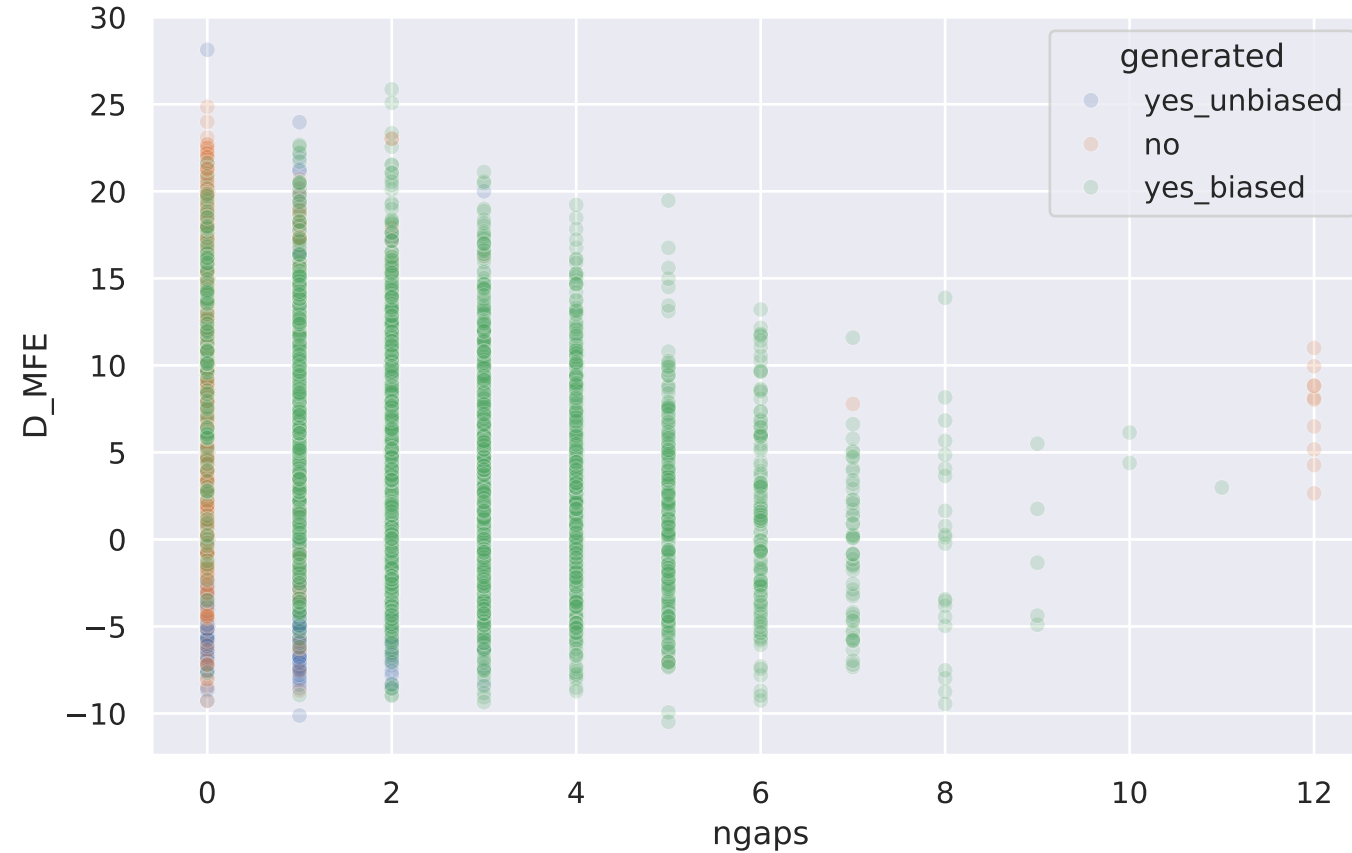
