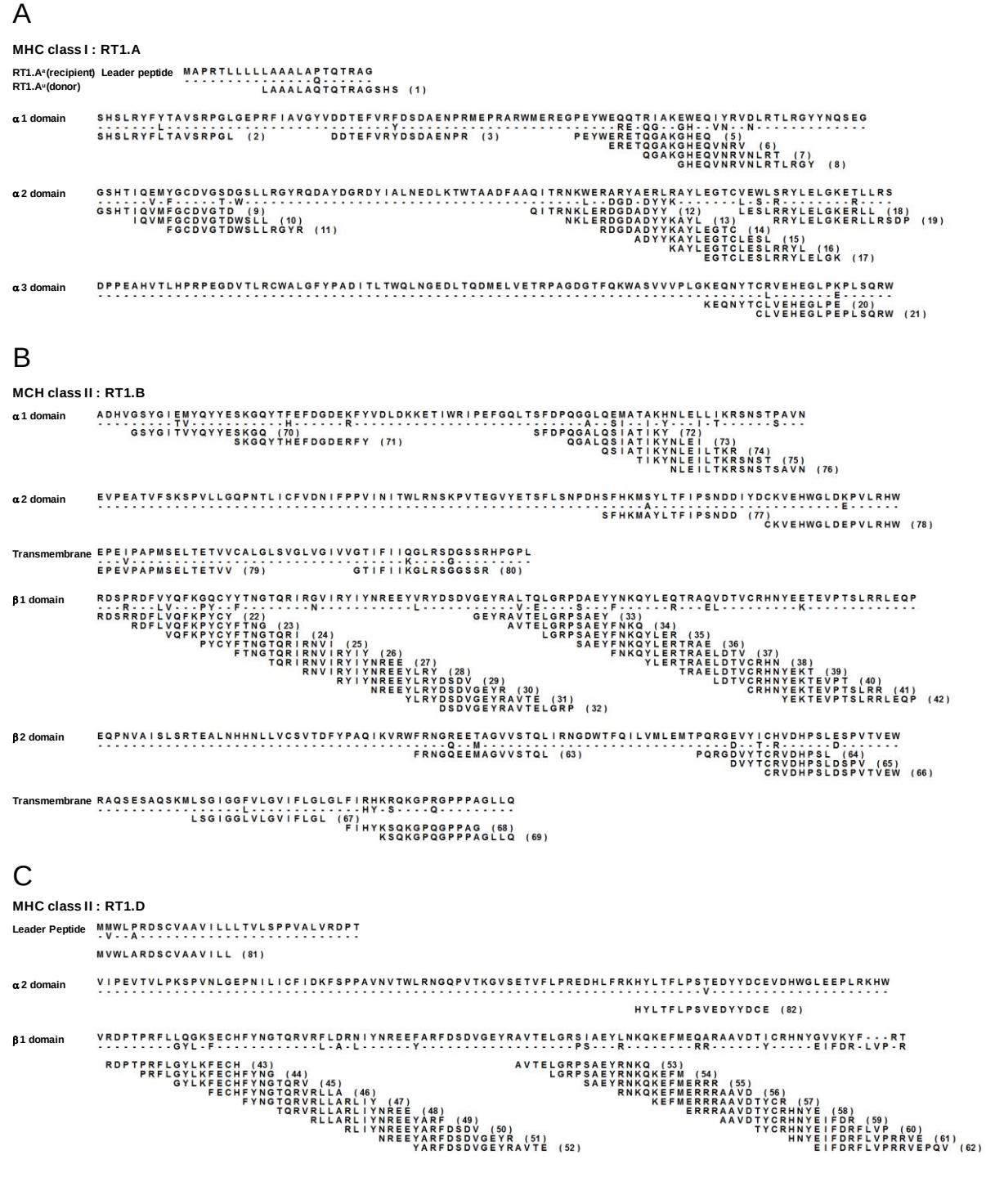
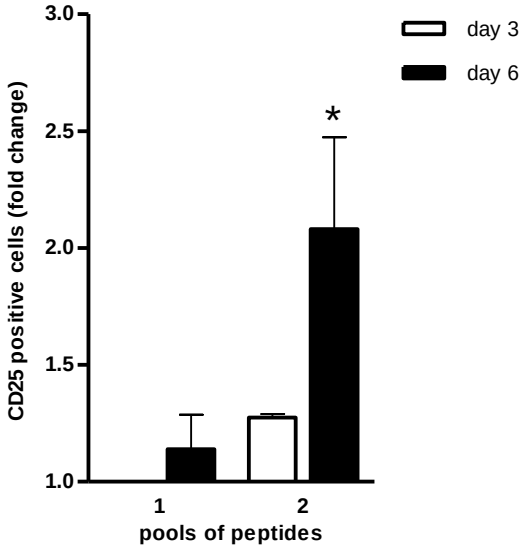
Suppl. Fig.1. Picarda et al.



