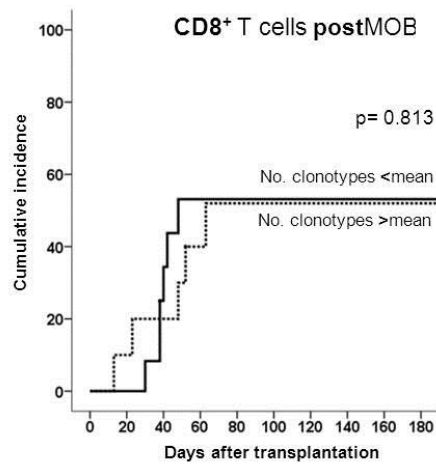
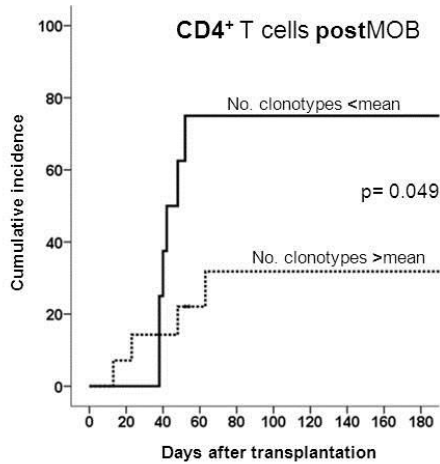


Supplementary Figures and Tables

Figure S1

A CMV reactivation



B EBV reactivation

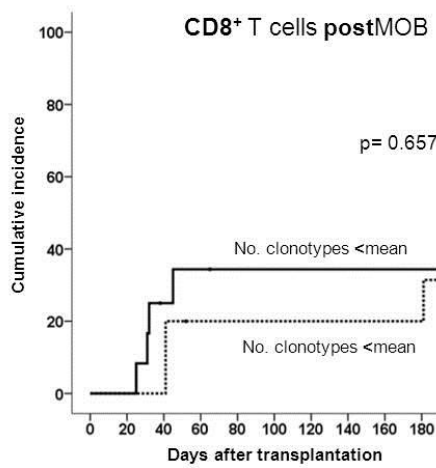
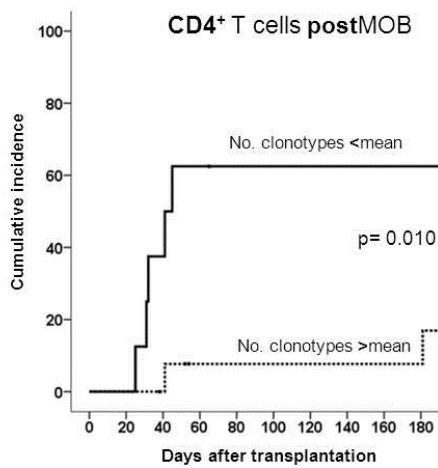


Fig S1. Cumulative incidence of viral reactivation after allogeneic stem cell transplantation. Reactivation was monitored weekly by PCR method. Number of clonotypes in donors after G-CSF mobilization were grouped in below and above mean value.

Figure S2: Control individuals

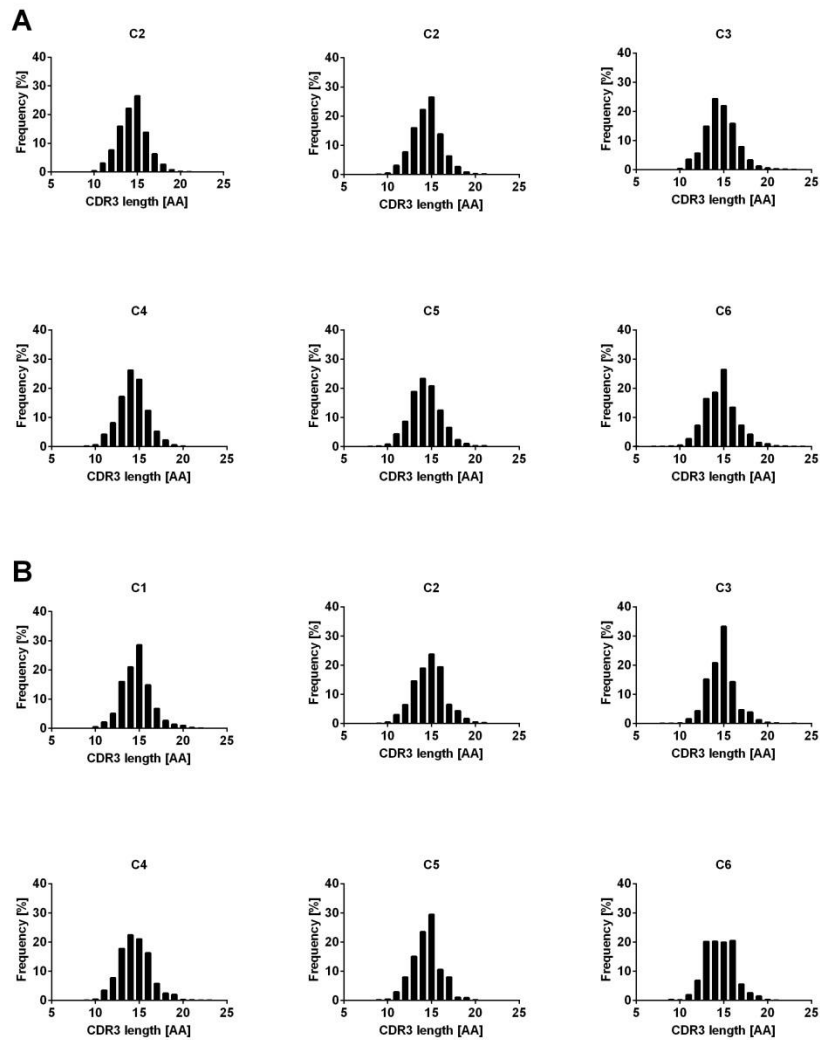


Fig S2. CDR3 length distribution in healthy control individuals. HTS derived CDR3 length distribution of (A) CD4⁺ or (B) CD8⁺ TCRβ sequences for every control donor (‘C1’ – ‘C6’). TCRβ CDR3 size is defined as all amino acids (AA) starting from the conserved 5’ cysteine in the V segment and ending at the conserved 3’ phenylalanine in the J segment.

