00	0.63	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.63	1.27	0.00	0.00	0.00	1.27	0.63	0.63	0.00	0.00	0.00	0.00	0.00	0.63	0.63	0.00	0.00	1.90	0.00	0.63	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.63	1.90	0.00	0.00	0.00	0.00	0.00	1.27	0.00	0.00	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.00
IgHV	272	0.37	0.37	0.37	0.00	0.00	0.37	0.00	0.00	0.37	0.00	0.00	0.74	0.37	0.00	0.37	0.37	0.37	0.00	0.37	0.00	0.74	0.37	0.74	0.00	0.37	0.74	0.00	0.00	0.00	0.00	0.37	0.00	0.00	0.00	0.37	0.74	0.37	0.00	0.00	0.37	0.00	1.10	0.00	0.00	0.74	0.37	0.00	0.00	0.37	0.37	0.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.37	0.00	0.37	0.00	0.37	0.74	0.37	0.00	0.00	0.00	0.37	0.74	0.00	0.00	0.00	0.00
NTRV	51	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	1.96	0.00	1.96	0.00	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	0.00	0.00	3.92	0.00	0.00	1.96	1.96	1.96	0.00	1.96	1.96	1.96	1.96
STRDV	62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	1.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Figure 4B Source Data. Proportion of motifs at each location along sequence length

B

V	n	FR1																																																																										
																																																																		C										
TRADV-TRAC	40	32.5	0.0	0.0	0.0	0.0	0.0	45.0	0.0	0.0	0.0	27.5	0.0	0.0	0.0	7.5	7.5	10.0	10.0	5.0	0.0	0.0	15.0	5.0	2.5	7.5	7.5	20.0	25.0	2.5	0.0	35.0	7.5	5.0	22.5	2.5	2.5	2.5	7.5	0.0	2.5	0.0	0.0	0.0	0.0	0.0	2.5	5.0	0.0	0.0	7.5	0.0	20.0	0.0	0.0	0.0	5.0	37.5	15.0	0.0	2.5	2.5	57.5	42.5	0.0	90.0	45.0	0.0	40.0	2.5	0.0	0.0	65.0	0.0	2.5	0.0	7.5	32.5	0.0
TRADV-TRDC	35	20.0	0.0	0.0	0.0	2.9	0.0	22.9	0.0	0.0	0.0	20.0	0.0	0.0	0.0	2.9	2.9	0.0	0.0	2.9	0.0	0.0	5.7	0.0	0.0	0.0	0.0	8.6	20.0	0.0	0.0	20.0	5.7	2.9	2.9	0.0	0.0	2.9	5.7	0.0	5.7	2.9	2.9	0.0	0.0	0.0	2.9	2.9	0.0	2.9	8.6	0.0	5.7	0.0	0.0	5.7	2.9	17.1	14.3	0.0	0.0	0.0	37.1	25.7	0.0	54.3	37.1	0.0	22.9	2.9	0.0	0.0	25.7	0.0	2.9	0.0	2.9	28.6	0.0
TRBV	8				0.00	12.50	0.00	0.00	0.00	0.00	12.50	0.00	0.00	0.00	0.00	37.50	50.00	0.00	0.00	12.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	37.50	0.00	0.00	0.00	12.50	0.00	0.00	0.00	0.00	0.00	25.00	0.00	0.00	25.00	25.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	25.00	0.00	0.00	0.00	25.00	12.50	0.00	0.00	37.50	12.50	0.00	0.00	37.50	37.50	0.00	0.00	0.00	100.00	75.00	0.00	0.00	62.50	12.50	0.00	0.00	0.00	0.00	0.00
TRGV	15				0.00	0.00	0.00	0.00	0.00	0.00	6.67	33.33	0.00	0.00	0.00	0.00	6.67	6.67	0.00	33.33	0.00	6.67	6.67	0.00	0.00	0.00	6.67	0.00	0.00	6.67	0.00	6.67	13.33	6.67	0.00	0.00	0.00	40.00	53.33	0.00	0.00	26.67	13.33	13.33	13.33	13.33	26.67	0.00	13.33	6.67	60.00	0.00	0.00	0.00	0.00	6.67	33.33	6.67	0.00	26.67	0.00	0.00	0.00	20.00	6.67	13.33	6.67	0.00	0.00	6.67	6.67	40.00	13.33	0.00	13.33	13.33	0.00	0.00	0.00
IgHV	10	0.00	0.00	0.00	0.00	0.00	10.00	70.00	0.00	0.00	0.00	70.00	10.00	0.00	0.00	0.00	30.00	0.00	0.00	0.00	0.00	0.00	80.00	0.00	0.00	30.00	0.00	0.00	70.00	10.00	0.00	0.00	0.00	0.00	0.00	0.00	30.00	30.00	0.00	20.00	0.00	0.00	0.00	20.00	10.00	0.00	0.00	0.00	0.00	0.00	60.00	10.00	0.00	10.00	10.00	0.00	0.00	0.00	0.00	0.00	0.00	10.00	30.00	0.00	10.00	30.00	0.00	0.00	70.00	0.00	0.00	0.00	0.00	0.00	70.00	40.00	0.00	0.00	0.00
NTRV	6										0.00	0.00	0.00	16.67	0.00	0.00	16.67	0.00	0.00	0.00	0.00	66.67	0.00	0.00	0.00	50.00	33.33	0.00	0.00	33.33	0.00	16.67	0.00	0.00	0.00	16.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	66.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	50.00	50.00	0.00	0.00	0.00	0.00	16.67	0.00	0.00	0.00	0.00	83.33	0.00	0.00	0.00	0.00	0.00	0.00	50.00	0.00
STRDV	7							0.00	0.00	0.00	14.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	28.57	0.00	0.00	0.00	0.00	0.00	0.00	42.86	28.57	0.00	42.86	0.00	0.00	100.00	0.00	0.00	0.00	85.71	0.00	0.00	0.00	0.00	57.14	14.29	0.00	71.43	85.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	42.86	0.00	0.00	14.29	57.14	0.00	0.00	0.00	0.00	0.00	71.43	85.71	0.00	14.29	0.00	0.00	14.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00

V	n	CDR1																															FR2																																																								
																																								W																																														
TRADV-TRAC	40										2.5	27.5	0.0	45.0	10.0	2.5	10.0	15.0	12.5	12.5	35.0	5.0	10.0	15.0	10.0	2.5	7.5	0.0							2.5	20.0	45.0	0.0	0.0	52.5	5.0	0.0	17.5	2.5	0.0	90.0	0.0	0.0	67.5	0.0	0.0	17.5	2.5	0.0	67.5	57.5	0.0	12.5	2.5	2.5	0.0	0.0	57.5	0.0	0.0	5.0	2.5	12.5	12.5	0.0	57.5	0.0	5.0	5.0	5.0	57.5	0.0	0.0	2.5	5.0	2.5	0.0	35.0	0.0	20.0	5.0	2.5	5.0
TRADV-TRDC	35										0.0	22.9	0.0	28.6	2.9	0.0	0.0	0.0	0.0	2.9	20.0	2.9	2.9	5.7	2.9	0.0	2.9	5.7							0.0	14.3	22.9	0.0	0.0	28.6	2.9	0.0	22.9	2.9	0.0	54.3	0.0	0.0	48.6	0.0	0.0	17.1	0.0	0.0	45.7	42.9	0.0	5.7	5.7	0.0	0.0	0.0	37.1	0.0	2.9	2.9	0.0	2.9	2.9	2.9	40.0	0.0	0.0	0.0	2.9	42.9	0.0	0.0	0.0	0.0	2.9	0.0	11.4	0.0	17.1	2.9	0.0	8.6
TRBV	8										0.00	0.00	0.00	0.00	50.00	0.00	25.00	50.00	25.00	0.00	0.00	25.00	0.00	25.00	37.50	0.00	0.00	50.00							0.00	0.00	75.00	0.00	0.00	62.50	0.00	0.00	100.00	0.00	0.00	100.00	0.00	0.00	12.50	12.50	0.00	50.00	62.50	12.50	12.50	37.50	12.50	0.00	0.00	0.00	37.50	37.50	37.50	0.00	50.00	0.00	12.50	12.50	0.00	25.00	25.00	0.00	37.50	87.50	50.00	0.00	12.50	0.00	12.50	25.00	25.00	25.00	0.00	25.00	50.00			
TRGV	15				0.00	6.67	6.67	0.00	0.00	0.00	33.33	6.67	0.00	0.00	33.33	0.00	0.00	0.00	6.67	0.00	33.33	20.00	0.00	13.33	20.00	6.67	33.33	26.67	0.00	13.33	20.00				20.00	0.00	0.00	0.00	0.00	13.33	0.00	0.00	13.33	0.00	0.00	86.67	0.00	0.00	73.33	0.00	0.00	73.33	60.00	0.00	0.00	0.00	6.67	6.67	40.00	0.00	6.67	6.67	6.67	0.00	6.67	6.67	0.00	46.67	6.67	0.00	0.00	0.00	0.00	13.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	26.67	6.67	0.00			
IgHV	10						0.00	0.00	100.00	0.00	0.00	0.00	0.00	30.00	20.00	0.00	20.00	20.00	0.00	30.00	20.00	0.00	60.00	70.00	0.00	0.00	30.00	30.00	50.00	10.00					0.00	0.00	10.00	10.00	50.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10.00	0.00	0.00	0.00	0.00	0.00	70.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10.00	0.00	0.00	0.00	0.00	0.00	40.00	0.00	0.00	40.00	0.00	0.00	10.00	40.00	30.00	10.00	0.00	20.00	0.00	70.00	0.00	10.00	20.00	50.00	60.00			
NTRV	6	0.00	0.00	0.00	0.00	16.67	16.67	0.00	0.00	0.00	0.00	16.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16.67	0.00	0.00	0.00	0.00																																0.00	0.00	0.00	0.00	0.00	0.00	0.00	16.67	16.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16.67	0.00	0.00	0.00	0.00	16.67
STRDV	7									14.29	42.86	0.00	0.00	0.00	0.00	0.00	0.00	14.29	0.00	0.00	100.00	0.00	0.00	85.71	14.29	14.29	0.00								14.29	0.00	0.00	0.00	0.00	100.00	0.00	0.00	100.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14.29	0.00	0.00	0.00	0.00	0.00	14.29	0.00	0.00	0.00	0.00	57.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	85.71	0.00	0.00	28.57	42.86	0.00	0.00	0.00	0.00	0.00			

V	n	CDR2																																								FR3																																																
TRADV-TRAC	40									0.0	2.5	10.0	0.0	15.0	32.5	0.0	22.5	2.5	2.5	22.5	30.0	0.0	32.5	27.5	5.0	25.0	0.0	32.5	35.0	0.0																	7.5	2.5	0.0	0.0	5.0	12.5	5.0	7.5	5.0	57.5	25.0	0.0	0.0	2.5	5.0	2.5	2.5	0.0	42.5	57.5	0.0	0.0	0.0	0.0	0.0	2.5	7.5	0.0	0.0	62.5	0.0	0.0	2.5	0.0	0.0	0.0	20.0	62.5	25.0	5.0	10.0	2.5
TRADV-TRDC	35									0.0	5.7	5.7	0.0	11.4	14.3	0.0	20.0	2.9	2.9	11.4	11.4	0.0	20.0	17.1	5.7	28.6	0.0	17.1	17.1	0.0																	2.9	2.9	0.0	0.0	5.7	5.7	0.0	0.0	0.0	45.7	25.7	0.0	0.0	5.7	2.9	2.9	2.9	0.0	25.7	40.0	5.7	5.7	0.0	0.0	0.0	2.9	2.9	0.0	0.0	22.9	0.0	0.0	0.0	0.0	0.0	0.0	14.3	34.3	17.1	2.9	2.9	0.0
TRBV	8												0.00	0.00	0.00	37.50	25.00	25.00	25.00	37.50	0.00	12.50	25.00	0.00	0.00	0.00	0.00																	0.00	25.00	0.00	25.00	25.00	12.50	25.00	12.50	12.50	12.50	12.50	0.00	0.00	50.00	0.00	0.00	0.00	0.00	0.00	25.00	62.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12.50	12.50	0.00	37.50	0.00	0.00	12.50	0.00	0.00	0.00	25.00	12.50	0.00	0.00	0.00	12.50
TRGV	15												0.00	0.00	0.00	0.00	6.67	0.00	0.00	26.67	13.33	26.67	53.33	13.33	0.00	0.00	6.67																	13.33	13.33	26.67	0.00	13.33	13.33	6.67	6.67	0.00	0.00	0.00	13.33	13.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.67	0.00	0.00	6.67	0.00	0.00	6.67	13.33	13.33	6.67	26.67	13.33	20.00	6.67	60.00	0.00	0.00	0.00	13.33	6.67	0.00	33.33	33.33	0.00
IgHV	10										0.00	30.00	60.00	0.00	0.00	0.00	10.00	90.00	0.00	0.00	20.00	30.00	0.00	0.00	20.00	0.00	50.00	90.00																		0.00	0.00	10.00	0.00	10.00	40.00	0.00	0.00	0.00	20.00	20.00	0.00	40.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10.00	0.00	0.00	0.00	0.00	0.00	70.00	0.00	10.00	10.00	0.00	0.00	10.00	0.00
NTRV	6	16.67	0.00	0.00	16.67	16.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16.67	16.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16.67	0.00	0.00	0.00	50.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	66.67	66.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
STRDV	7										0.00	57.14	0.00	0.00	0.00	28.57	0.00	14.29	0.00	14.29	14.29	0.00	0.00	0.00	0.00	0.00	0.00	71.43																		71.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14.29	0.00	0.00	71.43	57.14	0.00	14.29	85.71	0.00	0.00	0.00	0.00	0.00	28.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	42.86	42.86	0.00	85.71	100.00	0.00	28.57	28.57	0.00

