Supplemental Figures

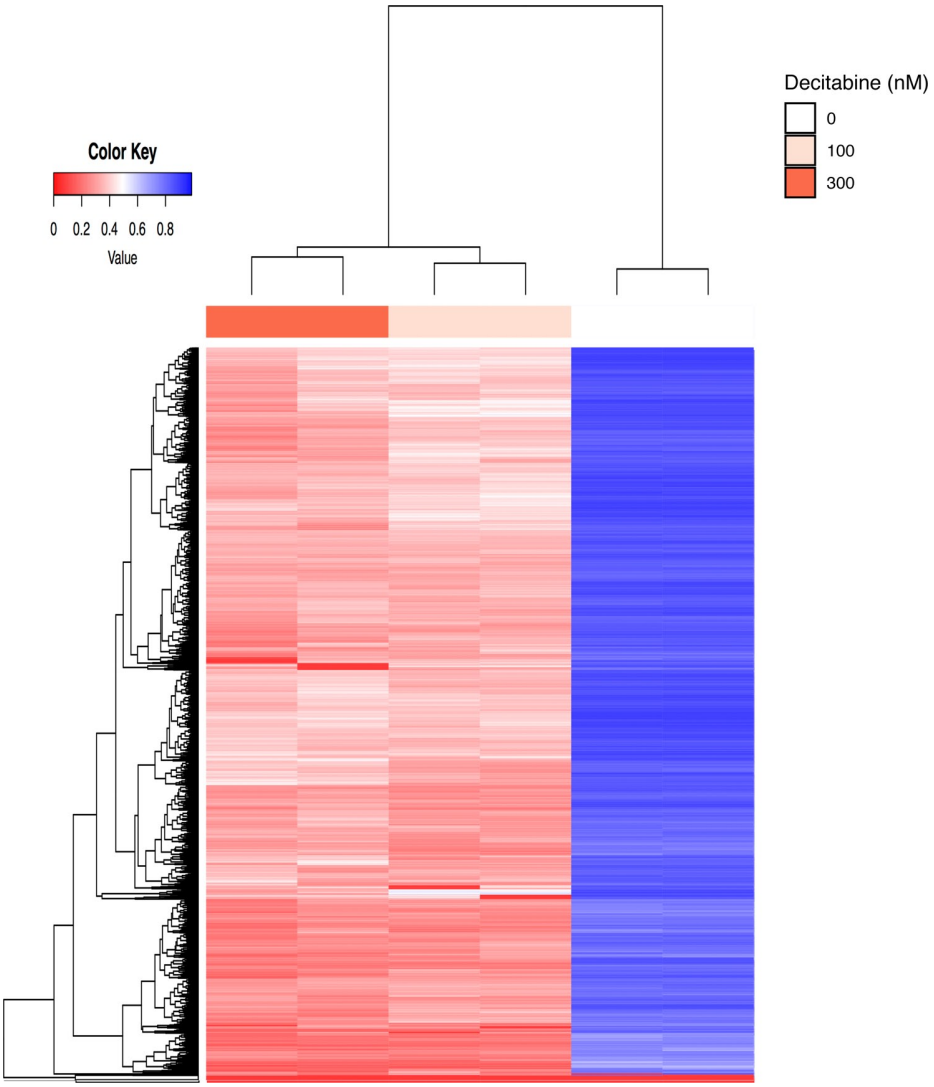

Figure S1. Decitabine produced dose-dependent decrease in DNA methylation in 786-0 cells. Heatmap show unsupervised cluster analysis of DNA methylation levels using the top 500 most variable probes.