Figure S3 (A): CD4⁺ T cells preMOB

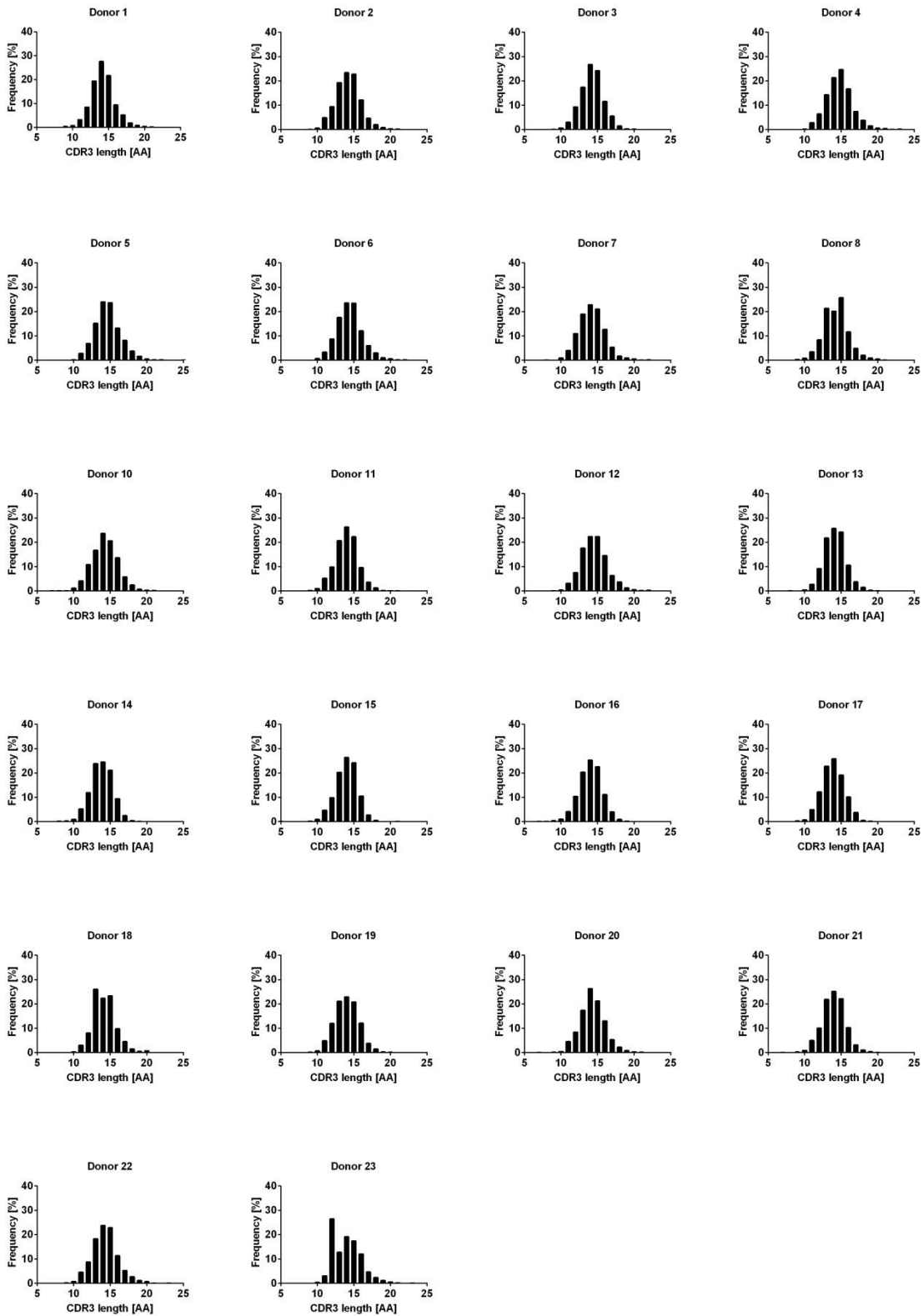


Figure S3 (B): CD4⁺ T cells postMOB

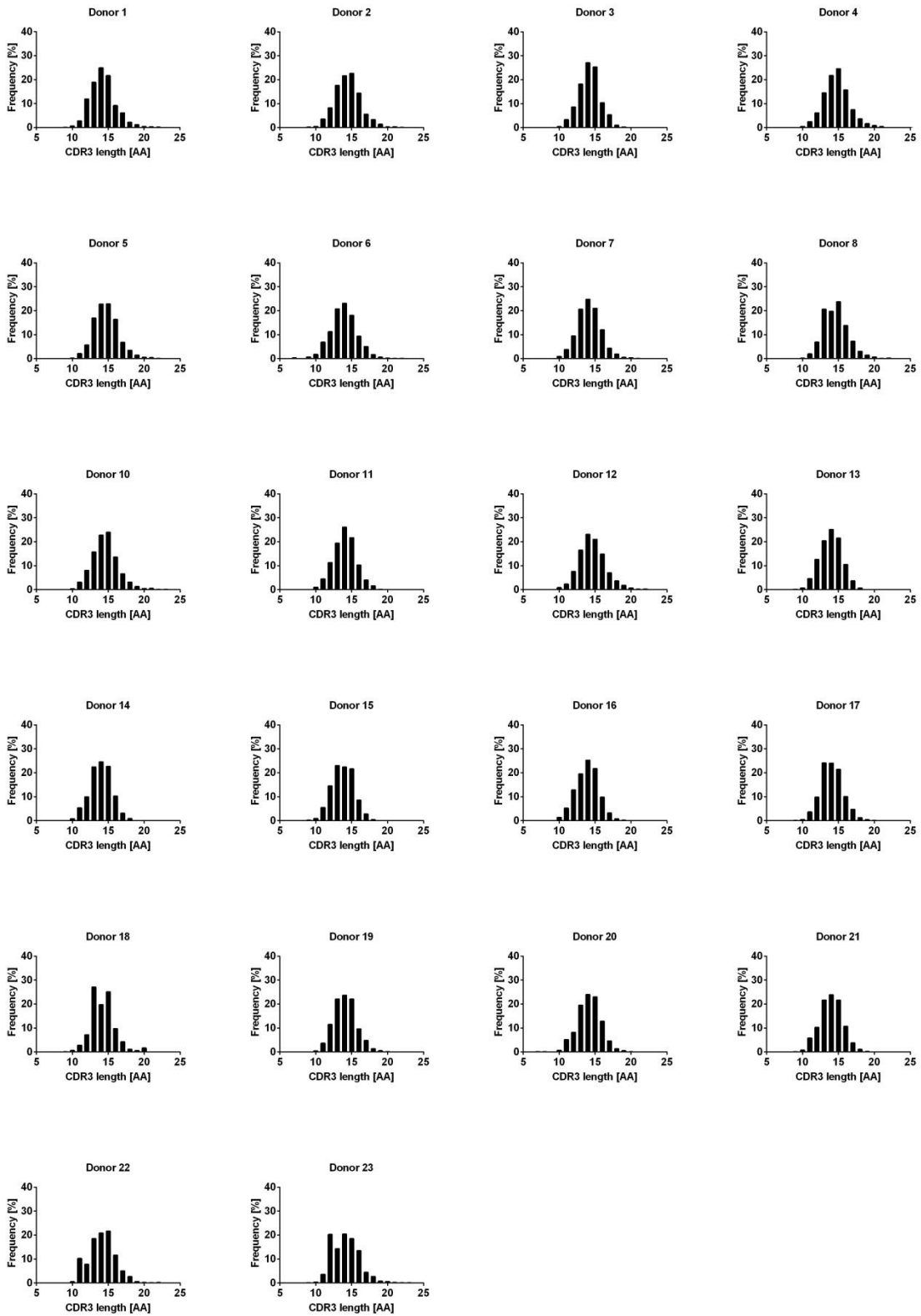


Figure S3 (C): CD8⁺ T cells preMOB

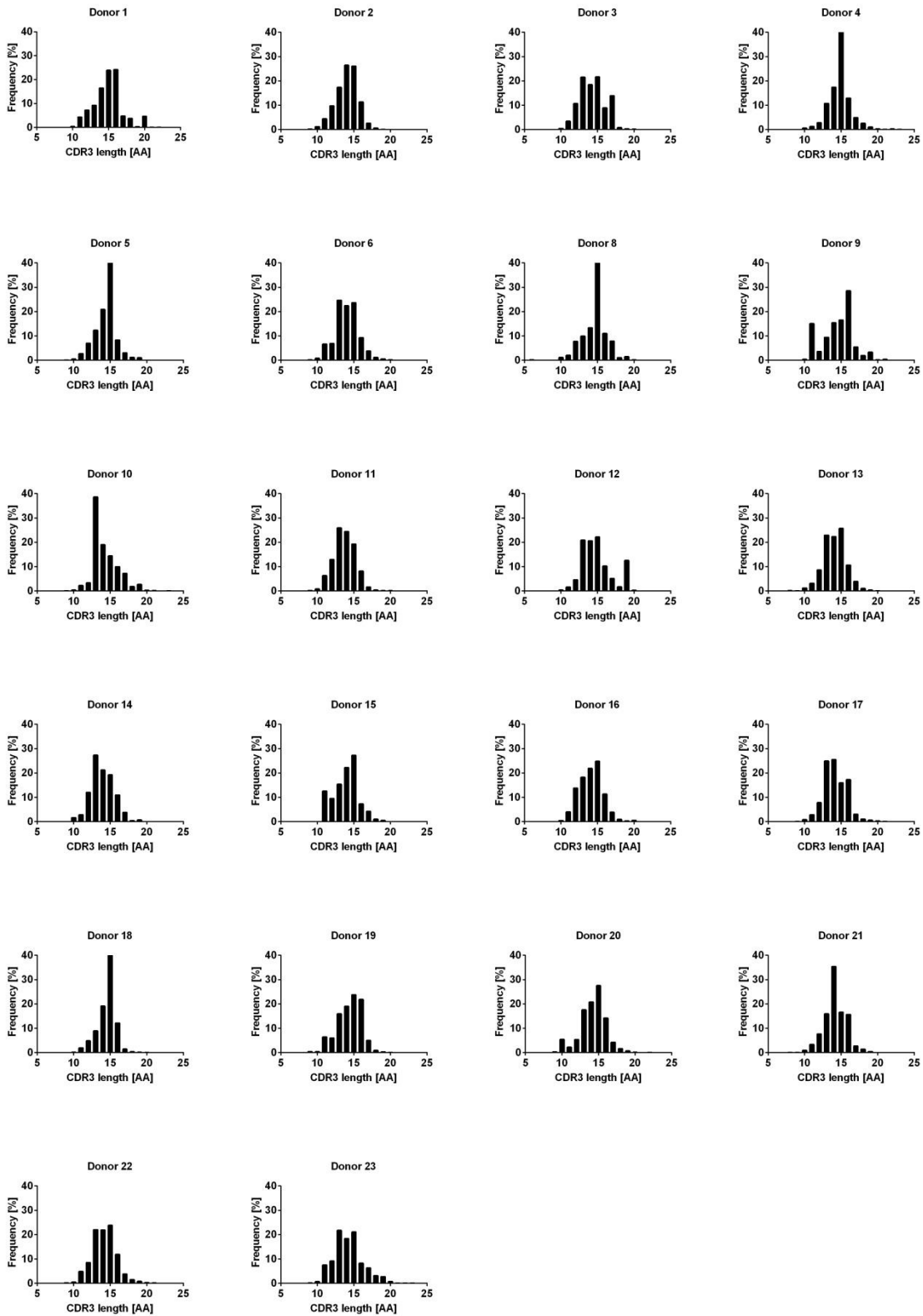


Figure S3 (D): CD8⁺ T cells postMOB

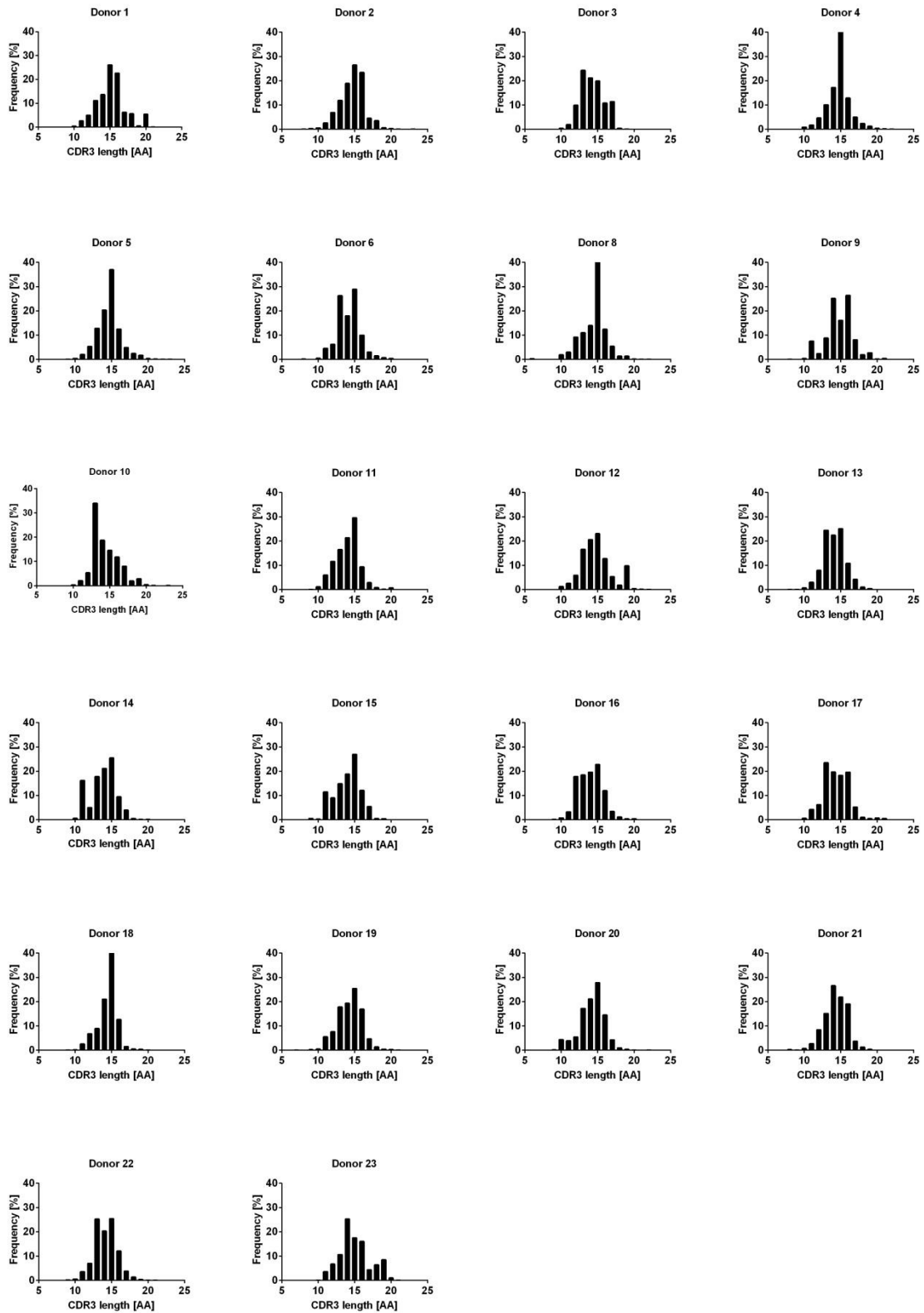


