

## Supplementary Table Legends

**Supplementary Table 1:** Oligonucleotide primers used in these studies.

**Supplementary Table 2:** Sequence diversity of PCR products obtained from Figure 1. Products shown in Figure 1 were cloned and their sequence determined. The number of unique direct V-to-D rearrangements is indicated above the total number of clones sequenced. WT and cR2 animals are compared.

**Supplementary Table 3: (Part 1)** Sequence characterization of a typical D $\beta$ 2 coding element (upper case) deletion amplified from thymocyte DNA from a cR2 animal resulting in a perfect signal joint between the RSS12 and RSS23 (lower case). Germline sequence is shown above the line for comparison purposes. **(Part 2)** Sequence characterization of the D $\beta$ 1 to D $\beta$ 2 deletional rearrangements amplified from WT and cR2 thymocyte DNA. Some the PCR products shown in Figure 6 were cloned and their sequence determined, demonstrating that the RSS12 of D $\beta$ 1 was joined to the RSS23 of D $\beta$ 2. Several of the joints included portions of the D $\beta$ 1 and D $\beta$ 2 coding sequence (upper case) and novel nucleotides (N) in between (also upper case). In one sequence (67-5-1) the short stretch of novel nucleotides has been joined to a sequence that is 106bps away from the D $\beta$ 2 and appears to be a cryptic RSS sequence. Germline sequences are shown above the line. **(Part 3)** Sequence characterization of various D $\beta$ -to-D $\delta$  chromosomal translocations. Some of the PCR products shown in Figure 7 were cloned and the sequences determined. RSS sequences and their adjacent coding sequence are shown in lower and upper case, respectively. Untemplated nucleotides (N) are shown between the D coding sequences. In one characterization (c5-F) from a cR2 animal, the D $\beta$ 1 sequence is 59bps away from the 3' end of the D $\beta$ 1 coding sequence and is likely a cryptic RSS. Germline sequences are shown above the line in each case.

## Supplementary Figure Legends

**Supplementary Figure 1.** Representation of the V $\beta$ 8.1 coding sequence (boxed) followed by its flanking RSS-23 sequence. Portions of the RSS-23 are labeled above (clear boxes). A cryptic RSS-12 sequence is shown by the shaded box and shares the RSS-23 heptamer sequence but in the reverse orientation. Solid vertical arrow represents the normal position of the coding and signal ends breaks when the RSS-23 is utilized. The hollow vertical arrow denotes the cryptic coding and signal end breaks when the cryptic RSS-12 is utilized.

**Supplementary Figure 2.** Frequency of direct V $\beta$ #-to-D $\beta$ # rearrangements in *cR2* and WT mice. DNA purified from the thymus of sets of four animals for each genotype was analyzed by real-time PCR for direct VD $\beta$ 1 and VD $\beta$ 2 (C) rearrangements and the mean values (bars) with standard errors (whiskers) are shown.

**Supplementary Figure 3.** Frequency of complete V<sub>H</sub>-to-D<sub>H</sub>-to-J<sub>H</sub> and direct V<sub>H</sub>-to-D<sub>H</sub> rearrangements in *cR2* and WT mice. Direct VD-del and VD-inv, deletion and inversion utilizing V<sub>H</sub>J558 and DFL16.1. DNA purified from the indicated tissues was analyzed for complete VDJ (upper) or direct VD joints (middle and lower; deletion or inversion). Hybrid joints (not illustrated) were excluded by placing the D segment primer just within that coding segment. Four animals from each of the three possible genotypes were examined and the mean values (bars) with standard errors (whiskers) are shown.

**Supplementary Figure 4.** Frequency of direct D to J rearrangements in the thymus of *cR2* and WT mice. DNA purified from the thymus were analyzed for direct deletional VD joints (upper) or direct inversional DJ joints (lower). Four animals from each of the three possible genotypes were examined and the mean values (bars) with standard errors (whiskers) are shown.