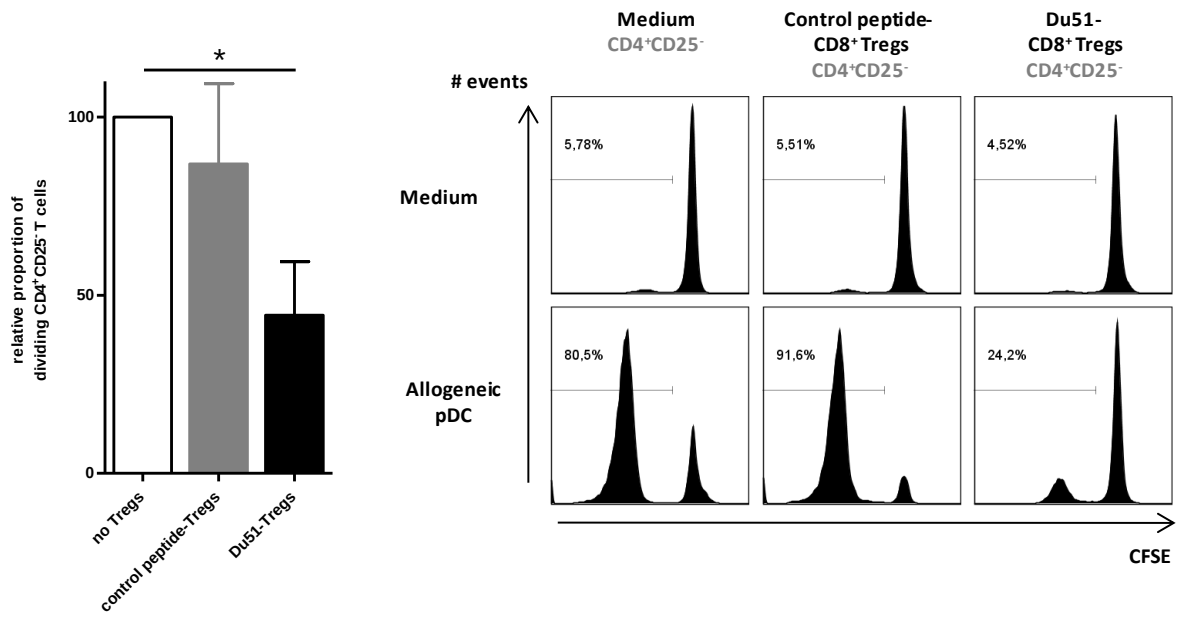
Suppl. Figure 1: Aa sequence alignment of the recipient a-haplotype (upper sequence) and donor u-haplotype (lower sequence) RT1 molecules. Sixteen aa-long overlapping peptides (82 synthetic peptides) were chosen along the polymorphic regions of the MHC-I RT1.A^u (α1, α2 and α3 domains) (**A**), MHC-II RT1.B^u (all domains) (**B**) and RT1.D^u (α2, β1 domains) (**C**).

Suppl. Fig. 2. Picarda et al.



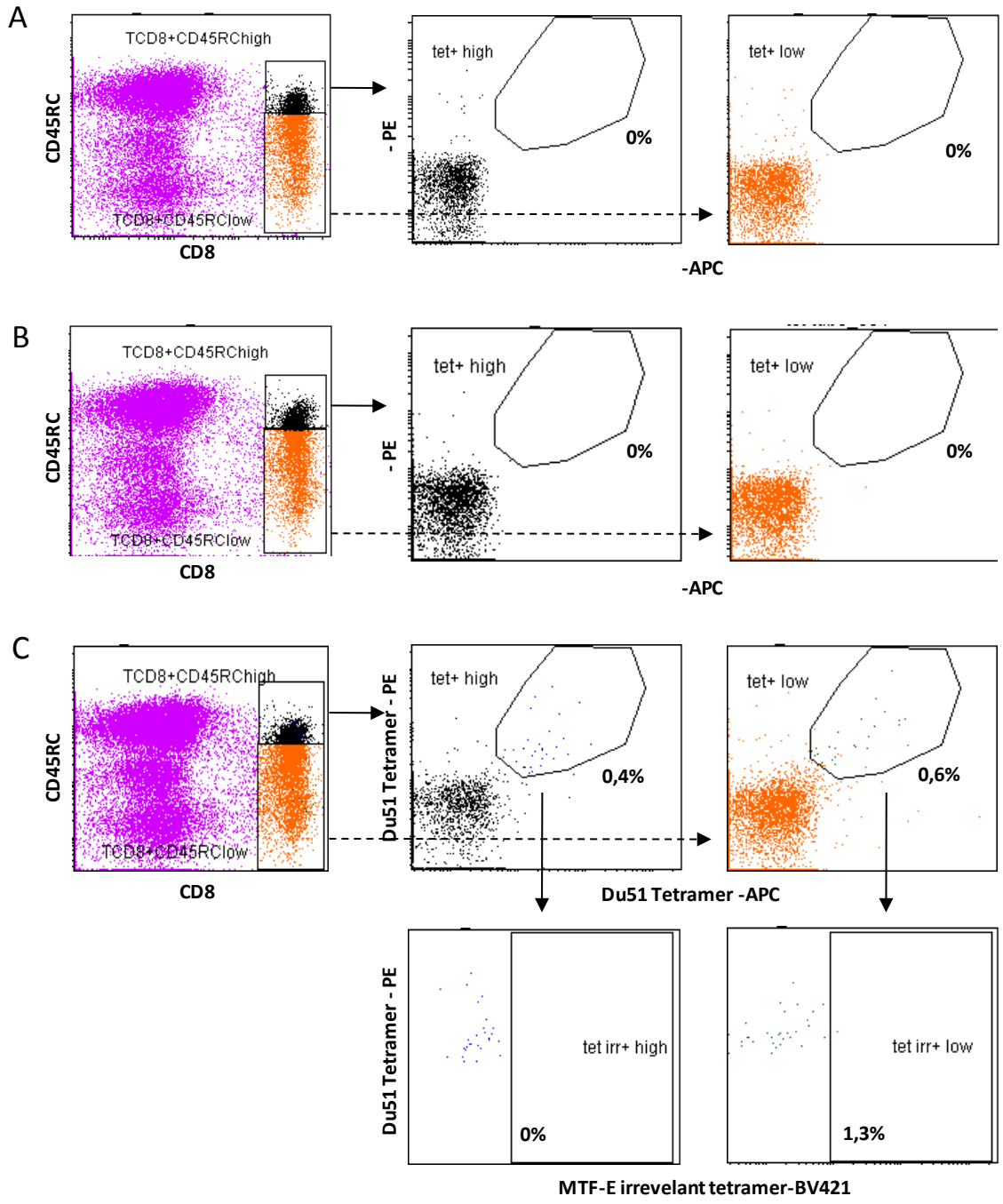
Suppl. Figure 2: 6 days of stimulation with matured pDCs and pools of peptides efficiently activates CD8$^+$ Tregs. Peptides were grouped into pools of peptides and tested in an *in vitro* assay where mature syngeneic recipient pDCs and sorted-CD8$^+$CD40Ig Treg cells from CD40Ig-treated long-term allograft bearing recipients were cocultured for 3 or 6 days. Results are expressed as the ratio ± SEM between the percentage of CD25 positive cells after peptide stimulation and percentage of CD25 positive cells in the control condition without peptide. *$p<0.05$, n=3 to 7.