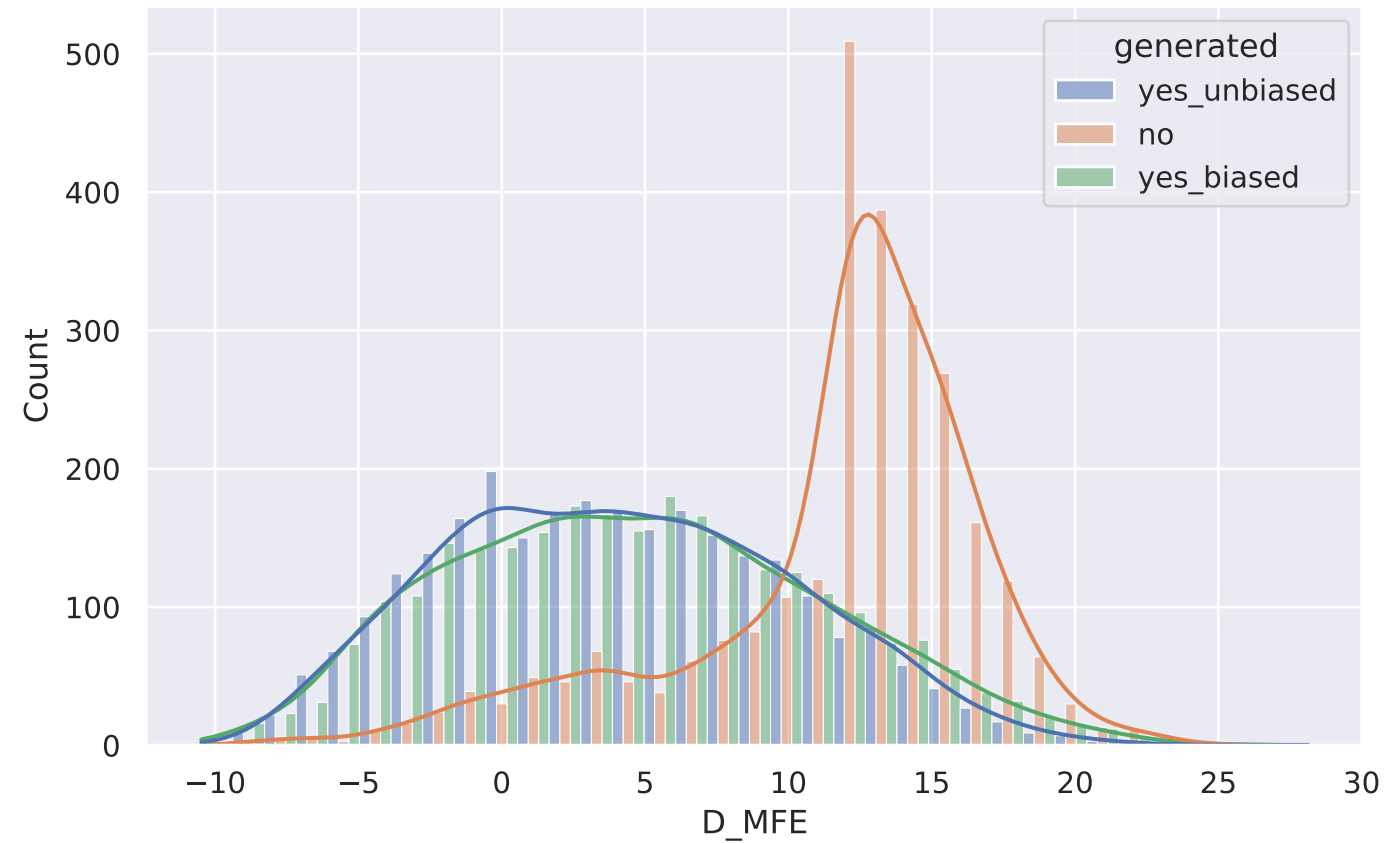
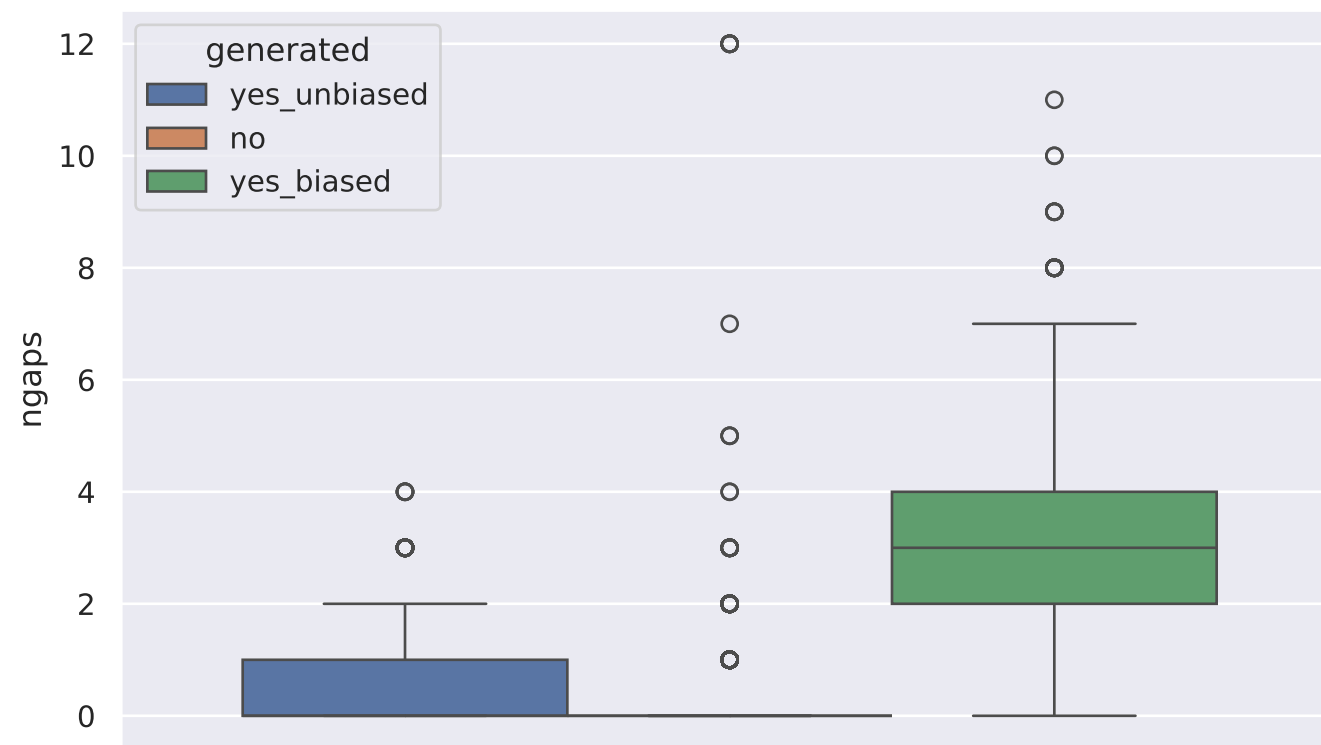
