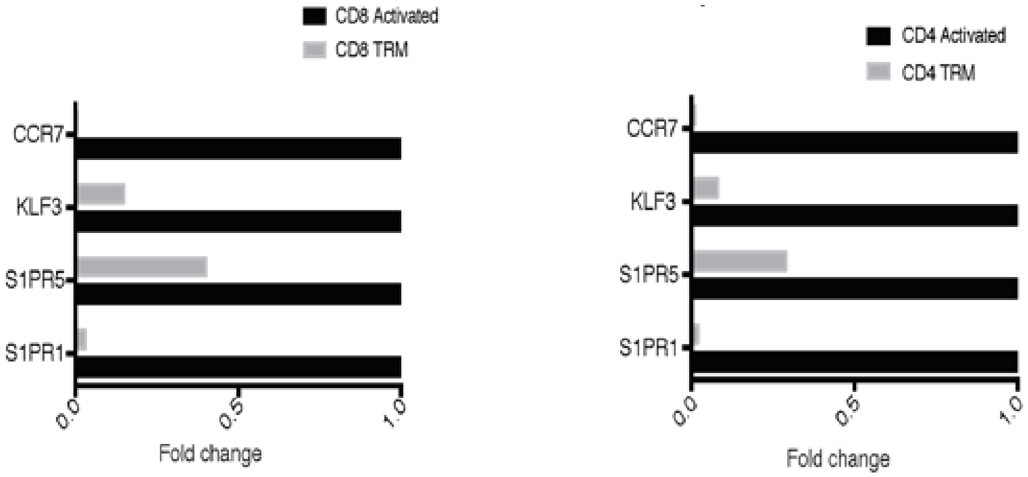
Supplementary Table S1. CyTOF antibody panel.

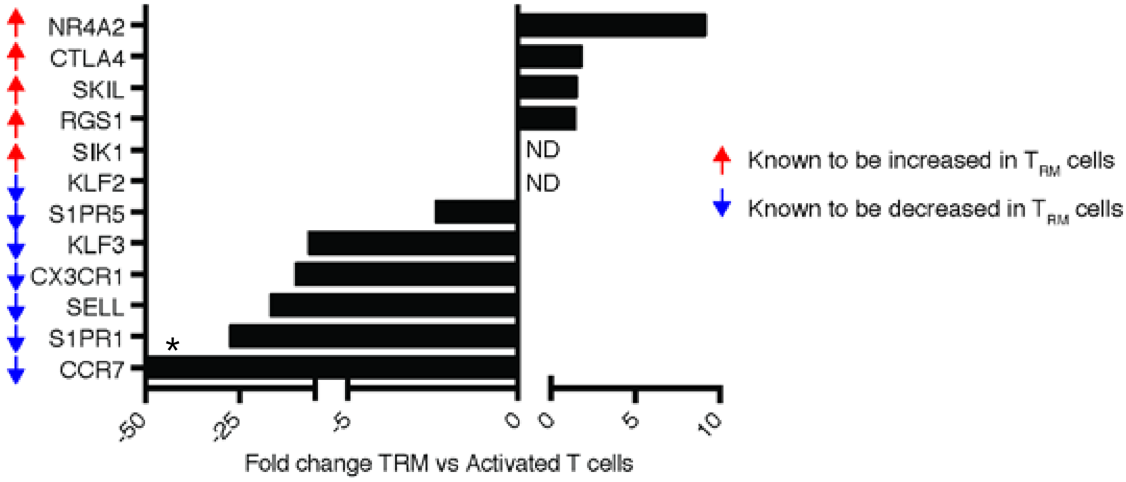
CyTOF Antibodies		
Name	**Clone**	**Metal**
CD45	HI30	89 Y
B7H3	MIH42	141 Pr
CD19	HIB19	142 Nd
C-kit	104D2	143 Nd
CD27	0323	144 Nd
CD4	RPA-T4	145 Nd
CD8	RPA-T8	146 Nd
CD11c	Bu15	147 Sm
CD14	RMO52	148 Nd
CD25	2A3	149 Sm
CD103	Ber-ACT8	151 Eu
TIM3	F38-2E2	153 Eu
CD3	UCHT1	154 Sm
CXCR5	J252D4	155 Gd
CD16	3G8	156 Gd
CD33	WM53	158 Gd
CCR7	GO43H7	159 Tb
41BB	4B4-1	161 Dy
BTLA	MIH26	163 Dy
CD95	DX2	164 Dy
CD45RO	UCHL1	165 Ho
HLADR	L243	166 Er
CD69	FN50	169 Tm
CTLA4	14D3	170 Er
CD38	HIT2	172 Yb
ICOS	DX29	173 Yb
PDL1	MIH1	174 Yb
PD1	EH12.2H7	175 Lu
CD56	CMSSB	176 Yb
PLZF	Mags.21F7	152 Sm
GATA3	TWAJ	167 Er
Ki67	Ki-67	168 Er
TBET	4B10	160 Gd
Foxp3	PCH101	162 Dy
Granzyme	GB11	171 Yb