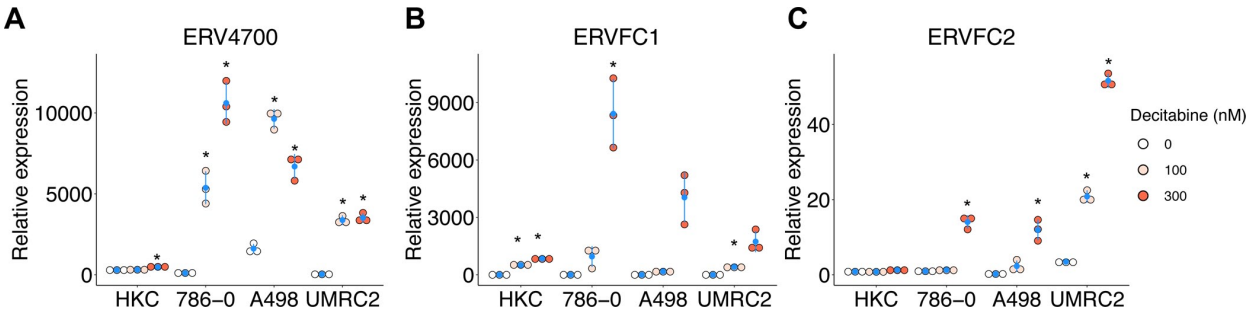

Figure S2. Additional ERVs upregulated by decitabine treatment. Panel of kidney cell lines were treated with decitabine for 3 days and ERV expression was assayed on day 5 by RT-qPCR. Barplots show expression values for indicated ERVs as means ± SE (N=3). Significance assessed by T-test, and p-values were adjusted via Holm's Bonferroni correction. Asterix (*) indicates Bonferroni corrected p-value < 0.05.

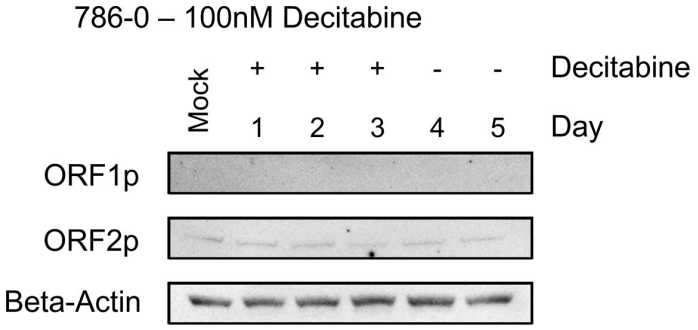

Figure S3. Expression of LINE-1 ORFp1 and ORFp2 proteins assessed by immunoblot analysis. Beta-Actin was used as a loading control. 786-0 cells were treated with 100nM decitabine for three days (day 0, 1 and 2) and protein was harvested at days 0 to 5. Mock treated cells were treated with DMSO for three days (day 0, 1 and 2) and protein was harvested at day 5.

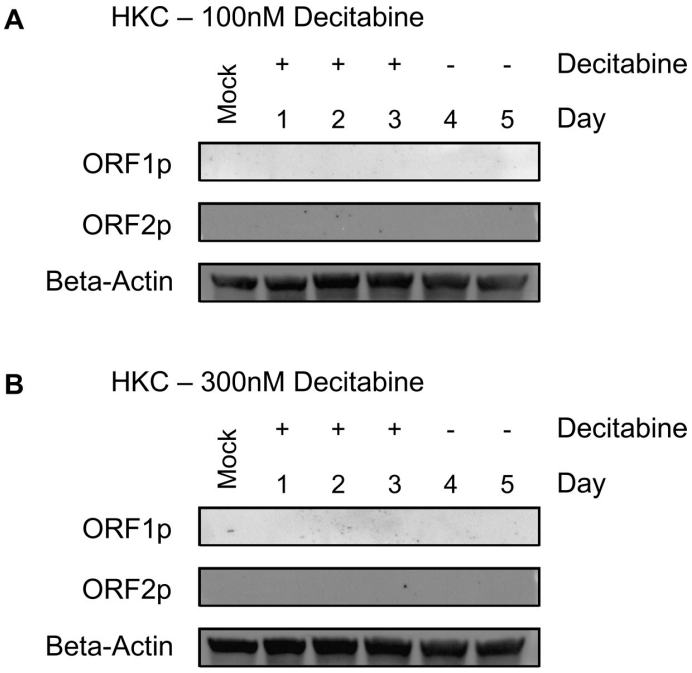

Figure S4. Expression of LINE-1 ORFp1 and ORFp2 proteins assessed by immunoblot analysis. Beta-Actin was used as a loading control. HKC cells were treated with A) 100nM or B) 300nM decitabine for three days (day 0, 1 and 2) and protein was harvested at days 0 to 5. Mock treated cells were treated with DMSO for three days (day 0, 1 and 2) and protein was harvested at day 5.

