SUPPLEMENTAL MATERIAL

Peaudecerf et al., http://www.jem.org/cgi/content/full/jem.20120845/DC1

A

TCRA diversity of DP thymocytes

	# of cells sorted	# of unique CDR3s
Control	200,000	96,449
Control	200,000	95,144
Graft	70,000	58,843

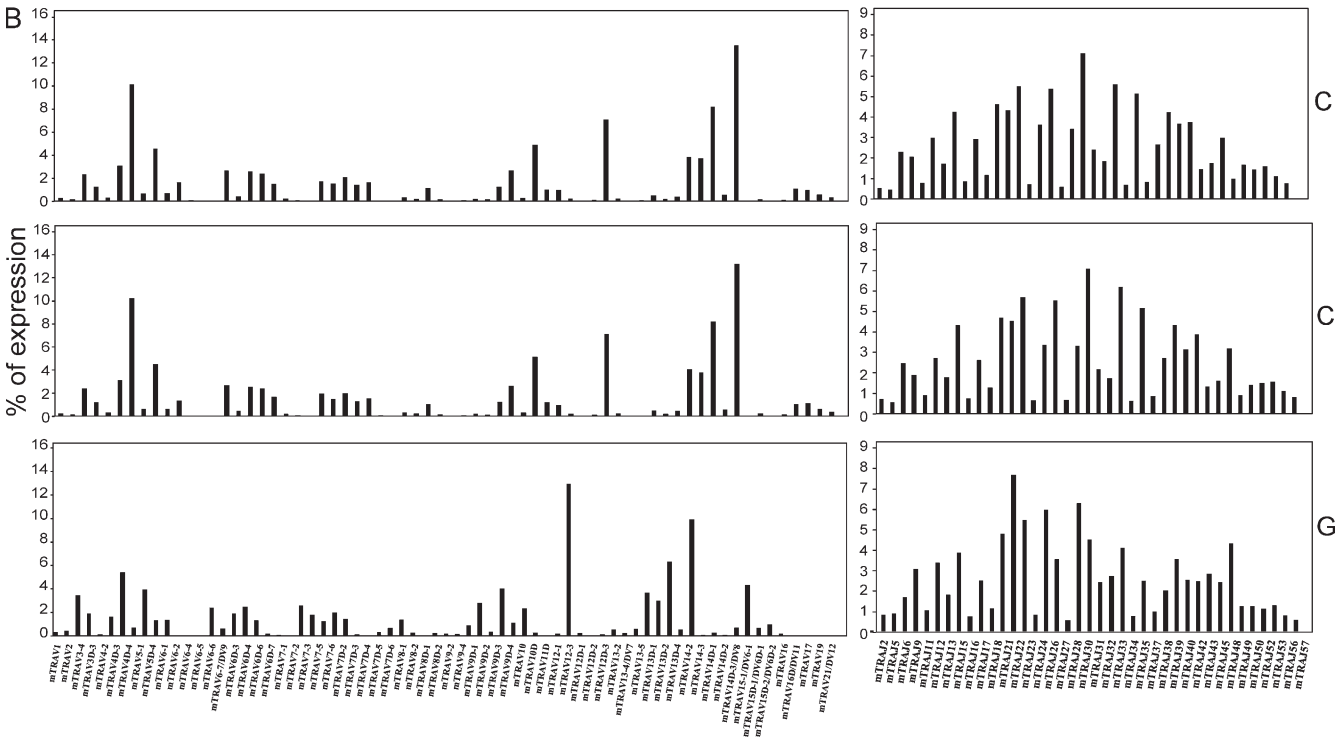

Figure S1. The CD4⁺CD8αβ⁺ (DP) populations persisting in the grafts. 6–8-wk-old CD45.2⁺ B6 Rag2γ_c^- mice were grafted with a single thymus lobe from CD45.1⁺ B6 WT neonatal mice. 2 mo later, DP cells from the graft or from age-matched controls were sorted and the TCRA repertoires were analyzed. (A) Numbers of cells sorted and of unique CDR3 regions identified. (B) TCRAV and TCRAJ usage in two controls (C, top graphs) and one transplanted thymus (G, bottom graph) from the four transplanted mice studied.

A TCR diversity of CD8 Tcells in the spleen

	# of cells sorted	# of unique CDR3s TCRB	TCRA
Control	200,000	113,032	140,070
Control	200,000	106,590	136,362
Graft (4w)	200,000	104,284	142,064
Graft (4w)	200,000	129,998	124,641
Graft (6w)	200,000	109,090	167,908
Graft (8w)	200,000	ND	185,346