Figure S1



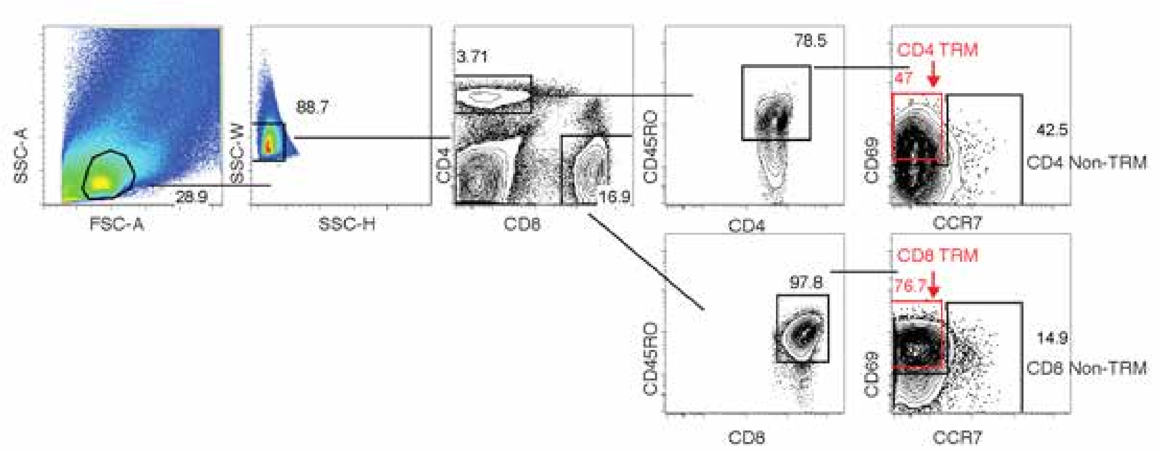
Supplementary Figure S1: Expression of genes implicated in tissue retention in T_{RM} cells versus circulating T cells activated in vitro. CD4 and CD8 T_{RM} cells were sorted from tumor tissue. T cells obtained from peripheral blood were stimulated in vitro with anti-CD3/28 beads and CD69+ activated CD4 and CD8 T cells were flowsorted. RNA was obtained and gene expression was analyzed using affymetrix U133 plus 2 array. Panel on the left shows expression of genes implicated in tissue retention in tumor CD8 T_{RM} cells versus circulating CD8 T cells activated in-vitro with CD3/28 (CD69+ sorted). Panel on the right shows expression of genes implicated in tissue retention in tumor CD4 T_{RM} cells compared to circulating CD4 T cells activated in-vitro with anti-CD3/28 (69+ sorted). Both panels shows fold change compared to activated T cells.

