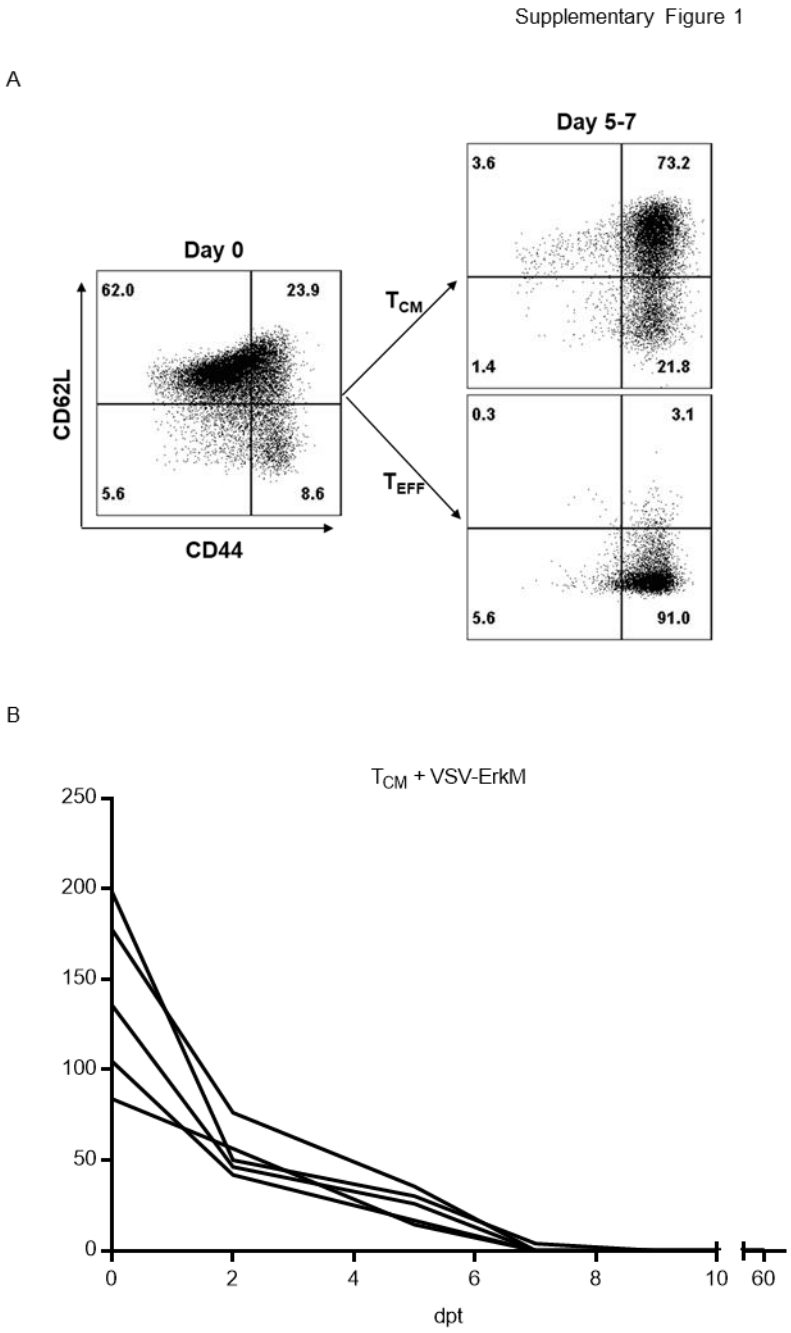

Figure S1. ***In vitro*** **differentiation/expansion of T_{CM} and T_{EFF} and tumor regression curve of T_{CM} + VSV-ErkM treated mice**. (A) DUC18 transgenic T cells were stimulated with corresponding ErkM peptide in the presence of IL-15 + IL-21 + rapamycin or IL-2 for 7 days in order to generate central memory (T_{CM}) or effector (T_{EFF}) phenotype cells, respectively. An

example of flow cytometry phenotypic analysis of cultured transgenic T cells is depicted. (B) Tumor regression curve of T_{CM} + VSV-ErkM treated mice from Figure 1A with expanded axes to display regression kinetics.

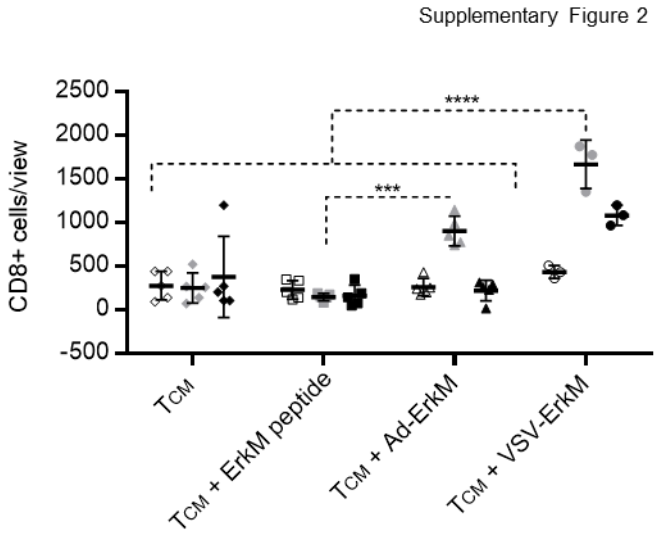

Figure S2. CD8 staining counts of treated tumor sections. CMS5 tumor tissues from mice receiving the indicated treatment were stained with an anti-CD8 antibody and multiple high magnification micrographs taken for counting of positive stained cells per view using the analyze particle function of the ImageJ software "(54)". Data are results of one independent experiment with 3 tumors analyzed per group and 5 images analyzed per tumor for the T_{CM} alone, T_{CM} + ErkM peptide and T_{CM} + Ad-ErkM groups and 3 images for the T_{CM} + VSV-ErkM group. Data were analyzed using a two-way ANOVA with Holm-Sidak correction for multiple comparisons. Significant results are denoted as *$P < 0.05$, ***$P < 0.001$, and ****$P < 0.0001$.

Supplementary Figure 3

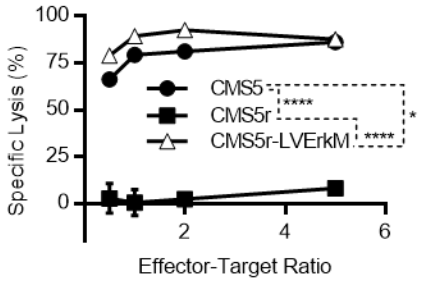

Figure S3. ErkM peptide expression rescues CMS5r susceptibility to DUC18 killing.

Cytotoxicity of DUC18 T_{EFF} cells on CMS5 cells and CMS5r cells engineered to express the ErkM peptide (CMS5r-LVErkM) but not on CMS5r cells (n=3). Data is derived from a single experiment. A two-way ANOVA with Holm-Sidak correction for multiple comparisons was used for statistical analysis and significant results are denoted as *P < 0.05 and ****P < 0.0001.