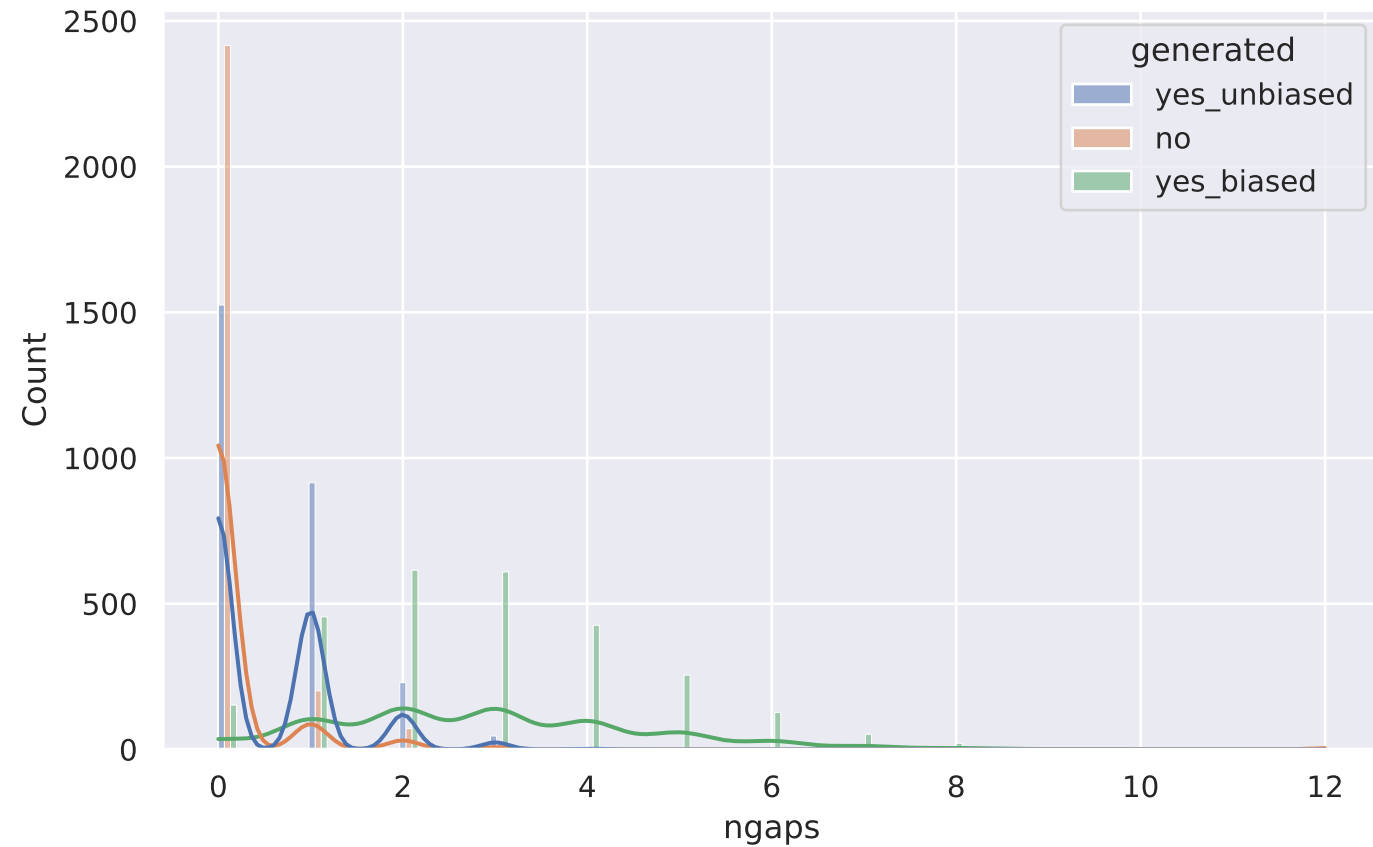