V	n	FR3																																																																							
																												L																										D												Y						C	
TRADV-TRAC	40	25.0	0.0	20.0	22.5	2.5	40.0	42.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	7.5	2.5	0.0	10.0	12.5	5.0	7.5	5.0	2.5	12.5	0.0	20.0	35.0	2.5	0.0	0.0	0.0	2.5	0.0	0.0	0.0	10.0	7.5	5.0	0.0	2.5	2.5	57.5	47.5	17.5	42.5	57.5	2.5	12.5	57.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	22.5	37.5	0.0	2.5	0.0	35.0	0.0	0.0	2.5	0.0	2.5	77.5	0.0	0.0	0.0
TRADV-TRDC	35	22.9	0.0	17.1	14.3	0.0	25.7	22.9	2.9	0.0	0.0	2.9	0.0	0.0	2.9	0.0	0.0	0.0	5.7	11.4	2.9	5.7	2.9	0.0	8.6	2.9	22.9	17.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.9	5.7	0.0	2.9	2.9	40.0	22.9	0.0	28.6	48.6	0.0	22.9	37.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	25.7	31.4	0.0	0.0	0.0	28.6	0.0	0.0	5.7	0.0	0.0	48.6	0.0	0.0	0.0
TRBV	8	0.00	0.00	12.50	0.00	0.00	0.00	0.00	0.00	12.50	0.00	0.00	25.00	0.00	0.00	0.00	0.00	25.00	12.50	0.00	0.00	25.00	0.00	37.50	37.50	0.00	25.00	50.00	12.50	0.00	0.00	0.00	0.00	0.00	37.50	0.00	0.00	25.00	0.00	0.00	0.00	25.00	25.00	0.00	25.00	25.00	25.00	0.00	12.50	37.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	25.00	0.00	62.50	37.50	0.00	12.50	0.00	0.00	0.00	0.00	25.00	0.00	0.00	25.00	0.00	0.00	0.00
TRGV	15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13.33	33.33	0.00	6.67	6.67	6.67	6.67	13.33	6.67	40.00	40.00	6.67	13.33	26.67	0.00	0.00	0.00	13.33	0.00	0.00	0.00	0.00	6.67	0.00	0.00	0.00	0.00	0.00	26.67	13.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.67	6.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	33.33	0.00	0.00	0.00	13.33	0.00	0.00	0.00	6.67	6.67	73.33	0.00	0.00	0.00
IgHV	10	0.00	0.00	0.00	0.00	10.00	10.00	0.00	0.00	20.00	0.00	0.00	10.00	20.00	0.00	70.00	0.00	0.00	30.00	0.00	0.00	0.00	0.00	0.00	30.00	30.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10.00	0.00	0.00	0.00	0.00	0.00	60.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10.00	0.00	0.00	0.00	10.00	0.00	0.00	0.00	0.00	0.00	30.00	0.00	0.00	0.00	10.00	10.00	70.00	0.00	10.00	0.00
NTRV	6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	66.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	50.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	66.67	0.00	66.67	0.00	0.00	0.00	0.00	66.67	16.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16.67	0.00	0.00	0.00	16.67	0.00
STRDV	7	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14.29	14.29	0.00	28.57	14.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	71.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14.29	14.29	0.00	28.57	42.86	0.00	42.86	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	71.43	57.14	0.00	57.14	0.00	42.86	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00

Supplemental Figure 6A. Source Data

Alpha Position	Alpha Mutation	Avg Alpha Mutation	Alpha Motifs	Avg Alpha Motifs	Delta Position	Delta Mutation	Avg Delta Mutation	Delta Motifs	Avg Delta Motifs
		n=422		**n=38**			**n=140**		**n=21**
53	1	0.24	2.00	5.26	53	1	0.71	1.00	4.76
54	2	0.47	0.00	0.00	54	1	0.71	0.00	0.00
55	2	0.47	1.00	2.63	55	1	0.71	1.00	4.76
56	3	0.71	0.00	0.00	56	0	0.00	0.00	0.00
57	3	0.71	0.00	0.00	57	0	0.00	0.00	0.00
58	6	1.42	0.00	0.00	58	3	2.14	0.00	0.00
59	2	0.47	5.00	13.16	59	0	0.00	1.00	4.76
60	2	0.47	1.00	2.63	60	0	0.00	0.00	0.00
61	4	0.95	0.00	0.00	61	0	0.00	0.00	0.00
62	2	0.47	1.00	2.63	62	0	0.00	0.00	0.00
63	1	0.24	0.00	0.00	63	1	0.71	0.00	0.00
64	5	1.18	1.00	2.63	64	0	0.00	1.00	4.76
65	3	0.71	4.00	10.53	65	0	0.00	2.00	9.52
66	3	0.71	0.00	0.00	66	0	0.00	0.00	0.00
67	0	0.00	13.00	34.21	67	0	0.00	7.00	33.33
68	4	0.95	0.00	0.00	68	0	0.00	0.00	0.00
69	5	1.18	0.00	0.00	69	0	0.00	0.00	0.00
70	13	3.08	0.00	0.00	70	1	0.71	0.00	0.00
71	2	0.47	0.00	0.00	71	0	0.00	1.00	4.76
72	0	0.00	0.00	0.00	72	0	0.00	0.00	0.00
73	0	0.00	18.00	47.37	73	0	0.00	8.00	38.10
74	1	0.24	0.00	0.00	74	0	0.00	0.00	0.00
75	5	1.18	0.00	0.00	75	0	0.00	0.00	0.00
76	2	0.47	0.00	0.00	76	0	0.00	0.00	0.00
77	2	0.47	11.00	28.95	77	0	0.00	7.00	33.33
78	0	0.00	0.00	0.00	78	0	0.00	0.00	0.00
79	0	0.00	0.00	0.00	79	0	0.00	0.00	0.00
80	0	0.00	0.00	0.00	80	1	0.71	0.00	0.00
81	0	0.00	3.00	7.89	81	1	0.71	1.00	4.76
82	2	0.47	3.00	7.89	82	1	0.71	1.00	4.76
83	4	0.95	4.00	10.53	83	0	0.00	0.00	0.00
84	8	1.90	4.00	10.53	84	0	0.00	0.00	0.00
85	1	0.24	2.00	5.26	85	0	0.00	1.00	4.76
86	1	0.24	0.00	0.00	86	0	0.00	0.00	0.00
87	4	0.95	0.00	0.00	87	0	0.00	0.00	0.00
88	4	0.95	6.00	15.79	88	0	0.00	2.00	9.52
89	4	0.95	2.00	5.26	89	0	0.00	0.00	0.00
90	2	0.47	1.00	2.63	90	0	0.00	0.00	0.00
91	2	0.47	3.00	7.89	91	0	0.00	0.00	0.00
92	3	0.71	3.00	7.89	92	0	0.00	0.00	0.00
93	3	0.71	8.00	21.05	93	1	0.71	3.00	14.29
94	2	0.47	10.00	26.32	94	0	0.00	7.00	33.33
95	5	1.18	1.00	2.63	95	0	0.00	0.00	0.00
96	4	0.95	0.00	0.00	96	0	0.00	0.00	0.00
97	8	1.90	14.00	36.84	97	0	0.00	7.00	33.33
98	5	1.18	3.00	7.89	98	1	0.71	2.00	9.52
99	6	1.42	2.00	5.26	99	0	0.00	1.00	4.76
100	2	0.47	9.00	23.68	100	0	0.00	1.00	4.76
101	2	0.47	1.00	2.63	101	1	0.71	0.00	0.00
102	1	0.24	1.00	2.63	102	2	1.43	0.00	0.00
103	0	0.00	1.00	2.63	103	1	0.71	1.00	4.76
104	4	0.95	3.00	7.89	104	2	1.43	2.00	9.52
105	3	0.71	0.00	0.00	105	0	0.00	0.00	0.00
106	1	0.24	1.00	2.63	106	1	0.71	2.00	9.52
107	1	0.24	0.00	0.00	107	0	0.00	1.00	4.76
108	3	0.71	0.00	0.00	108	0	0.00	1.00	4.76
109	0	0.00	0.00	0.00	109	1	0.71	0.00	0.00
110	1	0.24	0.00	0.00	110	0	0.00	0.00	0.00

Supplemental Figure 6A. Source Data

Alpha Position	Alpha Mutation	Avg Alpha Mutation	Alpha Motifs	Avg Alpha Motifs	Delta Position	Delta Mutation	Avg Delta Mutation	Delta Motifs	Avg Delta Motifs
111	1	0.24	0.00	0.00	111	0	0.00	0.00	0.00
112	1	0.24	1.00	2.63	112	0	0.00	1.00	4.76
113	1	0.24	2.00	5.26	113	1	0.71	1.00	4.76
114	0	0.00	0.00	0.00	114	0	0.00	0.00	0.00
115	1	0.24	0.00	0.00	115	1	0.71	1.00	4.76
116	1	0.24	3.00	7.89	116	0	0.00	3.00	14.29
117	2	0.47	0.00	0.00	117	0	0.00	0.00	0.00
118	1	0.24	8.00	21.05	118	1	0.71	2.00	9.52
119	2	0.47	0.00	0.00	119	0	0.00	0.00	0.00
120	2	0.47	0.00	0.00	120	0	0.00	0.00	0.00
121	0	0.00	0.00	0.00	121	0	0.00	2.00	9.52
122	4	0.95	2.00	5.26	122	0	0.00	1.00	4.76
123	8	1.90	15.00	39.47	123	0	0.00	6.00	28.57
124	2	0.47	6.00	15.79	124	1	0.71	5.00	23.81
125	0	0.00	0.00	0.00	125	0	0.00	0.00	0.00
126	2	0.47	1.00	2.63	126	0	0.00	0.00	0.00
127	1	0.24	1.00	2.63	127	0	0.00	0.00	0.00
128	2	0.47	23.00	60.53	128	1	0.71	13.00	61.90
129	5	1.18	17.00	44.74	129	2	1.43	9.00	42.86
130	0	0.00	0.00	0.00	130	0	0.00	0.00	0.00
131	2	0.47	36.00	94.74	131	0	0.00	19.00	90.48
132	1	0.24	18.00	47.37	132	1	0.71	13.00	61.90
133	3	0.71	0.00	0.00	133	1	0.71	0.00	0.00
134	0	0.00	16.00	42.11	134	0	0.00	8.00	38.10
135	4	0.95	1.00	2.63	135	0	0.00	1.00	4.76
136	1	0.24	0.00	0.00	136	0	0.00	0.00	0.00
137	2	0.47	0.00	0.00	137	1	0.71	0.00	0.00
138	2	0.47	26.00	68.42	138	1	0.71	9.00	42.86
139	3	0.71	0.00	0.00	139	0	0.00	0.00	0.00
140	1	0.24	1.00	2.63	140	0	0.00	1.00	4.76
141	3	0.71	0.00	0.00	141	2	1.43	0.00	0.00
142	6	1.42	3.00	7.89	142	1	0.71	1.00	4.76
143	8	1.90	13.00	34.21	143	2	1.43	10.00	47.62
144	6	1.42	0.00	0.00	144	1	0.71	0.00	0.00
145	4	0.95	1.00	2.63	145	0	0.00	0.00	0.00
146	7	1.66	11.00	28.95	146	1	0.71	8.00	38.10
147	4	0.95	0.00	0.00	147	2	1.43	0.00	0.00
148	2	0.47	18.00	47.37	148	0	0.00	10.00	47.62
149	3	0.71	4.00	10.53	149	0	0.00	1.00	4.76
150	6	1.42	1.00	2.63	150	0	0.00	0.00	0.00
151	4	0.95	4.00	10.53	151	0	0.00	0.00	0.00
152	11	2.61	6.00	15.79	152	0	0.00	0.00	0.00
153	2	0.47	5.00	13.16	153	0	0.00	0.00	0.00
154	4	0.95	5.00	13.16	154	0	0.00	1.00	4.76
155	8	1.90	14.00	36.84	155	1	0.71	7.00	33.33
156	6	1.42	2.00	5.26	156	0	0.00	1.00	4.76
157	4	0.95	4.00	10.53	157	0	0.00	1.00	4.76
158	3	0.71	6.00	15.79	158	0	0.00	2.00	9.52
159	4	0.95	4.00	10.53	159	1	0.71	1.00	4.76
160	2	0.47	1.00	2.63	160	0	0.00	0.00	0.00
161	5	1.18	3.00	7.89	161	2	1.43	1.00	4.76
162	4	0.95	0.00	0.00	162	0	0.00	2.00	9.52
163	5	1.18	1.00	2.63	163	0	0.00	0.00	0.00
164	9	2.13	8.00	21.05	164	1	0.71	5.00	23.81
165	5	1.18	18.00	47.37	165	1	0.71	8.00	38.10
166	1	0.24	0.00	0.00	166	2	1.43	0.00	0.00
167	0	0.00	0.00	0.00	167	0	0.00	0.00	0.00
168	1	0.24	21.00	55.26	168	0	0.00	10.00	47.62
169	1	0.24	2.00	5.26	169	0	0.00	1.00	4.76

