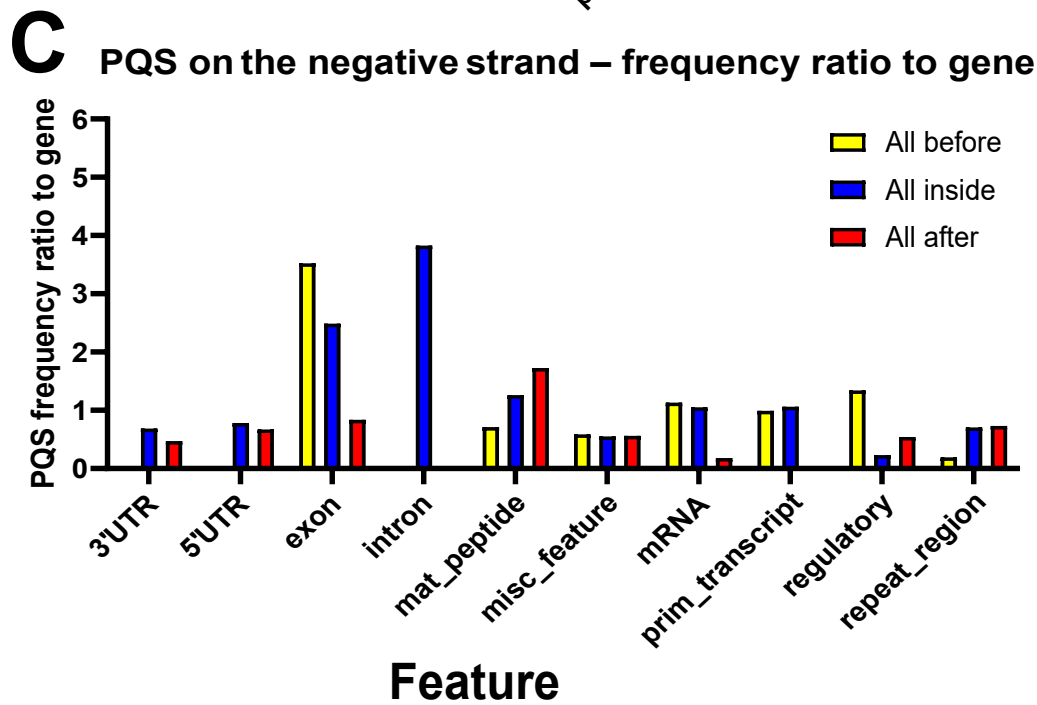
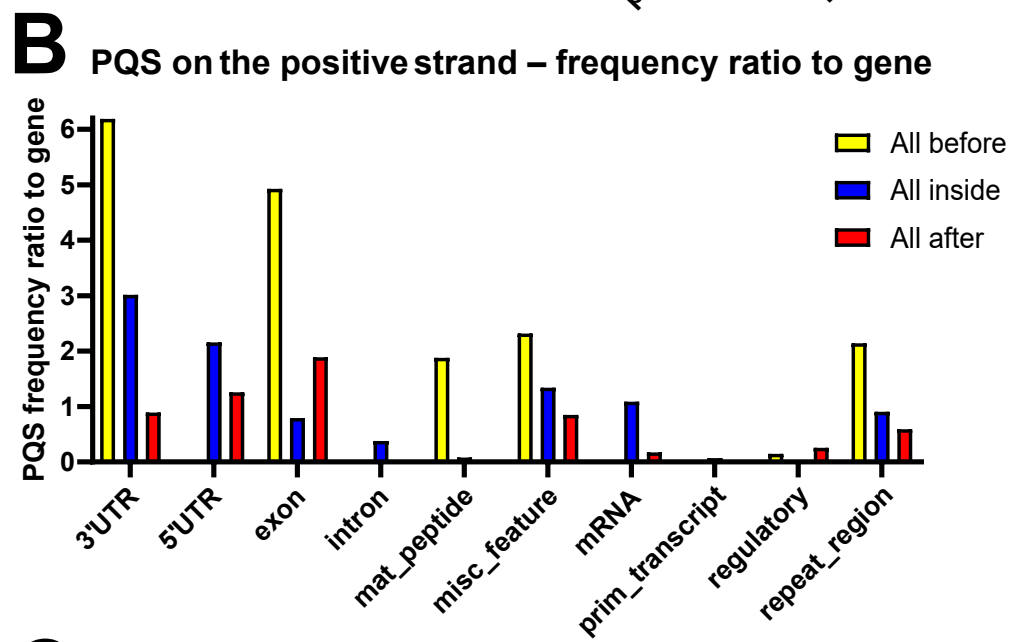
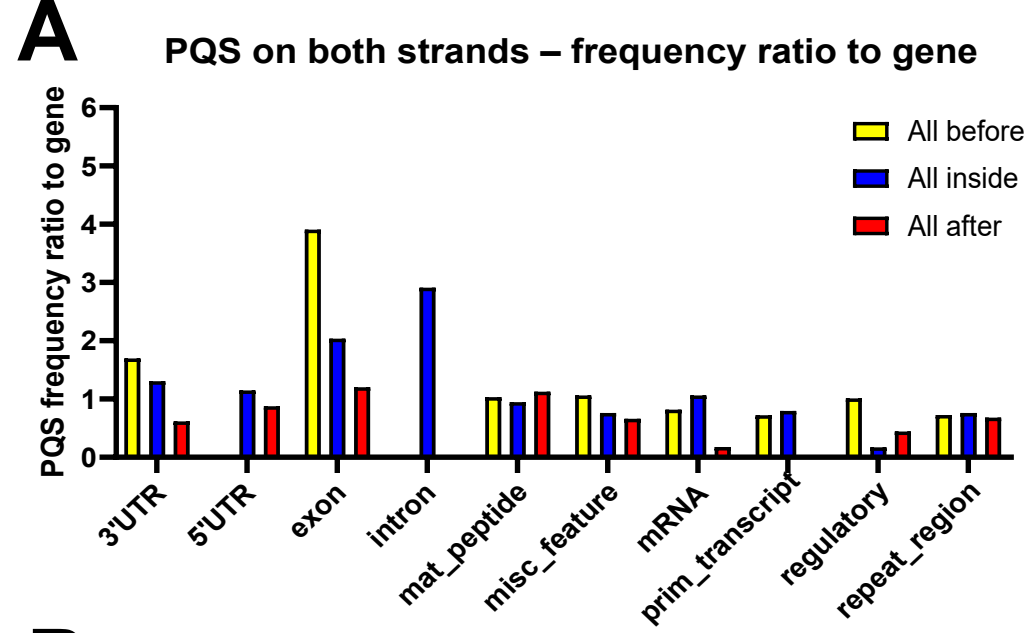
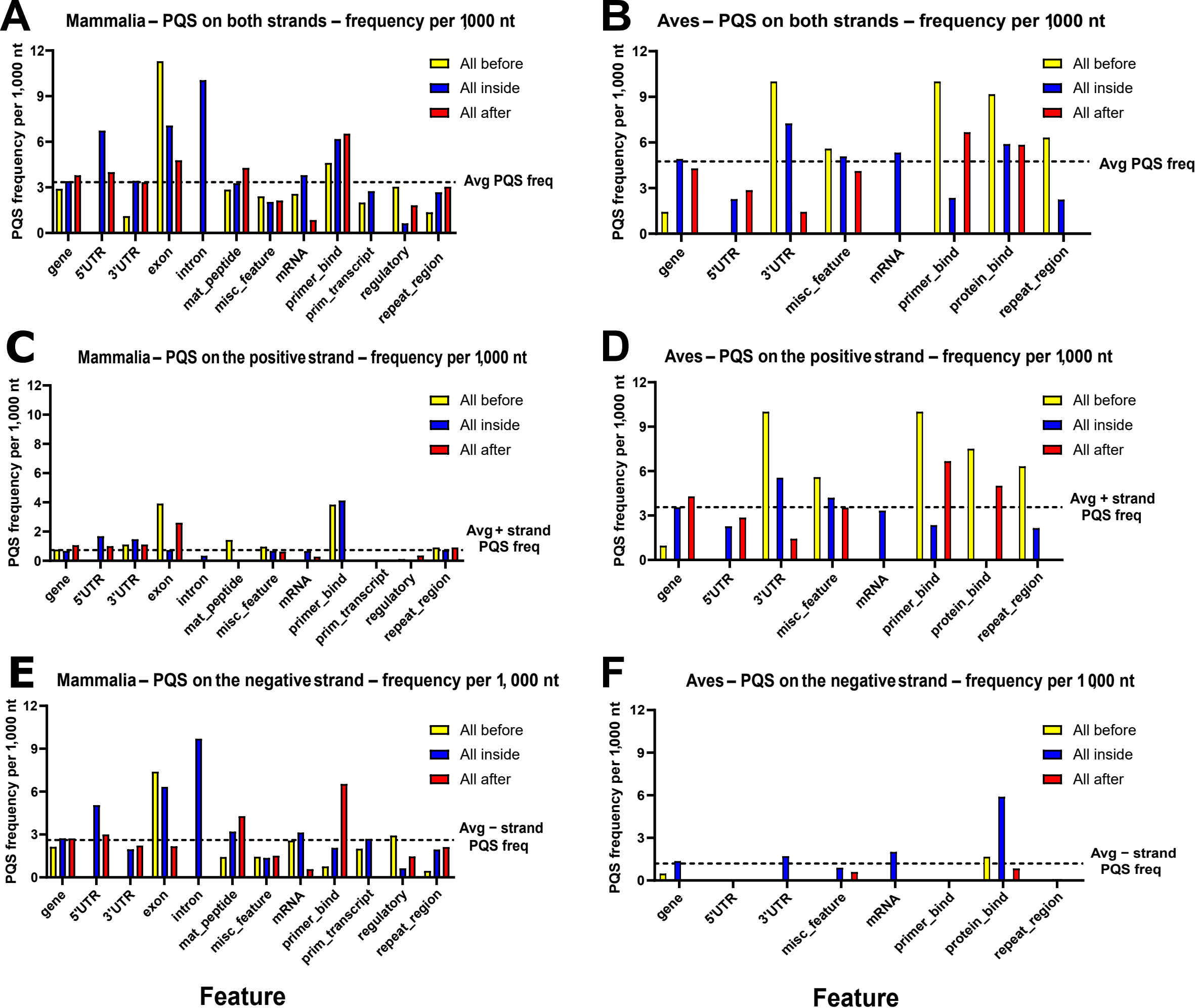




SM 03. Feature analysis – frequency ratio to gene. We analysed the total counts and frequencies of all PQS (total PQS on both strands and PQS on each strand) within (All Inside), before (100 nt) and after (100 nt) annotated features from the NCBI database. The charts show the ratio of PQS frequencies per 1,000 nt between gene annotation and other annotated features. (A) PQS on both strands; (B) PQS on the positive strand; (C) PQS on the negative strand.



SM 04. Features analysis – mammalian and avian retroviruses. We analysed the frequencies of all PQS (total PQS on both strands and PQS on each strand) within (All Inside), before (100 nt) and after (100 nt) annotated features in all mammalian (121 genomes, including all mammalian retroviruses) and avian retroviral genomes (16 genomes). PQS frequencies normalized per 1,000 nt annotated locations: **(A)** PQS on both strands in mammalian retroviruses; **(B)** PQS on both strands in avian retroviruses; **(C)** PQS on the positive strand in mammalian retroviruses; **(D)** PQS on the positive strand in avian retroviruses; **(E)** PQS on the negative strand in mammalian retroviruses; **(F)** PQS on the negative strand in avian retroviruses. Dashed lines denote the average (Avg) PQS frequencies (freq) for the corresponding strands (both, positive and negative strands, respectively).