Supplementary Table 1.

Conventional Primers	
Oligo Name	Sequence
Vβ8-F1	GTGGCAGTAACAGGAGGAAAGGTGAC
Vβ8-F2	CATGTAAGGATCGGCAGGACACG
Dβ1-F1	CCAGAGGAGCAGCTTATCTGGTGGT
Dβ1-F2	CAAGGGGTAGACCTATGGGAGGGTC
Dβ1-R1	GAGTAATCGCTTTGTGTGCATCACA
Dβ1-R2	CATTCTGGATCTAAACACATCTAGGCTTGC
Dβ2-F1	AAGCTGAACATTGTCCAGTAAGCAACAGG
Dβ2-F2	TCCTGGTAGGGACCTTATCACTTCACTCC
Dβ2-R1	CCCTGGATAGCCTTTCACACTCGTG
Dβ2-R2	CACATAGACTCCTCCTCACATGTAAATGCA
Dδ2-F1	CAAAGCACTGGCTGGTTAATGGC
Dδ2-F2	CCAAGTTTGATAACAGGTGAGTCTCTGTGC
Dδ2-R1	GTCAGTGTAGTCCGCTTGATCAATATTGAGG
Dδ2-R2	TTCTTGCAGTGACAATACAGACCAAATATACAGC
Dβ2-SJ-R1	GCACCTCTCCAGTTGAATCATTGTGCACA
Vh101-F1	ATGGCTGTCTTAGGGCTGCTCTTC
Vh101-F2	GCCAGTCTCCAGGAAAGGGTCTG
DhFL16.1-R1	AGTAGTTCTTATCATTCTCCCAAAGCA
DhFL16.1-R2	GCTGTTGGGAGGTCAGCCTAGAG
Dδ1-R1	GTCAGTGTAGTCCGCTTGATCAATATTGAGG
Dδ1-R2	TTCTTGCAGTGACAATACAGACCAAATATACAGC
Dδ1-F1	CAAAGCACTGGCTGGTTAATGGC
Dδ1-F2	CCAAGTTTGATAACAGGTGAGTCTCTGTGC
Dδ2-R1	CCAGGAAACAGATGAGAGACAGAGGC
Dδ1-R2	GCAAGTGGAGGTCATATCTTGTCAGTC
qPCR Primers	
Oligo Name	Sequence
APRT-F1	TGACTGAGGAGCTGGCTAGATG
APRT-R1	GAGCCACCAAGCAGTTCCTG
APRT-TaqMan	TCACACCCCTGCTCCAGCAGC
Vβ2-F	CCACACGGGTCACTGATACG
Vβ2-R	AGGTTCTGCCCTGGCTCAT
Vβ2-TaqMan	TGGCCACTTGCAGCCTCAGCT
Vβ7-F	GGAAGAAGCGGGAGCATTTC
Vβ7-R	GTAGAGCTGTGGATAAACTGCTAGCA
Vβ7-TaqMan	CCCTGATTCTGGATTCTGCTAAAACAAACCA
Vβ8-F	AGAAAGGAGATATCCCTGATGGATAC
Vβ8-R	GGGTAGCCAACTCCAGAATGAG
Vβ8-TaqMan	AGGCCTCCAGACCAAGCCAAGAGAACTT
Vβ14-F	GCCGAAGGACGACCAATTC
Vβ14-R	GGCACAGAGGTAGAAGCCAGAGT