Supplemental Figure 6A. Source Data

Alpha Position	Alpha Mutation	Avg Alpha Mutation	Alpha Motifs	Avg Alpha Motifs	Delta Position	Delta Mutation	Avg Delta Mutation	Delta Motifs	Avg Delta Motifs
170	0	0.00	0.00	0.00	170	1	0.71	0.00	0.00
171	2	0.47	7.00	18.42	171	1	0.71	8.00	38.10
172	0	0.00	1.00	2.63	172	0	0.00	1.00	4.76
173	0	0.00	0.00	0.00	173	0	0.00	0.00	0.00
174	0	0.00	36.00	94.74	174	0	0.00	19.00	90.48
175	0	0.00	0.00	0.00	175	0	0.00	0.00	0.00
176	0	0.00	0.00	0.00	176	1	0.71	0.00	0.00
177	3	0.71	27.00	71.05	177	1	0.71	17.00	80.95
178	1	0.24	0.00	0.00	178	0	0.00	0.00	0.00
179	1	0.24	0.00	0.00	179	1	0.71	0.00	0.00
180	0	0.00	7.00	18.42	180	1	0.71	6.00	28.57
181	0	0.00	1.00	2.63	181	0	0.00	0.00	0.00
182	3	0.71	0.00	0.00	182	0	0.00	0.00	0.00
183	4	0.95	27.00	71.05	183	1	0.71	16.00	76.19
184	8	1.90	23.00	60.53	184	0	0.00	15.00	71.43
185	6	1.42	0.00	0.00	185	0	0.00	0.00	0.00
186	2	0.47	5.00	13.16	186	1	0.71	2.00	9.52
187	2	0.47	1.00	2.63	187	0	0.00	2.00	9.52
188	2	0.47	1.00	2.63	188	1	0.71	0.00	0.00
189	1	0.24	0.00	0.00	189	1	0.71	0.00	0.00
190	0	0.00	0.00	0.00	190	0	0.00	0.00	0.00
191	2	0.47	23.00	60.53	191	0	0.00	13.00	61.90
192	5	1.18	0.00	0.00	192	0	0.00	0.00	0.00
193	3	0.71	0.00	0.00	193	1	0.71	1.00	4.76
194	1	0.24	2.00	5.26	194	1	0.71	1.00	4.76
195	2	0.47	1.00	2.63	195	0	0.00	0.00	0.00
196	7	1.66	5.00	13.16	196	0	0.00	1.00	4.76
197	3	0.71	5.00	13.16	197	0	0.00	1.00	4.76
198	0	0.00	0.00	0.00	198	0	0.00	1.00	4.76
199	4	0.95	23.00	60.53	199	0	0.00	14.00	66.67
200	3	0.71	0.00	0.00	200	1	0.71	0.00	0.00
201	2	0.47	2.00	5.26	201	2	1.43	0.00	0.00
202	1	0.24	2.00	5.26	202	0	0.00	0.00	0.00
203	4	0.95	2.00	5.26	203	0	0.00	1.00	4.76
204	14	3.32	23.00	60.53	204	0	0.00	15.00	71.43
205	0	0.00	0.00	0.00	205	0	0.00	0.00	0.00
206	0	0.00	0.00	0.00	206	0	0.00	0.00	0.00
207	0	0.00	1.00	2.63	207	0	0.00	0.00	0.00
208	4	0.95	2.00	5.26	208	1	0.71	0.00	0.00
209	1	0.24	1.00	2.63	209	1	0.71	1.00	4.76
210	8	1.90	0.00	0.00	210	0	0.00	0.00	0.00
211	14	3.32	14.00	36.84	211	0	0.00	4.00	19.05
212	0	0.00	0.00	0.00	212	0	0.00	0.00	0.00
213	3	0.71	8.00	21.05	213	0	0.00	6.00	28.57
214	2	0.47	2.00	5.26	214	0	0.00	1.00	4.76
215	5	1.18	1.00	2.63	215	0	0.00	0.00	0.00
216	2	0.47	2.00	5.26	216	0	0.00	3.00	14.29
217	0	0.00	0.00	0.00	217	0	0.00	0.00	0.00
218	3	0.71	1.00	2.63	218	1	0.71	2.00	9.52
219	0	0.00	4.00	10.53	219	1	0.71	2.00	9.52
220	4	0.95	0.00	0.00	220	0	0.00	0.00	0.00
221	8	1.90	6.00	15.79	221	0	0.00	4.00	19.05
222	8	1.90	13.00	34.21	222	0	0.00	5.00	23.81
223	0	0.00	0.00	0.00	223	0	0.00	0.00	0.00
224	1	0.24	9.00	23.68	224	0	0.00	7.00	33.33
225	5	1.18	1.00	2.63	225	0	0.00	1.00	4.76
226	0	0.00	1.00	2.63	226	0	0.00	1.00	4.76
227	5	1.18	9.00	23.68	227	0	0.00	4.00	19.05
228	3	0.71	12.00	31.58	228	0	0.00	4.00	19.05

Supplemental Figure 6A. Source Data

Alpha Position	Alpha Mutation	Avg Alpha Mutation	Alpha Motifs	Avg Alpha Motifs	Delta Position	Delta Mutation	Avg Delta Mutation	Delta Motifs	Avg Delta Motifs
229	9	2.13	0.00	0.00	229	0	0.00	0.00	0.00
230	4	0.95	13.00	34.21	230	0	0.00	7.00	33.33
231	3	0.71	11.00	28.95	231	0	0.00	6.00	28.57
232	2	0.47	2.00	5.26	232	0	0.00	2.00	9.52
233	0	0.00	10.00	26.32	233	0	0.00	10.00	47.62
234	1	0.24	0.00	0.00	234	1	0.71	0.00	0.00
235	5	1.18	13.00	34.21	235	0	0.00	6.00	28.57
236	4	0.95	14.00	36.84	236	1	0.71	6.00	28.57
237	2	0.47	0.00	0.00	237	0	0.00	0.00	0.00
238	3	0.71	3.00	7.89	238	0	0.00	1.00	4.76
239	5	1.18	1.00	2.63	239	0	0.00	1.00	4.76
240	2	0.47	0.00	0.00	240	1	0.71	0.00	0.00
241	6	1.42	0.00	0.00	241	0	0.00	0.00	0.00
242	2	0.47	2.00	5.26	242	0	0.00	2.00	9.52
243	5	1.18	5.00	13.16	243	0	0.00	2.00	9.52
244	2	0.47	2.00	5.26	244	0	0.00	0.00	0.00
245	8	1.90	3.00	7.89	245	1	0.71	0.00	0.00
246	8	1.90	2.00	5.26	246	0	0.00	0.00	0.00
247	0	0.00	23.00	60.53	247	0	0.00	16.00	76.19
248	2	0.47	10.00	26.32	248	0	0.00	9.00	42.86
249	0	0.00	0.00	0.00	249	0	0.00	0.00	0.00
250	1	0.24	0.00	0.00	250	1	0.71	0.00	0.00
251	1	0.24	1.00	2.63	251	0	0.00	2.00	9.52
252	17	4.03	2.00	5.26	252	3	2.14	1.00	4.76
253	1	0.24	1.00	2.63	253	0	0.00	1.00	4.76
254	3	0.71	1.00	2.63	254	0	0.00	1.00	4.76
255	2	0.47	0.00	0.00	255	0	0.00	0.00	0.00
256	1	0.24	17.00	44.74	256	0	0.00	9.00	42.86
257	2	0.47	23.00	60.53	257	0	0.00	14.00	66.67
258	1	0.24	0.00	0.00	258	0	0.00	2.00	9.52
259	1	0.24	0.00	0.00	259	0	0.00	2.00	9.52
260	6	1.42	0.00	0.00	260	0	0.00	0.00	0.00
261	1	0.24	0.00	0.00	261	1	0.71	0.00	0.00
262	1	0.24	0.00	0.00	262	1	0.71	0.00	0.00
263	1	0.24	1.00	2.63	263	0	0.00	1.00	4.76
264	3	0.71	3.00	7.89	264	0	0.00	1.00	4.76
265	2	0.47	0.00	0.00	265	0	0.00	0.00	0.00
266	1	0.24	0.00	0.00	266	0	0.00	0.00	0.00
267	6	1.42	25.00	65.79	267	0	0.00	8.00	38.10
268	2	0.47	0.00	0.00	268	0	0.00	0.00	0.00
269	1	0.24	0.00	0.00	269	0	0.00	0.00	0.00
270	2	0.47	1.00	2.63	270	1	0.71	0.00	0.00
271	0	0.00	0.00	0.00	271	0	0.00	0.00	0.00
272	0	0.00	0.00	0.00	272	0	0.00	0.00	0.00
273	0	0.00	0.00	0.00	273	1	0.71	0.00	0.00
274	1	0.24	8.00	21.05	274	0	0.00	5.00	23.81
275	1	0.24	25.00	65.79	275	1	0.71	12.00	57.14
276	0	0.00	10.00	26.32	276	0	0.00	6.00	28.57
277	2	0.47	2.00	5.26	277	0	0.00	1.00	4.76
278	0	0.00	4.00	10.53	278	0	0.00	1.00	4.76
279	3	0.71	1.00	2.63	279	0	0.00	0.00	0.00
280	4	0.95	10.00	26.32	280	0	0.00	8.00	38.10
281	0	0.00	0.00	0.00	281	0	0.00	0.00	0.00
282	2	0.47	8.00	21.05	282	1	0.71	6.00	28.57
283	3	0.71	9.00	23.68	283	0	0.00	5.00	23.81
284	0	0.00	1.00	2.63	284	0	0.00	0.00	0.00
285	0	0.00	16.00	42.11	285	0	0.00	9.00	42.86
286	0	0.00	17.00	44.74	286	0	0.00	8.00	38.10
287	1	0.24	0.00	0.00	287	0	0.00	1.00	4.76

