Supplementary Figure and Table Legends

Table S1: Expression levels of immunogenic tumor antigens as reported by Cheevers *et al.*[23] translated to murine gene names (Mouse Genome Informatics) in KPC3, AE17 and B16 with a minimal threshold of 1 RPKM (reads per kilo base per million mapped reads).

Fig. S1: Venn diagram illustrating overlapping and non-overlapping genes of the tumor cell lines KPC3 (pancreatic cancer), AE17 (mesothelioma), B16F10 (melanoma) and MC38 (colon adenocarcinoma).

Fig. S2: MFI of CD11c, CD40, PD-L1, MHCII, CD80 and CD86 on cultered DCs for vaccination. Control non-loaded DCs were not stimulated with CpG.

Fig. S3: Percentage of CD69+, Ki67+ and CD44+CD62L- subsets of circulating CD4+ and CD8+ T cells at day -3, 4 and 20. N=8 per group. Significance was determined using the non-parametric Mann-Whitney U test. Data presented as the mean ± s.e.m. *P<0.05.

Fig. S4: Relative production of IFNγ, IL-2 and TNFα by by CD8+ splenocytes of AE17 lysate-DC/αCD40-treated and untreated after stimulation with DCs loaded with KPC3, AE17 or B16F10, or non-loaded DCs, normalized for untreated mice. N=6-10 per group. Significance was determined using the non-parametric Mann-Whitney U test. Data presented as the mean±s.e.m. **P<0.01, **P<0.01, ***P<0.001, ****P<0.0001.

Fig. S5: Lysate-DC is not effective as monotherapy in tumor-bearing mice. (A) CD3+, CD4+ and CD8+ circulating T cells as a percentage of alive CD45+ cells, four days after DC vaccination. (B) Percentage of CD44+CD62L- and Ki67+ subsets of CD4+ and CD8+ circulating T cells, four days after DC vaccination. (C) Tumor volume measured over time, and tumor size at the day of sacrifice (day 22). (D) CD3+, CD4+ and CD8+ TILs as a percentage of alive CD45+ cells. N=5-9 per group. Significance was determined using the non-parametric Mann-Whitney U test. Data presented as the mean ± s.e.m. *P<0.05, **P<0.01, ***P<0.001.

Fig. S6: (A) Study setup (B) Tumor volume measured over time, and tumor size at day of sacrifice (day 18). (C) Percentage of CD69+, Ki67+, PD-1+ and CD44+CD62L- subsets of CD4+ and CD8+ circulating T cells, four days after treatment initiation. (D) Memory status of CD4+ and CD8+ circulating T cells at day 9 and day 16. (E) Number of CD3+, CD4+, CD8+, CD4+CD25+FoxP3+ TILs per mg tumor. (F) MFI of PD-1 and Lag-3 of CD4+ and CD8+ TILs. N=7-8 per group. Significance was determined using the non-parametric Mann-Whitney U test. Data presented as the mean ± s.e.m. *P<0.05, **P<0.01, ***P<0.001.

Fig. S7: (A) Study setup in mesothelioma model. (B) Kaplan-Meier analysis of treated and untreated animals. (C) Percentage of PD-1+ and Ki67 subsets of CD4+ and CD8+ circulating T cells, on day 16. N=5 per group. Significance was determined using the non-parametric Mann-Whitney U test. Data presented as the mean ± s.e.m. *P<0.05, **P<0.01.

Fig. S8: Tumor outgrowth curves of treated and untreated tumor-bearing mice.

Fig. S9: (A) Interim blood analysis on day 14. Percentage of CD4+ and CD8+ of CD3+ T cells. (B) Absolute number of CD3+, CD4+, CD8+, CD335+ and CD19+ cells per μL blood drawn on day 14.

Fig. S10: Orthotopic tumors taken out on day 17.

Fig. S11: Fraction of non-myeloid (CD45-), monocyte (CD45+F4/80-CD11b+Ly6C+Ly6G-), granulocyte (CD45+F4/80-CD11b+Ly6C-Ly6G+), cDC1 (CD45+F4/80-CD11b+CD11b-CD11c+MHCII+CD103+), cDC2 (CD45+F4/80-CD11b+CD11c+MHCII+), MDSC (CD45+F4/80-CD11b+Ly6CintLy6Gint) and TAM (CD45+F4/80+CD11b+) as part of a whole of treated and untreated tumors.

Fig. S12: Hierarchical clustering of individual tumor samples based on genes significantly different between groups.

Fig. S13: Vulcano plots of differentially expressed genes between DC vaccination vs combination therapy (A) or αCD40 vs combination therapy (B). The X-axis is log2 fold change and the Y-axis is -log10 of the original *p*-value. Markers with *p*-values < 0.05 and log2 fold change > 0.5 are marked in red, while markers with *p*-values < 0.05 and log2 fold change < -0.5 are marked in green. The two vertical lines

indicate the log2 fold change threshold of 0.5 and -0.5. The horizontal line indicates the original *p*-value threshold of 0.05.

Fig. S14: (A) GSEA of T-cell exhaustion gene sets in tumors of αCD40 or DC therapy versus combination therapy treated mice, presented as the normalized enrichment score (NES). (B) GSEA of T-cell exhaustion and glycolysis gene sets in tumors of combination therapy versus αCD40 treated mice, presented as the normalized enrichment score (NES).

Fig. S15: Hematoxylin and Eosin, Serius Red and Trichromic staining on tumor tissue.

Fig. S16: CD31 immunohistochemistry staining on tumor tissue of treated and untreated mice.

Fig. S17: (A) Number and percentage of PD-1+, Tim-3+, VISTA+, CD39+ and NKG2A+ subsets of CD4+ TILs. (B) Number and percentage of IFNγ+, Granzyme B+, IL-10+ and Ki67+ subsets of CD4+ TILs. (C) Detection of co-expression of inhibitory receptors (PD-1, Tim-3 and CD39) on CD4+ and CD8+ TILs. Numbers within circles represent percentage of TILs with 0 inhibitory receptors. (D) Percentage of PD-1/TIM-3 double positive and negative cells of CD4+ and CD8+ TILs. N=7-8 per group. Significance was determined using the non-parametric Mann-Whitney U test. Data presented as the mean ± s.e.m. *P<0.05, **P<0.01, ***P<0.001.

Fig. S18: ELISA-based IL-12p40 detection in supernatant of bone-marrow derived DCs stimulated with FGK45 or isotype. Significance was determined using the Student's t-test. Data presented as the mean ± s.e.m. ***P<0.001.