Supplementary Figures:

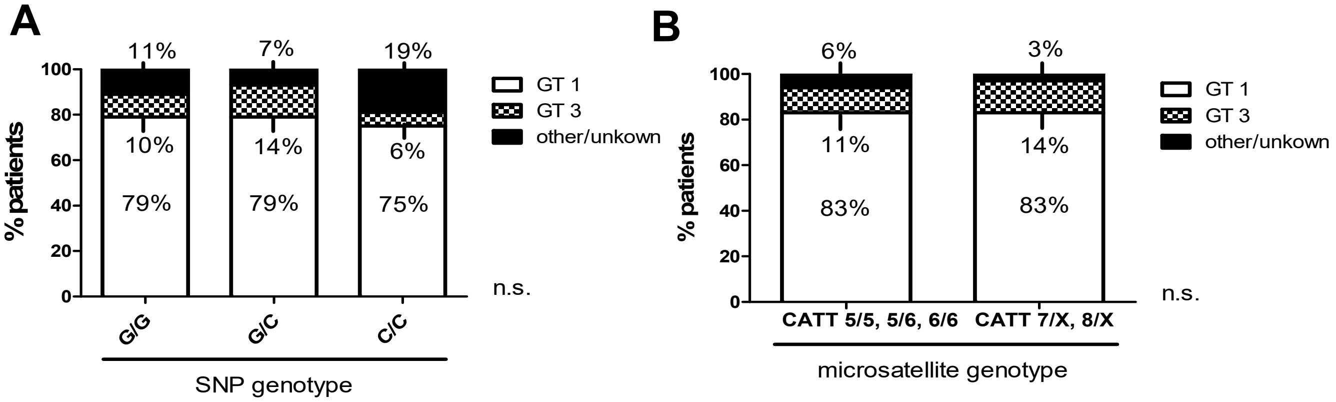

Figure S1. HCV genotype frequency does not differ significantly in SNP and microsatellite genotype subgroups of the HCV 2018 cohort. **(A)** The prevalence of the HCV genotype is depicted in the three SNP genotype subgroups "G/G", "G/C" and "C/C". Here no significant difference concerning HCV genotype 1 ("GT 1"), 3 ("GT 3") or patients infected with HCV genotype 2 or 4 or unkown HCV genotype ("other/unkown") is observed. **(B)** The prevalence of the HCV genotype is depicted in the two microsatellite genotype subgroups "CATT 5/5, 5/6, 6/6" and "CATT 7/X, 8/X". Here no significant difference concerning the HCV genotype 1 ("GT 1"), 3 ("GT 3") or patients infected with HCV genotype 2 or 4 or unkown HCV genotype ("other/unkown") is observed.

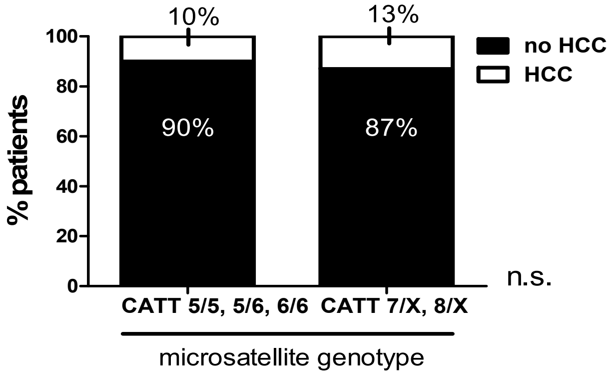

Figure S2. High microsatellite repeat counts in the -794 CATT$_{5\text{-}8}$ are not associated with prevalence of HCC: The HCC prevalence does not differ significantly between the two microsatellite repeat genotype subgroups. Data are expressed as contingency.