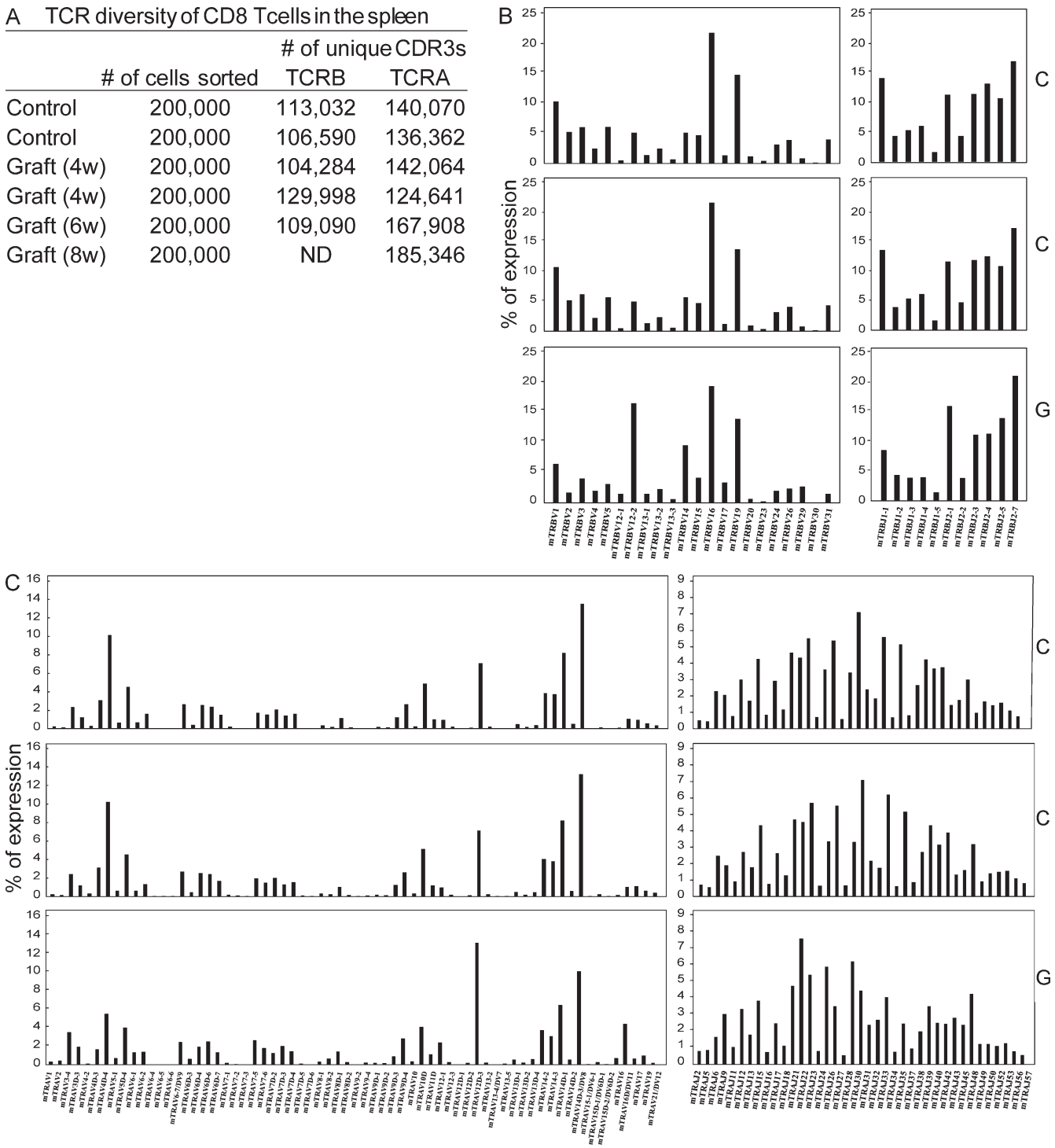

Figure S2. The repertoire of the peripheral T cell pools 1 mo after grafting. 6–8-wk-old CD45.2+ B6 Rag2γ_c^- mice were grafted with a single thymus lobe from CD45.1+ B6 WT neonatal mice. At different time points after surgery, 2 × 10^4 CD8 T cells were sorted from their spleen or from the spleen of age-matched controls and TCRB and TCRA repertoires were analyzed. (A) Numbers of unique CDR3 regions identified in the spleen. (B) TCRVB and TCRBJ usage (C) TCRVA and TCRJA usage in two WT mice (C, top graphs) and one transplanted mouse (G, bottom graph) at 1 mo after grafting. 4 mice were studied at different time points with the equivalent results.

Table S1. Primer sequences used for single-cell genetic profiling

Genes	Primer sequences
Bcl11b	A: GGCGATGCCAGAATAGATGC
	B: TTGTCCAGGACCTTGTCGTA
	C: TTGTCCCAGAGGGAACTCAT
Gata3	A: TCGGCCATTCGTACATGGAA
	B: TGGATGGACGTCTTGGAGAA
	C: ATCGATGGTCAAGGCAACCA
Notch1	A: GCTACGAATGTGCCTGTGAA
	B: CATACGTAGCCACTGGTCAT
	C: CAACGAGTGCAACAGTAACC
Rag1	A: CAACCAAGCTGCAGACATTC
	B: CTACTGGAGACTGTTCTAGG
	C: GCAGACATTCTAGCACTCTG

All primer sequences are in 5′→ 3′ direction. B primers are anti-sense, and were used for gene-specific reverse transcription. This was followed by a first RT-PCR associating primers A and B. A second, seminested PCR was performed by adding primers B and C. Primers for the house keeping gene were as described (Peixoto et al., 2004).

REFERENCE

Peixoto, A., M. Monteiro, B. Rocha, and H. Veiga-Fernandes. 2004. Quantification of multiple gene expression in individual cells. *Genome Res.* 14:1938–1947. http://dx.doi.org/10.1101/gr.2890204