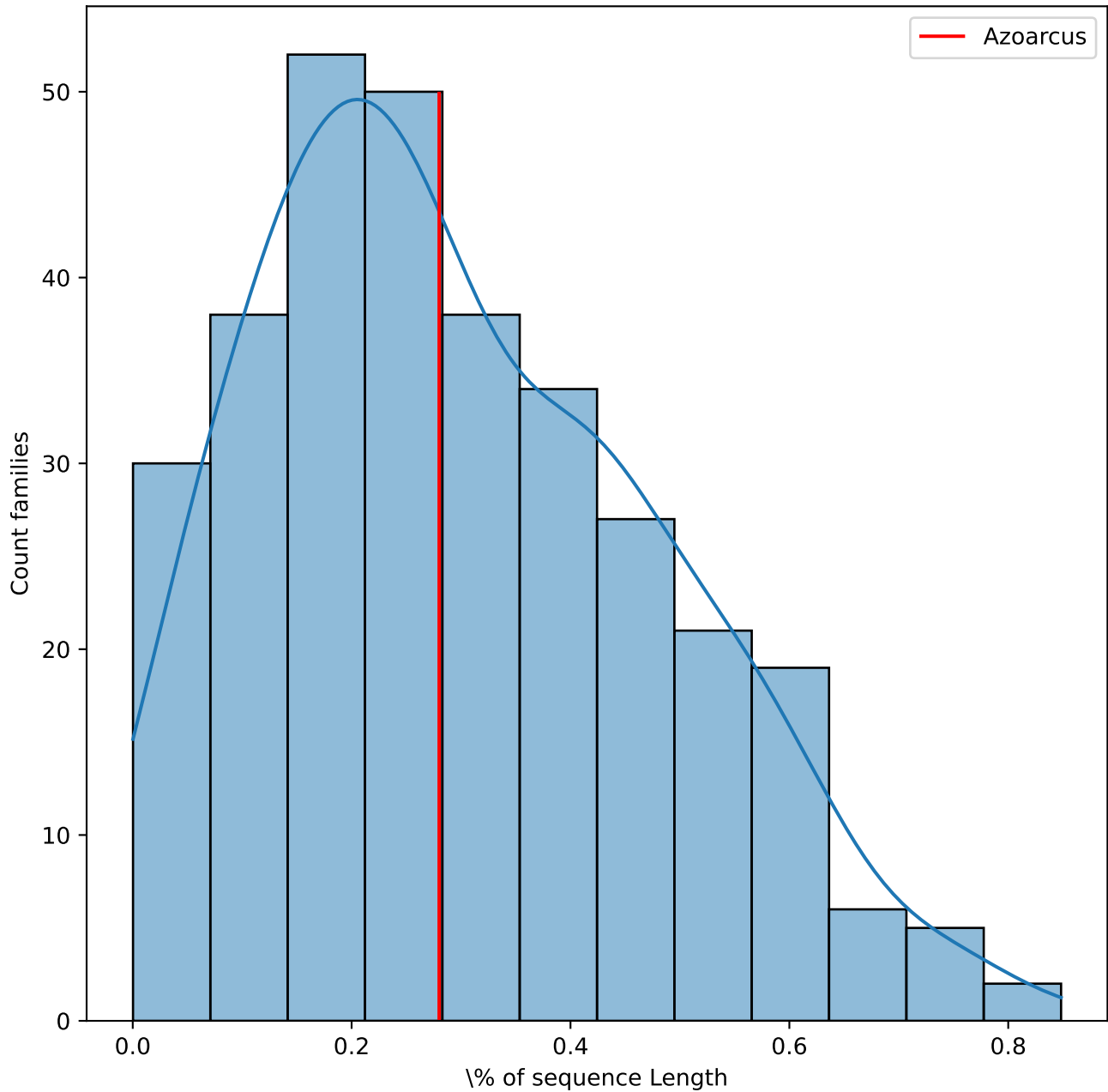
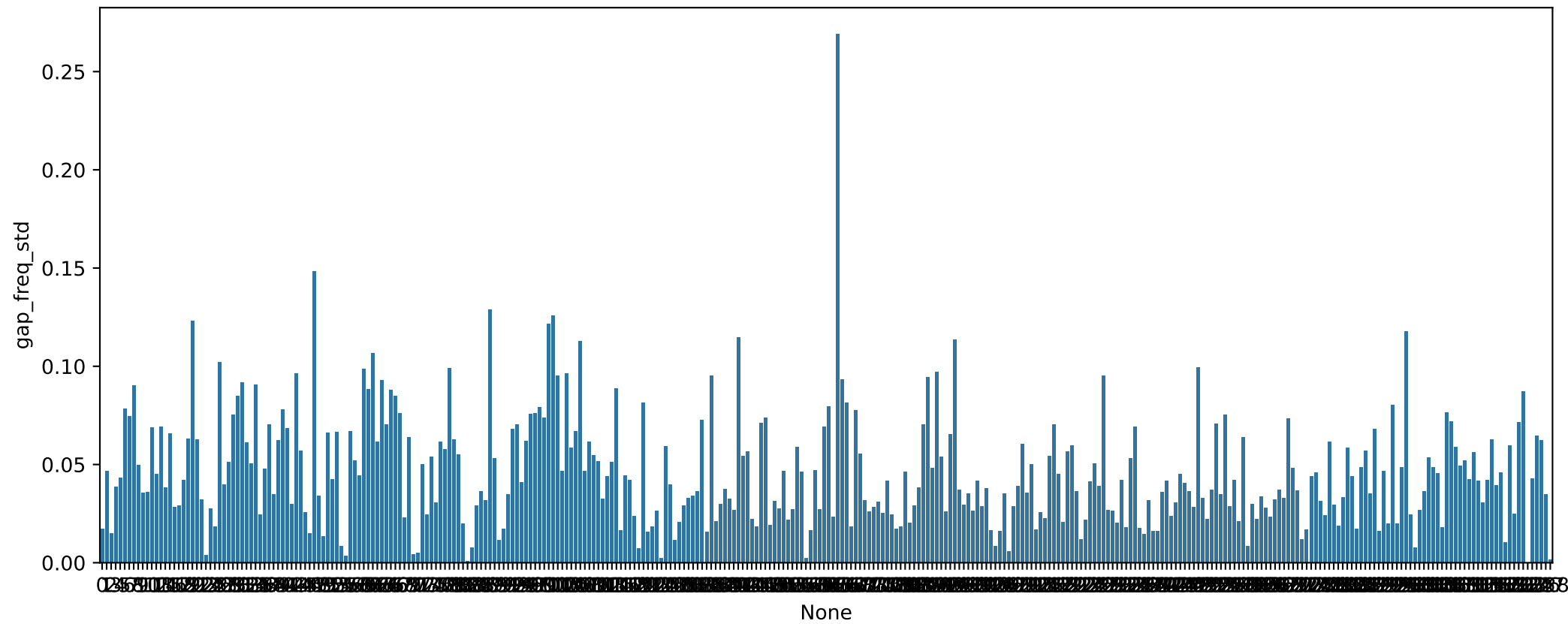


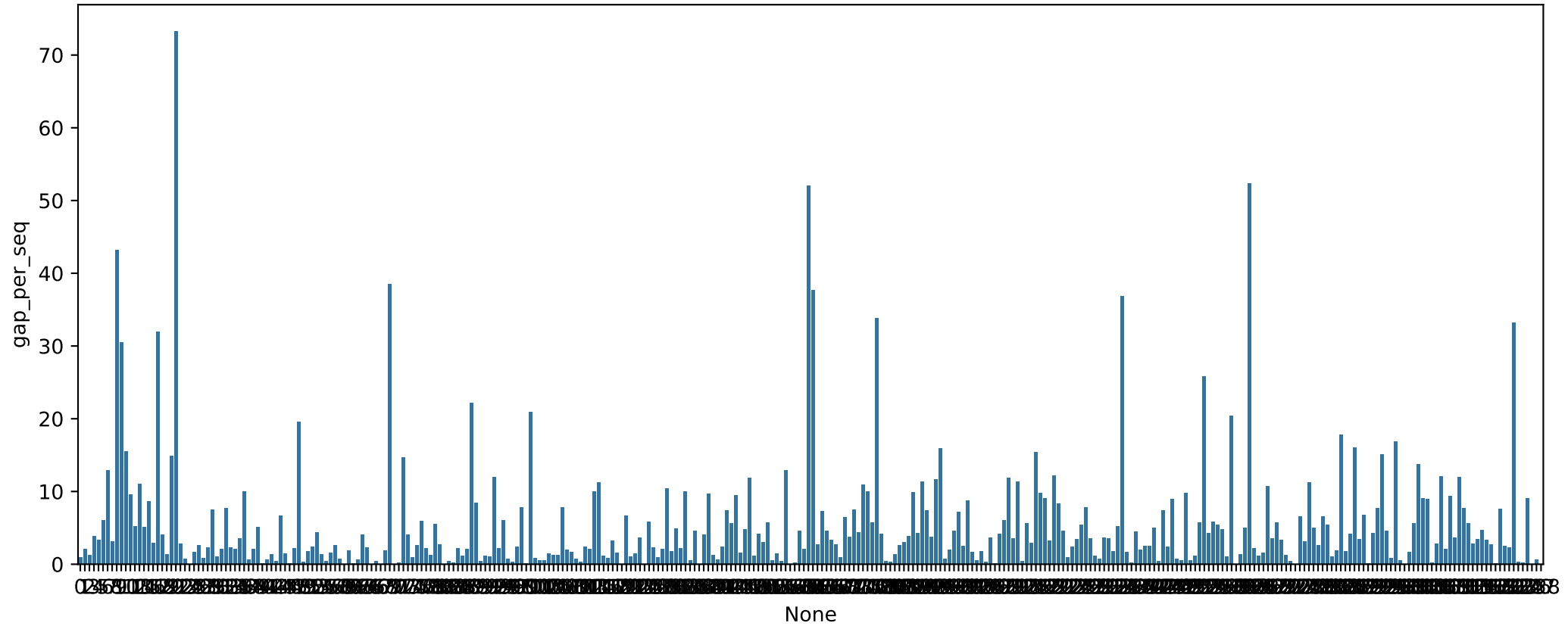