Fig S3. HTS derived CDR3 length distribution of TCR β sequences in G-CSF mobilized stem cell donors. HTS derived CDR3 length distribution of CD4⁺ TCR β sequences before (pre, **A**) or after (post, **B**) G-CSF induced stem cell mobilization as well as the HTS derived CDR3 length distribution of CD8⁺ TCR β sequences pre (**C**) or post (**D**) G-CSF administration for every stem cell donor. TCR β CDR3 size is defined as all amino acids (AA) starting from the conserved 5' cysteine in the V segment and ending at the conserved 3' phenylalanine in the J segment.

Figure S4

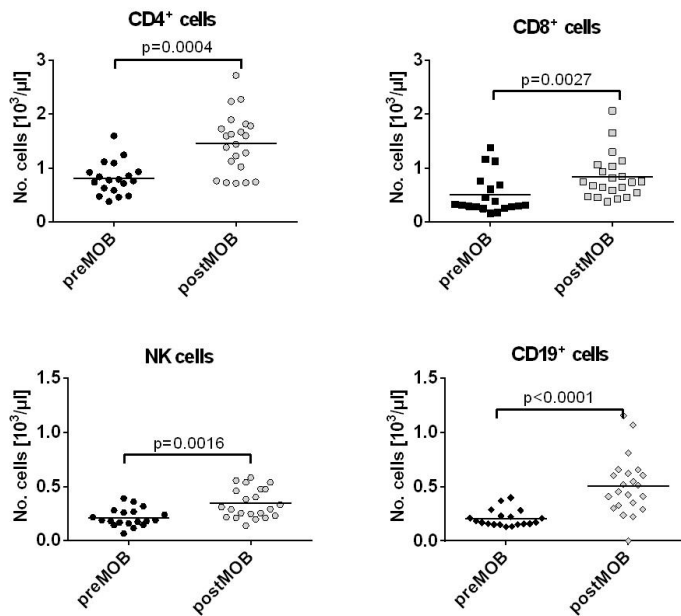
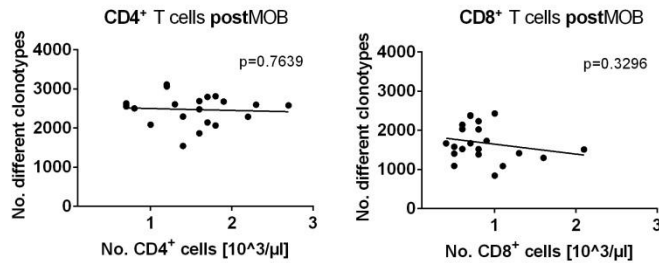


