Supplementary Figure S2  G-test statistics for each mitochondrial genome region for PB changes using as expectation the size of the features. Dashed line indicates 0.05 significance level with a Bonferroni correction, while dotted line indicates an uncorrected 0.05 significance level. Negative signs on top of bars indicate that observed values were lower than expected. Gray bar indicates noncoding or synonymous changes, while black bars indicate non-synonymous changes. The name of the genomic region follows the names used on accession NC_012920.1, with the only exception of HSV-I, HSV-II, HSV-III and D-Loop, that split the original region annotated as D-Loop in the three hyper-variable regions and the remnant of the D-Loop, respectively.