Rfam families distribution depending on the gap frequencies



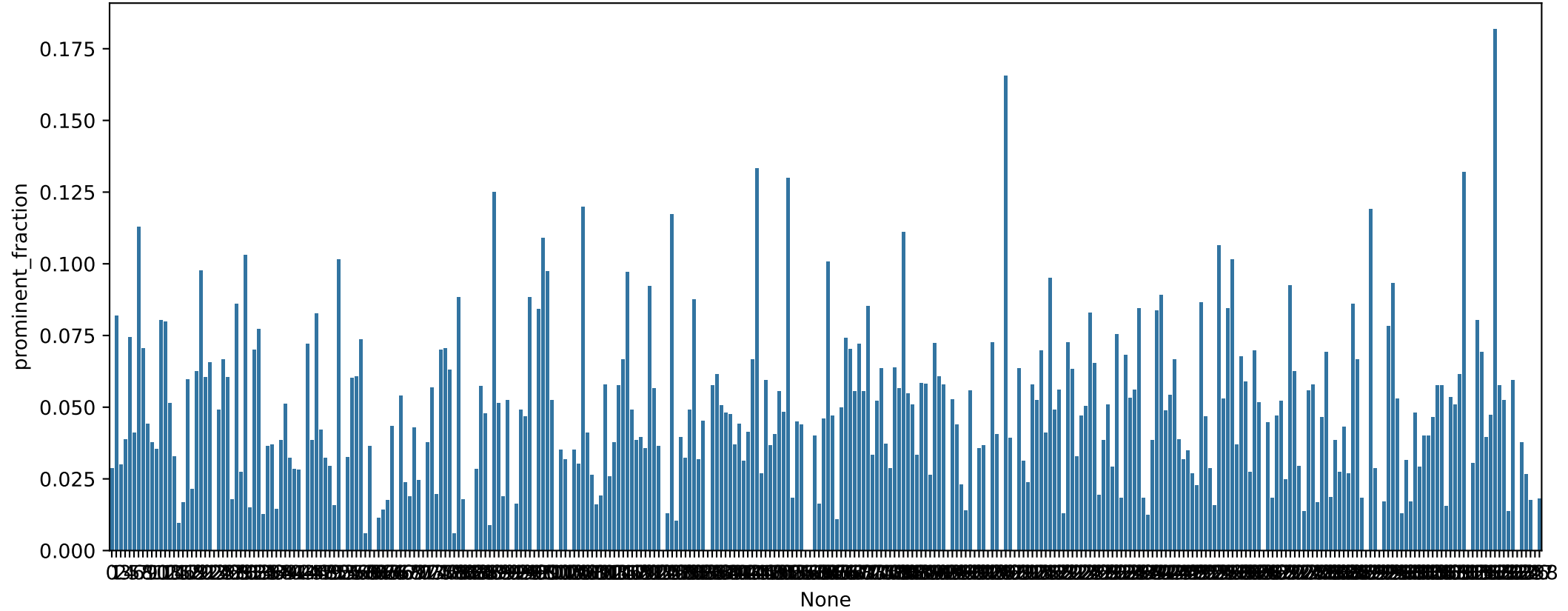
Numeric Feature : gap_freq_std