Suppl. Fig. 3. Picarda et al.



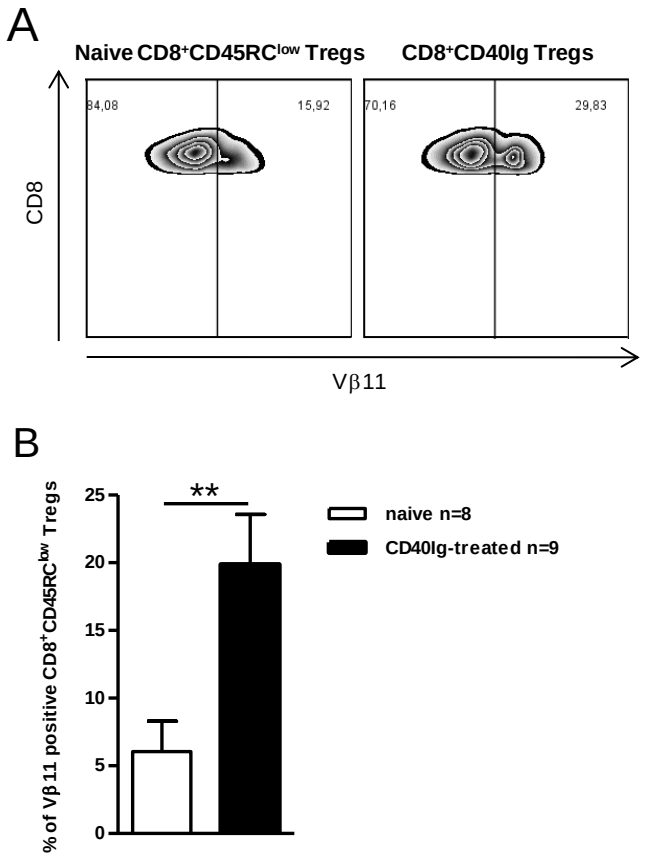
Suppl. Figure 3: Du51-activated Tregs maintained efficient suppressive activity. Fresh $CD8^+$CD40Ig Tregs and syngeneic CpG-matured pDCs were cocultured for 6 days with either Du51 or a control peptide. At day 6, Tregs were isolated by cell sorting (TCR^+) and their regulatory function was analyzed by measuring their capacity to suppress MLR assay. The relative proportion of naive CFSE-labeled dividing LEW.1A $CD4^+CD25^-$ T cells after stimulation with donor LEW.1W pDCs was analyzed at day 6 of culture, in the absence or presence of 6 days peptide-stimulated $CD8^+$ Tregs at a 1:1 ratio effector:suppressor. Graphs represent the mean±SEM. *$p<0.05$ (left). Plots are representative of four independent experiments (right).

Suppl. Fig. 4. Picarda et al.