Fig S4. Cell counts in peripheral blood of donors before and after G-CSF administration. Diversity dot blots of cell counts of peripheral blood lymphocyte subsets before (preMOB) stem cell mobilization via G-CSF and at the day of apheresis (postMOB). Leukocytes were gated as CD45^+ and lymphocytes as $\text{CD45}^{\text{high}}\text{CD14}^-$ cells. Within the lymphocytic population, T cells were determined as CD3^+ , B cells as CD19^+ , NK cells as $\text{CD56}^+ \text{CD3}^-$ cell populations. T-cell subpopulations were analyzed upon CD4 and CD8 expression. Cell counts/ μl whole blood were calculated based on the number of beads and the sample volume in TruCount tubes (BD Bioscience). The numbers of all lymphocytic subsets increased significantly after G-CSF administration (Mann-Whitney U test).

Figure S5

A Peripheral blood



B Graft

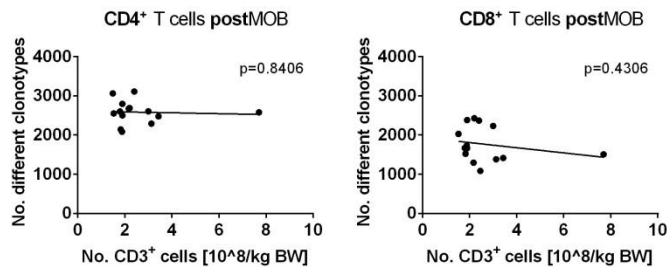


Fig S5. TCR diversity in correlation with cell numbers of the donor peripheral blood or the stem cell graft. Scatter plots of CD4⁺ and CD8⁺ T-cell diversity and (A) absolute T-cell counts (CD4⁺ and CD8⁺ T cells) in peripheral blood of stem cell donors post G-CSF mobilization and (B) cell counts of CD3⁺ cells (per kg recipient bodyweight) in the graft. There was no correlation of TCRβ diversity with peripheral blood cell counts.

Figure S6

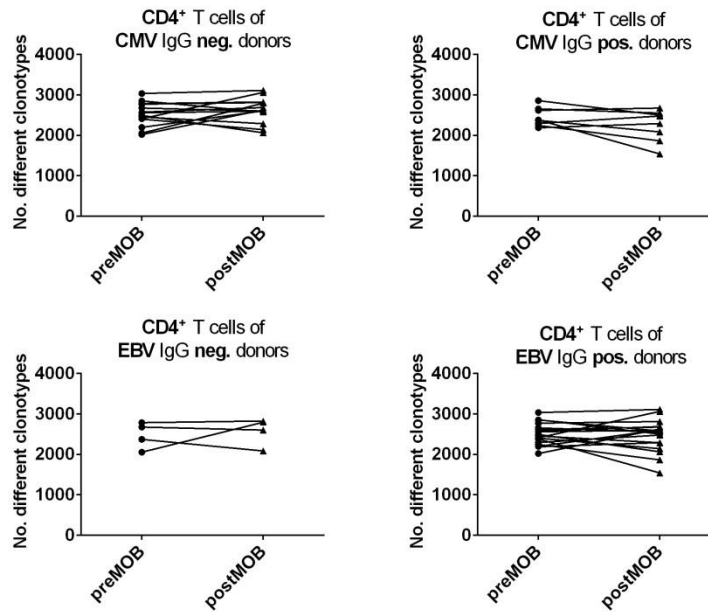
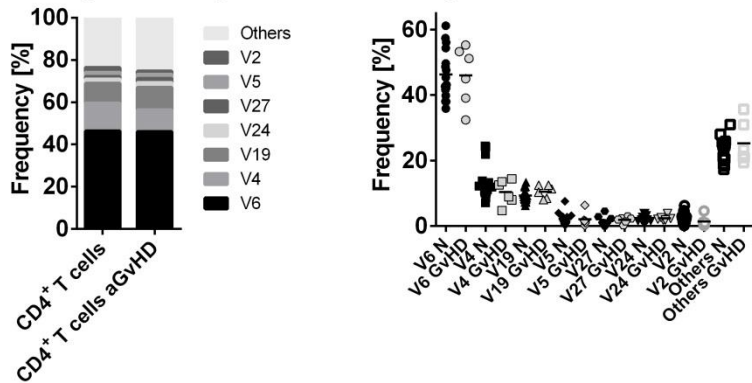


Fig S6. CD4⁺ TCR repertoire diversity of CMV/EBV seropositive or seronegative donors before and after G-CSF mobilization. Diversity dot blots of CMV and/or EBV seronegative (left panel) and seropositive donors (right panel). Changes in CD4⁺ T-cell diversity after G-CSF treatment are independent of the serostatus of the donor.

