

Table S2: mutations identified in SBI-0090799-resistant virus. List of mutations specifically identified in the genomes of ZIKV MR766 selected for 5 passages in Huh-7.5 cells, in the presence of SBI-0090799 at a concentration of 10 μ M. Reads were aligned to the ZIKV genome NC_012532.1. The list had been filtered for nucleotides deviating from the reference sequence but shared with the virus selected in the presence of DMSO.

Sheet “Variants Unique to 10 μ M”: list of all the nucleotide variants specifically identified in the virus selected in the presence of SBI-0090799 [10 μ M]. POS (Position in the Reference Sequence), REF (Nucleotide in the Reference Sequence), ALT (Nucleotide in the Alternative Sequence), QUAL (Genotype Quality), AD (Allele Depth), DP (Total Depth used for Variant Calling), VF (Variant Frequency), SB (Strand Bias Score). Variants with a frequency above 5% are highlighted with a black square.

Sheet “Variants with frequency >5%”: list of all the nucleotide and amino acid variants identified with a frequency above 5%. Variants with a frequency above 10% are highlighted with a black square. The protein involved (col E), the codon change (col D), the specific amino acid (col F), and the corresponding mutations (col C) are also indicated.