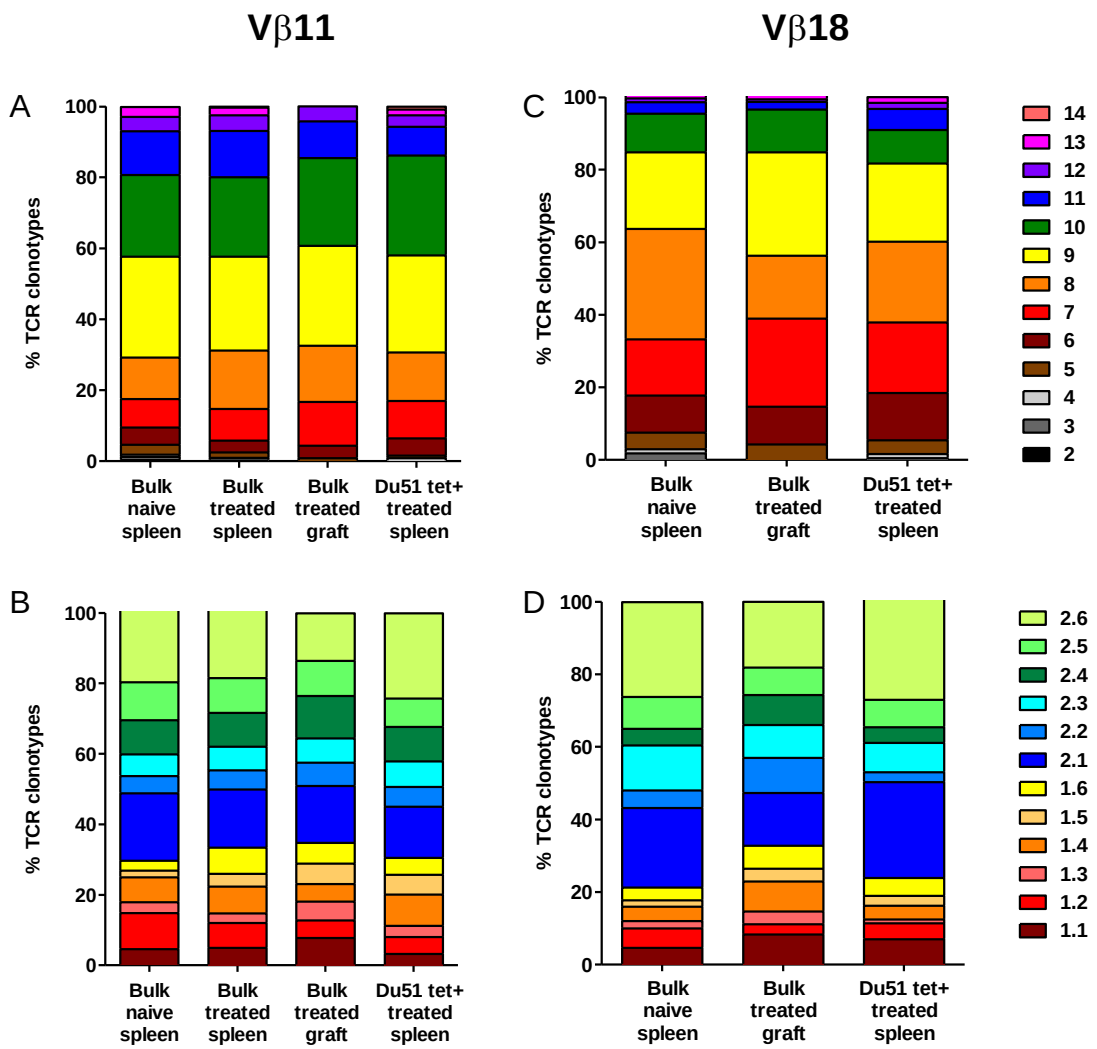
Suppl. Figure 4: Du51-specific Tregs identification in naive animals. T cells-enriched spleens of naive animals were incubated with no tetramer **(A)**, irrelevant RT1.A^a/MTF-E tetramer labeled with BV421 **(B),** or both RT1.A^a/MTF-E-BV421 and RT1.A^a/Du51 tetramers labeled with streptavidin conjugated to PE and APC **(C)**. Panels show representative plots.

Suppl. Fig. 5. Picarda et al.



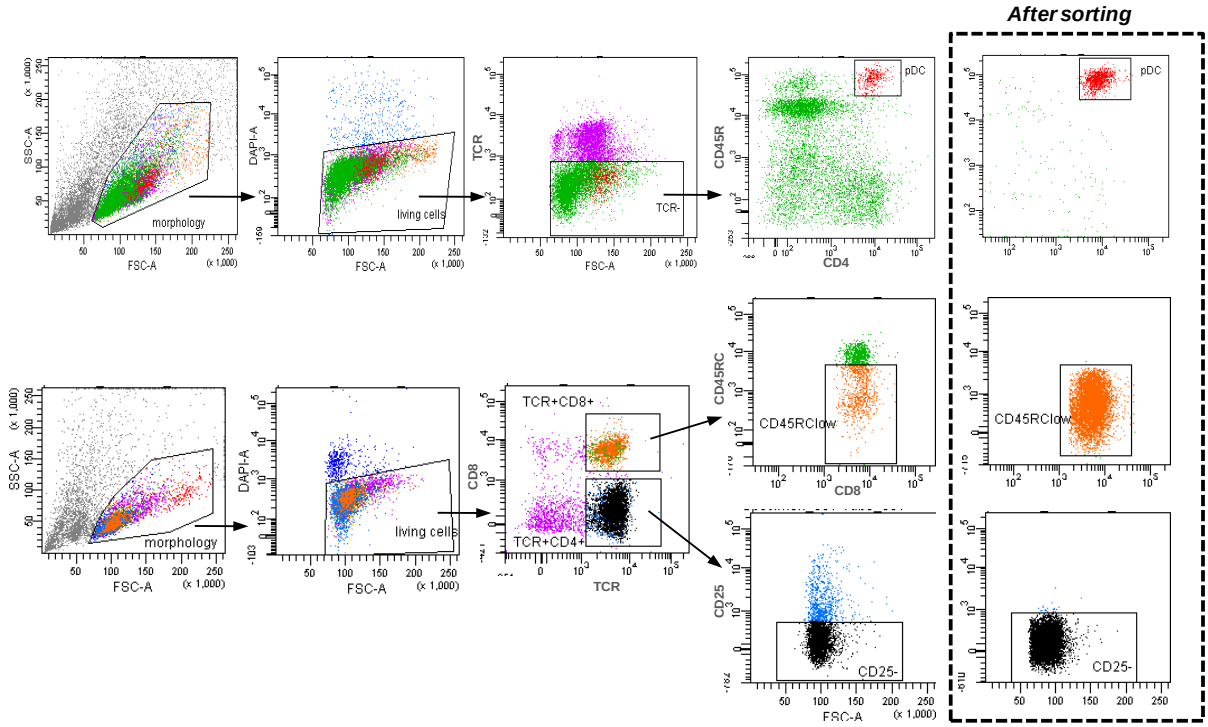
Suppl. Figure 5: Vbeta 11 chain was preferentially recombined in CD8$^+$CD45RC^{low} T cells. (A) Vβ11 chain protein expression by CD8$^+$CD45RC^{low} T cells from naive LEW.1A and CD40Ig-treated rats. Background was measured with a control isotype antibody and is less than 9%. Data are representative of nine independent experiments. (**B**) Data are summarized and background non-specific staining was subtracted, plotting mean ± SEM of Vβ11 positive cells. **p<0.01, n=8 and 9 for naive and CD40Ig-treated rats respectively.