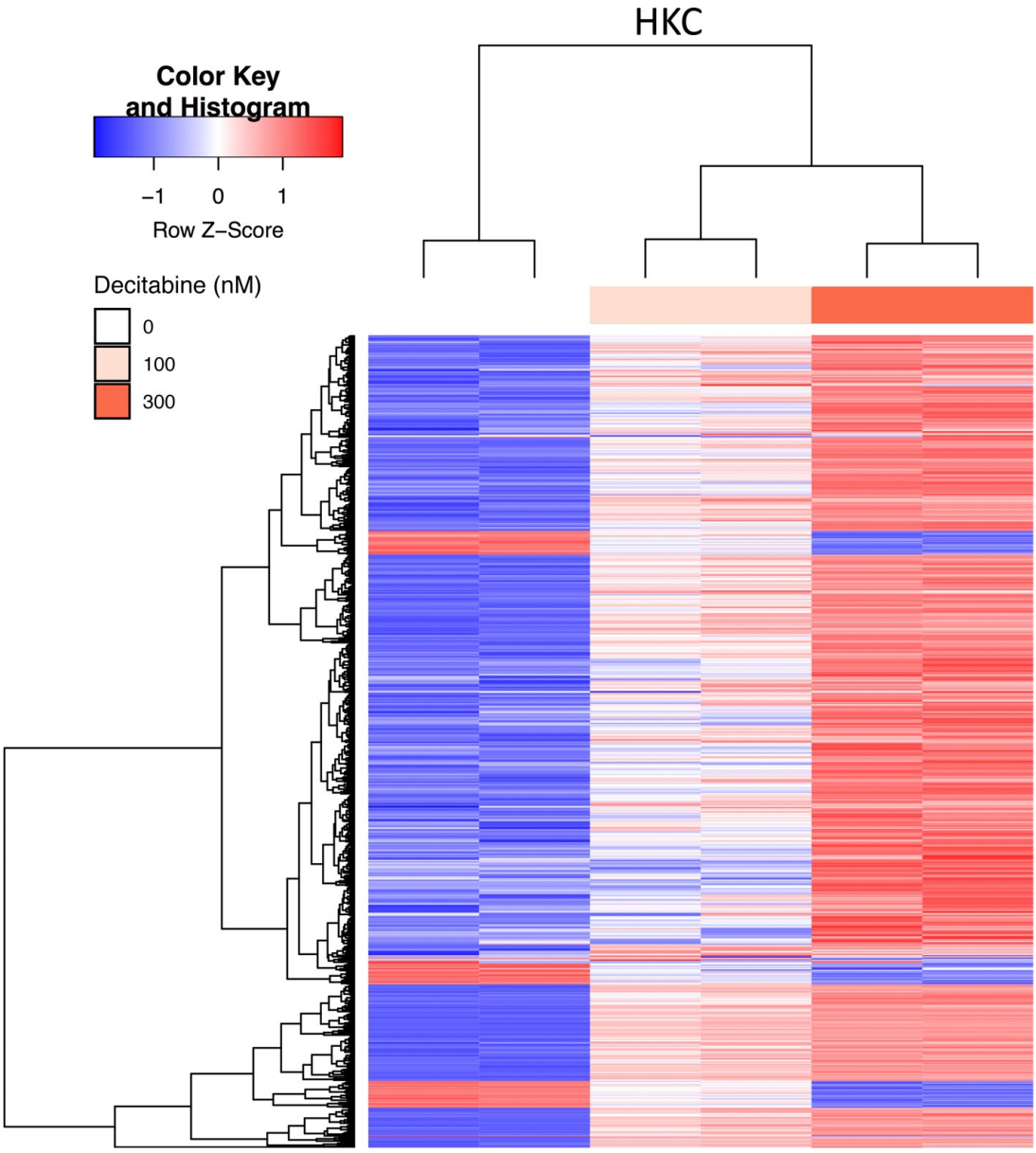

Figure S5. Heatmap showing unsupervised cluster analysis performed using the top 500 most variably expressed genes in HKC cells treated with (100nM and 300nM) or without (0nM) decitabine.