Vβ14-TaqMan	TCCTAAGCACGGAGAAGCTGCTTCTCAG
Dβ1-R	GCGACCCAGGAGAAGAGTAGAG
Dβ2-R	GCTGAGAGTTGGTGTTTTTTTGG
Jβ2.7-R	GGAAGCGAGAGATGTGAATCTTACC
Vh81X-F	CCATGGAGAGACGATTCATCATC
Vh81X-R	GTCCTCAGACCTCAGACTGCTCAT
Vh81X-TaqMan	CCAGAGACAATACCAAGAAGACCCTGTACCTGC
Vh101-F	CAAGGCCACAYTSACTGTAGACA
Vh101-R	AGGCTGMTGAGCTGCATGT
Vh101-MGB	AYCCTCCAGCACAGCC
JhS1-R	GCCAGCTTACCTGAGGAAACG
JhS4-F	CCAGGGGTGATTCTAGTCAGACTCT
JhS4-R	AGACCTGGAGAGGCCATTCTTAC
JhS4-TaqMan	TCAAGGAACCTCAGTCACCGTCTCCTCA
DhFL16.1-F	TACGGTAGTAGCTACCACAGTGCTATATCCATC
DhFL16.1-R	CCGTAGTAATAAACACAGTAGTAGATCCCTTCACAA
DhSP2.9-F	TTTTTGTCAAGGGATCTACTACTGTGTCT
DhSP2.9-R	TTTTTGTAGCTGGATATATCACTGTGGTA
DhQ52-F	GCGGAGCACCCACAGTGCTA
DhQ52-R	CCACGTGTCACCGTGGTC

LM-PCR Primers

Oligo Name	Sequence
JhS2-F1	TCACTGGGTCTATAATTACTCTGATGTCTAGGAC
JhS2-F2	GTCAGGTGAGTCTCATCTGGG
Vα7.2-F1	CAACCAAACCGGTAATGTGCCTTTC
Vα7.2-F2	CTGTGTAGCGTGTGCTCTATCTCAGGC
Vβ18-R1	CATTTCTCGTACTGGTGTCTGTAGTAAGTCCT
Vβ18-R2	TGAACAGGTGTCAGCCGAATCTGTG
Vβ14-F1	ATGTTGTTTTCCAGACTTCAACTTGAC
Vβ14-F2	GACTATCAGCCAGAAATTCAGTGGCAA
Vδ4-R1	CCAACTCAGCTCCAGCCTTTCTTATCAG
Vδ4-R2	AGGAGGTCTCATCTCAGATGTGCTGC
Vδ5-F1	CCCATTGAACCCAGAGTGAGAGGTG
Vδ5-F2	GAAGCCAGTCTTTCCTGTGCCAGG
β-Glob-F1	TTTGGCTAGTCACTTCGGCA
B-Glob-R2	GTGTGTCCGCTATGCCTCCT

**Supplementary Table 2:** Sequence diversity of products obtained from Figure 1.

		WT	cR2
V $\beta$ 8/D $\beta$ 1	Unique	8	12
	Total	18	16
V $\beta$ 8/D $\beta$ 2	Unique	12	14
	Total	12	15
Vh101/DhFL16.1	Unique	1	8
	Total	8	11

	D $\beta$ 2 RSS12	D $\beta$ 2 Coding	D $\beta$ 2 RSS23
cR2 4-13	ctttttgtatcacgatgtaacattgtg	GGGACTGGGGGGGC	cacaatgattcaactggaagaggtgcttttataaaa
	ctttttgtatcacgatgtaacattgtg		cacaatgattcaactggaagaggtgcttttataaaa