Suppl. Fig. 6. Picarda et al.



Suppl. Figure 6: Summary of the features of Vβ11 (A, B) and Vβ18 (C, D) TCR aa repertoires obtained from CD8^{+}CD45RC^{low} Tregs of naive spleens versus Bulk or Du51 tetramer^{+} CD8^{+}CD40IgTregs from spleens or GITCs of CD40Ig-treated grafts. Shown are the percentages of the TCRβ aa clonotypes pooled across all animals per group using a particular CDR3 length (**A, C**) and Jβ gene usage (**B, D**).

Suppl. Fig. 7. Picarda et al.



Suppl. Figure 7: Sorting strategy for coculture experiments. After gating cells by their morphology, dead cells were excluded by DAPI expression. pDCs were sorted by FACS Aria by gating on TCR negative cells, and CD4 and CD45Rhigh double positive cells. $CD4^{+}$T cells were sorted by gating on TCR and CD4 positive expression and CD25 negative expression. $CD8^{+}$Tregs were sorted according to $CD8^{+}CD45RC^{low}$ markers expression. Purity after cell sorting was greater than 99%.

Suppl. Table 1. Picarda et al.

Vβ	CDR3β region	Jβ	CDR3 length	Bulk naive spleen					Bulk treated graft							Du51 Tet$^+$ treated spleen				Bulk treated spleen						No. animals
				1	2	3	4	5	1	2	3	4	5	6	7	1	2	3	4	1	2	3	4	5	6	
11	SLVGYEQ	2.6	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2
11	SLDGGYEQ	2.6	8	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
11	SPGGAGDKI	2.3	9	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
11	SSQGNDY	1.2	7	0	3	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
11	SLGDGSYAEQ	2.1	10	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
11	SLQGNTGQL	2.2	9	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
11	SLRGETQ	2.5	7	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	2
11	SLTGGRQNTL	2.4	10	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	2
11	SLVGAEQ	2.1	7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
11	SPGGSYAEQ	2.1	9	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	8	0	0	0	0	2
11	SSPTGENTL	2.4	9	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	2
11	SLAVANQAQ	1.5	9	0	0	0	0	0	0	0	4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
11	SLETQ	2.5	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
11	SQNYDY	1.2	6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	0	2
11	SLAWGGYAEQ	2.1	10	0	0	0	1	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
11	SQGQQNTL	2.4	8	0	0	0	0	0	0	12	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	2
Total number of TCR sequences				68	72	73	70	75	44	76	69	87	77	80	77	76	54	67	84	119	103	99	113	116	96	

Vβ	CDR3β region	Jβ	CDR3 length	Bulk naive spleen					Bulk treated graft						Du51 Tet$^+$ treated spleen				No. animals
				1	2	3	4	5	1	2	3	4	5	6	1	2	3	4	
18	GDSSYEQ	2.6	7	0	0	0	0	0	0	0	0	0	1	0	1	1	0	1	4
18	GGWEETQ	2.5	7	0	0	0	0	0	23	3	4	0	0	0	0	0	0	0	3
18	GDGSYAEQ	2.1	8	1	0	0	0	1	0	0	0	0	0	0	0	0	2	0	3
18	GDSYEQ	2.6	6	0	0	0	1	2	0	0	0	0	0	0	0	0	4	0	3
18	GEGSYAEQ	2.1	8	0	0	4	0	1	0	0	0	0	0	0	0	0	0	0	2
18	GERGSYEQ	2.6	8	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
18	GNTEV	1.1	5	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	2
18	GTGSYAEQ	2.1	8	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	2
18	GVGEQ	2.6	5	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
18	GTGLNTL	2.4	7	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0	2
18	KDSNNQAQ	1.5	8	0	0	0	0	0	0	0	0	0	0	0	0	1	0	4	2
18	GAGNERL	1.4	7	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	2
18	GDGYEQ	2.6	6	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
18	GTGNAEQ	2.1	7	0	0	0	3	0	45	0	0	0	0	0	0	0	0	0	2
18	GFGYEQ	2.6	6	0	0	0	0	1	0	0	0	0	27	0	0	0	0	0	2
18	GTDYAEQ	2.1	7	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	2
18	GGPGESSYEQ	2.6	10	0	0	0	0	0	6	0	0	0	0	0	0	0	2	0	2
18	DRGLGTL	2.4	7	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	2
18	LQGAGYDY	1.2	8	0	0	0	0	0	0	0	0	13	0	0	0	2	0	0	2
18	GEGGFYAEQ	2.1	9	0	0	0	0	0	0	0	0	0	2	0	0	2	0	0	2
Total number of TCR sequences				62	69	75	58	62	88	54	80	94	89	77	55	70	81	79	

Suppl. Table 1: Aa sequence, Jβ usage and CDR3 length of inter-individually shared clonotypes from the Vβ11 and Vβ18 repertoires in spleen and graft of naive and CD40Ig-treated rats 120 days after transplantation.

Suppl. Table 2. Picarda et al.

