

In-host flat-like quasispecies, methods and clinical implications

Supplementary material - Near-flat quasispecies examples

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Near-flat quasispecies - HCV treatment failures

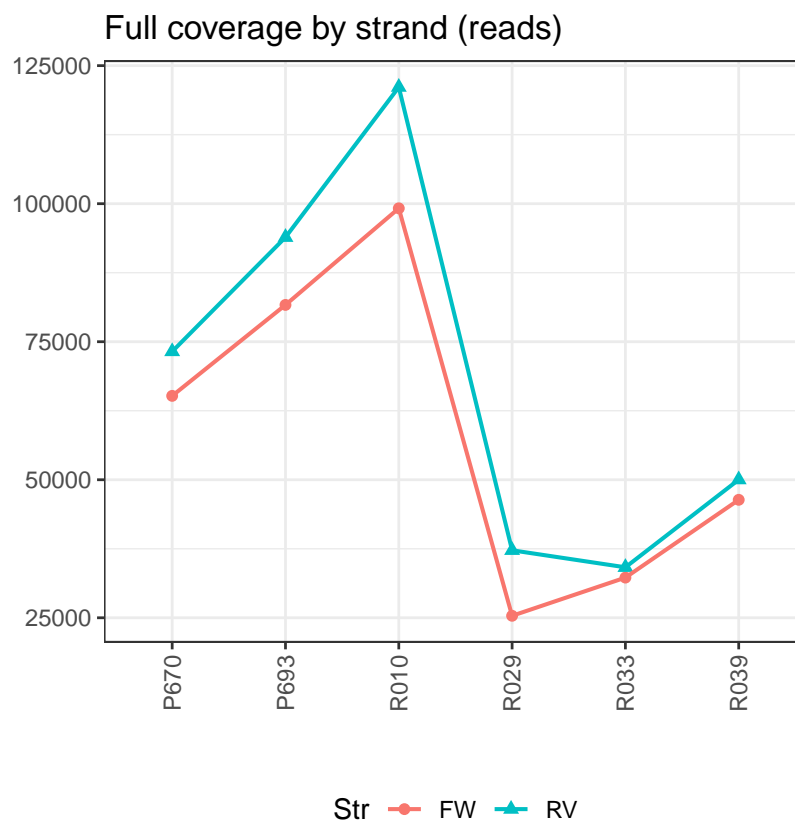


Figure NF-1: Coverage by amplicon and strand in read number.

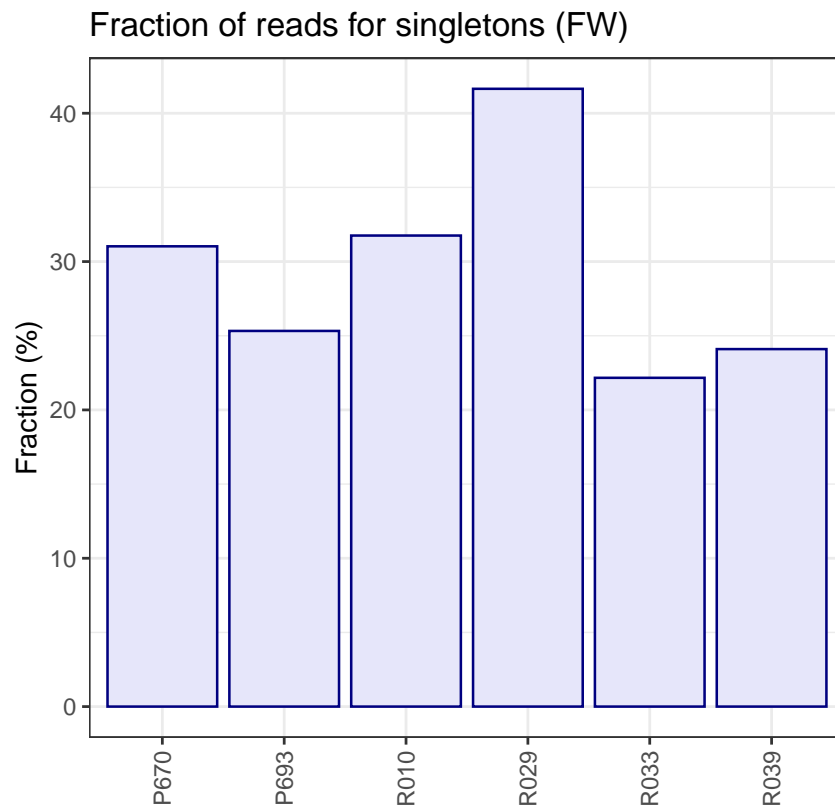


Figure NF-2: Fraction of reads for singletons observed with forward strand reads.

