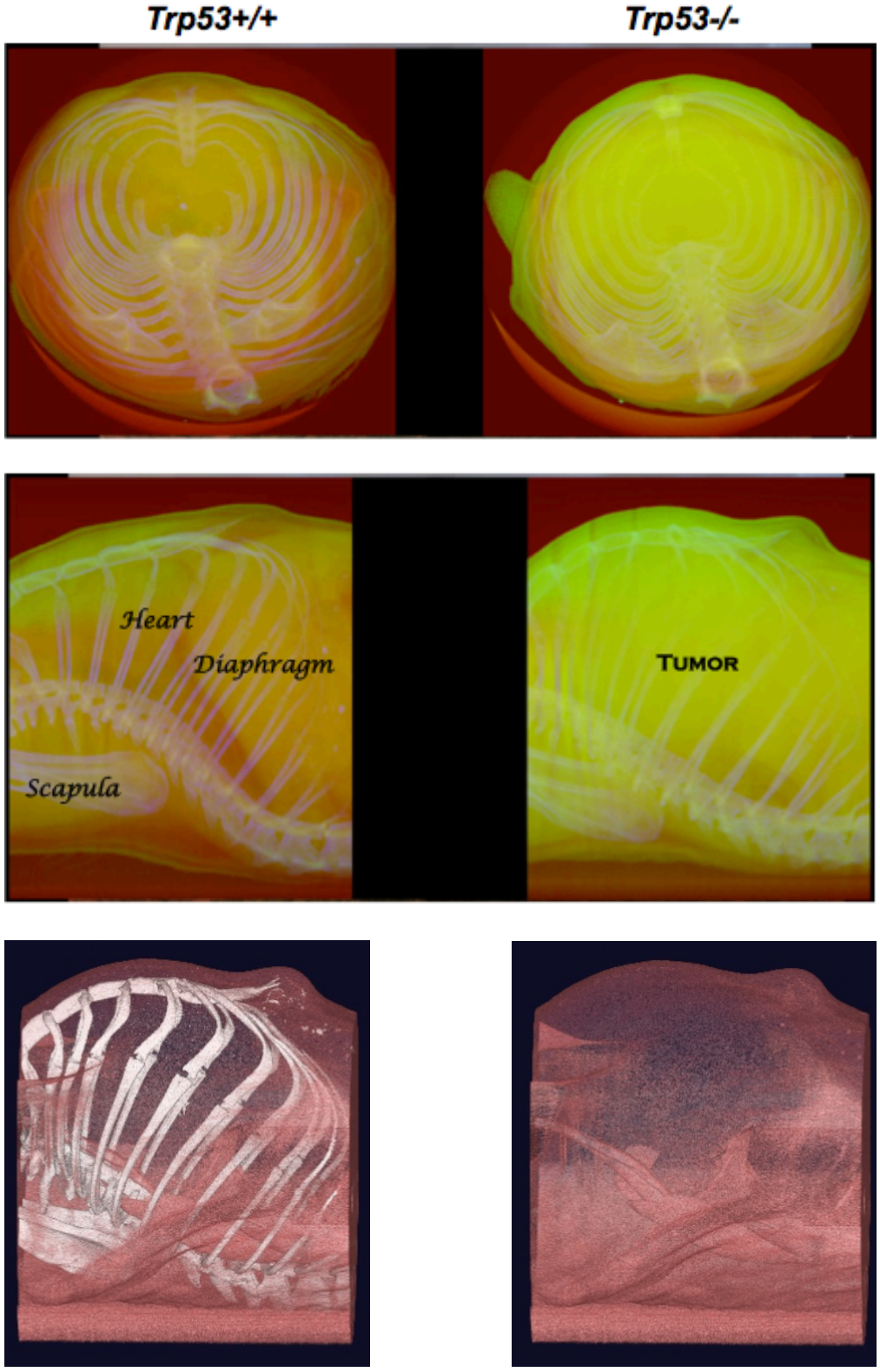
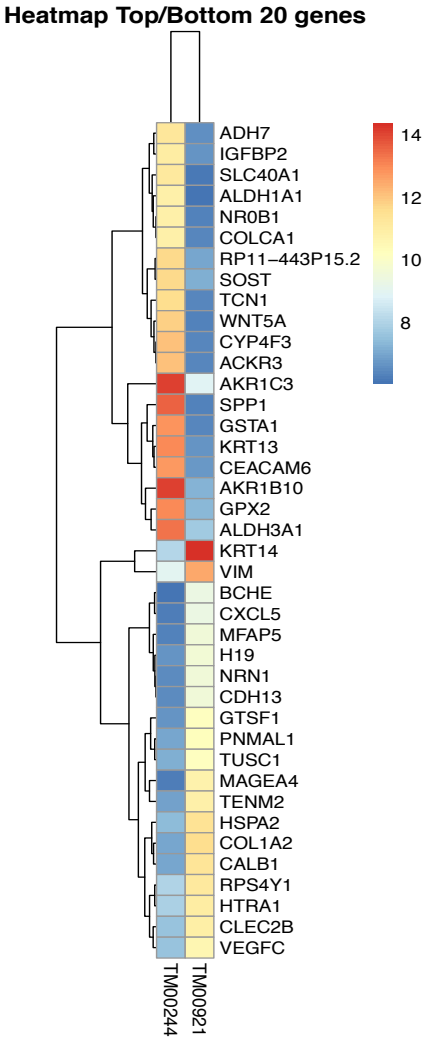
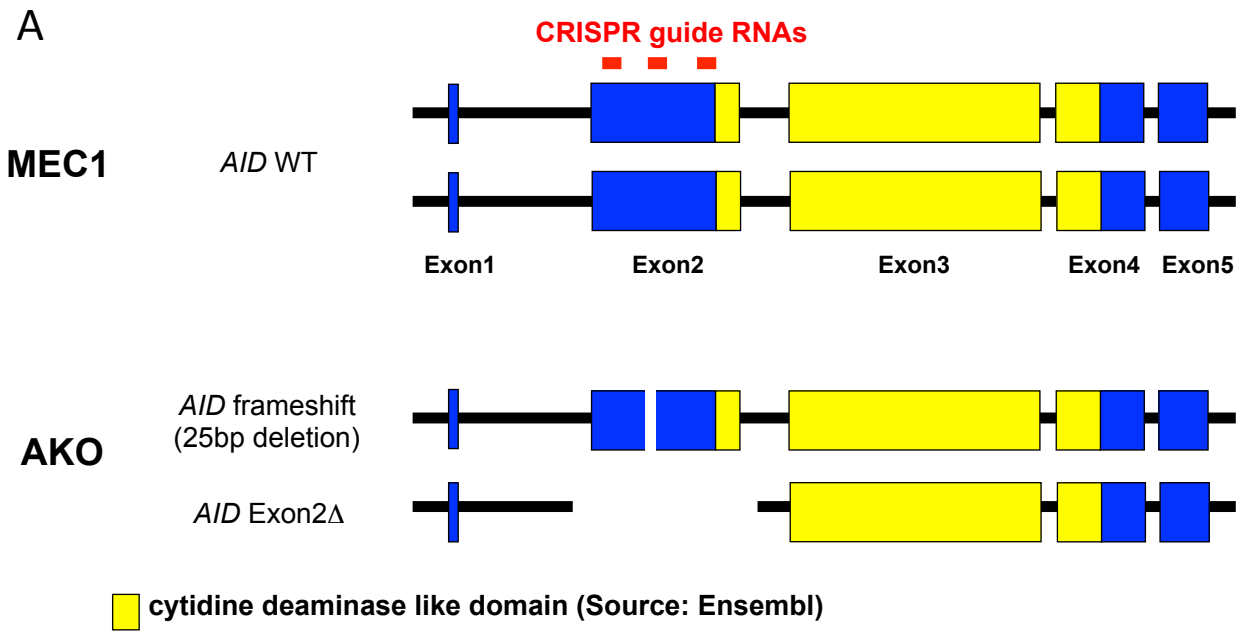
Supplementary Figure 1: Colorized 3D rendering of the micro-computed tomography of a control *Trp53+/+* and a *Trp53-/-* mouse with a thymic lymphoma tumor.