Figure S7

A V segment usage in CD4⁺ T cells postMOB



B V segment usage in CD8⁺ T cells postMOB

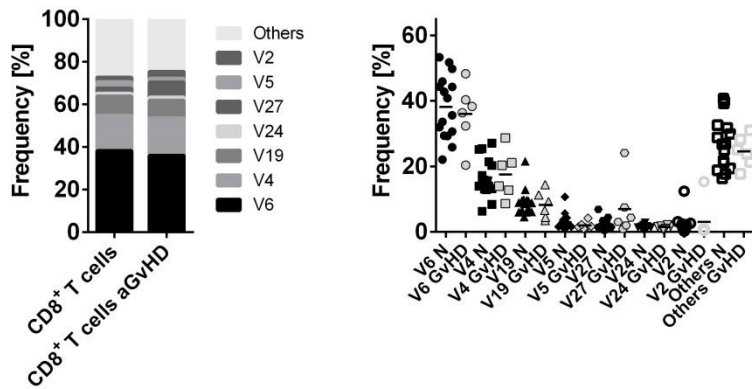
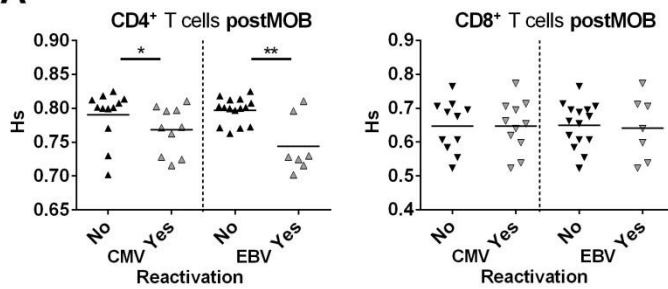


Fig S7. Vβ subgroup usage in donors whose recipients later suffered from GvHD. Mean frequencies of Vβ subgroup usage of TCRs from CD4⁺ (A) or CD8⁺ (B) T cells in donors segregated by appearance of aGvHD in recipients. Seven of the most frequent Vβ subgroups were illustrated individually in the bar plot (left panel). The remaining subgroups were compiled. The nomenclature according to the international ImMunoGeneTics information system (IMGT) was used. The right panel shows the individual frequencies of all donors. No significant differences could be shown between these two groups.

Figure S8

A



B

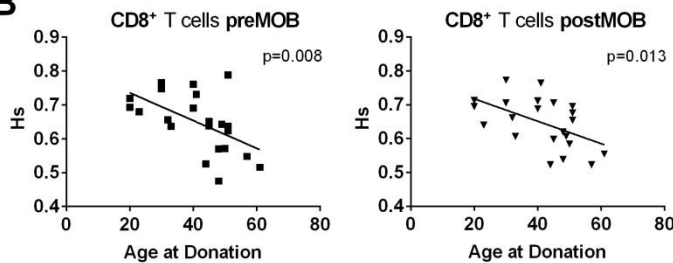


Fig S8. Donor TCR β analyses using Shannon entropy (H_s). (A) Diversity dot plots of CD4⁺ and CD8⁺ T-cell preparation from G-CSF mobilized grouped according to reactivation of CMV or EBV. Donors of patients without CMV and/or EBV reactivation showed significant higher diversity in the CD4⁺ T-cell compartment post G-CSF mobilization (*p=0.034; **p=0.003). In CD8⁺ T cells, no significant difference could be detected. (B) Scatter plots of CD8⁺ T-cell diversity and the age for stem cell donors pre and post G-CSF mobilization. The diversity of CD8⁺ T cells decreases with increasing donor age irrespective of G-CSF mobilization (preMOB: $r=-0.55$; $p=0.008$; postMOB: $r=-0.52$; $p=0.013$; $n=22$).

Table S1. Characteristics of 23 stem cell recipients.

Recipient													Graft	Donor	
No.	Sex	Age	Dis.	Conditioning regime	IgG		acute GvHD	Reactivation		Relapse	Chimerism		CD3 ⁺ [10 ⁸ /kg BW]	CD4 ⁺ [10 ³ /μl PB]	CD8 ⁺
					CMV	EBV		CMV (max. copies)	EBV (max. copies)		Day	Donor %			
1	M	60	MM	RIC / FBM	pos.	pos.	Yes	No	Yes (70000)	No	30	99.9	N.A.	2.2	1.0
2	M	62	MM	RIC / FBM	neg.	pos.	Yes	No	No	No	60	100	2.4	1.2	0.7
3	M	60	MM	RIC / FBM	pos.	pos.	Yes	Yes (42000)	No	No	38	99.9	3.0	1.3	0.8
4	M	27	AML	MAB / TreoFlu	neg.	pos.	No	No	No	Yes	60	99.3	N.A.	N.A.	N.A.
5	F	57	CLL	RIC / TTFuCy	neg.	pos.	No	No	No	Yes	60	99.7	N.A.	2.3	0.6
6	M	50	CML	MAB /TreoFlu	pos.	pos.	Yes	Yes (23000)	Yes (430000)	Yes	30	100	N.A.	1.4	0.5
7	M	57	AML	RIC / FBM	neg.	pos.	Yes	No	No	No	30	100	1.5	1.2	0.4
8	F	47	AML	RIC / FBM	pos.	pos.	No	No	No	No	30	100	2.2	1.9	1.6
9	M	67	MDS	RIC / FBM	pos.	pos.	Yes	Yes (24000)	No	No	35	100	2.5	0.7	1.1
10	M	57	ALL	RIC / BusFlu	neg.	pos.	Yes	No	No	No	37	100	N.A.	0.7	0.5
11	M	56	OMF	RIC / BusFlu	neg.	N.A.	Yes	No	No	No	30	81.6	N.A.	1.8	0.8
12	F	51	AML	RIC / FBM	pos.	pos.	Yes	Yes (12000)	Yes (320000)	Yes	30	100	1.5	0.7	0.6
13	M	66	AML	RIC / FBM	pos.	pos.	No	Yes (3800)	Yes (28000)	Yes	40	100	2.2	1.6	1.0
14	M	60	MDS	RIC / FBM	pos.	pos.	Yes	Yes (75000)	No	No	36	100	1.8	1.7	0.6
15	M	56	AML	RIC / FBM	pos.	pos.	No	Yes (26000)	No	No	39	93	N.A.	1.8	0.5
16	M	59	MDS	RIC / FBM	pos.	pos.	Yes	Yes (140000)	No	No	30	100	1.9	1.0	0.9
17	M	46	AML	RIC / FBM	pos.	pos.	Yes	Yes (23000)	No	No	30	100	1.9	0.8	0.4
18	M	52	MDS	RIC / FBM	pos.	pos.	Yes	Yes (30000)	Yes (42000)	No	30	100	3.1	1.4	0.8
19	F	33	AML	RIC / FBM	neg.	pos.	Yes	No	No	No	N.A.	N.A.	1.8	0.7	0.7
20	M	22	AML	RIC / FBM	neg.	neg.	Yes	No	No	No	29	100	1.9	1.7	0.7
21	M	69	AML	RIC / FBM	neg.	pos.	Yes	No	No	No	29	100	7.7	2.7	2.1
22	M	33	AML	MAB / TreoFlu	pos.	pos.	Yes	No	Yes (83000)	Yes	48	100	N.A.	1.6	0.8
23	M	59	MDS	RIC / FBM	pos.	pos.	No	Yes (16000)	Yes (27000)	No	30	99.3	3.4	1.6	1.3