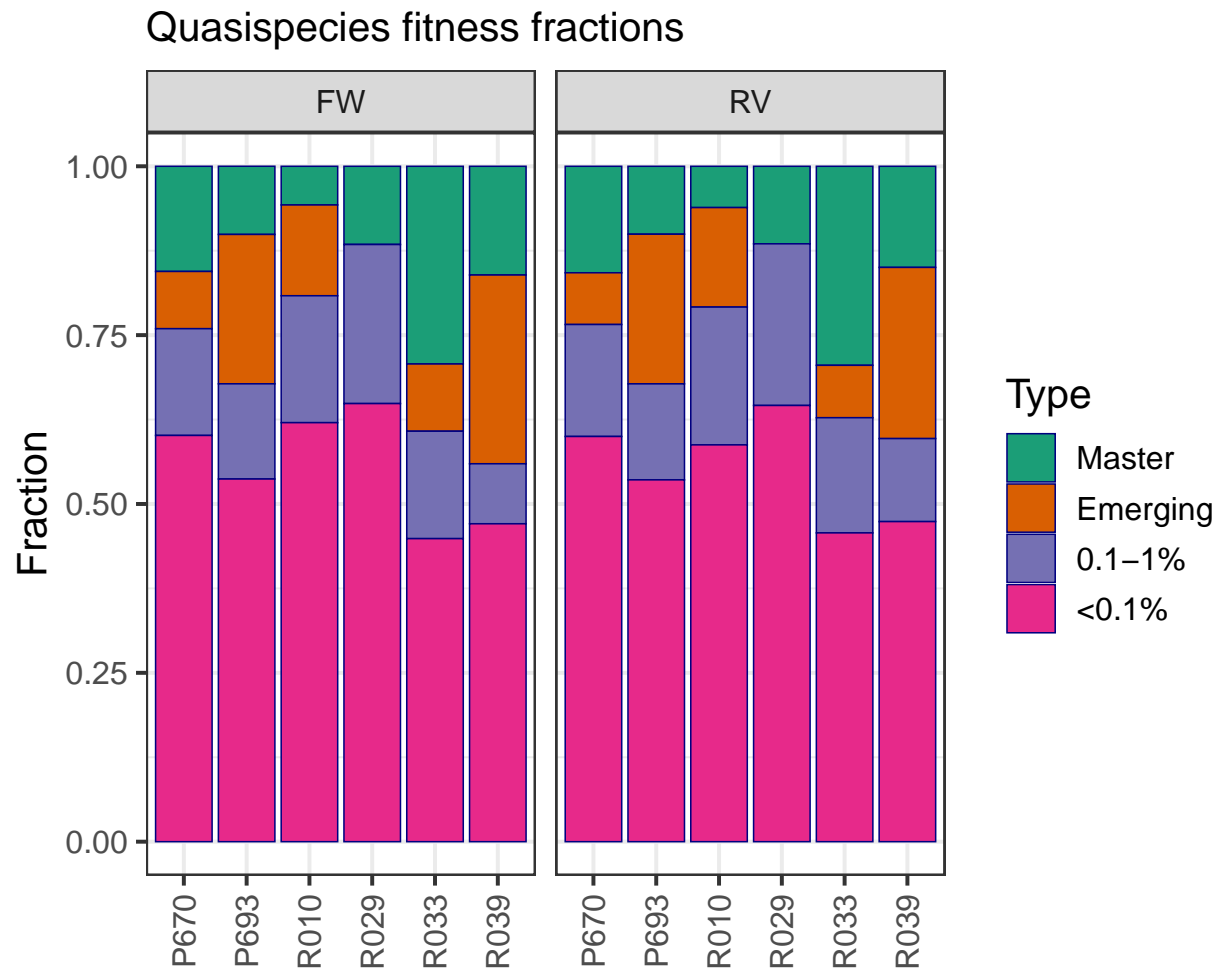


Figure NF-3: Quasispecies fitness fractions.