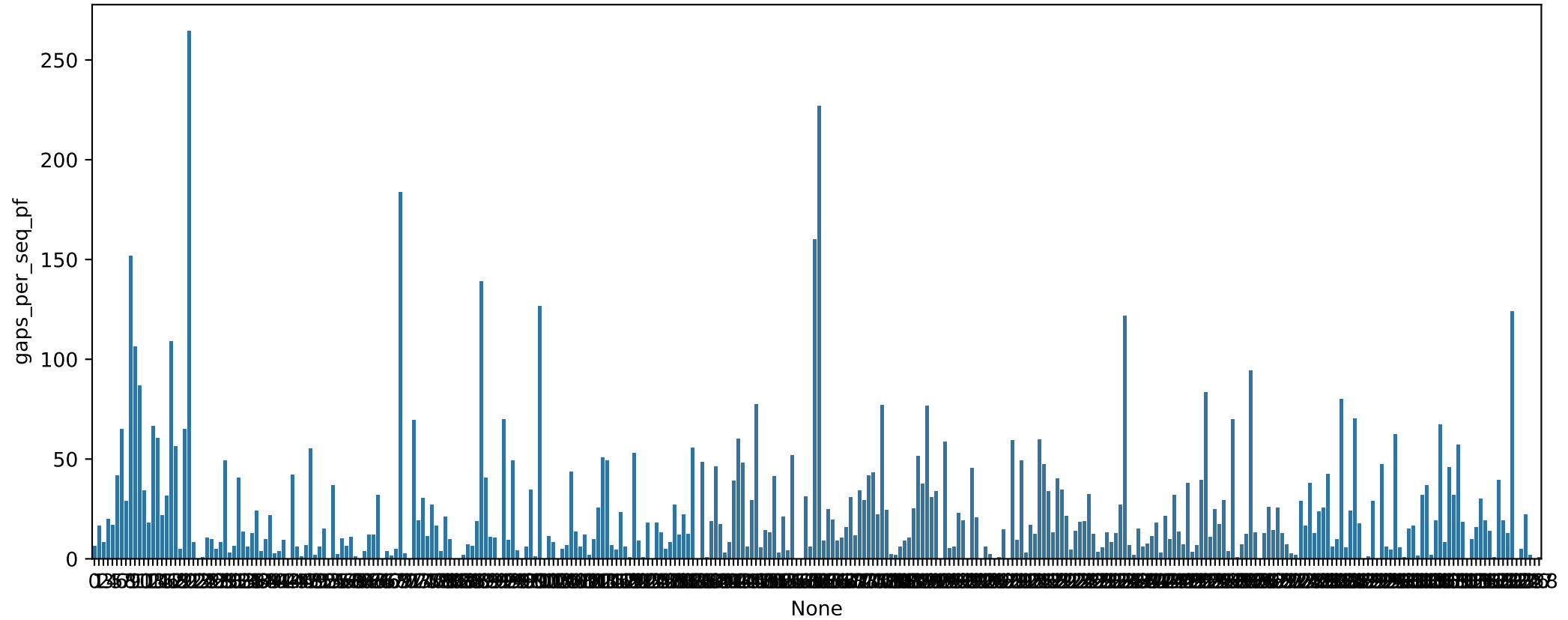
Numeric Feature : gap_per_seq



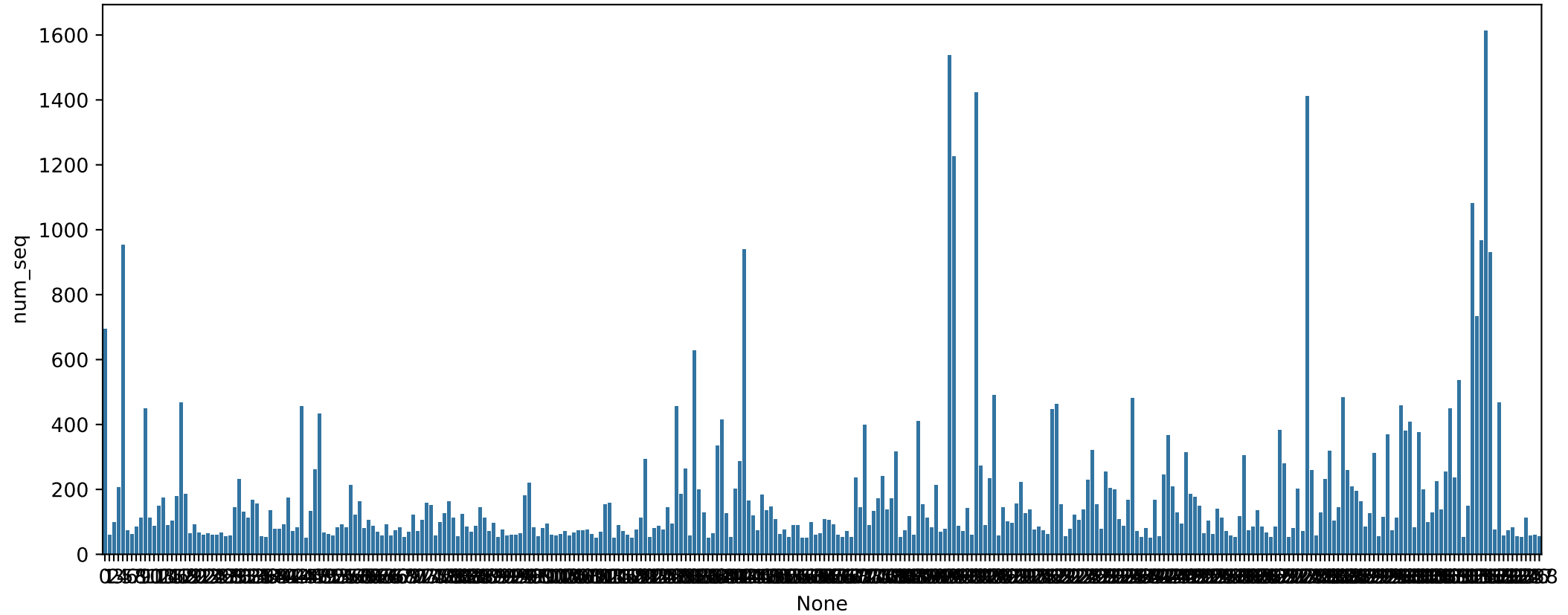