Supplementary Table 3 Part 2

D $\beta$ 1 to D $\beta$ 2 Deletions

	D $\beta$ 1 RSS12	D $\beta$ 1 Coding		D $\beta$ 2 Coding	D $\beta$ 2 RSS23
	cttttttgataaaagctgtaacattgtg	GGGACAGGGGGC	N	GGGACTGGGGGGGC	cacaatgatt
WT 5-1	cttttttgataaaagctgtaacattgtg				cacaatgatt
25-3-10	cttttttgataaaagctgtaacattgtg				cacaatgatt
13-2-2	cttttttgataaaagctgtaacattgtg		A	C	cacaatgatt
14-2-3	cttttttgataaaagctgtaacattgtg		T		cacaatgatt
16-3-1	cttttttgataaaagctgtaacattgtg		T		cacaatgatt
21-3-6	cttttttgataaaagctgtaacattgtg		TC		cacaatgatt
22-3-7	cttttttgataaaagctgtaacattgtg	GG			cacaatgatt
24-3-9	cttttttgataaaagctgtaacattgtg	GG			cacaatgatt
5-2	cttttttgataaaagctgtaacattgtg	GGGACAGGGGG	TTG	GGGACTGGGGGGGC	cacaatgatt
15-2-4	cttttttgataaaagctgtaacattgtg	GGGACAGGG			atgatt
17-3-2	cttttttgataaaagctgtaacattgtg	GGGACA	T	GACTGGGGGGGC	cacaatgatt
18-3-3	cttttttgataaaagctgtaacattgtg	GGGACAGGGG	ATGA	GGGACTGGGGGGGC	cacaatgatt
20-3-5	cttttttgataaaagctgtaacattgtg	GGGACAGGGGG	AG	TGGGGGGGC	cacaatgatt
23-3-8	cttttttgataaaagctgtaacat			ACTGGGGGGGC	cacaatgatt
cR2 6-1	cttttttgataaaagctgtaacattgtg				cacaatgatt
73-5-7	cttttttgataaaagctgtaacattgtg				cacaatgatt
62-4-6	cttttttgataaaagctgtaacattgtg		AGA		cacaatgatt
64-4-8	cttttttgataaaagctgtaacattgtg			C	cacaatgatt
66-4-10	cttttttgataaaagctgtaacattgtg			GC	cacaatgatt
70-5-4	cttttttgataaaagctgtaacattgtg		AG		cacaatgatt
57-4-1	cttttttgataaaagctgtaacattgtg	GGGACAGGG	TATTGTGGGGACACA	GGACTGGGGGGGC	cacaatgatt
58-4-2	cttttttgataaaagctgtaacattgtg	GGGACAGGGG		ACTGGGGGGGC	cacaatgatt
68-5-2	cttttttgataaaagctgtaacattgtg	GGGACAGGGG		ACTGGGGGGGC	cacaatgatt
60-4-4	cttttttgataaaagctgtaacattgtg	GGGACAGGG		ACTGGGGGGGC	cacaatgatt
63-4-7	cttttttgataaaagctgtaacattgtg	GGGACAGGGG		CTGGGGGGGC	cacaatgatt
69-5-3	cttttttgataaaagctgtaacattgtg		T	GACTGGGGGGGC	cacaatgatt
71-5-5	cttttttgataaaagctgtaacattgtg	GGGACAGGGGGC	G	CTGGGGGGGC	cacaatgatt
74-5-8	cttttttgataaaagctgtaacattgtg	GGGACAGGGGGC		TGGGGGGGC	cacaatgatt
67-5-1	cttttttgataaaagctgtaacattgtg	GGGACAGGG	CCT		<u>agtggactca</u>

Cryptic RSS +106bps from D $\beta$ 2 is shown underlined

Supplementary Table 3, Part 3

**D $\delta$ 2 > to < D $\beta$ 1 Translocations**

	RSS	D $\delta$ 2 Coding		D $\beta$ 1 Coding	RSS
	ggtttttgcaaagctctgtagcaccgtg	ATCGGAGGGGATACGAG	N	GGGACAGGGGGC	cacggtgatt
cR2 c1-F	ggtttt		AGG		cacggtgatt
cR2 c2-F	ggtttttgcaaagctctgtagcac		GAG		acggtgatt
cR2 c6-F	ggtttttgcaaagctctgtagcaccg				cggtgatt
cR2 c5-F	ggtttt		CCTC		*cacagtcctctac