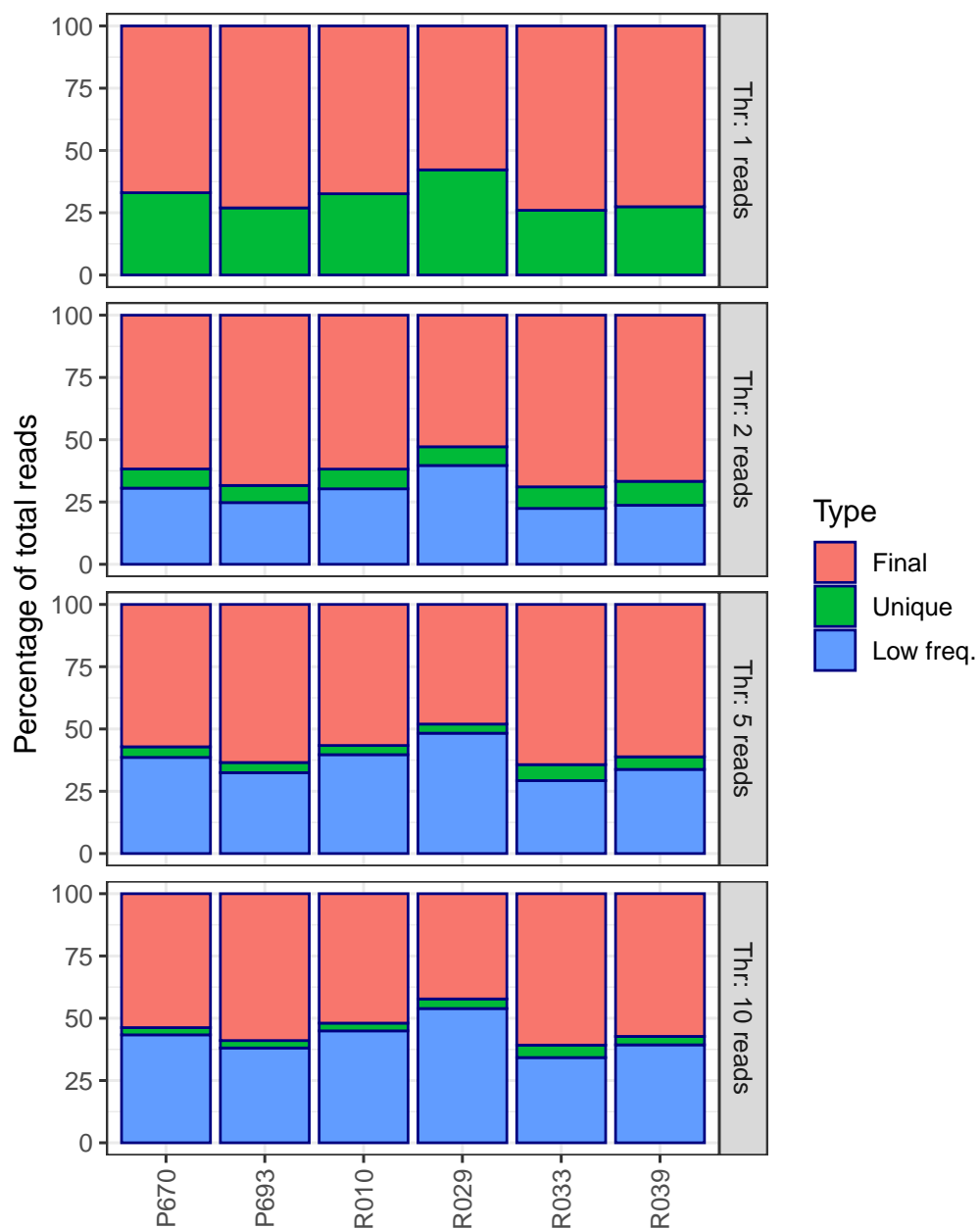


Figure NF-4: Impact of abundance filter followed by haplotype strand intersection. Abundance thresholds at 1, 2, 5 and 10 reads.