Numeric Feature : prominent_fraction



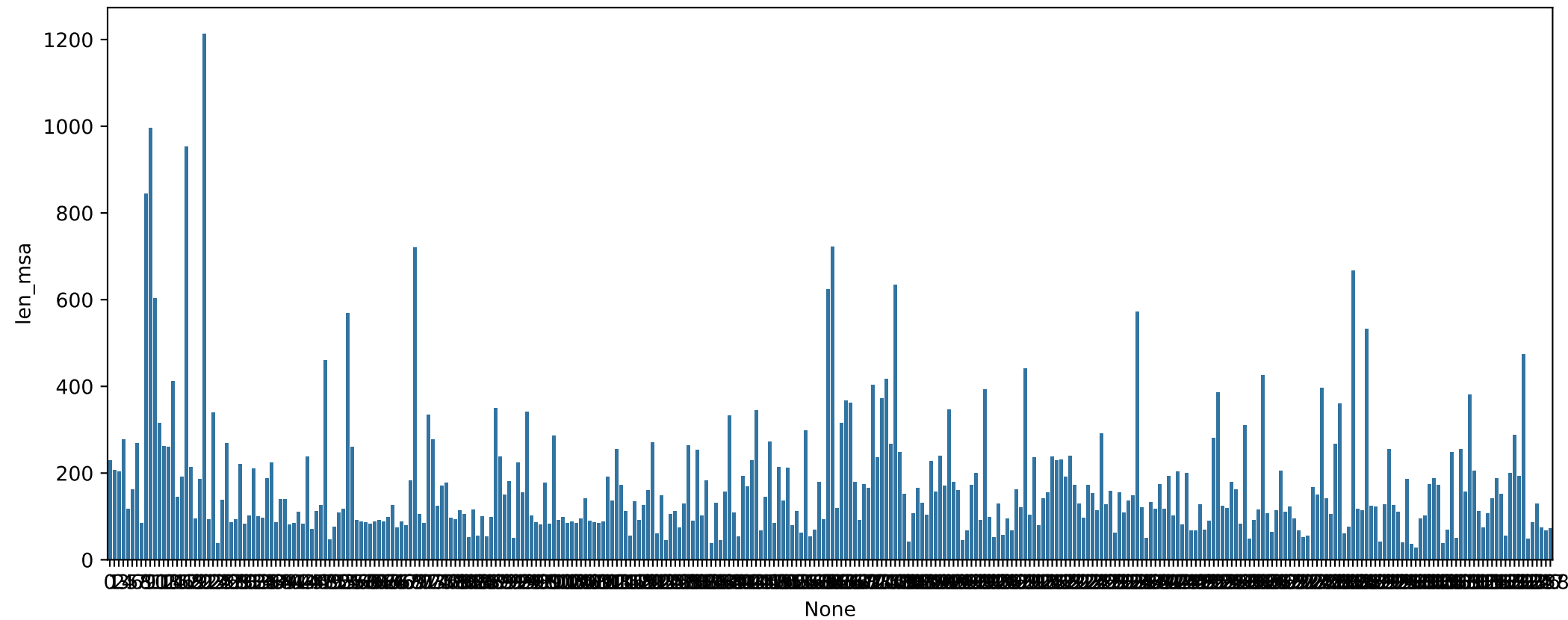
Numeric Feature : gaps_per_seq_pf