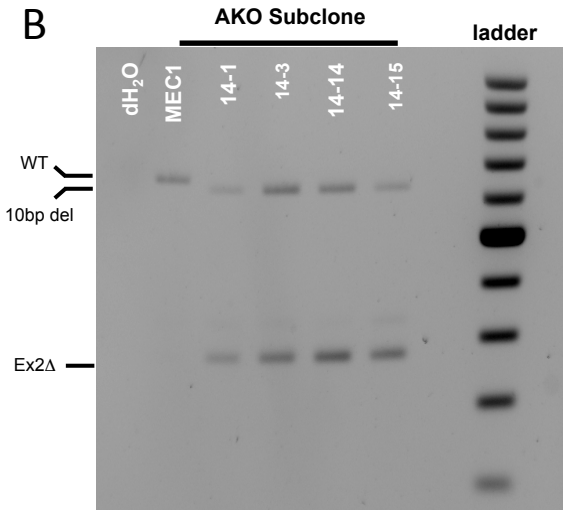


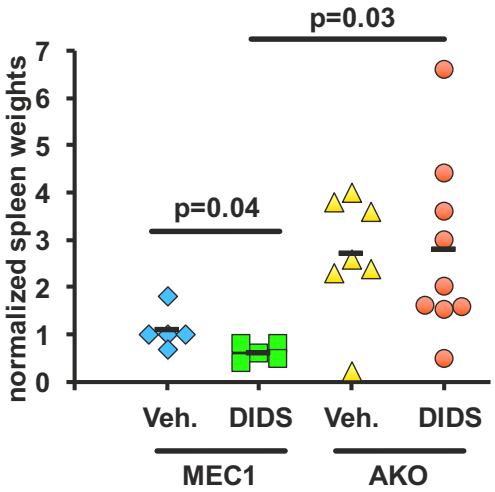
Supplementary Figure 2: Heatmap of the top and bottom 20 differentially expressed genes in two PDX human lung carcinomas, TM00244 and TM00921.

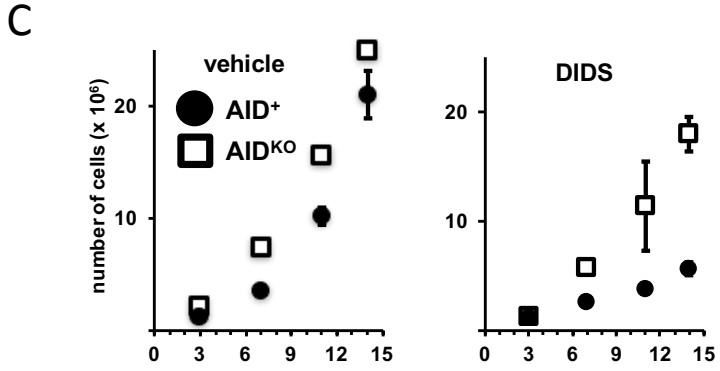


Supplementary Figure 3: Generation and Validation of AID Knock-out (AKO) MEC1 cells (A) schematic of the knock-out (B) PCR validation of AKO (C) Sensitivity of AKO to DIDS (D) Spleen weights of MEC1 and AKO with DIDS treatment.

