				Activated with anti-CD3 and anti-CD28					
Treatment				medium	medium + IL-12	+1,25D3	+1,25D3 + IL-12	+1,25D3 + IL-12	+ RA
Sorted phenotype		Memory T cells (fresh CD45RO$^+$)		CLA+ (sorted after treatment)					
	Sorted for ->	CLA$^+$	$?_4?_7^{hi}$	CCR10$^?$	CCR10$^?$	CCR10$^?$	CCR10$^?$	CCR10$^+$	$?_4?_7^{hi}$
Gene	Systemic name								
CCR4	208376_at	175	204	A	A	A	A	A	A
CCR6	206983_at	2601	1267	A	A	89	101	A	57
CCR7	206337_at	2911	3571	3914	3616	3056	1845	2189	5480
CCR8	208059_at	A	A	A	A	A	A	A	A
CCR9	207445_s_at	84	2997	A	A	65	A	65	955
CCR10	220565_at	A	A	A	A	A	130	482	A
VDR	204254_s_at	446	240	2008	2042	1446	1302	1093	4246
CYP27A1	203979_at	244	A	A	A	A	A	A	A
CYP27B1	205676_at	116	208	248	273	290	210	191	414

Supplemental Figure 3. Chemokine receptor expression by circulating memory and *in vitro* activated T cell subsets. Memory $CLA^+CD45RO^+$ and $\alpha_4\beta_7^{hi}CD45RO^+$ $CD3^+$ T cells were sorted from buffy coats and used to isolate RNA. Naïve T cells (0.7×10^6) were isolated by magnetic beads and activated for 2 days with anti-CD3 (1 μg/ml) and anti-CD28 (1 μg/ml) in the presence of medium, $1,25(OH)_2D_3$ (10 nM) or 10 nM retinoic acid (RA), and with or without IL-12 (2.5 ng/ml). After 2 days the cells were transferred to new wells and fresh medium containing IL-2 (12.5 ng/ml) added every two days. After 4 additional days, T cells were sorted by FACS according to their expression of CLA, CCR10 and $\alpha_4\beta_7$ as indicated and used to isolate RNA for microarray analysis. Total RNA from each FACS-sorted subset was isolated using RNeasy mini kit (Invitrogen), and the quality of total RNA was determined by Agilent Bioanalyzer.

The probe generation, hybridization and scanning were performed by the Stanford Protein and Nucleic Acid Biotechnology (PAN) Facility (http://cmgm.stanford.edu/pan/gene/index.html), and the Affymetrix human chip HG_U133_plus_2 was used for this study. Microarray data was analyzed using Affymetrix GeneChip Operating Software (GCOS) in combination with GeneSpring software (Agilent). TaqMan-based quantitative Data represent the raw Affymetrix signals: signal strength depends on the probe as well as the mRNA expression abundance, so that comparisons between a given gene among different cell samples is warranted, but differences in values between genes do not correlate with absolute mRNA expression. Experiments were repeated 3 times with similar results (except for the memory T cells and CLA^+ T cells activated without IL-12 or $1,25(OH)_2D_3$, which was performed once);

representative results are shown. A=absent. The expression of *CCR4–CCR10* are shown, as well as *VDR*, *CYP27A1* and *CYP27B*.