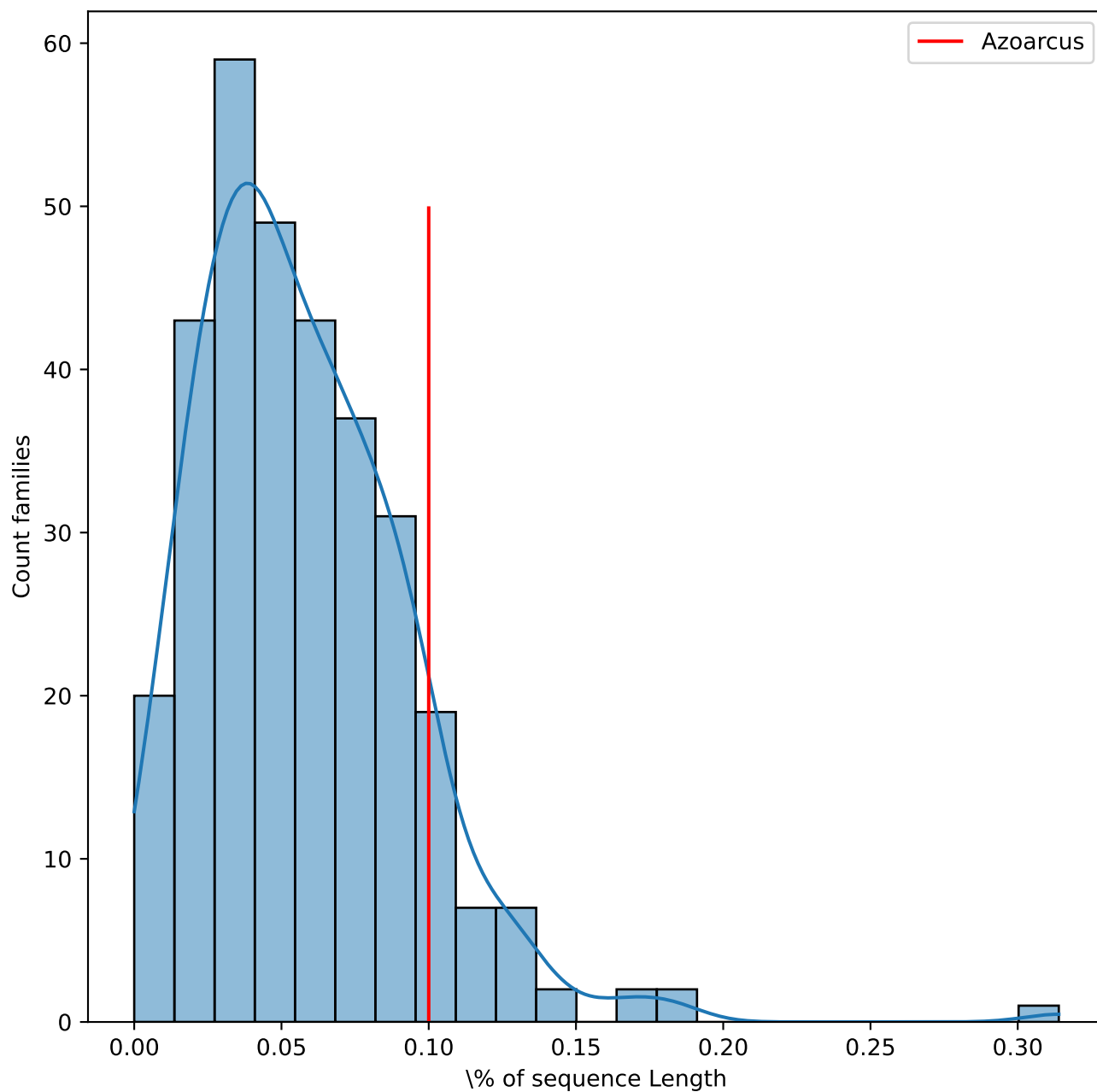
Numeric Feature : num_seq



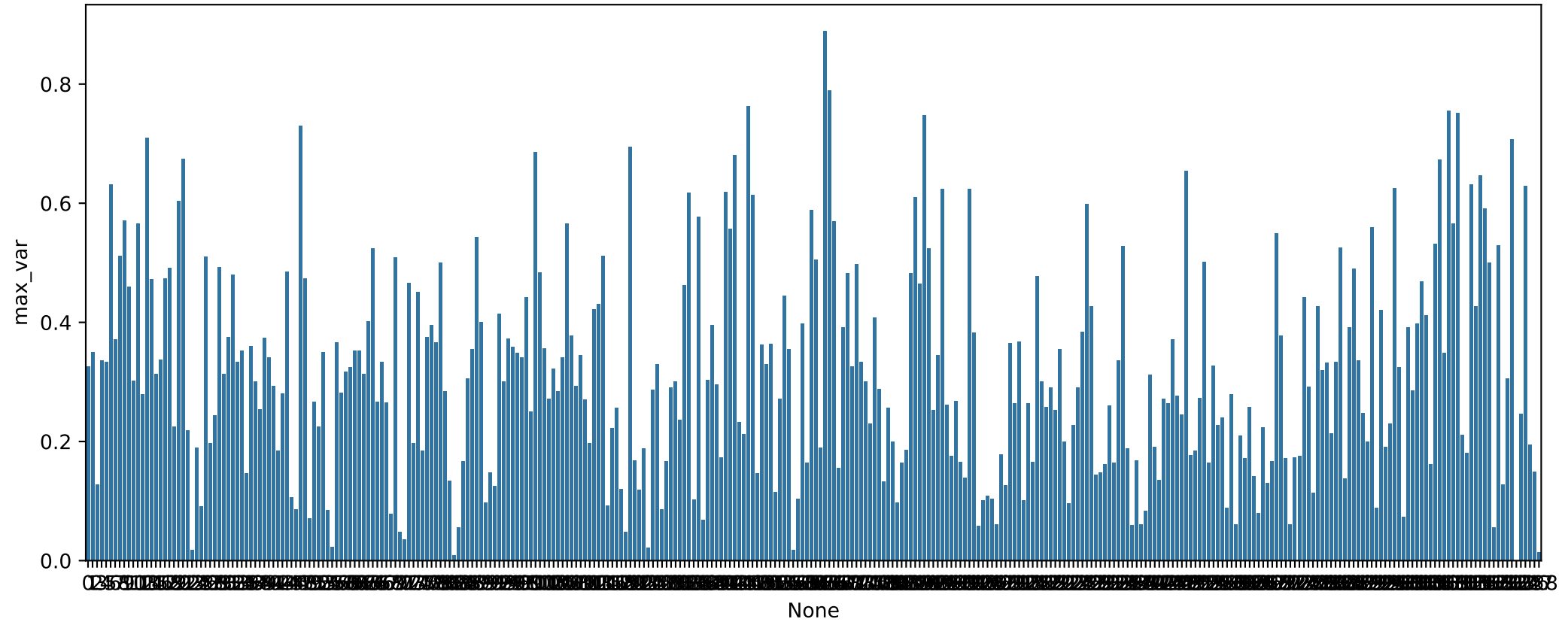
Numeric Feature : len_msa