\*not RSS sequence

**D $\delta$ 2 > to < D $\beta$ 2 Translocations**

	RSS	D $\delta$ 2 Coding		D $\beta$ 2 Coding	RSS
	ggtttttgcaaagctctgtagcaccgtg	ATCGGAGGGGATACGAG	N	GGGACTGGGGGGGC	cacaatgatt
WT d1-F	ggtttttgcaaagctctgtagcaccgtg				cacaatgatt
WT d2-F	ggtttttgcaaagctctgtagcacg			GGGACTGGGGGGGC	cacaatgatt
WT d3-F	ggtttttgcaaagctctgtagcaccgtg				cacaatgatt
cR2 d4-F	ggtttttgcaaagctctgtagcaccgtg				cacaatgatt
cR2 d6-F	ggtttttgcaaagctctg		GA		gatt

**D $\beta$ 2 > to < D $\delta$ 1 Translocations**

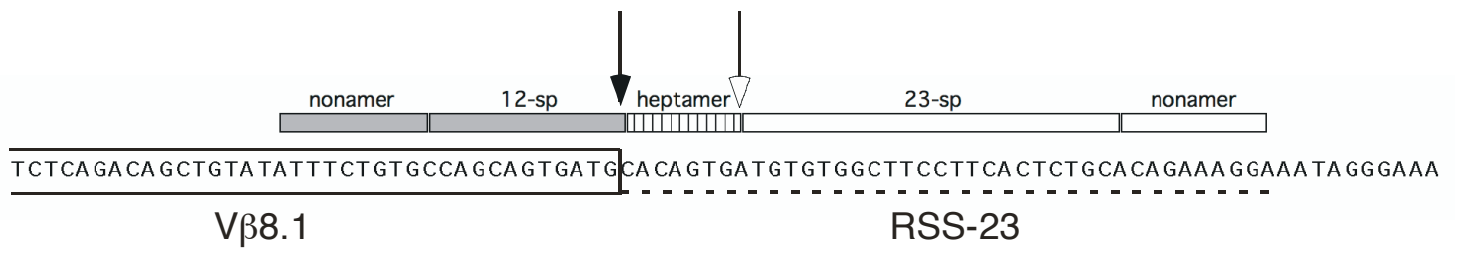
	RSS	D $\beta$ 2 Coding		D $\delta$ 1 Coding	RSS
	cttttttgtagcaccgatgtaacattgtg	GGGACTGGGGGGGC	N	GTGGCATATCA	cacaggttga
WT a1-F	cttttttgtagcaccgatg		AACCCCCNN		caggttga
cR2 a2-F	cttttttgtagcaccgatgtaacattgtg	GGGACTGGGGGGC	C		acaggttga
cR2 a4-F	cttttttgtagcaccgatgtaacattgtg	GGGACTGGGGGGC		CATATCA	cacaggttga