Vβ	Du51 Tet$^+$ treated #1	Jβ	Length	Frequency
11	SSSRGTEV	1.1	8	1
11	RFGV	1.1	4	1
11	SWDRAWCDY	1.2	9	1
11	SSNYDY	1.2	6	1
11	SPRRYDY	1.2	7	1
11	SLVRGIYDY	1.2	9	1
11	SLWGCERL	1.4	8	1
11	SFLTLSNERL	1.4	10	1
11	SSRDSSNERL	1.4	10	1
11	SWDNNNQAQ	1.5	9	1
11	SPGTHNNQAQ	1.5	10	1
11	SHPGTDNQAQ	1.5	10	1
11	SSLRDRDNSPL	1.6	11	1
11	SSTGSHNSPL	1.6	10	1
11	SRTDSYAEQ	2.1	9	2
11	SLELWGELSYAEQ	2.1	13	1
11	SFGGRGAEQ	2.1	9	1
11	SLLDRGFAEQ	2.1	10	1
11	SPQGAYAEQ	2.1	9	1
11	SHYAEQ	2.1	6	1
11	SDREGDTGQL	2.2	10	1
11	SLTANTGQL	2.2	9	1
11	SSSGDGQL	2.2	8	1
11	SFLPGGNTGQL	2.2	11	1
11	SPGLTDKI	2.3	8	1
11	SPPGHYTDKI	2.3	10	39
11	SLVRNTL	2.4	7	1
11	SLDRLGSQNTL	2.4	11	1
11	SSPTGENTL	2.4	9	2
11	SFPGTFQETQ	2.5	10	1
11	SLVRRIYEQ	2.6	9	1
11	SPYCYEQ	2.6	7	1
11	PLRDPPRDEQ	2.6	10	1
11	SLVRGASYEQ	2.6	10	1
11	SESGTGNEQ	2.6	9	1
11	SLLGGVYEQ	2.6	9	1
			total =	76
Vβ	**Du51 Tet$^+$ treated #2**	**Jβ**	**Length**	**Frequency**
11	SFFREV	1.1	6	1
11	SLAGSGAYDY	1.2	10	1
11	SSDSSGNVL	1.3	9	1
11	MTASGNVL	1.3	8	2
11	VDSGNVL	1.3	7	1
11	SLWDRGGERL	1.4	10	1
11	SEDISNERL	1.4	9	1
11	SSNQAQ	1.5	6	1
11	SLAVANQAQ	1.5	9	1
11	SLRKANNQAQ	1.5	10	1
11	SLDSADSPL	1.6	9	1
11	SVGDSSYAEQ	2.1	10	2
11	SLYHWSSYAEQ	2.1	11	1
11	SQELGGSAEQ	2.1	10	1
11	SLDRTSYAEQ	2.1	10	2
11	SFSAEQ	2.1	6	2
11	SARDFLTYAEQ	2.1	11	1
11	SFAGNTGQL	2.2	9	1
11	SFVSNTGQL	2.2	9	1
11	SKGPLTGQL	2.2	9	1
11	SLFTGRSDKI	2.3	10	1
11	SPRDGTTDKI	2.3	10	1
11	SFGDSTTDKI	2.3	10	1
11	SDALGGYTDKI	2.3	11	1
11	TTGTENTL	2.4	8	1
11	SFRWKNTL	2.4	8	1
11	SENYRGQNTL	2.4	10	1
11	SLPLQGSNTL	2.4	10	1

11	SQGQQNTL	2.4	8	3
11	SERYRGR	2.4	7	1
11	SLDWDPFQETQ	2.5	11	1
11	SNGTFQETQ	2.5	9	1
11	SPPGLGKETQ	2.5	10	3
11	SHGRGGQETQ	2.5	10	1
11	SRLGGGYEQ	2.6	9	1
11	SLPWDSPSSYEQ	2.6	12	1
11	SSRDSSYEQ	2.6	9	1
11	SLDSGNEQ	2.6	8	1
11	SLDWWGGPSSYEQ	2.6	13	1
11	SLEGQGSYEQ	2.6	10	1
11	SLDNVDRGQYEQ	2.6	12	1
11	SLDVTGIWEQ	2.6	10	2
11	SSIRGTYEQ	2.6	9	1
11	SLDSDRGPYEQ	2.6	11	1
11	SVKGAYEQ	2.6	8	1
			total =	54
Vβ	**Du51 Tet$^+$ treated #3**	**Jβ**	**Length**	**Frequency**
11	SLNTALNTEV	1.1	10	2
11	SQNYDY	1.2	6	6
11	SLDPTYNSPL	1.6	10	4
11	FASYAEQ	2.1	7	9
11	SLDRDWGGGSQNTL	2.4	13	1
11	SLGTKETQ	2.5	8	9
11	SLNSGGGNQETQ	2.5	12	4
11	SLTDSYEQ	2.6	8	3
11	SWTLSYEQ	2.6	8	27
11	SSNRDWREQ	2.6	9	2
			total =	67
Vβ	**Du51 Tet$^+$ treated #4**	**Jβ**	**Length**	**Frequency**
11	STSDAGNVL	1.3	9	1
11	SSGDERL	1.4	7	2
11	SLAHPISNERL	1.4	11	1
11	SLFAGEL	1.4	7	1
11	SFWTISNERL	1.4	10	1
11	SLGGVSNERL	1.4	10	1
11	SLSGVGERL	1.4	9	1
11	SLDRGEAQ	1.5	8	1
11	STPRQNSPL	1.6	9	1
11	SSGTANSPL	1.6	9	32
11	SLRDWGGFYAEQ	2.1	12	1
11	SLDLGGPYAEQ	2.1	11	13
11	RGEGAEQ	2.1	7	2
11	SLRPTEQ	2.1	7	2
11	SLVPAEQ	2.1	7	2
11	SLDRGVDKI	2.3	9	1
11	SLAGGGTDKI	2.3	10	2
11	SLVGSTDKI	2.3	9	1
11	SFRDSQNTL	2.4	9	1
11	SLDWGRL	2.4	7	2
11	SPRDRETQ	2.5	8	1
11	SSDRVGQETQ	2.5	10	1
11	SLETQ	2.5	5	1
11	SLRDSDSYEQ	2.6	10	2
11	SGQGIGYEQ	2.6	9	1
11	SKGAGEQ	2.6	7	1
11	SLDFRGYEQ	2.6	9	2
11	SLEGAYEQ	2.6	8	1
11	YRGGSSYEQ	2.6	9	1
11	SLGTSYEQ	2.6	8	1
11	SSNPTGNYEQ	2.6	10	1
11	DGNRGDYEH	2.6	9	1
11	SLVGTGFYEQ	2.6	10	1
			total =	84