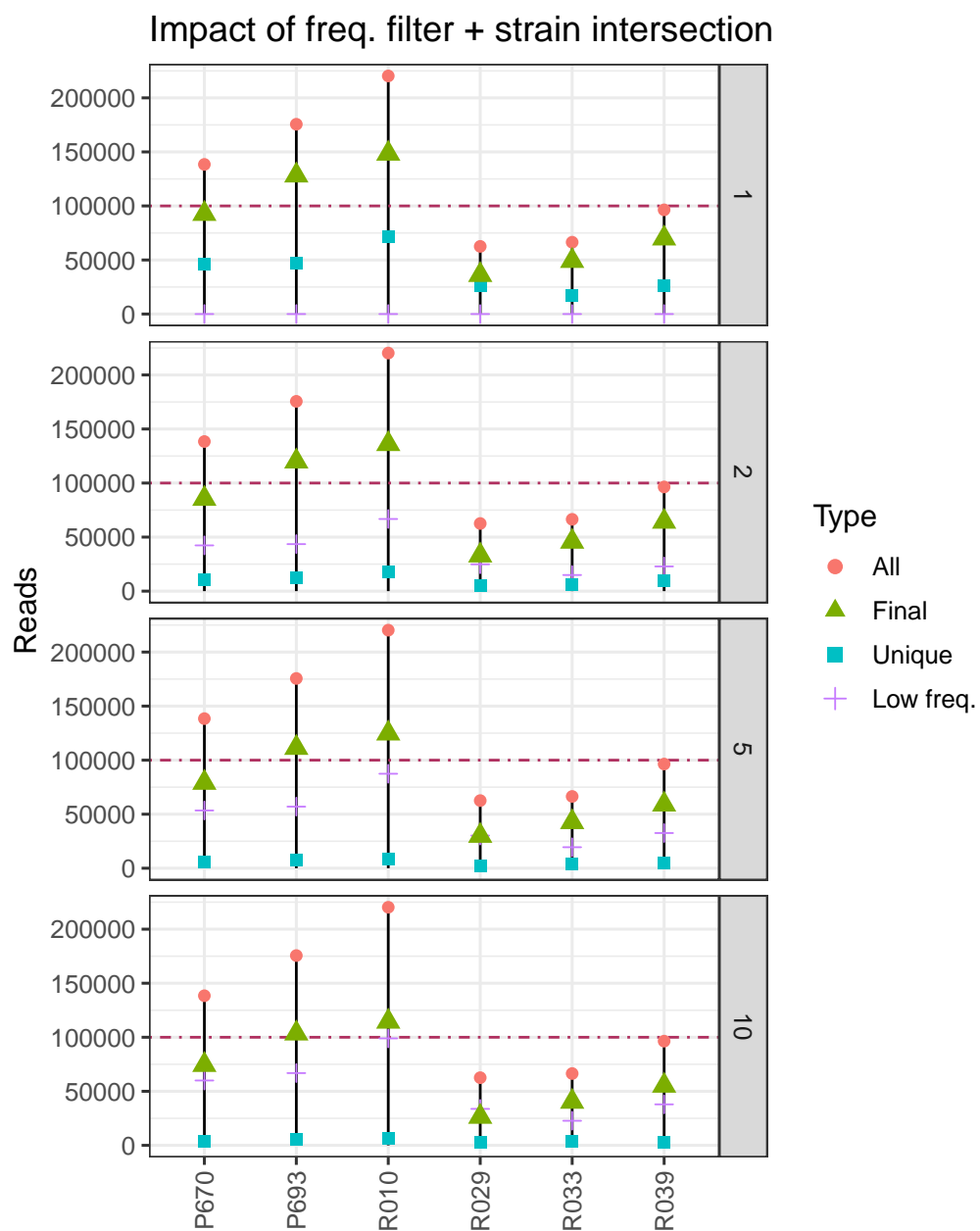


Figure NF-5: Impact of abundance filter followed by haplotype strand intersection. Abundance thresholds at 1, 2, 5 and 10 reads.

