Supplementary Figure 4. Mutational repertoire of the two colon cancer *patient-derived xenograft* (PDX) lines used in this study (red box: KUC1; blue box: KUC2). WT: wild-type (no mutation). Mis: missense mutation. Frm: frameshift mutation. SpD: splice donor site mutation. The schematic for the representation of the mutational repertoire, with mutations grouped based on their impact on specific signaling pathways, was based on a template developed by the *The Cancer Genome Atlas* (TCGA) consortium (Nature 487:330-337, 2012).