Suppl. Table 2: Aa sequences, Jβ usage, CDR3 length and frequency of clonotypes from the Vβ11 repertoire in spleen of Du51 Tet$^+$ CD8$^+$CD40Ig-treated rats 120 days after transplantation.

Suppl. Table 3. Picarda et al.

Vβ	Du51 Tet$^+$ treated #1	Jβ	Length	Frequency
18	ASGSAEV	1.1	7	1
18	GRGRV	1.1	5	1
18	STGSTEV	1.1	7	1
18	GVGGNYDY	1.2	8	1
18	GQGLNYDY	1.2	8	1
18	GRDRANYDY	1.2	9	1
18	GGGSNERL	1.4	8	2
18	TQGSNERL	1.4	8	1
18	GEGSNERL	1.4	8	1
18	GDRQSISNERL	1.4	11	1
18	GQGKERL	1.4	7	1
18	GGTVPV	1.4	6	1
18	GQGERAEQ	2.1	8	1
18	EEGSRYAEQ	2.1	9	1
18	GPGLSYAEQ	2.1	9	1
18	GATGDSYAEQ	2.1	10	1
18	GDSGGFPYAEQ	2.1	11	1
18	GDSGDYAEQ	2.1	9	1
18	GVGFSYAEQ	2.1	9	3
18	GEDGYSYAEQ	2.1	10	1
18	FGQGFAEQ	2.1	8	1
18	LDRVYAEQ	2.1	8	2
18	GTGTYAEQ	2.1	8	1
18	APGTGGPSYAEQ	2.1	12	1
18	GYDSDKI	2.3	7	1
18	GRTDKI	2.3	6	1
18	GTGGSTDKI	2.3	9	2
18	GAPGLPTDKI	2.3	10	1
18	TGTDKI	2.3	6	2
18	GWGVQNTL	2.4	8	3
18	GDWGLGQETQ	2.5	10	2
18	GGLGEETQ	2.5	8	1
18	GFETGGVNSYEQ	2.6	12	1
18	RHFSYEQ	2.6	7	1
18	GSDGSSYEQ	2.6	9	1
18	GDWGAEQ	2.6	7	1
18	GGLGGASYEQ	2.6	10	1
18	GDGTLRSYEQ	2.6	10	1
18	GDSSYEQ	2.6	7	1
18	GPNLQGGYEQ	2.6	10	1
18	GVGRSYEQ	2.6	8	1
18	GEGTASYEQ	2.6	9	4
18	GVVYEQ	2.6	6	1
			total =	55
Vβ	**Du51 Tet$^+$ treated #2**	**Jβ**	**Length**	**Frequency**
18	GRSGGLTEV	1.1	9	1
18	GEGNTEV	1.1	7	4
18	LQGAGYDY	1.2	8	2
18	GQGRYDY	1.2	7	2
18	GERDERL	1.4	7	1
18	RGHNQAQ	1.5	7	1
18	KDSNNQAQ	1.5	8	1
18	GGTGDNSPL	1.6	9	1
18	GDGYNSPL	1.6	8	1
18	GDRENNSPL	1.6	9	2
18	GRDRSYAEQ	2.1	9	1
18	GTDYAEQ	2.1	7	2
18	GAEQ	2.1	4	2
18	GGQGYSYAEQ	2.1	10	2
18	AGGDAEQ	2.1	7	1
18	GAVWGARYAEQ	2.1	11	1
18	GFVSYTEQ	2.1	8	1
18	GEGGFYAEQ	2.1	9	2
18	GDRVAEQ	2.1	7	4
18	GDSAEQ	2.1	6	1
18	GDRLSYAEQ	2.1	9	1
18	GRGRVGAEQ	2.1	9	1
18	GDRLGGPYAEQ	2.1	11	1

