



Figure S5: Identity check of paired samples from competitive growth experiments. (a-b) Sequencing analysis of minor and dominant clones **(a)** 17BC-D.1 and **(b)** 33BC-D.2, respectively. Paired minor and dominant samples contained the same barcode sequence as well as identical 3'LTR-genome boundaries. **(c)** Exome sequencing verified identical mutations in the DHFR loci for paired minor and dominant 17BC-D.1 and 33BC-D.2 clones, respectively. VAF, variant allele frequency.