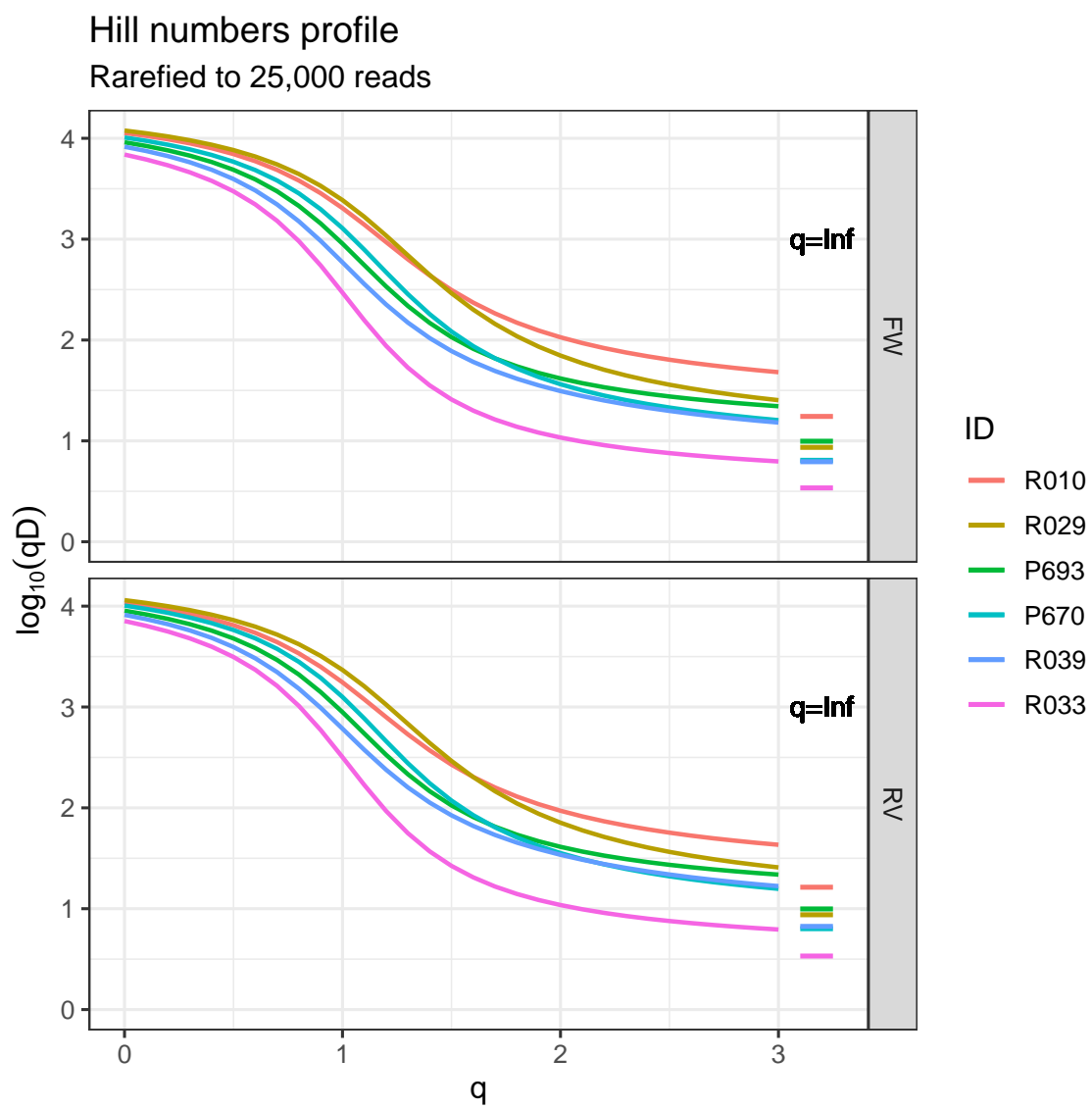


Figure NF-6: Hill numbers (HN) profiles rarefied to 25,000 reads.

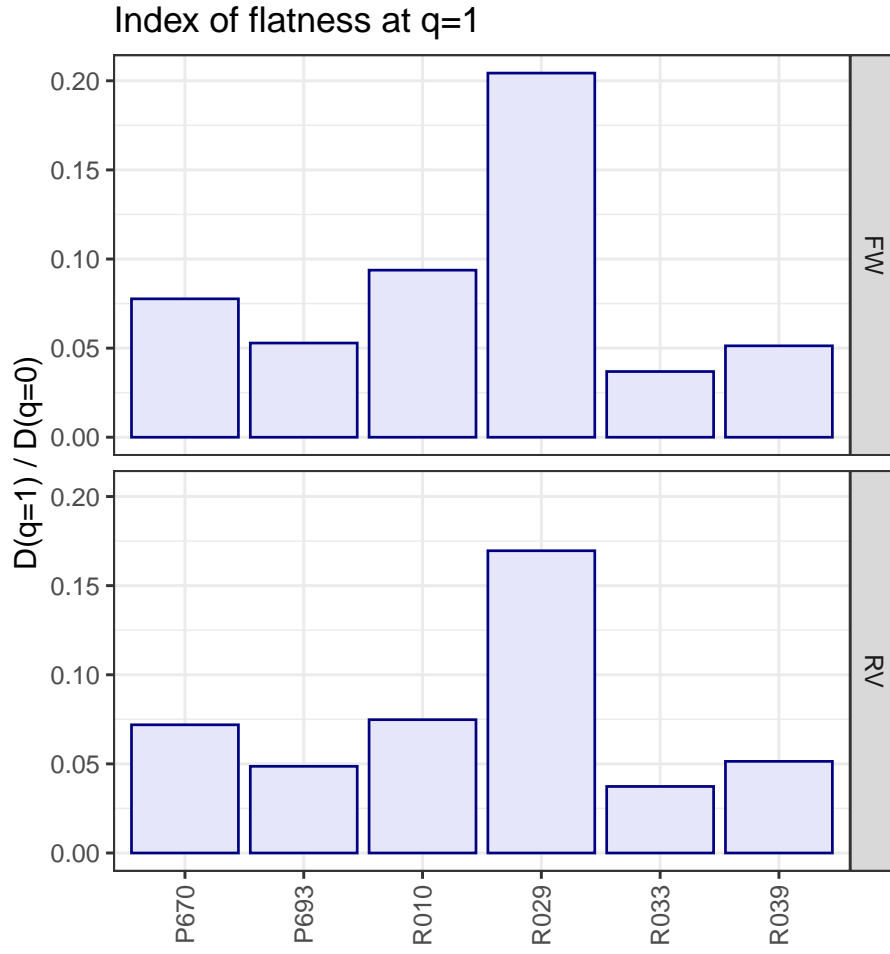


Figure NF-7: Evenness index ${}^1E = {}^1D/{}^0D$.

