

Table S1. Impact of NS5A Mutations associated with HCC on protein stability and their localization.

| # | Mutation | $\Delta\Delta G^a$ | Location in NS5A | | Interacting Protein/Nucleic Acid |
|----|--------------|--------------------|------------------|------------|---------------------------------------|
| 1 | S3T | -0.36 | Alpha-helix | N-terminal | p53, p85-PI3K, β -catenin |
| 2 | C13S | -1.86 | | | |
| 3 | C13R | -1.74 | | | |
| 4 | T122M | 0.06 | Beta-sheet | Domain-1 | NS5B, p53, p85-PI3K, β -catenin |
| 5 | F127L | -0.43 | | | |
| 6 | F127S | -1.08 | | | |
| 7 | M133I | -0.31 | | | |
| 8 | N137D | 0.54 | Coil-turn | | |
| 9 | N137K | 0.16 | | | |
| 10 | Q181E | 0.62 | Beta-sheet | | Viral RNA genome |
| 11 | Q181G | 0.52 | | | |
| 12 | Q181H | 0.53 | | | |
| 13 | Q181P | 0.22 | | | |

^a $\Delta\Delta G$ (kcal/ mol) = (ΔG wt fold - ΔG mutant fold) was calculated by STRUM algorithm. A negative $\Delta\Delta G$ value indicates a decrease in protein stability.

The mutations with $\Delta\Delta G < -1.0$, indicating a relevant decrease in protein stability is reported in bold