Supplemental Figure 6A. Source Data

Alpha Position	Alpha Mutation	Avg Alpha Mutation	Alpha Motifs	Avg Alpha Motifs	Delta Position	Delta Mutation	Avg Delta Mutation	Delta Motifs	Avg Delta Motifs
288	1	0.24	0.00	0.00	288	0	0.00	0.00	0.00
289	0	0.00	0.00	0.00	289	2	1.43	0.00	0.00
290	0	0.00	0.00	0.00	290	1	0.71	1.00	4.76
291	0	0.00	0.00	0.00	291	1	0.71	0.00	0.00
292	2	0.47	0.00	0.00	292	0	0.00	0.00	0.00
293	1	0.24	0.00	0.00	293	0	0.00	1.00	4.76
294	0	0.00	3.00	7.89	294	0	0.00	0.00	0.00
295	0	0.00	1.00	2.63	295	0	0.00	0.00	0.00
296	0	0.00	0.00	0.00	296	0	0.00	0.00	0.00
297	1	0.24	4.00	10.53	297	0	0.00	2.00	9.52
298	1	0.24	5.00	13.16	298	0	0.00	4.00	19.05
299	4	0.95	2.00	5.26	299	0	0.00	1.00	4.76
300	4	0.95	3.00	7.89	300	0	0.00	2.00	9.52
301	1	0.24	2.00	5.26	301	0	0.00	1.00	4.76
302	0	0.00	1.00	2.63	302	0	0.00	0.00	0.00
303	5	1.18	5.00	13.16	303	0	0.00	3.00	14.29
304	1	0.24	0.00	0.00	304	0	0.00	1.00	4.76
305	1	0.24	8.00	21.05	305	0	0.00	8.00	38.10
306	3	0.71	14.00	36.84	306	0	0.00	6.00	28.57
307	4	0.95	1.00	2.63	307	0	0.00	0.00	0.00
308	0	0.00	0.00	0.00	308	0	0.00	0.00	0.00
309	4	0.95	0.00	0.00	309	0	0.00	0.00	0.00
310	3	0.71	0.00	0.00	310	0	0.00	0.00	0.00
311	0	0.00	1.00	2.63	311	0	0.00	0.00	0.00
312	3	0.71	0.00	0.00	312	1	0.71	0.00	0.00
313	1	0.24	0.00	0.00	313	0	0.00	0.00	0.00
314	0	0.00	0.00	0.00	314	0	0.00	0.00	0.00
315	8	1.90	4.00	10.53	315	1	0.71	0.00	0.00
316	7	1.66	3.00	7.89	316	1	0.71	1.00	4.76
317	5	1.18	2.00	5.26	317	1	0.71	2.00	9.52
318	2	0.47	0.00	0.00	318	1	0.71	0.00	0.00
319	2	0.47	1.00	2.63	319	0	0.00	1.00	4.76
320	4	0.95	1.00	2.63	320	0	0.00	1.00	4.76
321	3	0.71	23.00	60.53	321	0	0.00	14.00	66.67
322	3	0.71	19.00	50.00	322	1	0.71	8.00	38.10
323	0	0.00	7.00	18.42	323	3	2.14	0.00	0.00
324	0	0.00	17.00	44.74	324	0	0.00	10.00	47.62
325	1	0.24	23.00	60.53	325	0	0.00	17.00	80.95
326	0	0.00	1.00	2.63	326	0	0.00	0.00	0.00
327	0	0.00	5.00	13.16	327	0	0.00	8.00	38.10
328	2	0.47	23.00	60.53	328	0	0.00	13.00	61.90
329	2	0.47	0.00	0.00	329	0	0.00	0.00	0.00
330	1	0.24	0.00	0.00	330	0	0.00	0.00	0.00
331	2	0.47	0.00	0.00	331	0	0.00	0.00	0.00
332	2	0.47	0.00	0.00	332	1	0.71	0.00	0.00
333	0	0.00	0.00	0.00	333	1	0.71	0.00	0.00
334	0	0.00	0.00	0.00	334	0	0.00	0.00	0.00
335	0	0.00	0.00	0.00	335	0	0.00	0.00	0.00
336	0	0.00	0.00	0.00	336	0	0.00	0.00	0.00
337	3	0.71	0.00	0.00	337	0	0.00	0.00	0.00
338	0	0.00	0.00	0.00	338	1	0.71	0.00	0.00
339	0	0.00	0.00	0.00	339	0	0.00	0.00	0.00
340	2	0.47	9.00	23.68	340	1	0.71	9.00	42.86
341	4	0.95	15.00	39.47	341	0	0.00	11.00	52.38
342	1	0.24	0.00	0.00	342	0	0.00	0.00	0.00
343	6	1.42	1.00	2.63	343	3	2.14	0.00	0.00
344	0	0.00	0.00	0.00	344	0	0.00	0.00	0.00
345	5	1.18	14.00	36.84	345	0	0.00	10.00	47.62
346	0	0.00	0.00	0.00	346	0	0.00	0.00	0.00

Supplemental Figure 6A. Source Data

Alpha Position	Alpha Mutation	Avg Alpha Mutation	Alpha Motifs	Avg Alpha Motifs	Delta Position	Delta Mutation	Avg Delta Mutation	Delta Motifs	Avg Delta Motifs
347	0	0.00	0.00	0.00	347	0	0.00	0.00	0.00
348	0	0.00	1.00	2.63	348	0	0.00	2.00	9.52
349	2	0.47	0.00	0.00	349	0	0.00	0.00	0.00
350	2	0.47	1.00	2.63	350	0	0.00	0.00	0.00
351	2	0.47	31.00	81.58	351	0	0.00	17.00	80.95
352	1	0.24	0.00	0.00	352	0	0.00	0.00	0.00
353	1	0.24	0.00	0.00	353	0	0.00	0.00	0.00
354	6	1.42	0.00	0.00	354	0	0.00	0.00	0.00

Supplemental Figure 6B. Source Data

Beta Position	Beta Sum	Avg Beta Mutation	Beta Motif	Avg Beta Motif	Gamma Position	Gamma Sum	Avg Gamma Mutation	Gamma Motif	Avg Gamma Motif
		n=228		n=8			n=158		n=15
69	0	0.00	0	0.00	69	0	0.00	0	0.00
70	2	0.88	0	0.00	70	0	0.00	0	0.00
71	1	0.44	1	12.50	71	0	0.00	0	0.00
72	1	0.44	0	0.00	72	0	0.00	0	0.00
73	0	0.00	0	0.00	73	0	0.00	1	6.67
74	0	0.00	0	0.00	74	0	0.00	1	6.67
75	0	0.00	0	0.00	75	0	0.00	0	0.00
76	0	0.00	1	12.50	76	0	0.00	5	33.33
77	0	0.00	0	0.00	77	0	0.00	0	0.00
78	1	0.44	0	0.00	78	0	0.00	1	6.67
79	1	0.44	0	0.00	79	0	0.00	1	6.67
80	1	0.44	0	0.00	80	0	0.00	0	0.00
81	1	0.44	3	37.50	81	0	0.00	0	0.00
82	1	0.44	4	50.00	82	0	0.00	0	0.00
83	0	0.00	0	0.00	83	0	0.00	1	6.67
84	0	0.00	0	0.00	84	1	0.63	0	0.00
85	0	0.00	1	12.50	85	0	0.00	0	0.00
86	0	0.00	0	0.00	86	0	0.00	1	6.67
87	0	0.00	0	0.00	87	1	0.63	0	0.00
88	0	0.00	0	0.00	88	0	0.00	1	6.67
89	0	0.00	0	0.00	89	1	0.63	2	13.33
90	0	0.00	0	0.00	90	0	0.00	1	6.67
91	0	0.00	0	0.00	91	0	0.00	0	0.00
92	0	0.00	0	0.00	92	1	0.63	0	0.00
93	0	0.00	3	37.50	93	0	0.00	0	0.00
94	0	0.00	0	0.00	94	0	0.00	6	40.00
95	0	0.00	0	0.00	95	0	0.00	8	53.33
96	0	0.00	0	0.00	96	0	0.00	0	0.00
97	1	0.44	1	12.50	97	0	0.00	0	0.00
98	0	0.00	0	0.00	98	1	0.63	4	26.67
99	0	0.00	0	0.00	99	0	0.00	2	13.33
100	0	0.00	0	0.00	100	1	0.63	2	13.33
101	0	0.00	0	0.00	101	1	0.63	2	13.33
102	0	0.00	0	0.00	102	2	1.27	2	13.33
103	0	0.00	2	25.00	103	1	0.63	4	26.67
104	0	0.00	0	0.00	104	1	0.63	0	0.00
105	0	0.00	0	0.00	105	0	0.00	2	13.33
106	0	0.00	2	25.00	106	0	0.00	1	6.67
107	0	0.00	2	25.00	107	1	0.63	9	60.00
108	0	0.00	0	0.00	108	0	0.00	0	0.00
109	0	0.00	0	0.00	109	0	0.00	0	0.00
110	0	0.00	0	0.00	110	0	0.00	0	0.00
111	0	0.00	0	0.00	111	0	0.00	0	0.00
112	0	0.00	0	0.00	112	0	0.00	1	6.67
113	0	0.00	0	0.00	113	0	0.00	5	33.33
114	0	0.00	0	0.00	114	0	0.00	1	6.67
115	0	0.00	0	0.00	115	0	0.00	0	0.00
116	1	0.44	0	0.00	116	0	0.00	4	26.67

Supplemental Figure 6B. Source Data

Beta Position	Beta Sum	Avg Beta Mutation	Beta Motif	Avg Beta Motif	Gamma Position	Gamma Sum	Avg Gamma Mutation	Gamma Motif	Avg Gamma Motif
117	0	0.00	2	25.00	117	0	0.00	0	0.00
118	1	0.44	0	0.00	118	0	0.00	0	0.00
119	4	1.75	0	0.00	119	0	0.00	0	0.00
120	1	0.44	0	0.00	120	0	0.00	3	20.00
121	1	0.44	2	25.00	121	0	0.00	1	6.67
122	2	0.88	1	12.50	122	0	0.00	2	13.33
123	2	0.88	0	0.00	123	0	0.00	1	6.67
124	1	0.44	0	0.00	124	0	0.00	0	0.00
125	0	0.00	3	37.50	125	0	0.00	0	0.00
126	2	0.88	1	12.50	126	0	0.00	1	6.67
127	1	0.44	0	0.00	127	0	0.00	1	6.67
128	0	0.00	0	0.00	128	0	0.00	6	40.00
129	0	0.00	3	37.50	129	0	0.00	2	13.33
130	0	0.00	3	37.50	130	0	0.00	0	0.00
131	0	0.00	0	0.00	131	0	0.00	2	13.33
132	0	0.00	0	0.00	132	0	0.00	2	13.33
133	0	0.00	0	0.00	133	0	0.00	0	0.00
134	0	0.00	8	100.00	134	0	0.00	0	0.00
135	1	0.44	6	75.00	135	0	0.00	0	0.00
136	0	0.00	0	0.00	136	0	0.00	0	0.00
137	0	0.00	0	0.00	137	0	0.00	1	6.67
138	0	0.00	5	62.50	138	0	0.00	1	6.67
139	1	0.44	1	12.50	139	0	0.00	0	0.00
140	0	0.00	0	0.00	140	0	0.00	0	0.00
141	0	0.00	0	0.00	141	0	0.00	0	0.00
142	0	0.00	0	0.00	142	0	0.00	5	33.33
143	2	0.88	0	0.00	143	0	0.00	1	6.67
144	1	0.44	0	0.00	144	1	0.63	0	0.00
145	0	0.00	0	0.00	145	0	0.00	0	0.00
146	0	0.00	0	0.00	146	1	0.63	5	33.33
147	0	0.00	0	0.00	147	0	0.00	0	0.00
148	0	0.00	0	0.00	148	0	0.00	0	0.00
149	2	0.88	4	50.00	149	0	0.00	0	0.00
150	0	0.00	0	0.00	150	0	0.00	1	6.67
151	0	0.00	2	25.00	151	0	0.00	0	0.00
152	0	0.00	4	50.00	152	2	1.27	5	33.33
153	0	0.00	2	25.00	153	1	0.63	3	20.00
154	2	0.88	0	0.00	154	0	0.00	0	0.00
155	0	0.00	0	0.00	155	1	0.63	2	13.33
156	0	0.00	2	25.00	156	0	0.00	3	20.00
157	0	0.00	0	0.00	157	0	0.00	1	6.67
158	1	0.44	2	25.00	158	0	0.00	5	33.33
159	0	0.00	3	37.50	159	0	0.00	4	26.67
160	0	0.00	0	0.00	160	0	0.00	0	0.00
161	0	0.00	0	0.00	161	1	0.63	2	13.33
162	0	0.00	4	50.00	162	0	0.00	3	20.00
163	0	0.00	0	0.00	163	0	0.00	3	20.00
164	0	0.00	0	0.00	164	0	0.00	0	0.00
165	0	0.00	6	75.00	165	0	0.00	0	0.00

Supplemental Figure 6B. Source Data

Beta Position	Beta Sum	Avg Beta Mutation	Beta Motif	Avg Beta Motif	Gamma Position	Gamma Sum	Avg Gamma Mutation	Gamma Motif	Avg Gamma Motif
166	0	0.00	0	0.00	166	0	0.00	0	0.00
167	1	0.44	0	0.00	167	0	0.00	0	0.00
168	1	0.44	5	62.50	168	1	0.63	2	13.33
169	0	0.00	0	0.00	169	0	0.00	0	0.00
170	0	0.00	0	0.00	170	0	0.00	0	0.00
171	0	0.00	8	100.00	171	0	0.00	2	13.33
172	0	0.00	0	0.00	172	0	0.00	0	0.00
173	0	0.00	0	0.00	173	0	0.00	0	0.00
174	0	0.00	8	100.00	174	0	0.00	13	86.67
175	0	0.00	0	0.00	175	0	0.00	0	0.00
176	0	0.00	0	0.00	176	0	0.00	0	0.00
177	0	0.00	1	12.50	177	1	0.63	11	73.33
178	0	0.00	1	12.50	178	0	0.00	0	0.00
179	1	0.44	0	0.00	179	0	0.00	0	0.00
180	0	0.00	4	50.00	180	0	0.00	11	73.33
181	1	0.44	5	62.50	181	0	0.00	9	60.00
182	1	0.44	1	12.50	182	0	0.00	0	0.00
183	3	1.32	1	12.50	183	0	0.00	0	0.00
184	1	0.44	3	37.50	184	0	0.00	0	0.00
185	1	0.44	1	12.50	185	0	0.00	1	6.67
186	1	0.44	0	0.00	186	0	0.00	1	6.67
187	0	0.00	0	0.00	187	0	0.00	6	40.00
188	0	0.00	0	0.00	188	1	0.63	0	0.00
189	2	0.88	3	37.50	189	1	0.63	1	6.67
190	2	0.88	3	37.50	190	1	0.63	1	6.67
191	0	0.00	3	37.50	191	1	0.63	1	6.67
192	1	0.44	0	0.00	192	1	0.63	0	0.00
193	0	0.00	4	50.00	193	0	0.00	1	6.67
194	0	0.00	0	0.00	194	0	0.00	1	6.67
195	0	0.00	1	12.50	195	0	0.00	0	0.00
196	0	0.00	1	12.50	196	1	0.63	7	46.67
197	0	0.00	0	0.00	197	0	0.00	1	6.67
198	0	0.00	2	25.00	198	0	0.00	0	0.00
199	1	0.44	2	25.00	199	0	0.00	0	0.00
200	0	0.00	0	0.00	200	0	0.00	0	0.00
201	1	0.44	3	37.50	201	1	0.63	0	0.00
202	1	0.44	7	87.50	202	0	0.00	2	13.33
203	0	0.00	4	50.00	203	0	0.00	0	0.00
204	0	0.00	0	0.00	204	0	0.00	0	0.00
205	1	0.44	1	12.50	205	0	0.00	0	0.00
206	0	0.00	0	0.00	206	1	0.63	0	0.00
207	0	0.00	1	12.50	207	0	0.00	0	0.00
208	0	0.00	2	25.00	208	0	0.00	0	0.00
209	0	0.00	2	25.00	209	0	0.00	0	0.00
210	1	0.44	2	25.00	210	0	0.00	0	0.00
211	0	0.00	0	0.00	211	0	0.00	4	26.67
212	0	0.00	2	25.00	212	0	0.00	1	6.67
213	0	0.00	4	50.00	213	0	0.00	0	0.00
214	0	0.00	0	0.00	214	0	0.00	0	0.00