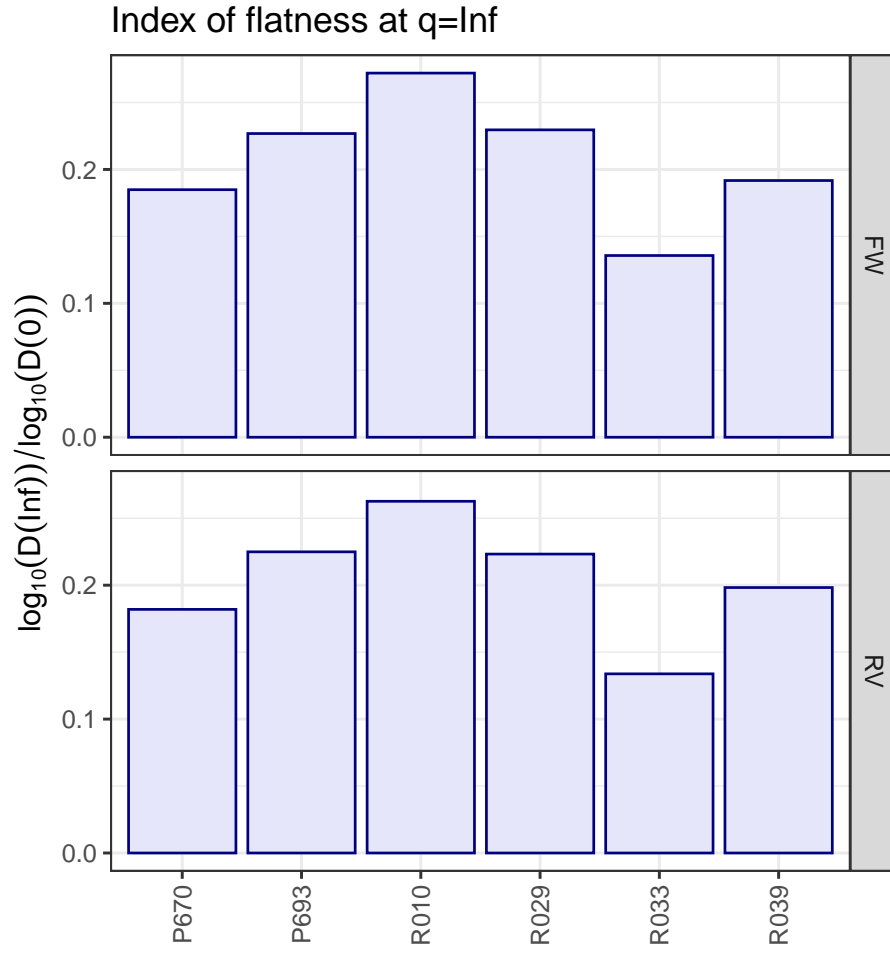


Figure NF-8: Evenness index $e\text{Inf}$, $\log_{10}({}^{\infty}D) / \log_{10}({}^0D)$.