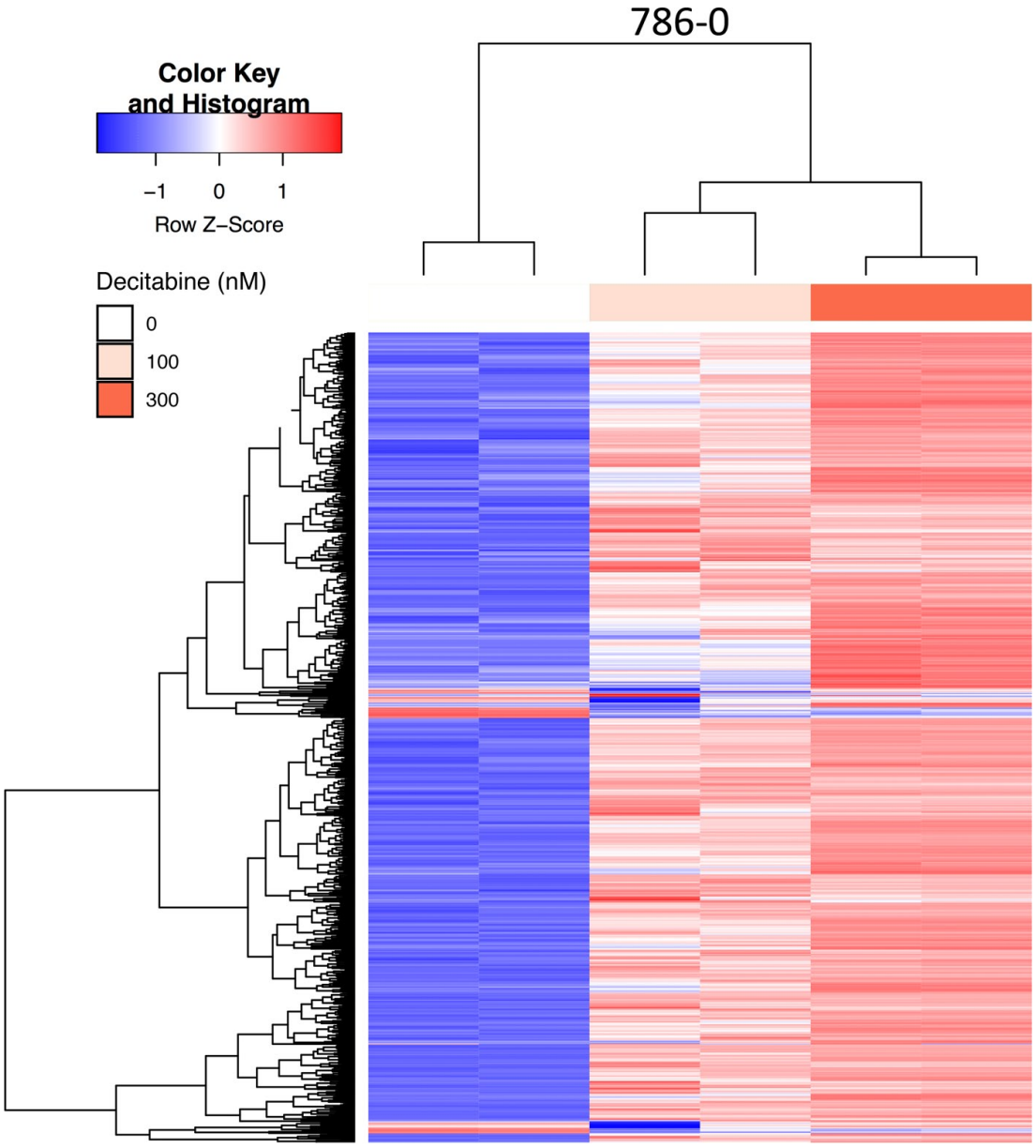

Figure S6. Heatmap showing unsupervised cluster analysis performed using the top 500 most variably expressed genes in 786-0 cells treated with (100nM and 300nM) or without (0nM) decitabine.