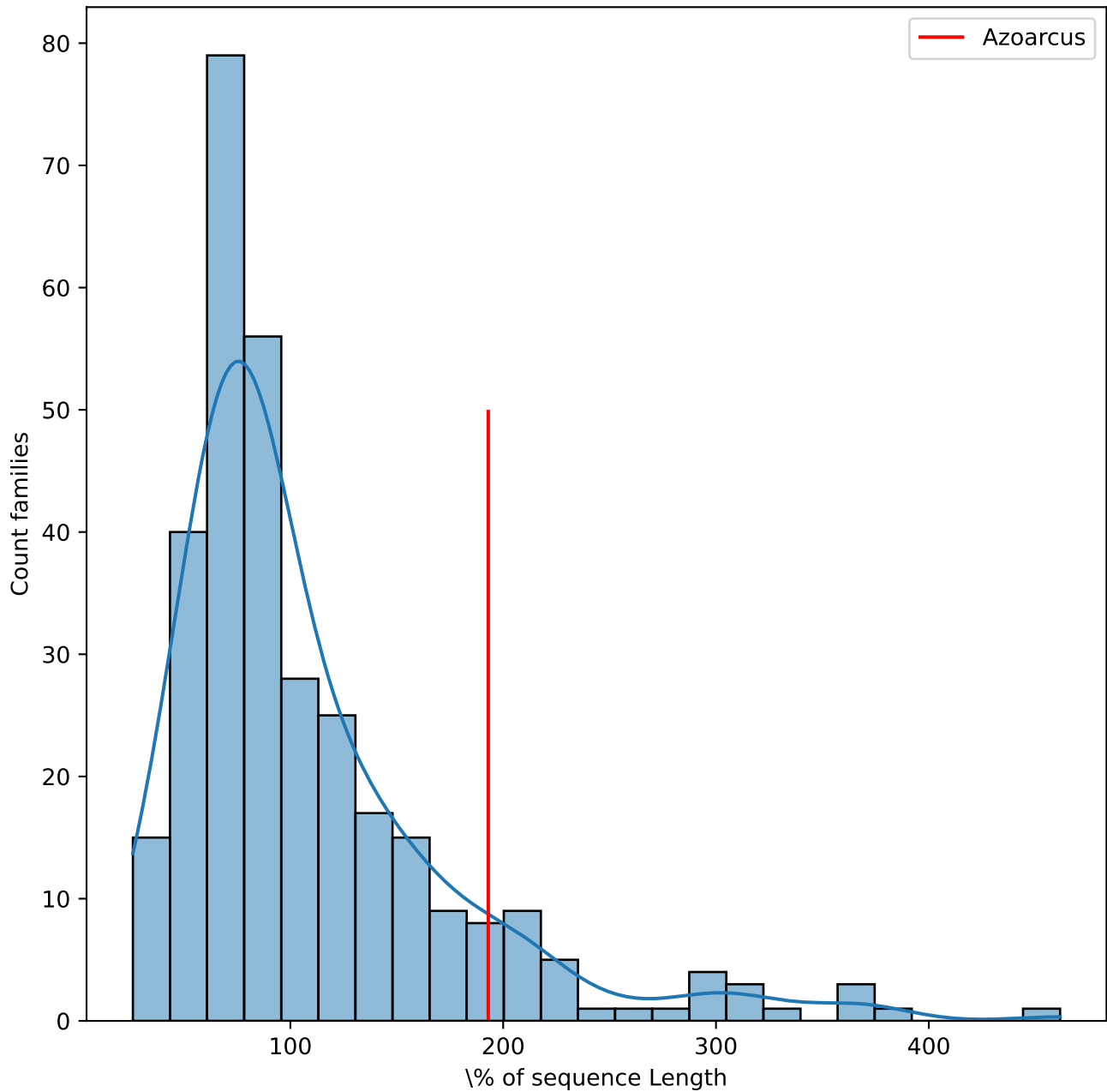
am families distribution for maximum variation of sequences si



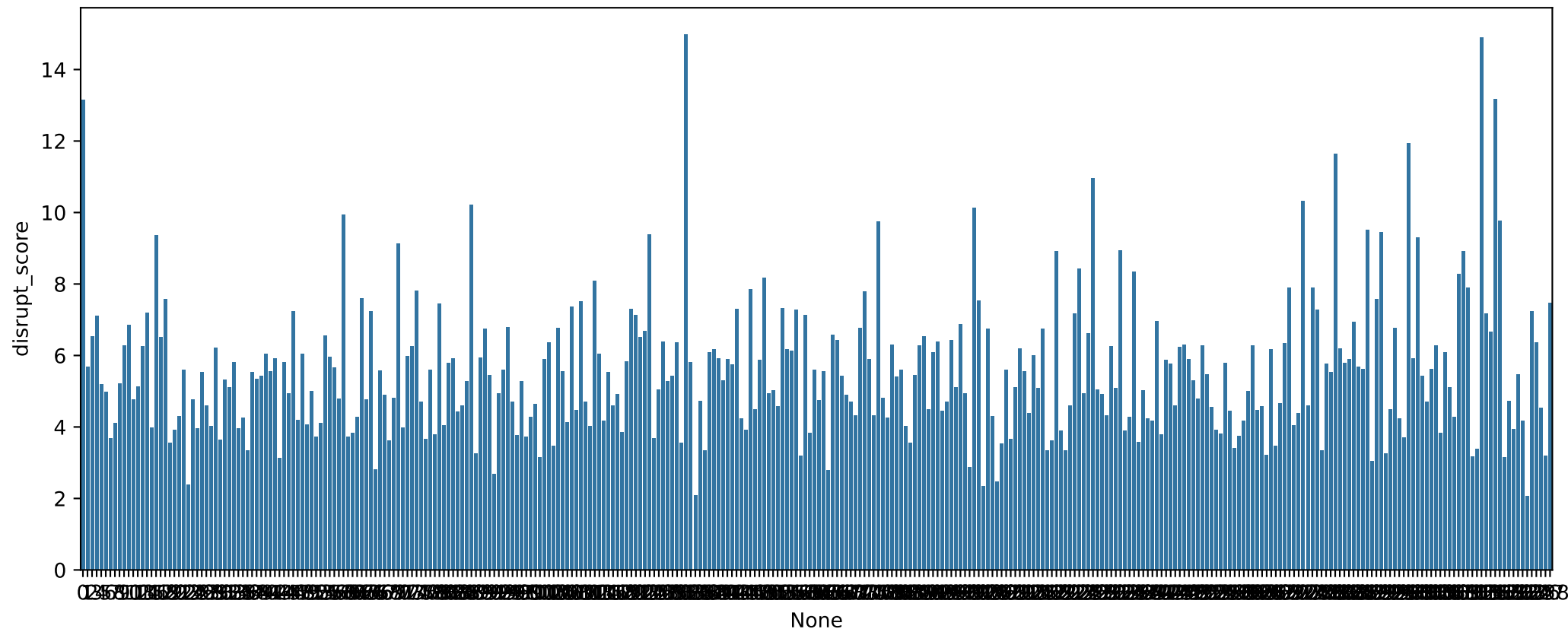