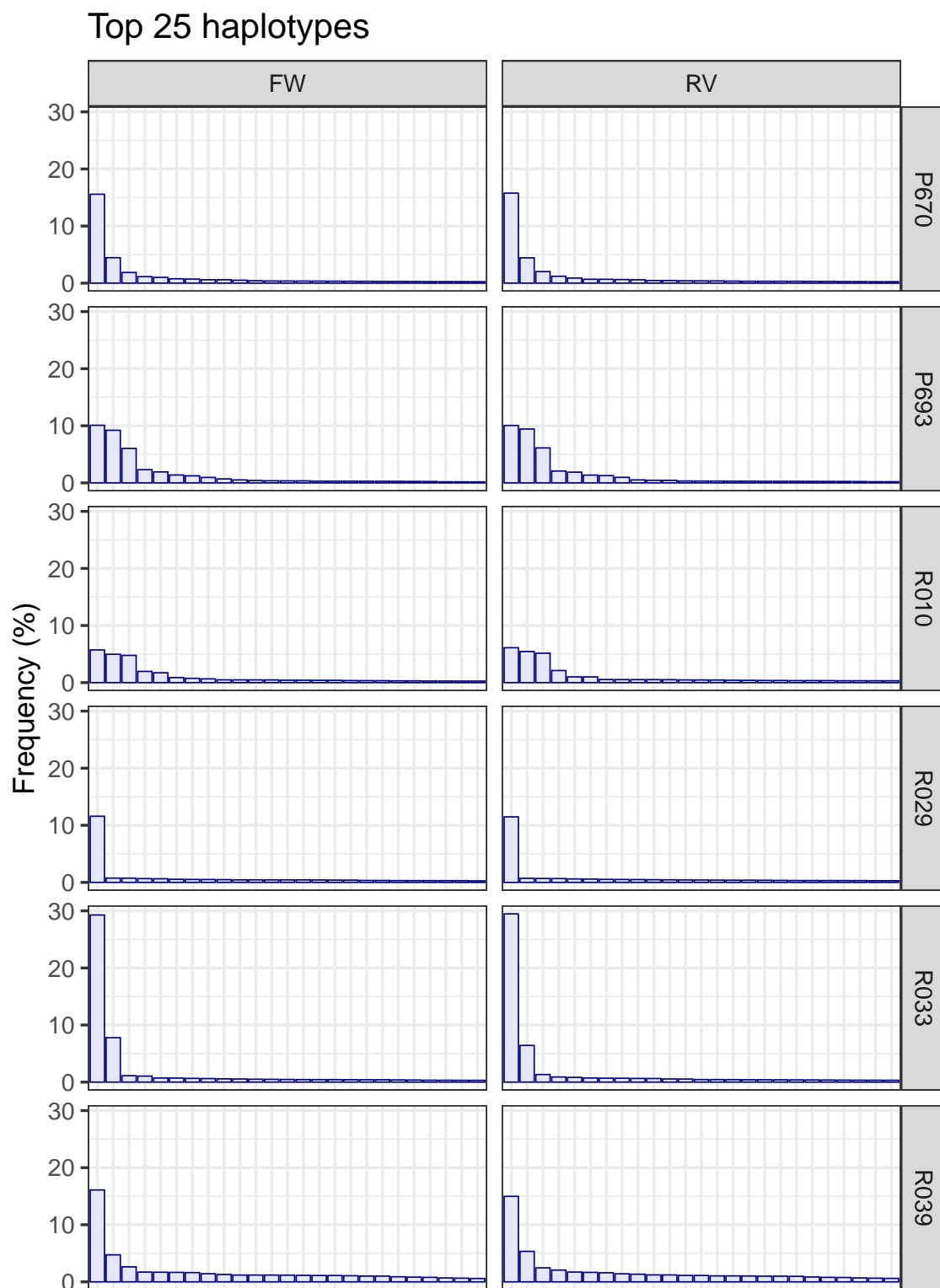


Figure NF-10: Frequencies of top 25 haplotypes.

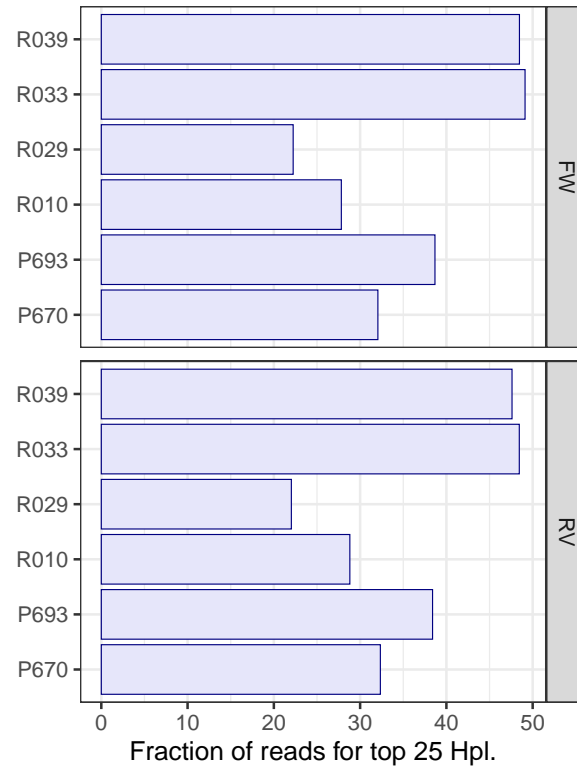


Figure NF-11: Fraction of reads for 25 top haplotypes.

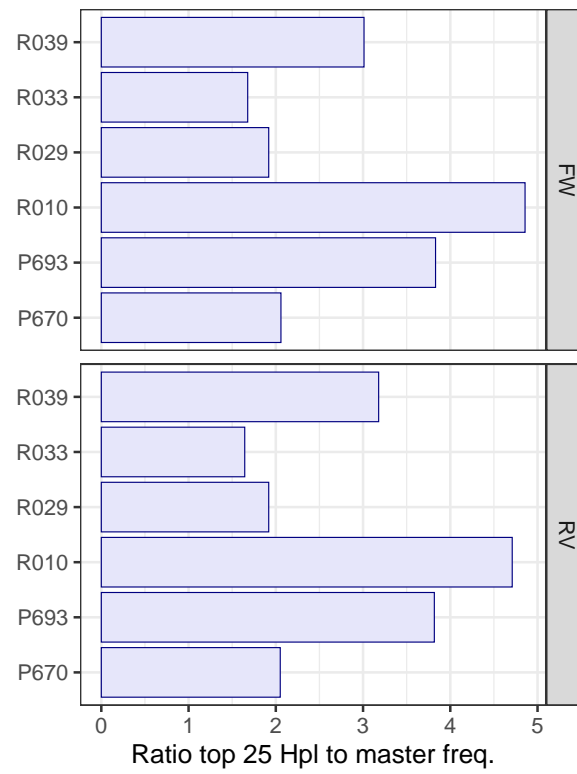


Figure NF-12: Ratio of reads for 25 top haplotypes to master haplotype.