18	GGLGGPYAEQ	2.1	10	1
18	GDRQGPDAEQ	2.1	10	2
18	GARRNAEQ	2.1	8	1
18	GGHPSYAEQ	2.1	9	1
18	SGSNYAEQ	2.1	8	1
18	GERRTGGVPYAEQ	2.1	13	1
18	GTGGHTGQL	2.2	9	1
18	GEQGLTDKI	2.3	9	2
18	GGRDDKI	2.3	7	3
18	DRGLGTL	2.4	7	1
18	GDWYSQNTL	2.4	9	1
18	GSGLGRNTL	2.4	9	2
18	ETGSQNTL	2.4	8	1
18	GQETQ	2.5	5	1
18	NQETQ	2.5	5	3
18	GGSLETQ	2.5	7	1
18	GDGYEQ	2.6	6	1
18	GSGEDSYEQ	2.6	9	1
18	GGRDRYYEQ	2.6	9	1
18	GLTLSYEQ	2.6	8	1
18	GAGQIYEQ	2.6	8	1
18	GRGGGGVYEQ	2.6	10	1
18	GNFYEQ	2.6	6	1
18	GEQGRNEQ	2.6	8	1
18	GESSYEQ	2.6	7	1
18	GDSSYEQ	2.6	7	1
18	GDRVYEQ	2.6	7	1
			total =	70
Vβ	**Du51 Tet^{+} treated #3**	**Jβ**	**Length**	**Frequency**
18	GDSRALV	1.1	7	1
18	DREGITEV	1.1	8	1
18	RVIGVEV	1.1	7	1
18	GTGSLNTEV	1.1	9	2
18	GRWRVGDY	1.2	8	1
18	GSTGDYDY	1.2	8	1
18	ANSGNVL	1.3	7	1
18	GEWGANQAQ	1.5	9	1
18	GGQGNQAQ	1.5	8	1
18	GSVDDL	1.6	6	1
18	GDVGAGYNSPL	1.6	11	2
18	CTPGLTINSPL	1.6	11	1
18	HSYAEQ	2.1	6	1
18	GAAEQ	2.1	5	2
18	GDGLYAEQ	2.1	8	1
18	GDGSYAEQ	2.1	8	2
18	GVRGGYAEQ	2.1	9	1
18	GETGVYAEQ	2.1	9	3
18	VVLETGGGAEQ	2.1	11	1
18	TTHTGQL	2.2	7	6
18	GPGQNTGQL	2.2	9	1
18	GAAGGDGQL	2.2	9	1
18	GDRDRGSDKI	2.3	10	1
18	APDWEESQNTL	2.4	11	2
18	GEWFGRGMETQ	2.5	11	1
18	GEGDPETQ	2.5	8	3
18	GDRGVQETQ	2.5	9	1
18	GEEGYEQ	2.6	7	4
18	GQGWYEQ	2.6	7	1
18	GDFRGNYEQ	2.6	9	1
18	NRDRGHEQ	2.6	8	1
18	GSGDSYEQ	2.6	8	1
18	EASGSYEQ	2.6	8	2
18	GEYEQ	2.6	5	2
18	GGPGESSYEQ	2.6	10	2
18	LAGYEQ	2.6	6	2
18	GDPLYEQ	2.6	7	1
18	GDFYEQ	2.6	6	1
18	GDSYEQ	2.6	6	4
18	GDAYEQ	2.6	6	17
18	GTGSYEQ	2.6	7	1
			total =	81

Vβ	Du51 Tet^{+} treated #4	Jβ	Length	Frequency
18	GEGDLNTEV	1.1	9	1
18	RDNTEV	1.1	6	1
18	GDAGEV	1.1	6	2
18	ATGSTEV	1.1	7	2
18	GDWYYDY	1.2	7	1
18	GESGPGNVL	1.3	9	1
18	GNQAQ	1.5	5	1
18	KDSNNQAQ	1.5	8	4
18	VTGINSPL	1.6	8	1
18	GDNSPL	1.6	6	1
18	GRGDNSPL	1.6	8	1
18	GQW	2.1	3	2
18	NDRAEQ	2.1	6	1
18	GLNSYAEQ	2.1	8	1
18	GSAGFAEQ	2.1	8	2
18	GGSSYAGQ	2.1	8	1
18	GLDSYAEQ	2.1	8	1
18	GGGAEEEDSYAEQ	2.1	13	2
18	GDSWTGGGAYAEQ	2.1	13	2
18	GDTGGQNSYAEQ	2.1	12	1
18	ERQAYAEQ	2.1	8	1
18	GGWGGVYAEQ	2.1	10	1
18	GGTLWGQL	2.2	8	1
18	GGATDKI	2.3	7	1
18	GERQGAGDKI	2.3	10	1
18	RNTDKI	2.3	6	5
18	VSGSDKI	2.3	7	1
18	LRDRLTDKI	2.3	9	1
18	GTQGFSDKI	2.3	9	1
18	ASGSDKI	2.3	7	2
18	EPGPSQNTL	2.4	9	1
18	RRDWGGKNTL	2.4	10	1
18	GEGRETQ	2.5	7	1
18	GETRRWQETQ	2.5	10	1
18	GDLETQ	2.5	6	1
18	GDLEGTGMETQ	2.5	11	1
18	GPDRGETQ	2.5	8	1
18	GRDWGGPQETQ	2.5	11	1
18	GEDWESYEQ	2.6	9	1
18	GLGGNSYEQ	2.6	9	1
18	GYEQ	2.6	4	1
18	GDRAEQ	2.6	6	7
18	GDRYEQ	2.6	6	1
18	GGDSYEQ	2.6	7	1
18	GDNYEQ	2.6	6	6
18	GDLVVPYEQ	2.6	9	1
18	GDSSYEQ	2.6	7	1
18	GEGQSSYEQ	2.6	9	1
18	GGRLEQ	2.6	6	1
18	DPRDRGPEQ	2.6	9	1
18	GDSQYEQ	2.6	7	1
18	GDREQ	2.6	5	1
18	GWDSYEQ	2.6	7	1
18	VVSYEQ	2.6	6	1
			total =	79

Suppl. Table 3: Aa sequences, Jβ usage, CDR3 length and frequency of clonotypes from the Vβ18 repertoire in spleen of Du51 Tet^{+} CD8^{+}CD40Ig-treated rats 120 days after transplantation.