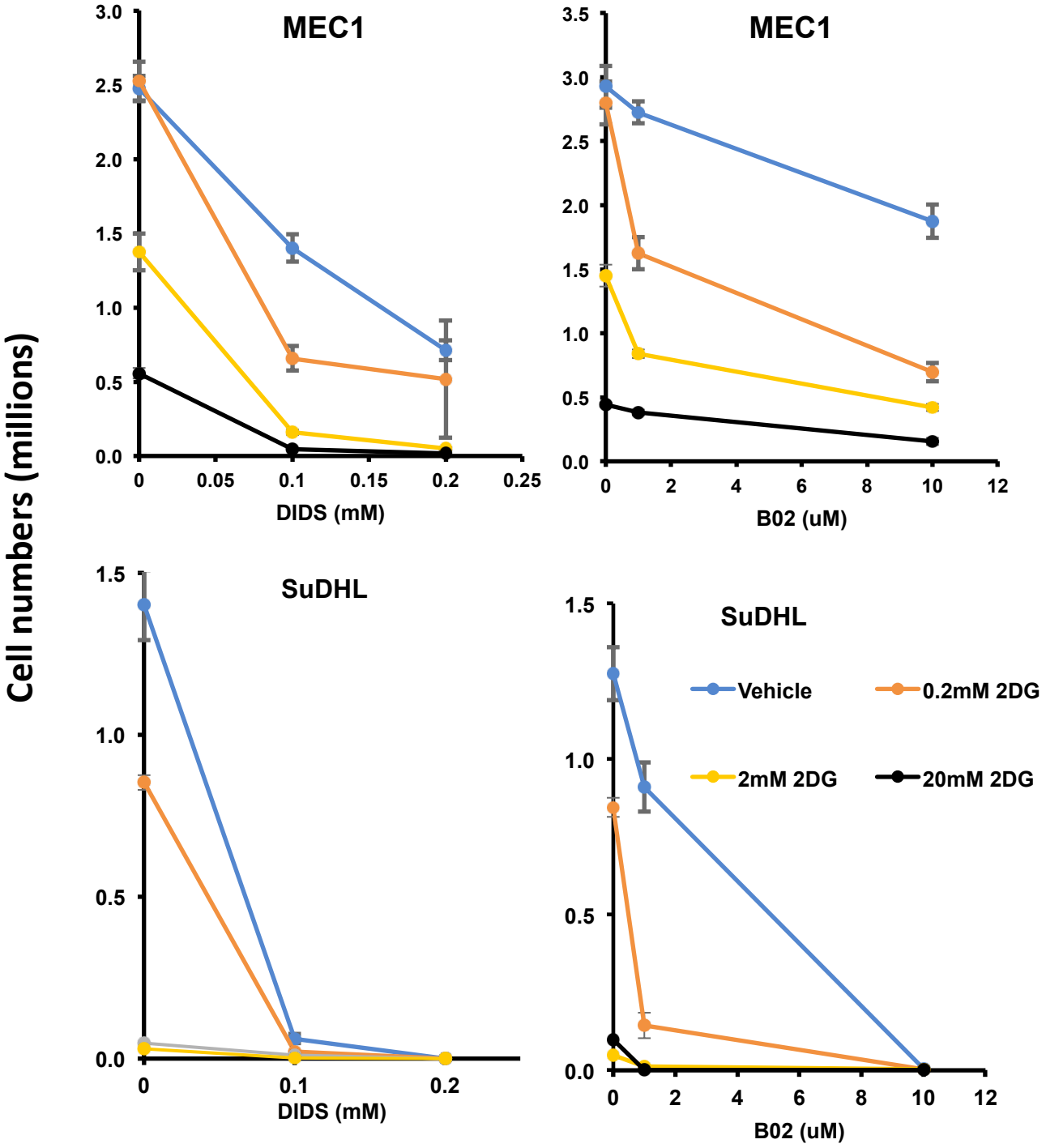




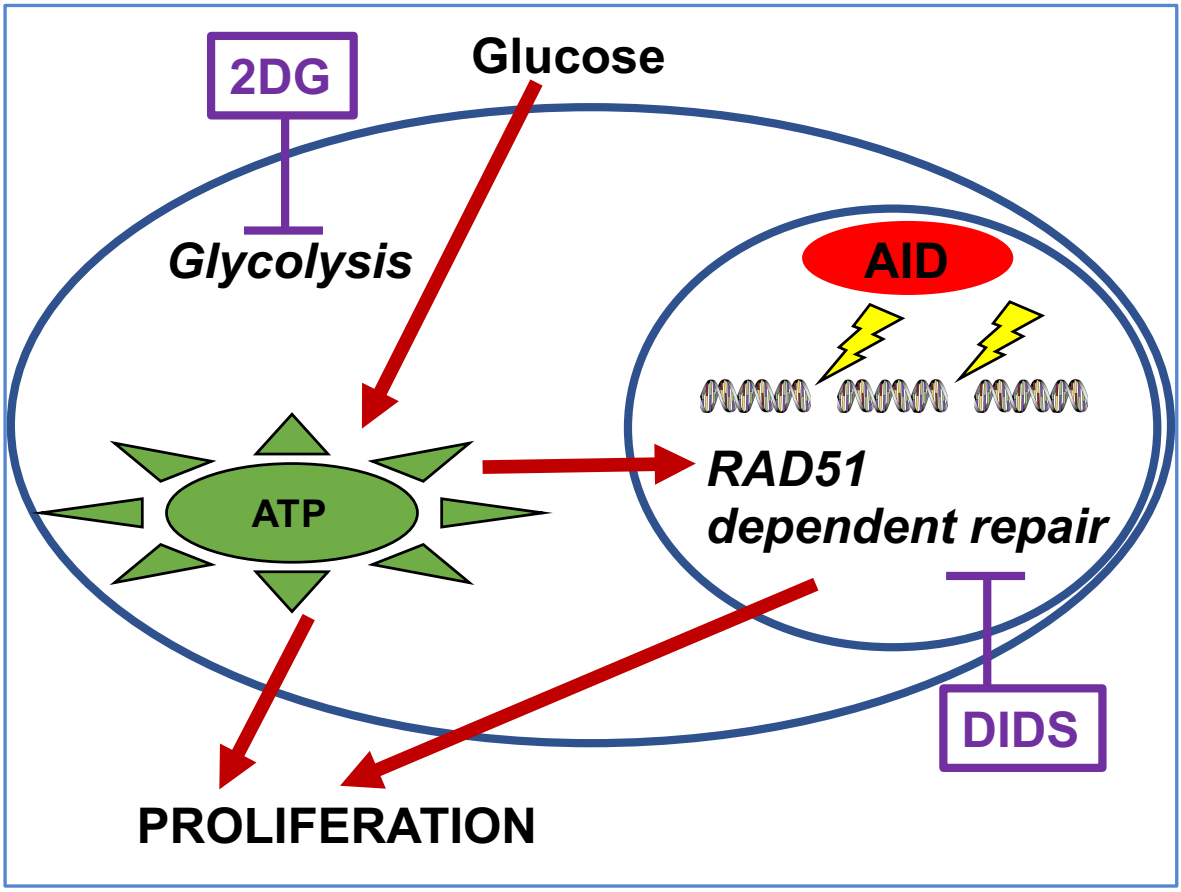




Supplementary Figure 4: Titration curves of MEC1 and SuDHL cells with DIDS and B02 RAD51 inhibitors.



Supplementary Figure 5: Visual concept of the study.



Supplementary table 1: Table of general gene functions of differentially expressed genes in two PDX human lung carcinomas, TM00244 and TM00921.

Gene	Function
ADH7	Phenylalanine metabolism, metabolism and oxidoreductase activity and retinol binding.
IGFBP2	Insulin-like growth factor binding and insulin-like growth factor II binding.
ALDH1A1	Glycosaminoglycan metabolism, oxidoreductase activity and acyl-CoA dehydrogenase activity.
TCN1	Innate Immune System and metabolism, and cobalamin binding.
CYP4F3	Arachidonic acid metabolism, iron ion binding and oxidoreductase activity with incorporation or reduction of molecular oxygen.
AKR1C3	Metabolism, oxidoreductase activity and aldo-keto reductase (NADP) activity.
GSTA1	Glutathione metabolism and drug metabolism, and glutathione transferase activity.
AKR1B10	Metabolism and acetone degradation, aldo-keto reductase (NADP) activity and indanol dehydrogenase activity.