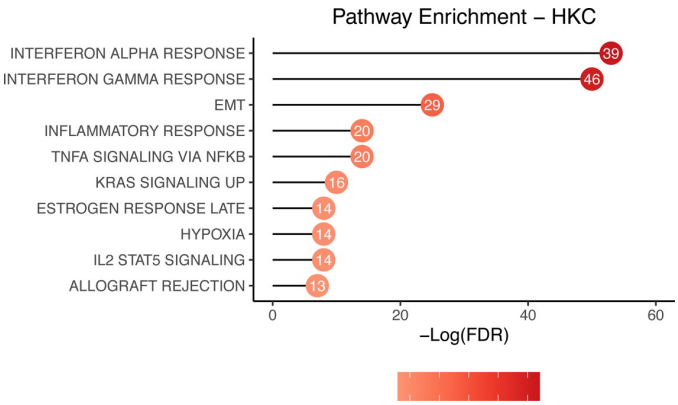

Figure S7. Lollipop representation of significantly enriched pathways for genes upregulated by decitabine treatment (300nM) in HKC cells as compared to DMSO vehicle (FDR<0.05 and Log2-fold > 1.5). Lollipop height and intensity color scale indicates magnitude -Log(FDR) of the enrichment for each pathway. The number of genes enriched in that pathway is indicated inside each lollipop genes enriched in that pathway.

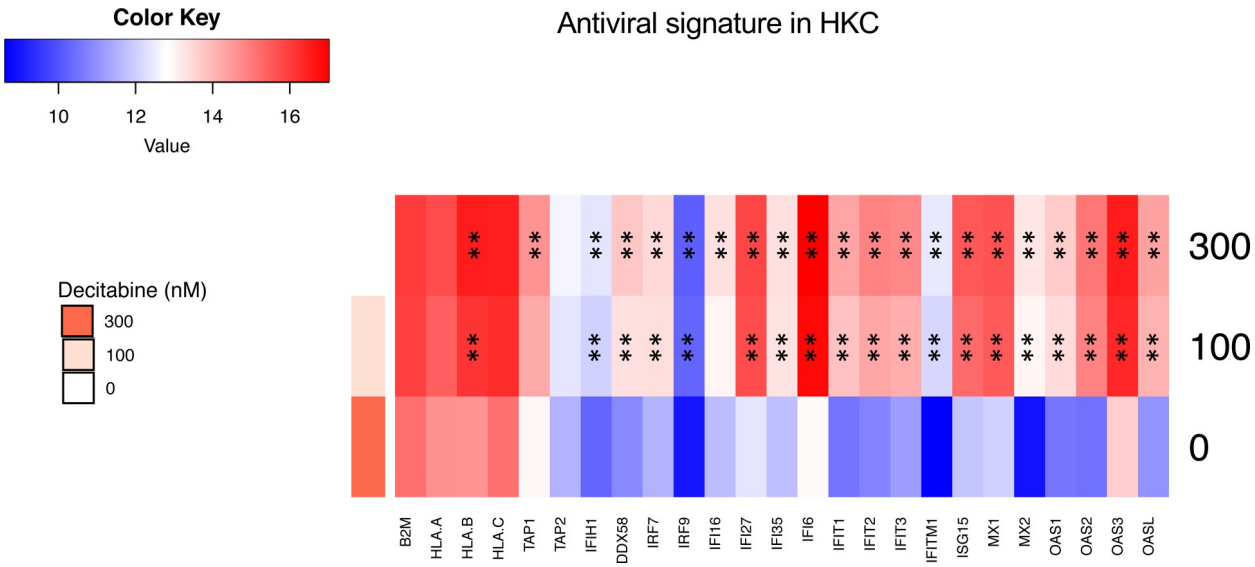

Figure S8. Expression levels of antiviral response genes in HKC cells treated with 0nM, 100nM and 300nM decitabine. Heatmap rows show mean expression of duplicate RNAseq measurements. Significance (100nM vs 0nM; 300nM vs 0nM) assessed by Wald test and corrected for multiple testing (FDR). Asterix (*) indicates FDR < 0.05, and double Asterix (**) indicates FDR < 0.001.

