



**Supplementary Figure 3.** A. Nonsynonymous somatic mutations identified by MSK-IMPACT in the parental and resistant RW7213 cancer cell line (top). Mutation types (left) and cancer cell fraction (CCF) of mutations identified (right) are color coded according to the legend. The length of the trunk and branches of the phylogenetic tree (bottom) is proportional to the number of shared and private mutations identified in the parental and resistant cell line. The somatic hotspot mutations, as well as the number of nonsynonymous mutations, are shown along their corresponding branches. B. Copy-number alterations (CNAs) of the parental and resistant RW7213 cancer line (top). Copy-number log<sub>2</sub> ratios are shown on the y-axis according to the chromosomes on the x-axis. The arrow shows KRAS amplification. Phylogenetic tree based on CNAs are shown (bottom). The numbers alongside the branches represent gains and losses shown in red and in blue, respectively.