Supplemental Figure 6B. Source Data

Beta Position	Beta Sum	Avg Beta Mutation	Beta Motif	Avg Beta Motif	Gamma Position	Gamma Sum	Avg Gamma Mutation	Gamma Motif	Avg Gamma Motif
215	0	0.00	0	0.00	215	1	0.63	0	0.00
216	0	0.00	0	0.00	216	0	0.00	0	0.00
217	0	0.00	3	37.50	217	0	0.00	0	0.00
218	0	0.00	2	25.00	218	0	0.00	1	6.67
219	1	0.44	2	25.00	219	0	0.00	0	0.00
220	0	0.00	2	25.00	220	0	0.00	0	0.00
221	0	0.00	3	37.50	221	0	0.00	4	26.67
222	0	0.00	0	0.00	222	0	0.00	2	13.33
223	0	0.00	1	12.50	223	0	0.00	4	26.67
224	1	0.44	2	25.00	224	2	1.27	8	53.33
225	1	0.44	0	0.00	225	1	0.63	2	13.33
226	1	0.44	0	0.00	226	0	0.00	0	0.00
227	0	0.00	0	0.00	227	0	0.00	0	0.00
228	0	0.00	0	0.00	228	1	0.63	1	6.67
229	0	0.00	0	0.00	229	0	0.00	2	13.33
230	1	0.44	2	25.00	230	0	0.00	2	13.33
231	0	0.00	0	0.00	231	0	0.00	4	26.67
232	1	0.44	2	25.00	232	0	0.00	0	0.00
233	0	0.00	2	25.00	233	0	0.00	2	13.33
234	0	0.00	1	12.50	234	0	0.00	2	13.33
235	1	0.44	2	25.00	235	0	0.00	1	6.67
236	1	0.44	1	12.50	236	1	0.63	1	6.67
237	1	0.44	1	12.50	237	0	0.00	0	0.00
238	0	0.00	1	12.50	238	1	0.63	0	0.00
239	1	0.44	1	12.50	239	2	1.27	0	0.00
240	0	0.00	0	0.00	240	1	0.63	2	13.33
241	3	1.32	0	0.00	241	0	0.00	2	13.33
242	0	0.00	4	50.00	242	0	0.00	0	0.00
243	0	0.00	0	0.00	243	1	0.63	0	0.00
244	0	0.00	0	0.00	244	1	0.63	0	0.00
245	0	0.00	0	0.00	245	0	0.00	0	0.00
246	0	0.00	0	0.00	246	0	0.00	0	0.00
247	0	0.00	0	0.00	247	0	0.00	0	0.00
248	0	0.00	2	25.00	248	0	0.00	0	0.00
249	0	0.00	5	62.50	249	0	0.00	0	0.00
250	0	0.00	0	0.00	250	1	0.63	1	6.67
251	0	0.00	0	0.00	251	0	0.00	0	0.00
252	0	0.00	0	0.00	252	0	0.00	0	0.00
253	0	0.00	0	0.00	253	3	1.90	1	6.67
254	0	0.00	0	0.00	254	0	0.00	0	0.00
255	0	0.00	0	0.00	255	0	0.00	0	0.00
256	0	0.00	0	0.00	256	0	0.00	1	6.67
257	1	0.44	0	0.00	257	0	0.00	2	13.33
258	0	0.00	1	12.50	258	0	0.00	2	13.33
259	0	0.00	1	12.50	259	0	0.00	1	6.67
260	0	0.00	0	0.00	260	0	0.00	4	26.67
261	0	0.00	3	37.50	261	0	0.00	2	13.33
262	1	0.44	0	0.00	262	0	0.00	3	20.00
263	0	0.00	0	0.00	263	0	0.00	1	6.67

Supplemental Figure 6B. Source Data

Beta Position	Beta Sum	Avg Beta Mutation	Beta Motif	Avg Beta Motif	Gamma Position	Gamma Sum	Avg Gamma Mutation	Gamma Motif	Avg Gamma Motif
264	0	0.00	1	12.50	264	0	0.00	9	60.00
265	1	0.44	0	0.00	265	1	0.63	0	0.00
266	0	0.00	0	0.00	266	0	0.00	0	0.00
267	0	0.00	0	0.00	267	0	0.00	0	0.00
268	0	0.00	2	25.00	268	0	0.00	2	13.33
269	0	0.00	1	12.50	269	1	0.63	1	6.67
270	0	0.00	0	0.00	270	2	1.27	0	0.00
271	0	0.00	0	0.00	271	2	1.27	5	33.33
272	0	0.00	0	0.00	272	1	0.63	5	33.33
273	0	0.00	1	12.50	273	1	0.63	0	0.00
274	0	0.00	0	0.00	274	0	0.00	0	0.00
275	0	0.00	0	0.00	275	0	0.00	0	0.00
276	0	0.00	1	12.50	276	0	0.00	0	0.00
277	0	0.00	0	0.00	277	0	0.00	0	0.00
278	0	0.00	0	0.00	278	1	0.63	0	0.00
279	0	0.00	0	0.00	279	1	0.63	0	0.00
280	0	0.00	0	0.00	280	0	0.00	0	0.00
281	0	0.00	0	0.00	281	0	0.00	0	0.00
282	0	0.00	1	12.50	282	0	0.00	0	0.00
283	0	0.00	0	0.00	283	0	0.00	0	0.00
284	1	0.44	0	0.00	284	1	0.63	0	0.00
285	0	0.00	2	25.00	285	0	0.00	0	0.00
286	0	0.00	0	0.00	286	0	0.00	0	0.00
287	1	0.44	0	0.00	287	0	0.00	2	13.33
288	0	0.00	0	0.00	288	0	0.00	5	33.33
289	0	0.00	0	0.00	289	1	0.63	0	0.00
290	0	0.00	2	25.00	290	0	0.00	1	6.67
291	0	0.00	1	12.50	291	1	0.63	1	6.67
292	0	0.00	0	0.00	292	0	0.00	1	6.67
293	0	0.00	0	0.00	293	0	0.00	1	6.67
294	0	0.00	2	25.00	294	1	0.63	2	13.33
295	0	0.00	0	0.00	295	0	0.00	1	6.67
296	0	0.00	3	37.50	296	0	0.00	6	40.00
297	0	0.00	3	37.50	297	0	0.00	6	40.00
298	0	0.00	0	0.00	298	0	0.00	1	6.67
299	1	0.44	2	25.00	299	1	0.63	2	13.33
300	2	0.88	4	50.00	300	2	1.27	4	26.67
301	0	0.00	1	12.50	301	0	0.00	0	0.00
302	0	0.00	0	0.00	302	0	0.00	0	0.00
303	0	0.00	0	0.00	303	0	0.00	0	0.00
304	0	0.00	0	0.00	304	2	1.27	2	13.33
305	0	0.00	0	0.00	305	1	0.63	0	0.00
306	1	0.44	0	0.00	306	1	0.63	0	0.00
307	0	0.00	3	37.50	307	0	0.00	0	0.00
308	0	0.00	0	0.00	308	0	0.00	0	0.00
309	1	0.44	0	0.00	309	0	0.00	1	6.67
310	0	0.00	2	25.00	310	0	0.00	0	0.00
311	0	0.00	0	0.00	311	0	0.00	0	0.00
312	0	0.00	0	0.00	312	1	0.63	0	0.00

Supplemental Figure 6B. Source Data

Beta Position	Beta Sum	Avg Beta Mutation	Beta Motif	Avg Beta Motif	Gamma Position	Gamma Sum	Avg Gamma Mutation	Gamma Motif	Avg Gamma Motif
313	0	0.00	0	0.00	313	1	0.63	0	0.00
314	0	0.00	2	25.00	314	0	0.00	0	0.00
315	1	0.44	2	25.00	315	0	0.00	4	26.67
316	0	0.00	0	0.00	316	3	1.90	2	13.33
317	0	0.00	2	25.00	317	0	0.00	0	0.00
318	1	0.44	2	25.00	318	1	0.63	0	0.00
319	0	0.00	2	25.00	319	0	0.00	0	0.00
320	0	0.00	0	0.00	320	0	0.00	0	0.00
321	1	0.44	1	12.50	321	0	0.00	0	0.00
322	1	0.44	3	37.50	322	1	0.63	0	0.00
323	0	0.00	0	0.00	323	0	0.00	0	0.00
324	0	0.00	0	0.00	324	0	0.00	0	0.00
325	0	0.00	0	0.00	325	0	0.00	1	6.67
326	0	0.00	0	0.00	326	1	0.63	1	6.67
327	1	0.44	0	0.00	327	3	1.90	0	0.00
328	0	0.00	0	0.00	328	0	0.00	0	0.00
329	0	0.00	0	0.00	329	0	0.00	0	0.00
330	1	0.44	0	0.00	330	0	0.00	0	0.00
331	0	0.00	0	0.00	331	0	0.00	0	0.00
332	0	0.00	2	25.00	332	0	0.00	0	0.00
333	0	0.00	0	0.00	333	2	1.27	0	0.00
334	0	0.00	5	62.50	334	0	0.00	0	0.00
335	3	1.32	3	37.50	335	0	0.00	5	33.33
336	0	0.00	0	0.00	336	0	0.00	0	0.00
337	0	0.00	1	12.50	337	0	0.00	0	0.00
338	0	0.00	0	0.00	338	0	0.00	0	0.00
339	0	0.00	0	0.00	339	1	0.63	2	13.33
340	0	0.00	0	0.00	340	0	0.00	0	0.00
341	0	0.00	0	0.00	341	0	0.00	0	0.00
342	0	0.00	2	25.00	342	0	0.00	0	0.00
343	0	0.00	0	0.00	343	1	0.63	1	6.67
344	0	0.00	0	0.00	344	0	0.00	1	6.67
345	0	0.00	2	25.00	345	0	0.00	11	73.33
346	0	0.00	0	0.00	346	0	0.00	0	0.00
347	0	0.00	0	0.00	347	0	0.00	0	0.00
348	0	0.00	0	0.00	348	0	0.00	0	0.00
349	0	0.00	0	0.00	349	1	0.63	2	13.33

Supplemental Figure 6C. Source Data

IgHV Position	IgHV Mutation	Avg mutation	IgHV Motifs	Avg Motif	TAILV Position	TAILV Mutation	Avg mutation	TAILV Motifs	Avg Motif
		n=237		n=14			n=11		n=2
61	0	0.00	0	0.00					
62	0	0.00	0	0.00					
63	0	0.00	0	0.00					
64	0	0.00	0	0.00					
65	0	0.00	0	0.00	65	0	0	1	50.00
66	0	0.00	1	7.14	66	0	0	0	0.00
67	0	0.00	7	50.00	67	0	0	0	0.00
68	0	0.00	0	0.00	68	0	0	0	0.00
69	0	0.00	0	0.00	69	0	0	0	0.00
70	0	0.00	0	0.00	70	0	0	0	0.00
71	1	0.42	7	50.00	71	0	0	0	0.00
72	0	0.00	1	7.14	72	0	0	2	100.00
73	0	0.00	0	0.00	73	0	0	1	50.00
74	0	0.00	0	0.00	74	0	0	0	0.00
75	2	0.84	0	0.00	75	0	0	0	0.00
76	0	0.00	3	21.43	76	0	0	0	0.00
77	0	0.00	0	0.00	77	0	0	0	0.00
78	0	0.00	0	0.00	78	0	0	0	0.00
79	0	0.00	0	0.00	79	0	0	0	0.00
80	1	0.42	0	0.00	80	0	0	0	0.00
81	0	0.00	0	0.00	81	0	0	0	0.00
82	0	0.00	8	57.14	82	0	0	1	50.00
83	0	0.00	0	0.00	83	0	0	0	0.00
84	0	0.00	0	0.00	84	0	0	0	0.00
85	0	0.00	3	21.43	85	0	0	0	0.00
86	0	0.00	0	0.00	86	0	0	0	0.00
87	0	0.00	0	0.00	87	0	0	0	0.00
88	1	0.42	7	50.00	88	0	0	1	50.00
89	0	0.00	1	7.14	89	0	0	0	0.00
90	0	0.00	0	0.00	90	0	0	0	0.00
91	0	0.00	0	0.00	91	0	0	0	0.00
92	0	0.00	0	0.00	92	0	0	0	0.00
93	0	0.00	0	0.00	93	0	0	0	0.00
94	0	0.00	0	0.00	94	0	0	0	0.00
95	0	0.00	0	0.00	95	0	0	0	0.00
96	0	0.00	3	21.43	96	0	0	0	0.00
97	0	0.00	3	21.43	97	0	0	0	0.00
98	0	0.00	0	0.00	98	0	0	1	50.00
99	0	0.00	2	14.29	99	0	0	0	0.00
100	0	0.00	0	0.00	100	0	0	0	0.00
101	0	0.00	0	0.00	101	0	0	0	0.00
102	0	0.00	0	0.00	102	0	0	0	0.00
103	0	0.00	2	14.29	103	0	0	0	0.00
104	0	0.00	1	7.14	104	0	0	1	50.00
105	1	0.42	0	0.00	105	0	0	2	100.00
106	1	0.42	0	0.00	106	0	0	0	0.00
107	1	0.42	0	0.00	107	0	0	0	0.00
108	0	0.00	0	0.00	108	0	0	0	0.00
109	1	0.42	0	0.00	109	0	0	0	0.00
110	0	0.00	6	42.86	110	0	0	0	0.00
111	2	0.84	1	7.14	111	0	0	0	0.00
112	0	0.00	0	0.00	112	0	0	1	50.00

