Figure S2. Average number of total SNVs distributed throughout RABV genome.
SNVs are plotted as the percentage per nucleotide per region (N, P, M, G and L genes and the non-coding (NC) regions) and are representative of the average number of mutations per region and per animal for *in vivo* passages (in black) or per cell culture for *in vitro* passages (in grey). Error bars correspond to standard deviations.