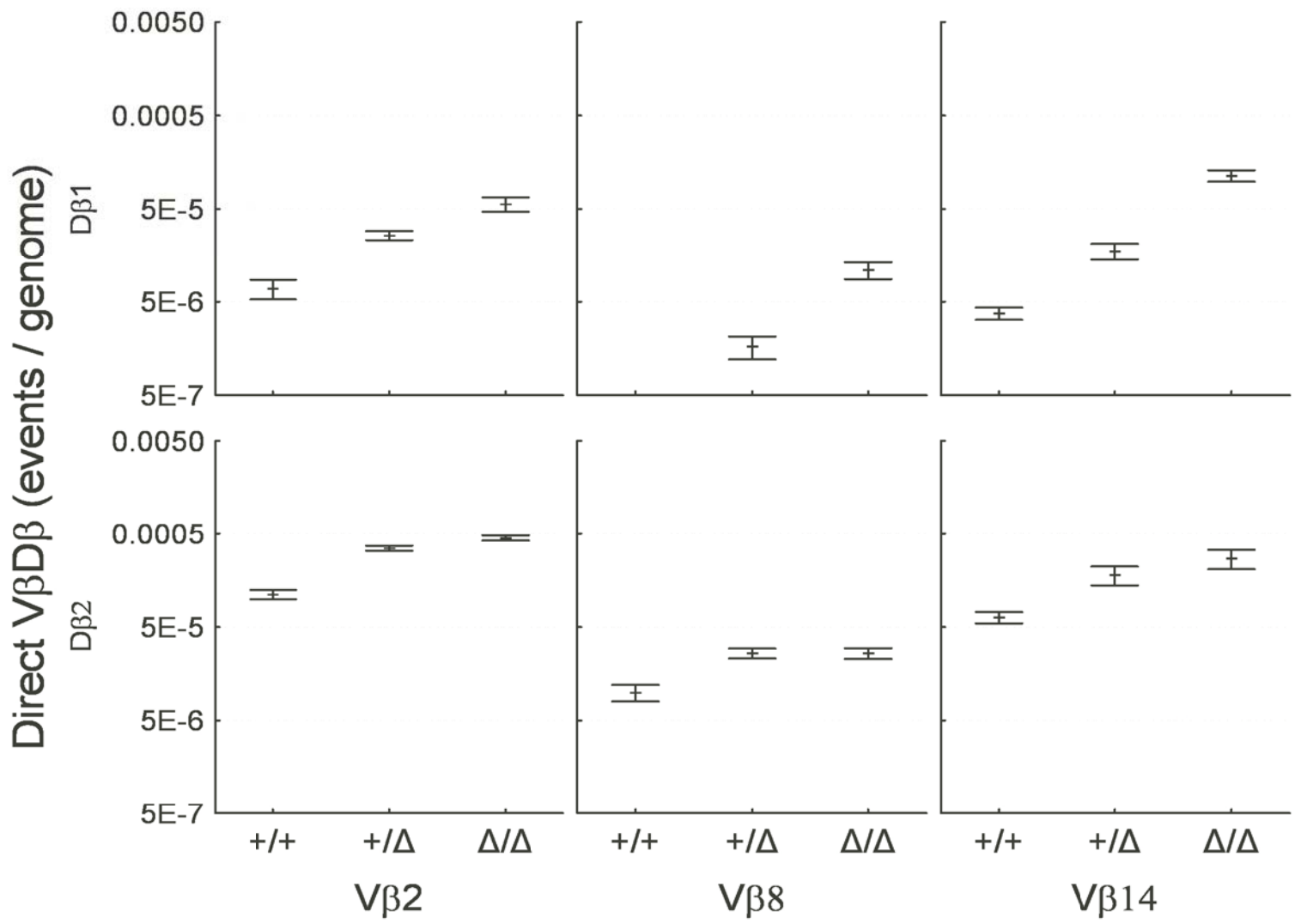
**D $\beta$ 2 > to < D $\delta$ 2 Translocations**

	RSS	D $\beta$ 2 Coding		D $\delta$ 2 Coding	RSS
	cttttttgtagcaccgatgtaacattgtg	GGGACTGGGGGGGC	N	ATCGGAGGGGATACGAG	cacagtgttg
WT b2-F	cttttttgtagcaccgatgtaacattgtg	GGGACTGGGGGGGC	GCG	TCGGAGGGGATACGAG	cacagtgttg
WT b4-F	cttttttgtagcaccgatgtaacattgtg		TC		cacagtgttg
cR2 b5-F	cttttttgtagcaccgatgtaacattgtg	GGGAC	TGGGTT		cacagtgttg
cR2 b6-F	cttttttgtagcaccgatgtaacattgtg	GGGACTGGGGGGC	ACGTGGCCCCGT		cagtgttg
cR2 b7-F	cttttttgtagcaccgatgtaacattgtg				cacagtgttg