Supplemental Figure 6C. Source Data

IgHV Position	IgHV Mutation	Avg mutation	IgHV Motifs	Avg Motif	TAILV Position	TAILV Mutation	Avg mutation	TAILV Motifs	Avg Motif
113	1	0.42	1	7.14	113	0	0	0	0.00
114	0	0.00	1	7.14	114	0	0	0	0.00
115	0	0.00	0	0.00	115	0	0	0	0.00
116	0	0.00	0	0.00	116	0	0	0	0.00
117	0	0.00	0	0.00	117	0	0	0	0.00
118	0	0.00	0	0.00	118	0	0	0	0.00
119	0	0.00	0	0.00	119	0	0	0	0.00
120	0	0.00	0	0.00	120	0	0	0	0.00
121	0	0.00	1	7.14	121	0	0	1	50.00
122	0	0.00	3	21.43	122	0	0	0	0.00
123	0	0.00	0	0.00	123	0	0	0	0.00
124	2	0.84	1	7.14	124	0	0	0	0.00
125	0	0.00	3	21.43	125	0	0	0	0.00
126	0	0.00	0	0.00	126	0	0	0	0.00
127	0	0.00	0	0.00	127	0	0	0	0.00
128	0	0.00	7	50.00	128	0	0	2	100.00
129	0	0.00	0	0.00	129	0	0	0	0.00
130	1	0.42	0	0.00	130	0	0	0	0.00
131	0	0.00	0	0.00	131	0	0	0	0.00
132	0	0.00	0	0.00	132	0	0	0	0.00
133	0	0.00	0	0.00	133	0	0	0	0.00
134	0	0.00	7	50.00	134	0	0	1	50.00
135	0	0.00	4	28.57	135	0	0	0	0.00
136	0	0.00	0	0.00	136	0	0	0	0.00
137	0	0.00	0	0.00	137	0	0	0	0.00
138	0	0.00	0	0.00	138	0	0	0	0.00
139	0	0.00	0	0.00	139	0	0	0	0.00
140	0	0.00	0	0.00	140	0	0	0	0.00
141	0	0.00	10	71.43	141	0	0	2	100.00
142	0	0.00	0	0.00	142	0	0	0	0.00
143	0	0.00	0	0.00	143	0	0	0	0.00
144	0	0.00	0	0.00	144	0	0	0	0.00
145	3	1.27	0	0.00	145	0	0	0	0.00
146	0	0.00	3	21.43	146	0	0	0	0.00
147	4	1.69	2	14.29	147	0	0	0	0.00
148	0	0.00	0	0.00	148	0	0	0	0.00
149	0	0.00	2	14.29	149	0	0	0	0.00
150	0	0.00	2	14.29	150	0	0	0	0.00
151	1	0.42	0	0.00	151	0	0	0	0.00
152	1	0.42	3	21.43	152	0	0	0	0.00
153	1	0.42	2	14.29	153	0	0	0	0.00
154	1	0.42	0	0.00	154	0	0	1	50.00
155	1	0.42	6	42.86	155	0	0	2	100.00
156	1	0.42	7	50.00	156	0	0	1	50.00
157	0	0.00	0	0.00	157	0	0	0	0.00
158	0	0.00	0	0.00	158	0	0	0	0.00
159	1	0.42	3	21.43	159	0	0	1	50.00
160	2	0.84	3	21.43	160	0	0	0	0.00
161	0	0.00	5	35.71	161	0	0	0	0.00
162	1	0.42	1	7.14	162	0	0	0	0.00
163	0	0.00	0	0.00	163	0	0	0	0.00
164	0	0.00	0	0.00	164	0	0	0	0.00
165	0	0.00	1	7.14	165	0	0	2	100.00

Supplemental Figure 6C. Source Data

IgHV Position	IgHV Mutation	Avg mutation	IgHV Motifs	Avg Motif	TAILV Position	TAILV Mutation	Avg mutation	TAILV Motifs	Avg Motif
166	2	0.84	1	7.14	166	0	0	0	0.00
167	3	1.27	5	35.71	167	0	0	0	0.00
168	0	0.00	0	0.00	168	0	0	1	50.00
169	0	0.00	0	0.00	169	0	0	0	0.00
170	0	0.00	0	0.00	170	0	0	0	0.00
171	0	0.00	0	0.00	171	0	0	2	100.00
172	0	0.00	0	0.00	172	0	0	0	0.00
173	0	0.00	0	0.00	173	0	0	0	0.00
174	0	0.00	0	0.00	174	0	0	2	100.00
175	0	0.00	1	7.14	175	0	0	0	0.00
176	0	0.00	0	0.00	176	0	0	0	0.00
177	0	0.00	0	0.00	177	0	0	0	0.00
178	0	0.00	0	0.00	178	0	0	0	0.00
179	0	0.00	0	0.00	179	0	0	0	0.00
180	0	0.00	0	0.00	180	0	0	0	0.00
181	0	0.00	7	50.00	181	0	0	0	0.00
182	0	0.00	0	0.00	182	0	0	0	0.00
183	0	0.00	0	0.00	183	0	0	0	0.00
184	0	0.00	0	0.00	184	0	0	0	0.00
185	0	0.00	0	0.00	185	0	0	0	0.00
186	1	0.42	0	0.00	186	0	0	0	0.00
187	1	0.42	0	0.00	187	0	0	0	0.00
188	2	0.84	0	0.00	188	0	0	1	50.00
189	1	0.42	1	7.14	189	0	0	1	50.00
190	1	0.42	0	0.00	190	0	0	0	0.00
191	0	0.00	0	0.00	191	0	0	0	0.00
192	0	0.00	0	0.00	192	0	0	0	0.00
193	0	0.00	0	0.00	193	0	0	0	0.00
194	0	0.00	0	0.00	194	0	0	0	0.00
195	3	1.27	4	28.57	195	0	0	0	0.00
196	0	0.00	0	0.00	196	0	0	0	0.00
197	0	0.00	0	0.00	197	0	0	0	0.00
198	1	0.42	4	28.57	198	0	0	0	0.00
199	1	0.42	0	0.00	199	0	0	1	50.00
200	0	0.00	0	0.00	200	0	0	0	0.00
201	0	0.00	1	7.14	201	0	0	0	0.00
202	0	0.00	4	28.57	202	0	0	0	0.00
203	0	0.00	3	21.43	203	0	0	0	0.00
204	4	1.69	1	7.14	204	0	0	2	100.00
205	0	0.00	0	0.00	205	0	0	0	0.00
206	0	0.00	2	14.29	206	0	0	0	0.00
207	0	0.00	0	0.00	207	0	0	0	0.00
208	0	0.00	7	50.00	208	0	0	2	100.00
209	0	0.00	0	0.00	209	0	0	0	0.00
210	0	0.00	1	7.14	210	0	0	0	0.00
211	1	0.42	2	14.29	211	0	0	0	0.00
212	0	0.00	5	35.71	212	0	0	0	0.00
213	0	0.00	6	42.86	213	0	0	1	50.00
214	1	0.42	0	0.00	214	0	0	0	0.00
215	0	0.00	3	21.43	215	0	0	0	0.00
216	1	0.42	6	42.86	216	0	0	2	100.00
217	0	0.00	0	0.00	217	0	0	0	0.00
218	0	0.00	0	0.00	218	0	0	0	0.00

Supplemental Figure 6C. Source Data

IgHV Position	IgHV Mutation	Avg mutation	IgHV Motifs	Avg Motif	TAILV Position	TAILV Mutation	Avg mutation	TAILV Motifs	Avg Motif
219	0	0.00	0	0.00	219	0	0	1	50.00
220	0	0.00	1	7.14	220	0	0	0	0.00
221	3	1.27	9	64.29	221	0	0	0	0.00
222	1	0.42	0	0.00	222	0	0	0	0.00
223	1	0.42	0	0.00	223	0	0	0	0.00
224	1	0.42	2	14.29	224	0	0	0	0.00
225	1	0.42	3	21.43	225	0	0	0	0.00
226	1	0.42	0	0.00	226	0	0	0	0.00
227	1	0.42	0	0.00	227	0	0	1	50.00
228	1	0.42	2	14.29	228	0	0	0	0.00
229	0	0.00	0	0.00	229	0	0	0	0.00
230	1	0.42	5	35.71	230	0	0	1	50.00
231	5	2.11	9	64.29	231	0	0	2	100.00
232	1	0.42	0	0.00	232	0	0	0	0.00
233	1	0.42	0	0.00	233	0	0	0	0.00
234	0	0.00	1	7.14	234	0	0	1	50.00
235	0	0.00	0	0.00	235	0	0	0	0.00
236	0	0.00	1	7.14	236	0	0	0	0.00
237	1	0.42	4	28.57	237	0	0	0	0.00
238	0	0.00	0	0.00	238	0	0	0	0.00
239	0	0.00	0	0.00	239	0	0	0	0.00
240	0	0.00	0	0.00	240	0	0	0	0.00
241	0	0.00	2	14.29	241	0	0	0	0.00
242	0	0.00	2	14.29	242	0	0	0	0.00
243	0	0.00	0	0.00	243	0	0	0	0.00
244	0	0.00	4	28.57	244	0	0	0	0.00
245	0	0.00	0	0.00	245	0	0	1	50.00
246	1	0.42	0	0.00	246	0	0	0	0.00
247	0	0.00	0	0.00	247	0	0	0	0.00
248	0	0.00	0	0.00	248	0	0	0	0.00
249	0	0.00	0	0.00	249	0	0	1	50.00
250	0	0.00	0	0.00	250	0	0	0	0.00
251	0	0.00	0	0.00	251	0	0	0	0.00
252	0	0.00	0	0.00	252	0	0	0	0.00
253	0	0.00	0	0.00	253	0	0	0	0.00
254	0	0.00	0	0.00	254	0	0	0	0.00
255	0	0.00	0	0.00	255	0	0	0	0.00
256	0	0.00	0	0.00	256	0	0	0	0.00
257	0	0.00	0	0.00	257	0	0	0	0.00
258	0	0.00	0	0.00	258	0	0	0	0.00
259	0	0.00	0	0.00	259	0	0	0	0.00
260	0	0.00	1	7.14	260	0	0	0	0.00
261	0	0.00	0	0.00	261	0	0	0	0.00
262	0	0.00	0	0.00	262	0	0	1	50.00
263	0	0.00	0	0.00	263	0	0	0	0.00
264	0	0.00	0	0.00	264	0	0	0	0.00
265	0	0.00	0	0.00	265	0	0	2	100.00
266	0	0.00	7	50.00	266	0	0	1	50.00
267	0	0.00	0	0.00	267	0	0	0	0.00
268	0	0.00	1	7.14	268	0	0	2	100.00
269	0	0.00	1	7.14	269	0	0	2	100.00
270	0	0.00	0	0.00	270	0	0	0	0.00
271	0	0.00	0	0.00	271	0	0	0	0.00