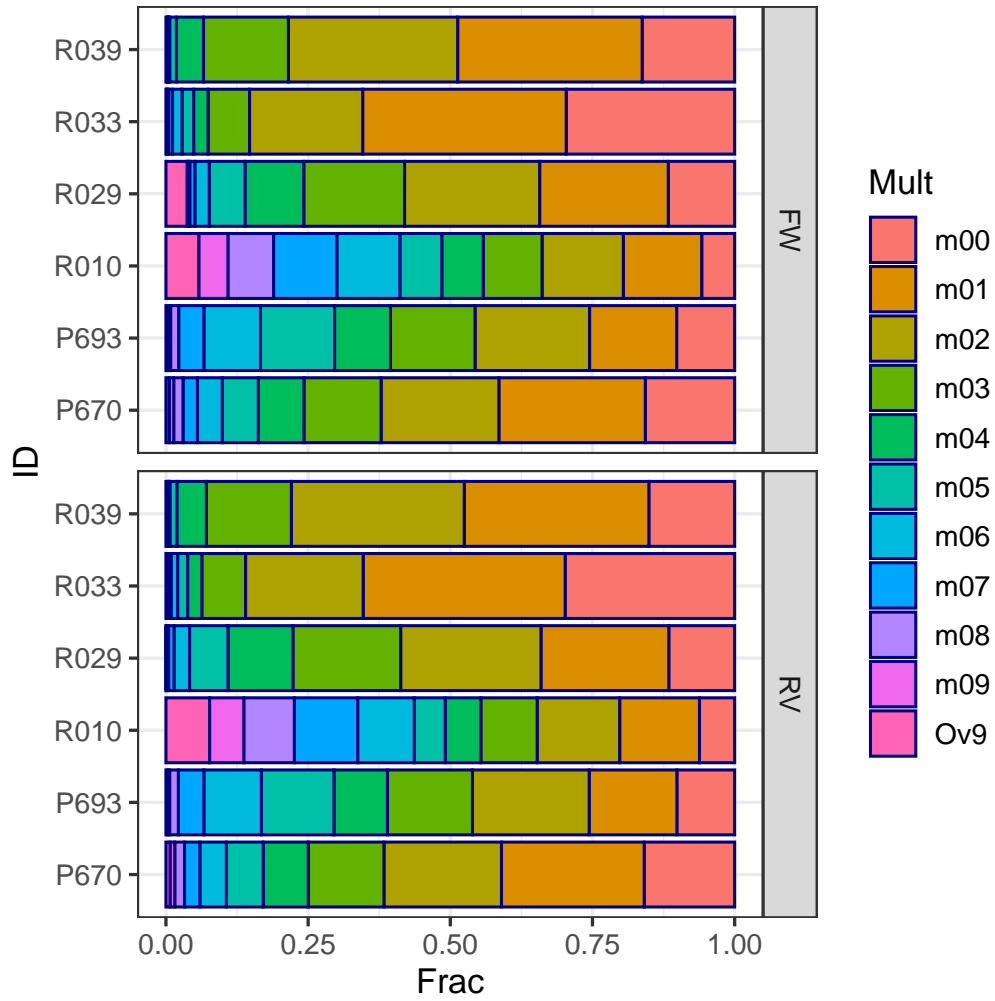


Figure NF-13: Fractions of reads with increasing number of substitutions with respect to the master haplotype in each sample. m00: fraction of reads for the master haplotype, m0x: fraction of reads for haplotypes showing x substitutions, Ov0: fraction of reads with over 9 substitutions.

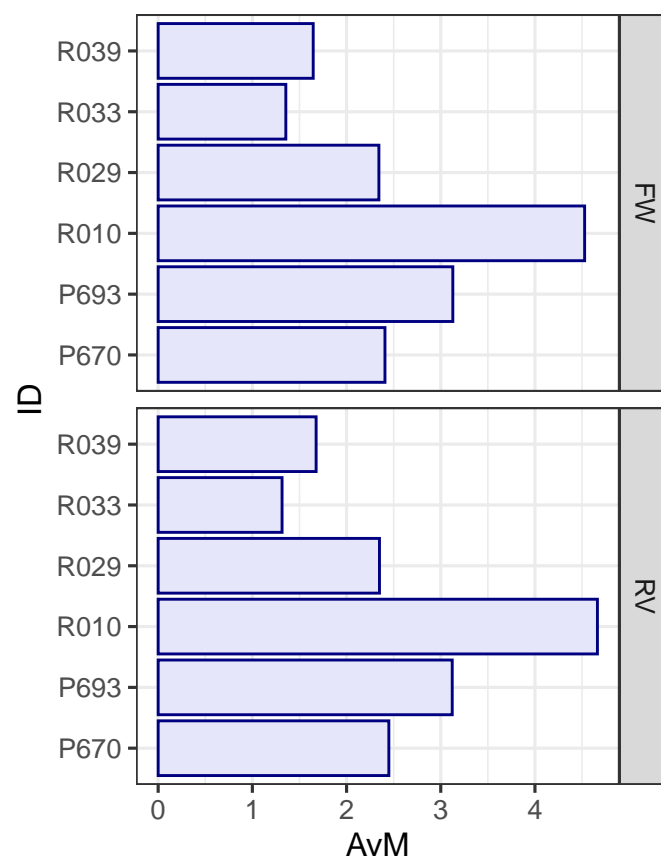


Figure NF-14: Mean number of substitutions per read with respect to the master haplotype in each amplicon and strand.