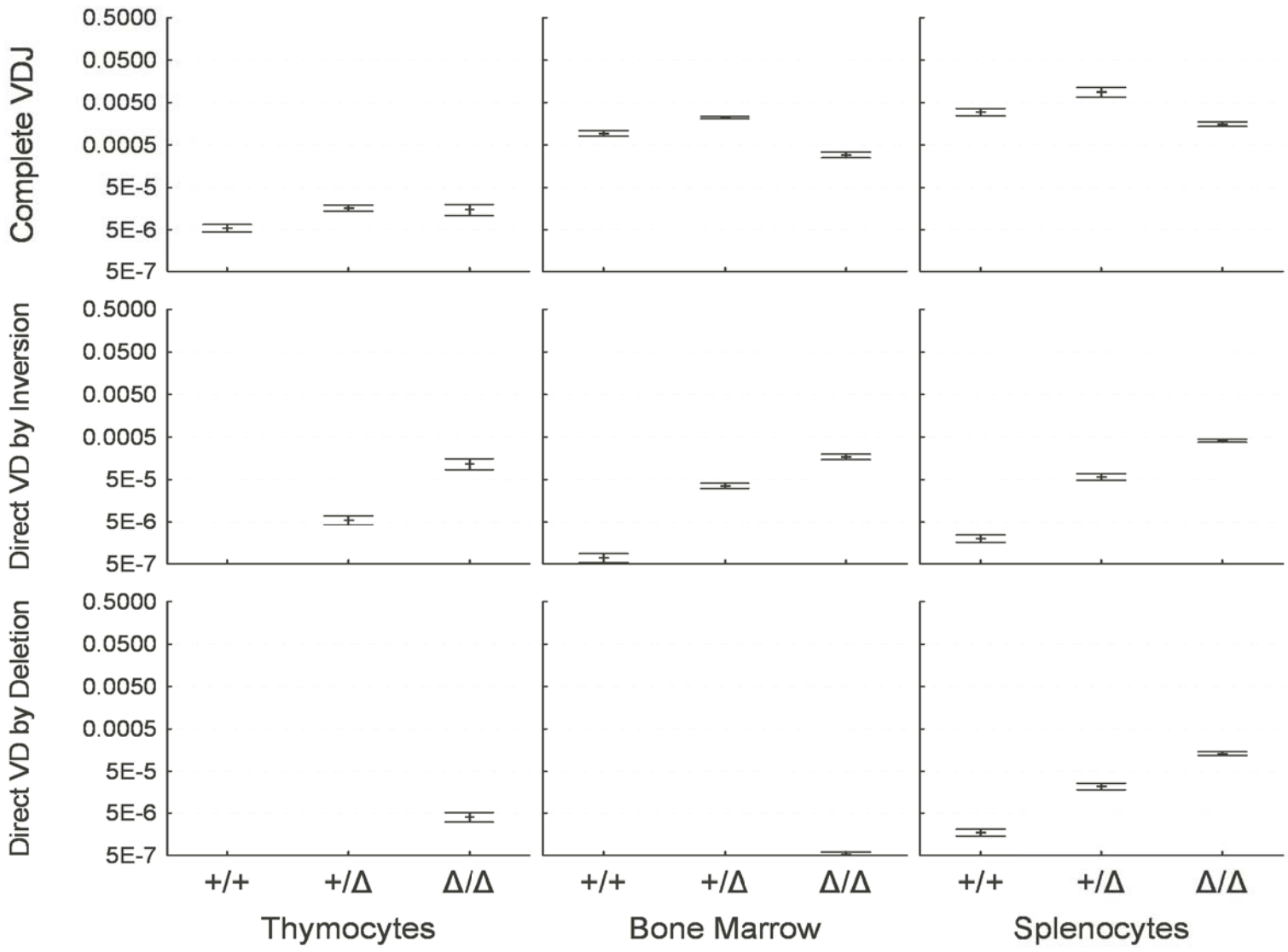
# Supplemental Figure 1



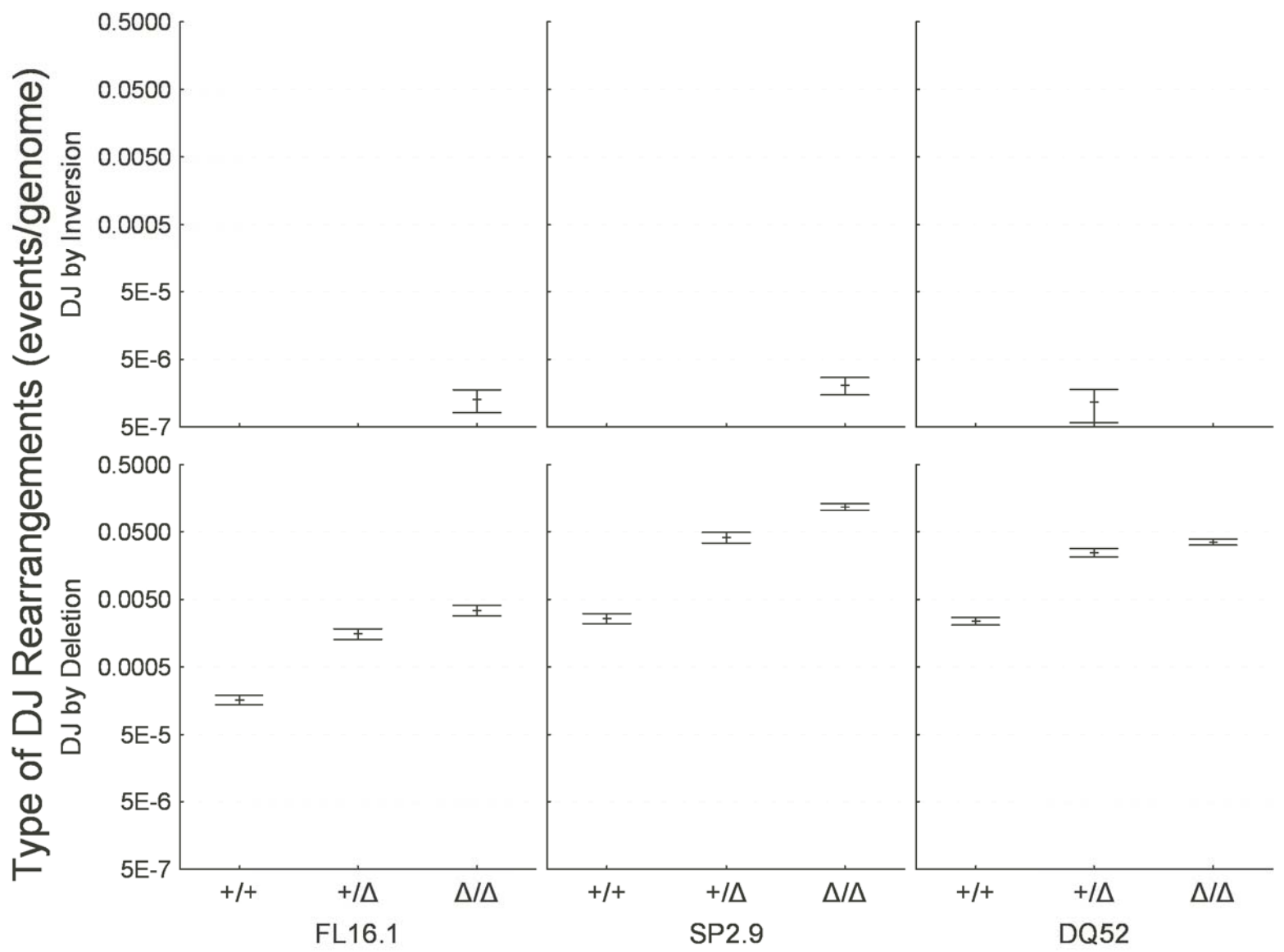


Supplemental Figure 2

# Type of Rearrangements (Events/Genome)



Supplemental Figure 3.



Supplemental Figure 4.