Supplementary Figure legends:

Figure S1:

Antigen-specific T-cell responses in the peripheral blood following CMV-specific T-cell infusion. (A) Representative longitudinal ex vivo analysis of CMV-specific CD8+ T-cells from GBM:03 patient before, during (before 3rd infusion) and after T-cell adoptive therapy. PBMC from each time point were incubated with HLA-peptide multimers and antibodies specific for CD3, CD4 and CD8 and then analysed using a LSR Fortessa with FACSDiva software. Post-acquisition analysis was conducted using FlowJo software. (B) Comprehensive analysis of CMV-specific T-cell frequencies in GBM patients before, during and after T-cell therapy. (C) Ex vivo polyfunctional profile of CMV-specific T-cells from GBM patients before, during and after T-cell infusions. PBMC from these patients were stimulated with pools of CMV epitopes for five hours in the presence of Monensin, Brefeldin and anti-CD107α. IFN-γ, IL-2 and TNF expression by CD8+ T-cells was assessed using intracellular cytokine assay. Data represents the percentage of T-cells expressing different combinations of CD107α, IFN-γ, IL-2 and/or TNF. Representative data from three recurrent GBM patients is shown.

Figure S2:

Molecular profiling of T-cell therapy (A) List of all genes that were significantly upregulated in the gene expression analysis of CMV-specific T-cells before and after in vitro expansion. (B) List of all significantly down-regulated genes. (C) Validation of selected genes from the gene array by flow cytometry.
Figure S3:

Longitudinal comparative phenotypic analysis of peripheral blood circulating and tumour infiltrating CD8+ T-cells from a GBM patient. Tumour infiltrating lymphoid cells and PBMC isolated before (d0), during (d38) and after (d78, d121) T cell therapy were incubated with antibodies specific for CD3, CD4, CD8 and specific markers (as indicated on the Y-axis of each box) and then analysed using a LSR Fortessa with FACSDiva software. Post-acquisition analysis was conducted using FlowJo software.