Gender, age, disease type, conditioning regime, virus status (CMV and EBV) and clinical data (incidence of aGvHD, CMV and EBV reactivation, relapse and chimerism) of the corresponding stem cell recipients. In addition cell numbers for CD4⁺ and CD8⁺ T cells in the peripheral blood of donors and CD34⁺ cells counts in the transplant are shown.

Threshold for antiviral treatment for CMV reactivation (Ganciclovir or Foscarnet) was >5000 copies/ml PB, for EBV reactivation (Rituximab) was >20000 copies/ml PB.

ALL indicates acute lymphatic leukemia; **AML**: acute myeloid leukemia; **CLL**: chronic lymphatic leukemia; **CML**: chronic myeloid leukemia; **MDS**: myelodysplastic syndrome; **MM**: multiple myeloma; **OMF**: osteomyelofibrosis; **MAB**: myeloablative conditioning; **RIC**: reduced intensity conditioning; **FBM**: Fludarabin 30mg/sqm d-9,-8,-7,-6,-5 + BCNU 150mg/sqm d-7,-6 + Melphalan 110mg/sqm d-4 + Thymoglobulin 2.5mg/kg (SIB), 7.5mg/kg (MUD); **TreoFlu**: Treosulfan 12g/sqm d-6,-5,-4 + Fludarabin 30mg/sqm d-6,-5,-4,-3,-2 + Thymoglobulin 2.5mg/kg (SIB), 7.5mg/kg (MUD); **BusFlu**: Busulfane i.v. 6.4mg/kg total dose + Fludarabin 30mg/sqm d-6,-5,-4 + Thymoglobulin 2.5mg/kg (SIB), 7.5mg/kg (MUD); **TTFuCy**: Thiotepa 10mg/kg d-6 + Fludarabin 30mg/kg d-4,-3 + Cyclophosphamide 30mg/kg d-4,-3 + Thymoglobulin 2.5mg/kg (SIB), 7.5mg/kg (MUD); **N.A.**: not available; **BW**: body weight; **PB**: peripheral blood

Table S2. Risk factors for aGvHD incidence.

Recipient follow up		acute GvHD			
		Yes	No	total	p-value x2-test
Donor type	MUD	12	3	15	0.3627
	SIB	5	3	8	
Donor age	<40	5	2	7	0.8576
	>40	12	4	16	
Patient					
Age	<40	3	1	4	0.9566
	>40	14	5	19	
CMV reactivation	Yes	8	3	11	0.9013
	No	9	3	12	
EBV reactivation	Yes	5	2	7	0.8576
	No	12	4	16	

Contingency table of the incidence of aGvHD in recipients after aHSCT in correlation with clinical parameters as donor age and type as well as Patient age and virus reactivation.

aGvHD: acute Graft-versus-host Disease; χ^2 -test: Chi-squared test

Table S3. Primer sequences.

TCRβ V segment(s)	Primer sequence
V2	CCCTACACGACGCTCTTCCGATCTCAAATTTCACTCTGAAGATCCGGTCCACAA
V3-1	CCCTACACGACGCTCTTCCGATCTCTCACTTAAATCTTCACATCAATTCCCTGG
V4-1	CCCTACACGACGCTCTTCCGATCTTTAAACCTTCACCTACACGCCCTGC
V4-2/3	CCCTACACGACGCTCTTCCGATCTTTATTCTTCACCTACACACCCTGC
V5-1	CCCTACACGACGCTCTTCCGATCTCTCTGAGATGAATGTGAGCACCTTG
V5-3	CCCTACACGACGCTCTTCCGATCTCTCTGAGATGAATGTGAGTGCCTTG
V5-4/5/6/7/8	CCCTACACGACGCTCTTCCGATCTCTCTGAGCTGAATGTGAACGCCTTG
V6-1	CCCTACACGACGCTCTTCCGATCTCGCTCAGGCTGGAGTCGGCTG
V6-2/3	CCCTACACGACGCTCTTCCGATCTCTGGGGTTGGAGTCGGCTG
V6-4	CCCTACACGACGCTCTTCCGATCTCCTCACGTTGGCGTCTGCTG
V6-5	CCCTACACGACGCTCTTCCGATCTCTCAGGCTGCTGTGGCTG
V6-6	CCCTACACGACGCTCTTCCGATCTGCTCAGGCTGGAGTTGGCTG
V6-7	CCCTACACGACGCTCTTCCGATCTCCCTCAAGCTGGAGTCAGCTG
V6-8	CCCTACACGACGCTCTTCCGATCTACTCAGGCTGGTGTGGCTG
V6-9	CCCTACACGACGCTCTTCCGATCTGCTCAGGCTGGAGTCAGCTG
V7-1	CCCTACACGACGCTCTTCCGATCTCACTCTGAAGTTCCAGCGCACAC
V7-2	CCCTACACGACGCTCTTCCGATCTACTCTGACGATCCAGCGCACAC
V7-3	CCCTACACGACGCTCTTCCGATCTTCTACTCTGAAGATCCAGCGCACAG
V7-4	CCCTACACGACGCTCTTCCGATCTCACTCTGAAGATCCAGCGCACAG
V7-6	CCCTACACGACGCTCTTCCGATCTACTCTGACGATCCAGCGCACAG
V7-7	CCCTACACGACGCTCTTCCGATCTCACTCTGACGATTCAGCGCACAG
V7-8	CCCTACACGACGCTCTTCCGATCTCACTCTGAAGATCCAGCGCACAC
V7-9	CCCTACACGACGCTCTTCCGATCTACCTTGGAGATCCAGCGCACAG
V9	CCCTACACGACGCTCTTCCGATCTCACTCTGAACTAAACCTGAGCTCTCTG
V10-1	CCCTACACGACGCTCTTCCGATCTCCCTCACTCTGGAGTCTGCTG
V10-2	CCCTACACGACGCTCTTCCGATCTCCCCTCACTCTGGAGTCAGCTA
V10-3	CCCTACACGACGCTCTTCCGATCTCTCCTCACTCTGGAGTCCGCTA
V11-1/3	CCCTACACGACGCTCTTCCGATCTCACTCTCAAGATCCAGCCTGCAG
V11-2	CCCTACACGACGCTCTTCCGATCTTCCACTCTCAAGATCCAGCCTGCAA
V12-3/4/5	CCCTACACGACGCTCTTCCGATCTCACTCTGAAGATCCAGCCCTCAG
V13	CCCTACACGACGCTCTTCCGATCTATTCTGAACTGAACATGAGCTCCTTGG
V14	CCCTACACGACGCTCTTCCGATCTTACTCTGAAGGTGCAGCCTGCAG
V15	CCCTACACGACGCTCTTCCGATCTATAACTTCCAATCCAGGAGGCCGAACA
V16	CCCTACACGACGCTCTTCCGATCTTGTAGCCTTGAGATCCAGGCTACGA
V17	CCCTACACGACGCTCTTCCGATCTTTCCACGCTGAAGATCCATCCCG
V18	CCCTACACGACGCTCTTCCGATCTCATCCTGAGGATCCAGCAGGTAG
V19	CCCTACACGACGCTCTTCCGATCTCTCTCACTGTGACATCGGCC
V20-1	CCCTACACGACGCTCTTCCGATCTTTGTCCACTCTGACAGTGACCAGTG
V23-1	CCCTACACGACGCTCTTCCGATCTAGCCTGGCAATCCTGTCTCAG

