





Figure S2. Results of germline and tumor profiling via exome sequencing. Shown is an overall view of chromosome 1 using a genome browser. The VAF pattern is split in a wide area of chromosome 1q in tumor tissue cells, suggesting that it is attributable to loss of heterozygosity. Furthermore, the CN ratio confirms the disappearance of the expression of the q23.1, q31.3, and q43 (including FH) regions (red arrows). CN, copy number; VAF, variant allele frequency; FH, gene encoding fumarate hydratase.