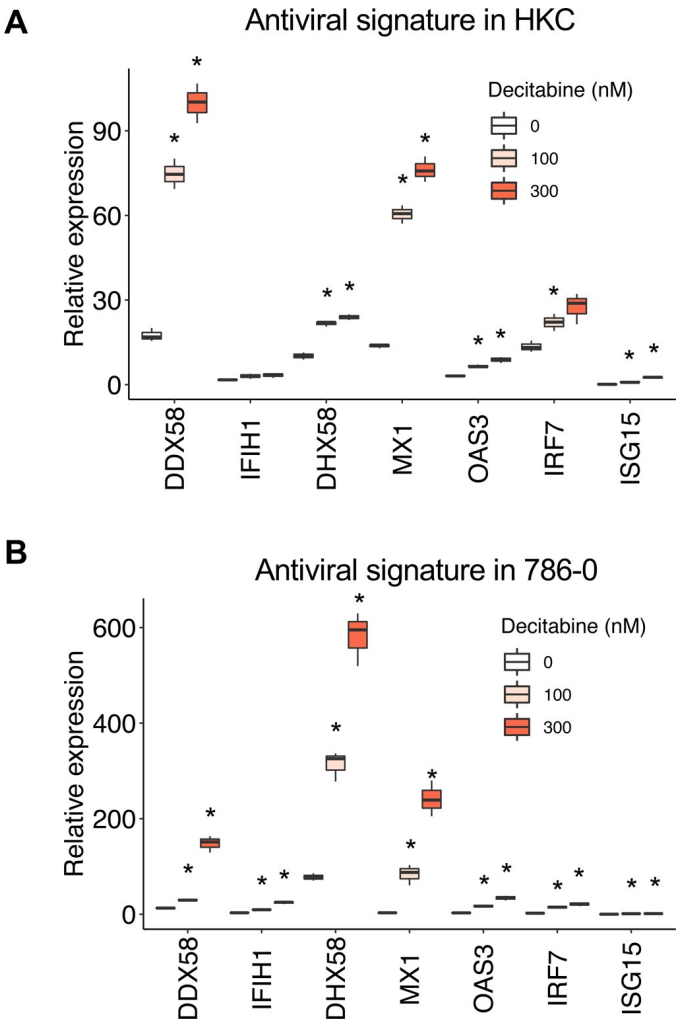

Figure S9. RT-qPCR assay to measure expression of antiviral response genes was measured in **A)** HKC or **B)** 786-0 cell lines. Cells were treated with DMSO or indicated doses of decitabine for 3 days, and RNA was harvested on day 5 to measure expression antiviral response genes. Barplots show expression values for indicated ERVs as means ± SE (N=3). Significance assessed by paired T-test. Asterix (*) indicates Bonferroni corrected p-value < 0.05.