Figure S2



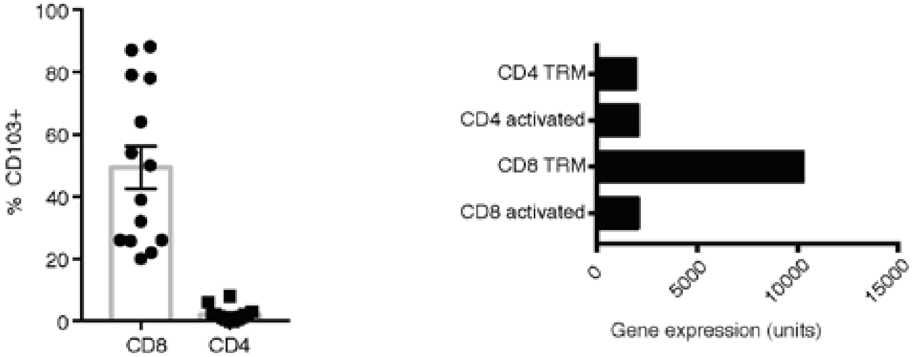
Supplementary Figure S2: Expression of core T_{RM} genes in CD8T_{RM} cells versus circulating CD8 T cells activated in vitro. CD8 T_{RM} cells were sorted from tumor tissue. T cells obtained from peripheral blood were stimulated in vitro with anti-CD3/28 beads and CD69+ activated CD8 T cells were flow sorted. RNA was obtained and gene expression was analyzed using affymetrix U133 plus 2 array. Figure shows expression (fold change) of previously described murine core T_{RM} genes in human CD8 T_{RM} cells isolated from melanoma tumor compared to circulating CD8 T cells activated in vitro using anti-CD3/28 beads (sorted 69+ CD8 T cells). * -157 fold, ND=no difference.

Figure S3



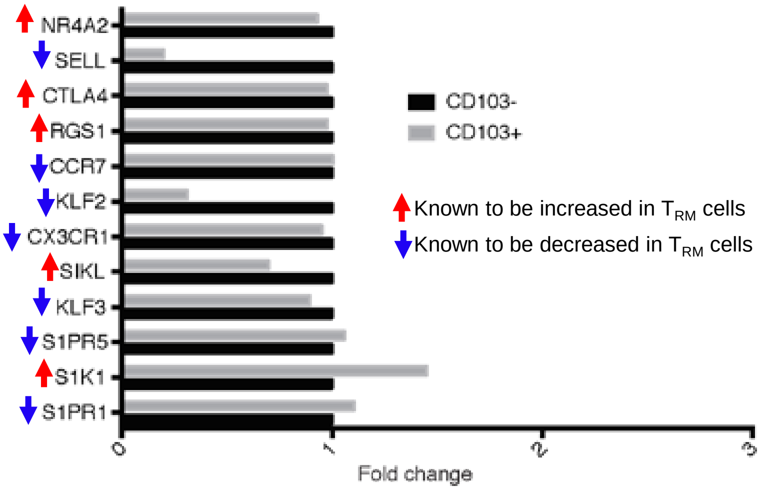
Supplementary Figure S3: Gating strategy used to sort T_{RM} and Non-T_{RM} cells from tumor tissue. Facs plot shows the sequential gating strategy used to sort T_{RM} and Non-T_{RM} cells from melanoma tumor tissue.

Figure S4



Supplementary Figure S4: **Expression of CD103 is enriched in tumor CD8 T_{RM} cells.** Panel on the left shows % of CD8 T_{RM} and CD4 T_{RM} cells from tumor tissue that express CD103 as determined using CyTOF. Panel on the right shows gene expression of ITGAE (CD103) in CD8 T_{RM} and CD4 T_{RM} from tumor compared to CD8 and CD4 circulating T cells activated in-vitro with anti-CD3/28.

Figure S5



Supplementary Figure S5: **Expression of core murine T_{RM} genes in CD103+ and CD103- tumor associated CD8 T_{RM} cells.** Bar graph shows expression of previously described murine core T_{RM} genes in human CD103+ and CD103- CD8 T_{RM} cells isolated from melanoma tumor. Figure shows fold change compared to CD103- cells T_{RM} cells.