Supplemental Figure 6C. Source Data

IgHV Position	IgHV Mutation	Avg mutation	IgHV Motifs	Avg Motif	TAILV Position	TAILV Mutation	Avg mutation	TAILV Motifs	Avg Motif
272	0	0.00	1	7.14	272	0	0	0	0.00
273	0	0.00	0	0.00	273	0	0	1	50.00
274	0	0.00	0	0.00	274	0	0	0	0.00
275	0	0.00	0	0.00	275	0	0	0	0.00
276	0	0.00	0	0.00	276	0	0	0	0.00
277	0	0.00	0	0.00	277	0	0	0	0.00
278	0	0.00	1	7.14	278	0	0	0	0.00
279	0	0.00	1	7.14	279	0	0	0	0.00
280	0	0.00	0	0.00	280	0	0	0	0.00
281	0	0.00	0	0.00	281	0	0	0	0.00
282	0	0.00	2	14.29	282	0	0	0	0.00
283	0	0.00	0	0.00	283	0	0	1	50.00
284	0	0.00	0	0.00	284	0	0	2	100.00
285	0	0.00	1	7.14	285	0	0	0	0.00
286	0	0.00	2	14.29	286	0	0	0	0.00
287	0	0.00	0	0.00	287	0	0	0	0.00
288	0	0.00	7	50.00	288	0	0	2	100.00
289	1	0.42	0	0.00	289	0	0	0	0.00
290	1	0.42	0	0.00	290	0	0	0	0.00
291	0	0.00	3	21.43	291	0	0	0	0.00
292	1	0.42	0	0.00	292	0	0	0	0.00
293	0	0.00	0	0.00	293	0	0	0	0.00
294	0	0.00	0	0.00	294	0	0	1	50.00
295	1	0.42	0	0.00	295	0	0	0	0.00
296	0	0.00	0	0.00	296	0	0	0	0.00
297	0	0.00	3	21.43	297	0	0	0	0.00
298	0	0.00	3	21.43	298	0	0	0	0.00
299	1	0.42	0	0.00	299	0	0	0	0.00
300	0	0.00	0	0.00	300	0	0	0	0.00
301	0	0.00	0	0.00	301	0	0	0	0.00
302	0	0.00	0	0.00	302	0	0	0	0.00
303	0	0.00	0	0.00	303	0	0	0	0.00
304	0	0.00	0	0.00	304	0	0	0	0.00
305	0	0.00	0	0.00	305	0	0	0	0.00
306	0	0.00	0	0.00	306	0	0	0	0.00
307	0	0.00	0	0.00	307	0	0	0	0.00
308	0	0.00	0	0.00	308	0	0	0	0.00
309	2	0.84	1	7.14	309	0	0	0	0.00
310	1	0.42	0	0.00	310	0	0	0	0.00
311	0	0.00	0	0.00	311	0	0	0	0.00
312	0	0.00	0	0.00	312	0	0	0	0.00
313	1	0.42	0	0.00	313	0	0	0	0.00
314	0	0.00	0	0.00	314	0	0	0	0.00
315	2	0.84	6	42.86	315	0	0	0	0.00
316	0	0.00	0	0.00	316	0	0	0	0.00
317	0	0.00	0	0.00	317	0	0	0	0.00
318	1	0.42	0	0.00	318	0	0	0	0.00
319	1	0.42	0	0.00	319	0	0	0	0.00
320	0	0.00	0	0.00	320	0	0	0	0.00
321	0	0.00	0	0.00	321	0	0	0	0.00
322	1	0.42	0	0.00	322	0	0	0	0.00
323	1	0.42	0	0.00	323	0	0	0	0.00
324	0	0.00	0	0.00	324	0	0	0	0.00

Supplemental Figure 6C. Source Data

IgHV Position	IgHV Mutation	Avg mutation	IgHV Motifs	Avg Motif	TAILV Position	TAILV Mutation	Avg mutation	TAILV Motifs	Avg Motif
325	0	0.00	0	0.00	325	0	0	0	0.00
326	0	0.00	0	0.00	326	0	0	0	0.00
327	0	0.00	0	0.00	327	0	0	0	0.00
328	0	0.00	0	0.00	328	0	0	0	0.00
329	0	0.00	1	7.14	329	0	0	0	0.00
330	0	0.00	0	0.00	330	0	0	0	0.00
331	0	0.00	0	0.00	331	0	0	0	0.00
332	0	0.00	0	0.00	332	0	0	0	0.00
333	1	0.42	1	7.14	333	0	0	0	0.00
334	0	0.00	0	0.00	334	0	0	1	50.00
335	0	0.00	0	0.00	335	0	0	1	50.00
336	0	0.00	0	0.00	336	0	0	0	0.00
337	0	0.00	0	0.00	337	0	0	0	0.00
338	2	0.84	0	0.00	338	0	0	1	50.00
339	0	0.00	3	21.43	339	0	0	0	0.00
340	0	0.00	0	0.00	340	0	0	0	0.00
341	1	0.42	0	0.00	341	0	0	0	0.00
342	1	0.42	0	0.00	342	0	0	0	0.00
343	1	0.42	1	7.14	343	0	0	0	0.00
344	0	0.00	1	7.14	344	0	0	0	0.00
345	1	0.42	7	50.00	345	0	0	0	0.00
346	1	0.42	0	0.00	346	0	0	0	0.00
347	1	0.42	1	7.14	347	0	0	0	0.00
348	1	0.42	0	0.00	348	0	0	0	0.00

Supplemental Figure 6D. Source Data

NTRV Position	NTRV Mutation	Avg NTRV Mutation	NTRV Motifs	Avg NTRV motif	STRDV Position	STRDV Position	STRDV Mutation	Avg STRDV Mutation	STRDV motifs	Avg STRDV motif
		n=51		n=6				n=62		n=7
61	0	0.00	0	0.00	61	13	0	0.00	0	0.00
62	0	0.00	0	0.00	62	14	0	0.00	0	0.00
63	0	0.00	0	0.00	63	15	0	0.00	0	0.00
64	0	0.00	1	16.67	64	16	0	0.00	1	14.29
65	0	0.00	0	0.00	65	17	0	0.00	0	0.00
66	0	0.00	0	0.00	66	18	0	0.00	0	0.00
67	0	0.00	1	16.67	67	19	0	0.00	0	0.00
68	0	0.00	0	0.00	68	20	0	0.00	0	0.00
69	0	0.00	0	0.00	69	21	0	0.00	0	0.00
70	0	0.00	0	0.00	70	22	0	0.00	0	0.00
71	1	1.96	0	0.00	71	23	0	0.00	0	0.00
72	0	0.00	4	66.67	72	24	0	0.00	2	28.57
73	0	0.00	0	0.00	73	25	0	0.00	0	0.00
74	0	0.00	0	0.00	74	26	0	0.00	0	0.00
75	0	0.00	0	0.00	75	27	0	0.00	0	0.00
76	0	0.00	3	50.00	76	28	0	0.00	0	0.00
77	0	0.00	2	33.33	77	29	0	0.00	0	0.00
78	0	0.00	0	0.00	78	30	0	0.00	0	0.00
79	0	0.00	0	0.00	79	31	1	1.61	3	42.86
80	1	1.96	2	33.33	80	32	0	0.00	2	28.57
81	1	1.96	0	0.00	81	33	0	0.00	0	0.00
82	0	0.00	1	16.67	82	34	0	0.00	3	42.86
83	0	0.00	0	0.00	83	35	0	0.00	0	0.00
84	0	0.00	0	0.00	84	36	0	0.00	0	0.00
85	0	0.00	0	0.00	85	37	0	0.00	7	100.00
86	0	0.00	1	16.67	86	38	0	0.00	0	0.00
87	0	0.00	0	0.00	87	39	0	0.00	0	0.00
88	0	0.00	0	0.00	88	40	0	0.00	0	0.00
89	1	1.96	0	0.00	89	41	0	0.00	6	85.71
90	0	0.00	0	0.00	90	42	0	0.00	0	0.00
91	0	0.00	0	0.00	91	43	0	0.00	0	0.00
92	0	0.00	0	0.00	92	44	0	0.00	0	0.00
93	0	0.00	0	0.00	93	45	0	0.00	0	0.00
94	0	0.00	0	0.00	94	46	0	0.00	4	57.14
95	0	0.00	0	0.00	95	47	0	0.00	1	14.29
96	0	0.00	0	0.00	96	48	0	0.00	0	0.00
97	0	0.00	0	0.00	97	49	1	1.61	5	71.43
98	0	0.00	0	0.00	98	50	0	0.00	6	85.71
99	0	0.00	4	66.67	99	51	0	0.00	0	0.00
100	0	0.00	0	0.00	100	52	0	0.00	0	0.00
101	0	0.00	0	0.00	101	53	0	0.00	0	0.00
102	0	0.00	0	0.00	102	54	1	1.61	0	0.00
103	0	0.00	0	0.00	103	55	0	0.00	0	0.00
104	0	0.00	0	0.00	104	56	0	0.00	0	0.00
105	1	1.96	0	0.00	105	57	0	0.00	0	0.00
106	0	0.00	0	0.00	106	58	0	0.00	0	0.00
107	0	0.00	0	0.00	107	59	0	0.00	0	0.00
108	0	0.00	0	0.00	108	60	0	0.00	0	0.00
109	0	0.00	0	0.00	109	61	0	0.00	3	42.86
110	0	0.00	3	50.00	110	62	0	0.00	0	0.00
111	0	0.00	3	50.00	111	63	1	1.61	0	0.00
112	0	0.00	0	0.00	112	64	1	1.61	1	14.29
113	0	0.00	0	0.00	113	65	0	0.00	4	57.14
114	0	0.00	0	0.00	114	66	0	0.00	0	0.00
115	0	0.00	0	0.00	115	67	0	0.00	0	0.00
116	0	0.00	1	16.67	116	68	0	0.00	0	0.00
117	0	0.00	0	0.00	117	69	0	0.00	0	0.00
118	0	0.00	0	0.00	118	70	0	0.00	0	0.00
119	0	0.00	0	0.00	119	71	1	1.61	5	71.43
120	0	0.00	0	0.00	120	72	0	0.00	6	85.71
121	1	1.96	5	83.33	121	73	0	0.00	0	0.00
122	2	3.92	0	0.00	122	74	0	0.00	1	14.29
123	1	1.96	0	0.00	123	75	0	0.00	0	0.00
124	0	0.00	0	0.00	124	76	0	0.00	0	0.00
125	0	0.00	0	0.00	125	77	0	0.00	1	14.29
126	0	0.00	0	0.00	126	78	1	1.61	0	0.00
127	0	0.00	0	0.00	127	79	0	0.00	0	0.00
128	0	0.00	3	50.00	128	80	0	0.00	0	0.00
129	0	0.00	0	0.00	129	81	0	0.00	0	0.00
130	0	0.00	0	0.00	130	82	0	0.00	0	0.00
131	0	0.00	0	0.00	131	83	0	0.00	0	0.00
132	0	0.00	0	0.00	132	84	0	0.00	0	0.00
133	0	0.00	0	0.00	133	85	0	0.00	1	14.29