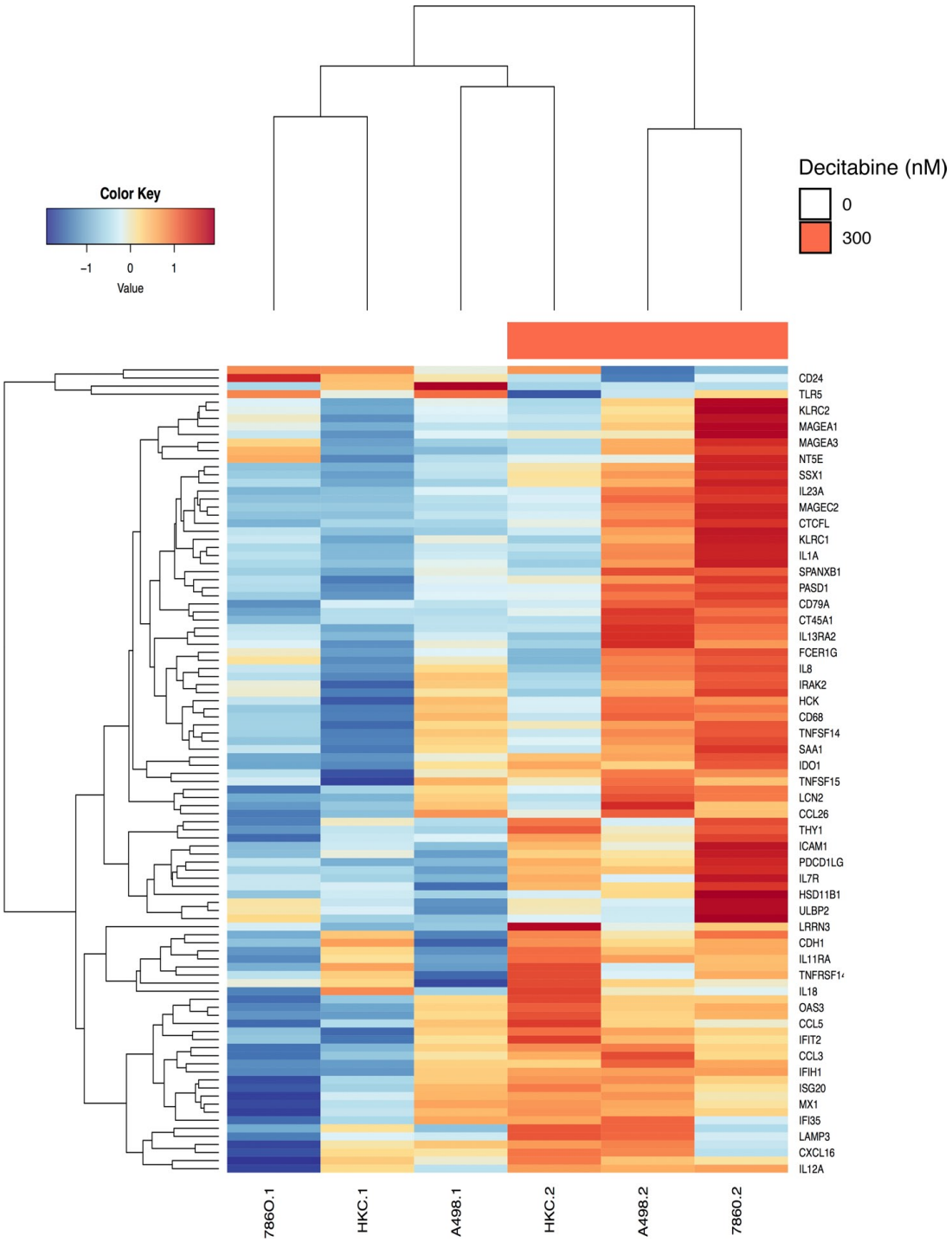

Figure S10. NanoString analysis using the pan-cancer immune panel was performed in kidney cell lines (HKC, A498 and 786-0) treated with 0nM or 300nM decitabine. Heatmap shows unsupervised analysis performed using the top 50 most variably expressed genes.

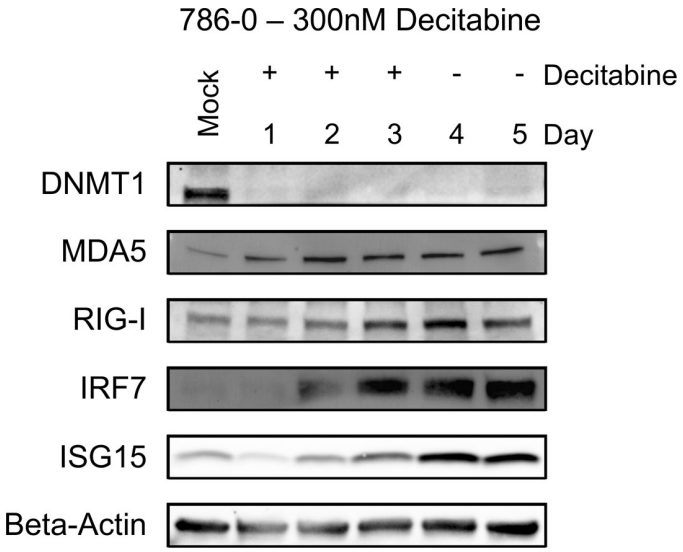

Figure S11. Antiviral protein levels were assessed by immunoblot analysis in 786-0 cells were treated with 300nM decitabine for three days (day 0, 1 and 2) and protein was harvested at days 0 to 5. Mock treated cells were treated with DMSO for three days (day 0, 1 and 2) and protein was harvested at day 5. Protein expression levels of DNMT1, RIG-I, DDX58, IRF7, ISG15, and Beta-Actin were assessed by immunoblot. Beta-Actin was used as a loading control.