Numeric Feature : max_var



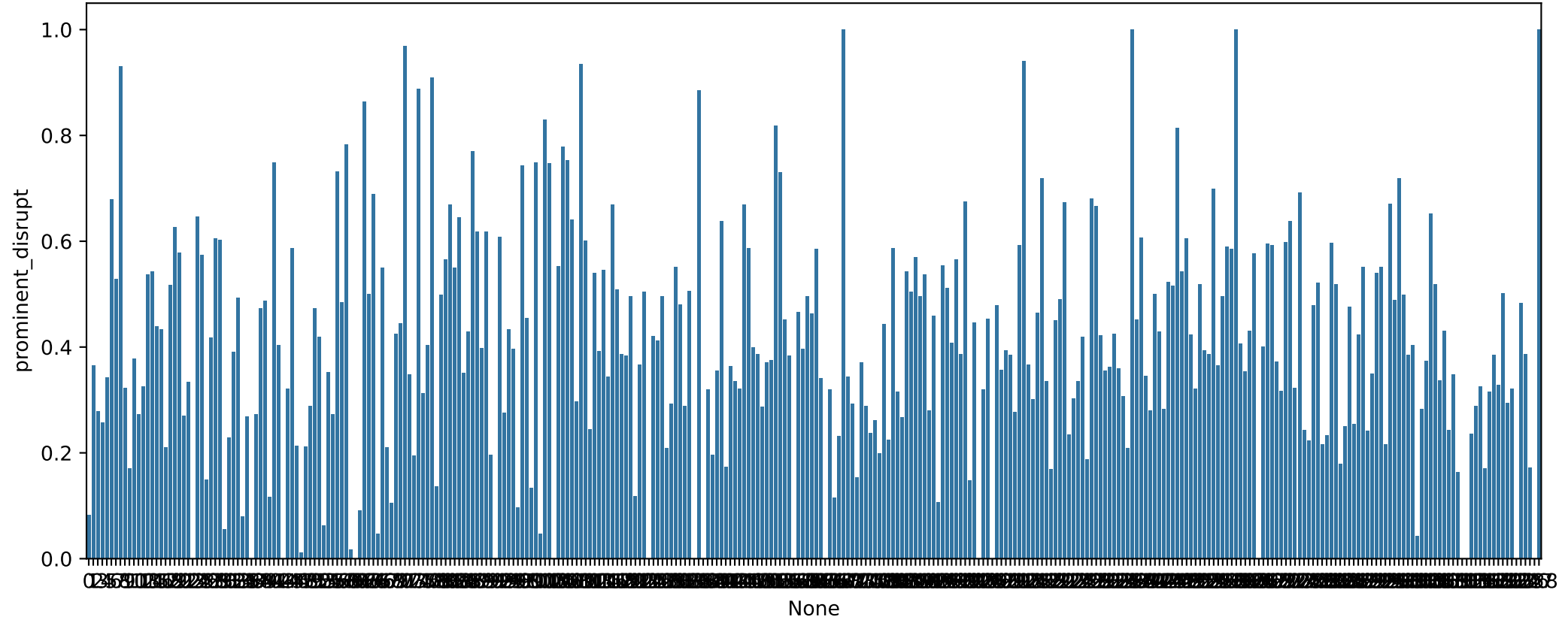
m families distribution depending on their sequences average s



Numeric Feature : disrupt_score



Numeric Feature : prominent_disrupt



Numeric Feature : concomitance_score