134	0	0.00	1	16.67	134	86	0	0.00	3	42.86
135	0	0.00	1	16.67	135	87	0	0.00	0	0.00
136	0	0.00	0	0.00	136	88	0	0.00	0	0.00
137	0	0.00	0	0.00	137	89	0	0.00	0	0.00
138	0	0.00	0	0.00	138	90	0	0.00	0	0.00
139	0	0.00	0	0.00	139	91	0	0.00	0	0.00
140	0	0.00	1	16.67	140	92	0	0.00	0	0.00
141	0	0.00	0	0.00	141	93	1	1.61	1	14.29
142	0	0.00	0	0.00	142	94	0	0.00	0	0.00
143	1	1.96	0	0.00	143	95	0	0.00	0	0.00
144	0	0.00	0	0.00	144	96	0	0.00	7	100.00
145	0	0.00	0	0.00	145	97	0	0.00	0	0.00
146	0	0.00	0	0.00	146	98	0	0.00	0	0.00
147	0	0.00	0	0.00	147	99	0	0.00	6	85.71
148	1	1.96	0	0.00	148	100	0	0.00	1	14.29
149	1	1.96	0	0.00	149	101	0	0.00	1	14.29
150	0	0.00	0	0.00	150	102	1	1.61	0	0.00
151	0	0.00	0	0.00	151	103	0	0.00	1	14.29
152	0	0.00	0	0.00	152	104	0	0.00	0	0.00
153	0	0.00	0	0.00	153	105	0	0.00	0	0.00
154	1	1.96	0	0.00	154	106	0	0.00	0	0.00
155	0	0.00	0	0.00	155	107	0	0.00	0	0.00
156	1	1.96	0	0.00	156	108	0	0.00	7	100.00
157	0	0.00	0	0.00	157	109	0	0.00	0	0.00
158	0	0.00	1	16.67	158	110	0	0.00	0	0.00
159	0	0.00	0	0.00	159	111	0	0.00	7	100.00
160	0	0.00	0	0.00	160	112	0	0.00	0	0.00
161	0	0.00	0	0.00	161	113	0	0.00	0	0.00
162	0	0.00	0	0.00	162	114	0	0.00	7	100.00
163	0	0.00	0	0.00	163	115	0	0.00	0	0.00
164	0	0.00	0	0.00	164	116	0	0.00	0	0.00
165	0	0.00	0	0.00	165	117	1	1.61	0	0.00
166	0	0.00	0	0.00	166	118	0	0.00	0	0.00
167	0	0.00	0	0.00	167	119	0	0.00	0	0.00
168	0	0.00	0	0.00	168	120	1	1.61	0	0.00
169	0	0.00	0	0.00	169	121	1	1.61	0	0.00
170	0	0.00	1	16.67	170	122	0	0.00	1	14.29
171	0	0.00	1	16.67	171	123	0	0.00	0	0.00
172	0	0.00	0	0.00	172	124	0	0.00	0	0.00
173	0	0.00	0	0.00	173	125	0	0.00	0	0.00
174	0	0.00	0	0.00	174	126	0	0.00	0	0.00
175	0	0.00	0	0.00	175	127	0	0.00	0	0.00
176	0	0.00	0	0.00	176	128	0	0.00	1	14.29
177	0	0.00	0	0.00	177	129	2	3.23	0	0.00
178	0	0.00	0	0.00	178	130	0	0.00	0	0.00
179	0	0.00	0	0.00	179	131	0	0.00	0	0.00
180	0	0.00	0	0.00	180	132	0	0.00	0	0.00
181	0	0.00	1	16.67	181	133	0	0.00	4	57.14
182	0	0.00	0	0.00	182	134	0	0.00	0	0.00
183	0	0.00	0	0.00	183	135	0	0.00	0	0.00
184	0	0.00	0	0.00	184	136	0	0.00	0	0.00
185	0	0.00	0	0.00	185	137	0	0.00	0	0.00
186	0	0.00	1	16.67	186	138	0	0.00	0	0.00
187	0	0.00	1	16.67	187	139	0	0.00	0	0.00
188	0	0.00	0	0.00	188	140	0	0.00	0	0.00
189	0	0.00	0	0.00	189	141	0	0.00	1	14.29
190	0	0.00	1	16.67	190	142	0	0.00	0	0.00
191	0	0.00	1	16.67	191	143	0	0.00	0	0.00
192	0	0.00	0	0.00	192	144	0	0.00	6	85.71
193	1	1.96	0	0.00	193	145	0	0.00	0	0.00
194	0	0.00	0	0.00	194	146	0	0.00	0	0.00
195	0	0.00	0	0.00	195	147	0	0.00	2	28.57
196	0	0.00	0	0.00	196	148	0	0.00	3	42.86
197	0	0.00	0	0.00	197	149	0	0.00	0	0.00
198	0	0.00	0	0.00	198	150	0	0.00	0	0.00
199	0	0.00	0	0.00	199	151	0	0.00	0	0.00
200	0	0.00	0	0.00	200	152	0	0.00	0	0.00
201	0	0.00	0	0.00	201	153	0	0.00	0	0.00
202	0	0.00	0	0.00	202	154	0	0.00	0	0.00
203	0	0.00	0	0.00	203	155	0	0.00	4	57.14
204	0	0.00	0	0.00	204	156	0	0.00	0	0.00
205	0	0.00	0	0.00	205	157	0	0.00	0	0.00
206	0	0.00	0	0.00	206	158	0	0.00	0	0.00
207	0	0.00	0	0.00	207	159	1	1.61	2	28.57
208	0	0.00	0	0.00	208	160	0	0.00	0	0.00
209	0	0.00	0	0.00	209	161	0	0.00	1	14.29
210	0	0.00	0	0.00	210	162	0	0.00	0	0.00
211	0	0.00	0	0.00	211	163	0	0.00	1	14.29

212	0	0.00	0	0.00	212	164	0	0.00	1	14.29
213	0	0.00	0	0.00	213	165	0	0.00	0	0.00
214	0	0.00	0	0.00	214	166	0	0.00	0	0.00
215	0	0.00	0	0.00	215	167	0	0.00	0	0.00
216	0	0.00	1	16.67	216	168	0	0.00	0	0.00
217	0	0.00	1	16.67	217	169	0	0.00	0	0.00
218	1	1.96	0	0.00	218	170	0	0.00	0	0.00
219	0	0.00	0	0.00	219	171	0	0.00	5	71.43
220	1	1.96	0	0.00	220	172	0	0.00	5	71.43
221	0	0.00	0	0.00	221	173	0	0.00	0	0.00
222	0	0.00	0	0.00	222	174	0	0.00	0	0.00
223	0	0.00	0	0.00	223	175	0	0.00	0	0.00
224	0	0.00	0	0.00	224	176	1	1.61	0	0.00
225	0	0.00	0	0.00	225	177	0	0.00	0	0.00
226	0	0.00	0	0.00	226	178	0	0.00	0	0.00
227	0	0.00	0	0.00	227	179	0	0.00	0	0.00
228	0	0.00	1	16.67	228	180	0	0.00	0	0.00
229	0	0.00	0	0.00	229	181	0	0.00	0	0.00
230	0	0.00	0	0.00	230	182	0	0.00	0	0.00
231	0	0.00	0	0.00	231	183	1	1.61	0	0.00
232	0	0.00	3	50.00	232	184	0	0.00	1	14.29
233	1	1.96	0	0.00	233	185	0	0.00	0	0.00
234	1	1.96	0	0.00	234	186	0	0.00	0	0.00
235	0	0.00	0	0.00	235	187	0	0.00	5	71.43
236	0	0.00	0	0.00	236	188	0	0.00	4	57.14
237	1	1.96	0	0.00	237	189	0	0.00	0	0.00
238	0	0.00	0	0.00	238	190	0	0.00	1	14.29
239	0	0.00	0	0.00	239	191	1	1.61	6	85.71
240	0	0.00	0	0.00	240	192	0	0.00	0	0.00
241	0	0.00	0	0.00	241	193	0	0.00	0	0.00
242	0	0.00	0	0.00	242	194	0	0.00	0	0.00
243	0	0.00	0	0.00	243	195	0	0.00	0	0.00
244	0	0.00	0	0.00	244	196	0	0.00	0	0.00
245	0	0.00	0	0.00	245	197	0	0.00	2	28.57
246	0	0.00	0	0.00	246	198	0	0.00	0	0.00
247	0	0.00	0	0.00	247	199	0	0.00	0	0.00
248	0	0.00	0	0.00	248	200	0	0.00	0	0.00
249	0	0.00	0	0.00	249	201	0	0.00	0	0.00
250	0	0.00	4	66.67	250	202	0	0.00	0	0.00
251	1	1.96	4	66.67	251	203	0	0.00	0	0.00
252	0	0.00	0	0.00	252	204	0	0.00	0	0.00
253	0	0.00	0	0.00	253	205	0	0.00	3	42.86
254	2	3.92	0	0.00	254	206	0	0.00	3	42.86
255	0	0.00	0	0.00	255	207	0	0.00	0	0.00
256	0	0.00	0	0.00	256	208	0	0.00	6	85.71
257	0	0.00	0	0.00	257	209	0	0.00	7	100.00
258	0	0.00	0	0.00	258	210	0	0.00	0	0.00
259	0	0.00	0	0.00	259	211	0	0.00	2	28.57
260	0	0.00	0	0.00	260	212	0	0.00	2	28.57
261	1	1.96	0	0.00	261	213	0	0.00	0	0.00
262	0	0.00	0	0.00	262	214	0	0.00	0	0.00
263	0	0.00	0	0.00	263	215	0	0.00	0	0.00
264	0	0.00	0	0.00	264	216	0	0.00	0	0.00
265	0	0.00	0	0.00	265	217	0	0.00	0	0.00
266	1	1.96	0	0.00	266	218	0	0.00	0	0.00
267	0	0.00	0	0.00	267	219	0	0.00	0	0.00
268	0	0.00	0	0.00	268	220	0	0.00	0	0.00
269	0	0.00	0	0.00	269	221	0	0.00	0	0.00
270	0	0.00	0	0.00	270	222	0	0.00	0	0.00
271	0	0.00	0	0.00	271	223	0	0.00	1	14.29
272	0	0.00	0	0.00	272	224	1	1.61	1	14.29
273	0	0.00	0	0.00	273	225	1	1.61	0	0.00
274	0	0.00	0	0.00	274	226	0	0.00	2	28.57
275	0	0.00	0	0.00	275	227	0	0.00	1	14.29
276	0	0.00	0	0.00	276	228	0	0.00	0	0.00
277	0	0.00	0	0.00	277	229	0	0.00	0	0.00
278	0	0.00	0	0.00	278	230	0	0.00	0	0.00
279	1	1.96	0	0.00	279	231	0	0.00	0	0.00
280	0	0.00	0	0.00	280	232	0	0.00	0	0.00
281	0	0.00	0	0.00	281	233	0	0.00	0	0.00
282	0	0.00	0	0.00	282	234	0	0.00	0	0.00
283	0	0.00	0	0.00	283	235	0	0.00	0	0.00
284	0	0.00	0	0.00	284	236	0	0.00	0	0.00
285	0	0.00	0	0.00	285	237	0	0.00	0	0.00
286	0	0.00	0	0.00	286	238	2	3.23	0	0.00
287	0	0.00	0	0.00	287	239	0	0.00	0	0.00
288	0	0.00	0	0.00	288	240	0	0.00	5	71.43
289	0	0.00	4	66.67	289	241	0	0.00	0	0.00

290	0	0.00	0	0.00	290	242	0	0.00	0	0.00
291	0	0.00	0	0.00	291	243	0	0.00	0	0.00
292	0	0.00	0	0.00	292	244	0	0.00	0	0.00
293	0	0.00	0	0.00	293	245	0	0.00	0	0.00
294	0	0.00	0	0.00	294	246	0	0.00	0	0.00
295	0	0.00	0	0.00	295	247	0	0.00	0	0.00
296	0	0.00	0	0.00	296	248	0	0.00	0	0.00
297	0	0.00	0	0.00	297	249	0	0.00	0	0.00
298	0	0.00	0	0.00	298	250	0	0.00	0	0.00
299	0	0.00	0	0.00	299	251	0	0.00	0	0.00
300	0	0.00	0	0.00	300	252	0	0.00	0	0.00
301	0	0.00	0	0.00	301	253	0	0.00	1	14.29
302	1	1.96	3	50.00	302	254	0	0.00	1	14.29
303	0	0.00	0	0.00	303	255	0	0.00	0	0.00
304	1	1.96	0	0.00	304	256	0	0.00	2	28.57
305	0	0.00	0	0.00	305	257	0	0.00	3	42.86
306	1	1.96	0	0.00	306	258	0	0.00	0	0.00
307	0	0.00	0	0.00	307	259	0	0.00	3	42.86
308	0	0.00	0	0.00	308	260	0	0.00	0	0.00
309	1	1.96	0	0.00	309	261	0	0.00	0	0.00
310	0	0.00	0	0.00	310	262	0	0.00	7	100.00
311	0	0.00	0	0.00	311	263	0	0.00	0	0.00
312	0	0.00	4	66.67	312	264	0	0.00	0	0.00
313	0	0.00	0	0.00	313	265	0	0.00	0	0.00
314	0	0.00	4	66.67	314	266	0	0.00	0	0.00
315	0	0.00	0	0.00	315	267	2	3.23	0	0.00
316	0	0.00	0	0.00	316	268	0	0.00	0	0.00
317	0	0.00	0	0.00	317	269	0	0.00	0	0.00
318	0	0.00	0	0.00	318	270	0	0.00	0	0.00
319	0	0.00	4	66.67	319	271	0	0.00	0	0.00
320	0	0.00	1	16.67	320	272	0	0.00	0	0.00
321	0	0.00	0	0.00	321	273	0	0.00	0	0.00
322	0	0.00	0	0.00	322	274	0	0.00	5	71.43
323	1	1.96	0	0.00	323	275	0	0.00	4	57.14
324	0	0.00	0	0.00	324	276	0	0.00	0	0.00
325	0	0.00	0	0.00	325	277	0	0.00	4	57.14
326	0	0.00	0	0.00	326	278	1	1.61	0	0.00
327	0	0.00	0	0.00	327	279	0	0.00	3	42.86
328	0	0.00	0	0.00	328	280	0	0.00	0	0.00
329	0	0.00	0	0.00	329	281	0	0.00	0	0.00
330	0	0.00	0	0.00	330	282	0	0.00	0	0.00
331	0	0.00	0	0.00	331	283	0	0.00	0	0.00
332	0	0.00	0	0.00	332	284	0	0.00	0	0.00
333	1	1.96	1	16.67	333	285	0	0.00	7	100.00
334	0	0.00	0	0.00	334	286	0	0.00	0	0.00
335	0	0.00	0	0.00	335	287	0	0.00	0	0.00
336	0	0.00	0	0.00	336	288	0	0.00	0	0.00
337	0	0.00	0	0.00	337	289	0	0.00	5	71.43
338	2	3.92	0	0.00	338	290	0	0.00	5	71.43
339	0	0.00	0	0.00	339	291	0	0.00	0	0.00
340	0	0.00	0	0.00	340	292	0	0.00	0	0.00
341	1	1.96	0	0.00	341	293	0	0.00	0	0.00
342	1	1.96	0	0.00	342	294	0	0.00	0	0.00
343	1	1.96	1	16.67	343	295	0	0.00	0	0.00