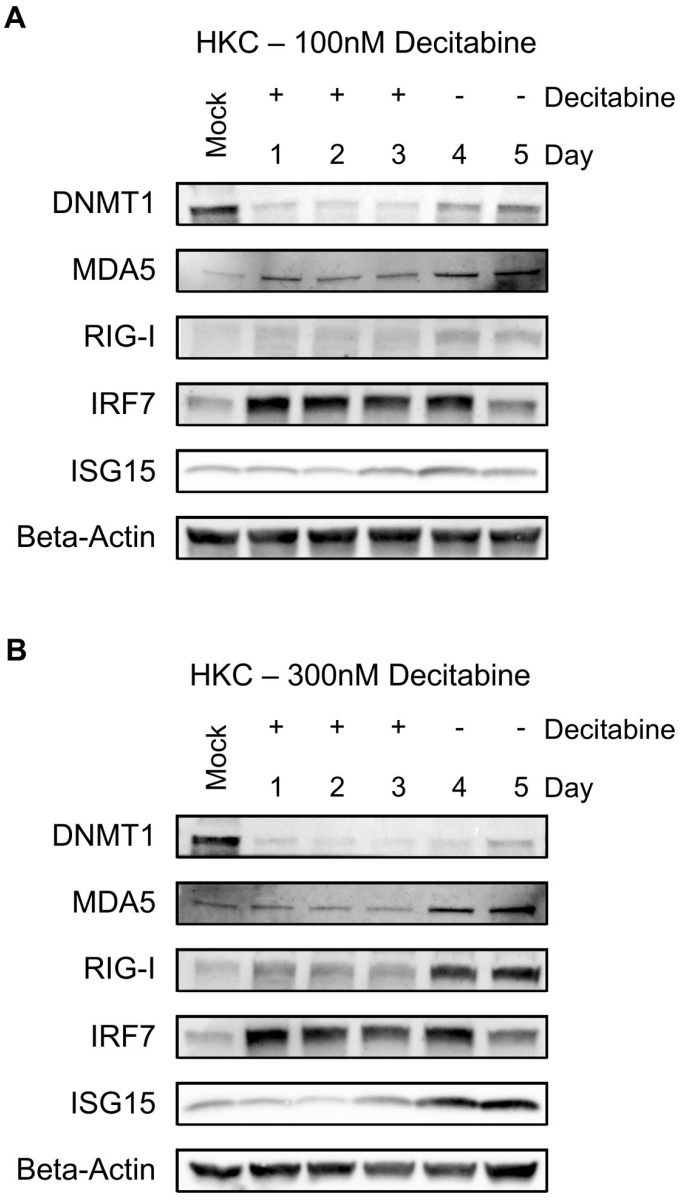

Figure S12. Antiviral protein levels were assessed by immunoblot analysis in HKC cells were treated with **A)** 100nM or **B)** 300nM decitabine for three days (day 0, 1 and 2) and protein was harvested at days 0 to 5. Mock treated cells were treated with DMSO for three days (day 0, 1 and 2) and protein was harvested at day 5. Protein expression levels of DNMT1, RIG-I, DDX58, IRF7, ISG15, and Beta-Actin were assessed by immunoblot. Beta-Actin was used as a loading control.

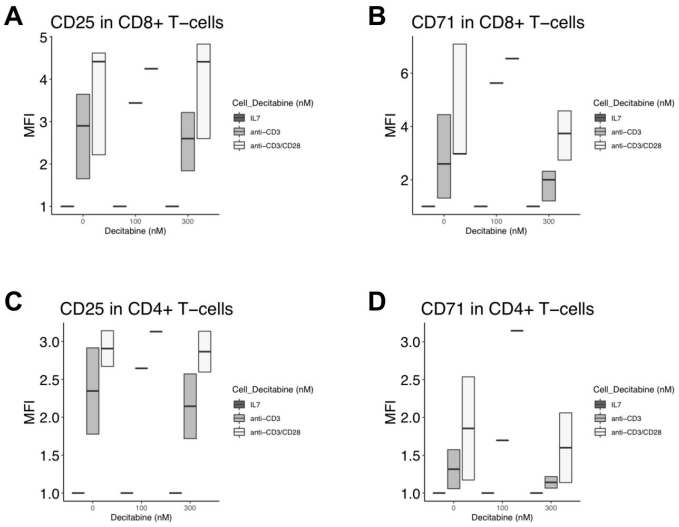

Figure S13. T-cell Activation assay was performed in healthy donor T-cells (Decitabine 0nM and 300nM n=5; Decitabine 100nM n=3) treated with 0nM, 100nm and 300nM decitabine. T-cells were stimulated with IL7, anti-CD3 or anti-CD3/CD28 for 5 days before measuring cell size and expression of CD4, CD8, CD25, and CD71 by flow cytometry.