Supplementary Table 1. Patient characteristics

Patient ID	Cancer type	Prior therapy	Months from end of last therapy to leukapheresis (mo)	%PD-1^{+} (of CD8^{+}) PBMC	# putative mutations[d]	Mutations evaluated[e]
NCI-3713	Mel[a]	IL-2, anti-CTLA-4	7 mo	4.1%	4359	7 minimal epitopes
NCI-3998	Mel	No treatment	-	1.9%	279	115 (TMG#1-7)
NCI-3784	Mel	Surgery, IFN	14 mo	2.1%	440	140 (TMG1-9)
NCI-3903	Mel	Surgery, MART-F5 TCR[b]	55 mo	3.4%	414	308 (TMG#1-26)
NCI-3926	Mel	IL-2, surgery, chemo.[c]	8 mo	7.4%	346	128 (TMG#1-11)
NCI-3759*	Mel	Surgery, IFN	1 mo	1.0%	n.d.[f]	n.e.[g]
NCI-3992*	Mel	Anti-PD-1, anti-CTLA-4	5 mo	8%	n.d.	n.e.

[a]Melanoma; [b] Adoptive transfer of autologous T cells that were gene-engineered to express a MART1 HLA-A*0201-restricted T cell receptor (TCR). [c]Chemotherapy NCI- 3926: dacarbazine and vinblastine. [d]Putative non-synonymous mutations were defined by: >2 exome variant reads, ≥ 10% variant frequency in the exome, ≥10 normal reads, and tumor/normal variant frequency ≥5. Common single nucleotide polymorphisms were filtered. [e]Mutations screened were selected based on whole-exome and transcriptome analysis. [f]Not deteremined. [g]Not evaluated.*NCI-3759 and 3992 were only included in Fig.4i

Nature Medicine: doi:10.1038/nm.4051