V24-1	CCCTACACGACGCTCTTCCGATCTTCCCTGTCCCTAGAGTCTGCCAT
V25-1	CCCTACACGACGCTCTTCCGATCTCCTGACCCTGGAGTCTGCCA
V27	CCCTACACGACGCTCTTCCGATCTCCTGATCCTGGAGTCGCCA
V28	CCCTACACGACGCTCTTCCGATCTTCCCTGATTCTGGAGTCGCCA
V29-1	CCCTACACGACGCTCTTCCGATCTTAACATTCTCAACTCTGACTGTGAGCAACA
V30	CCCTACACGACGCTCTTCCGATCTGGCAGTTCATCCTGAGTTCTAAGAAGC
TCRβ J segment	Primer sequence
J1-1	TTCAGACGTGTGCTCTTCCGATCTCTTACCTACAACCTGTGAGTCTGGTGCC
J1-2	TTCAGACGTGTGCTCTTCCGATCTCTTACCTACAACGGTTAACCTGGTCCCCG
J1-3	TTCAGACGTGTGCTCTTCCGATCTCTCACCTACAACAGTGAGCCAACCTTCCCT
J1-4	TTCAGACGTGTGCTCTTCCGATCTACCCAAGACAGAGAGCTGGGTTCCTACT
J1-5	TTCAGACGTGTGCTCTTCCGATCTCTTACCTAGGATGGAGAGTCGAGTCC
J1-6	TTCAGACGTGTGCTCTTCCGATCTACCTGTCACAGTGAGCCTGGTCCCCG
J2-1	TTCAGACGTGTGCTCTTCCGATCTTACCTAGCACGGTGAGCCGTGTCCC
J2-2	TTCAGACGTGTGCTCTTCCGATCTCTTACCCAGTACGGTCAGCCTAGAGC
J2-3	TTCAGACGTGTGCTCTTCCGATCTGAGCACTGTCAGCCGGGTGCCTGG
J2-4	TTCAGACGTGTGCTCTTCCGATCTCAGCACTCAGAGCCGGGTCCC
J2-5	TTCAGACGTGTGCTCTTCCGATCTACCGAGCACCAGGAGCCGCGTGC
J2-6	TTCAGACGTGTGCTCTTCCGATCTAGCACGGTCAGCCTGCTGCCGGC
J2-7	TTCAGACGTGTGCTCTTCCGATCTGTGACCGTGAGCCTGGTGCCCGG
Adapter primer	Primer sequence
FW	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTC
REV1	CAAGCAGAAGACGGCATAACGAGATCGTGATGTGACTGGAGTTCAGACGTGTGC
REV2	CAAGCAGAAGACGGCATAACGAGATACATCGGTGACTGGAGTTCAGACGTGTGC
REV3	CAAGCAGAAGACGGCATAACGAGATGCCTAAGTGACTGGAGTTCAGACGTGTGC
REV4	CAAGCAGAAGACGGCATAACGAGATTGGTCAGTGACTGGAGTTCAGACGTGTGC
REV5	CAAGCAGAAGACGGCATAACGAGATCACTGTGTGACTGGAGTTCAGACGTGTGC
REV6	CAAGCAGAAGACGGCATAACGAGATATTGGCGTGACTGGAGTTCAGACGTGTGC
REV7	CAAGCAGAAGACGGCATAACGAGATGATCTGGTGACTGGAGTTCAGACGTGTGC
REV8	CAAGCAGAAGACGGCATAACGAGATTCAAGTGACTGGAGTTCAGACGTGTGC
REV9	CAAGCAGAAGACGGCATAACGAGATCTGATCGTGACTGGAGTTCAGACGTGTGC
REV10	CAAGCAGAAGACGGCATAACGAGATAAGCTAGTGACTGGAGTTCAGACGTGTGC