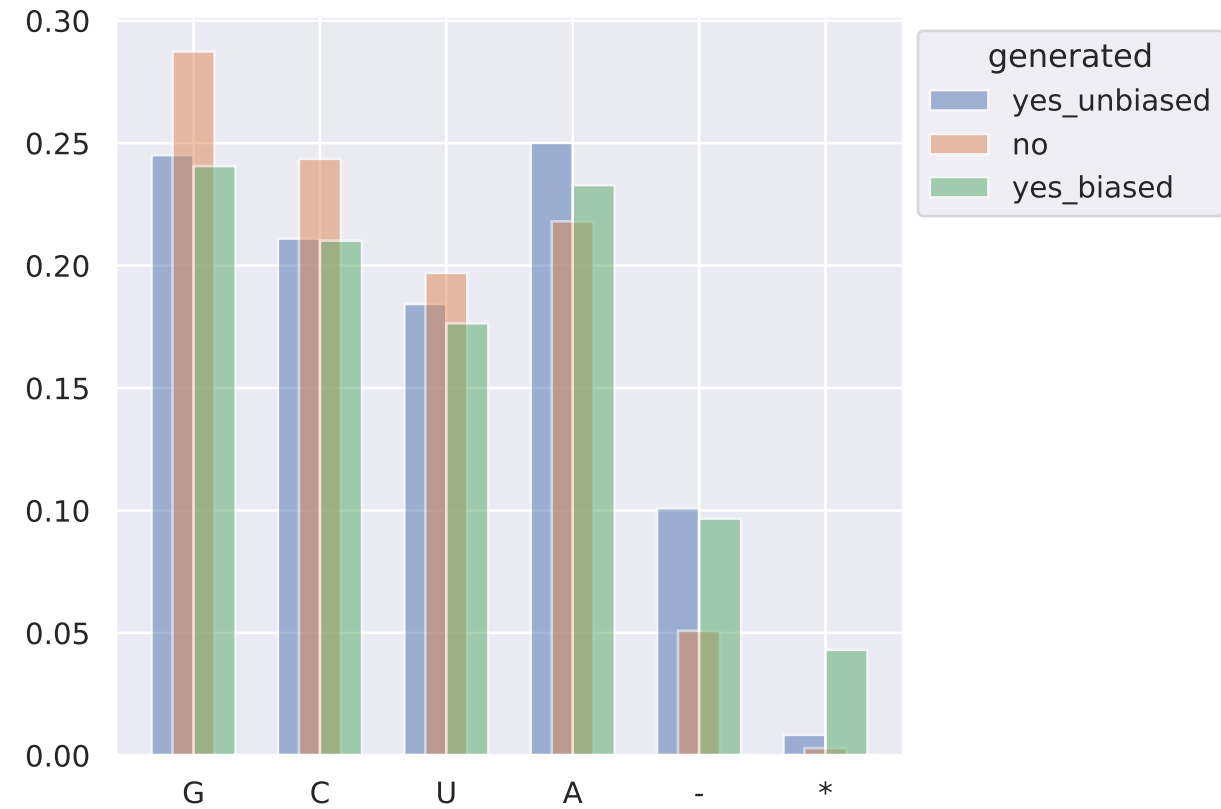
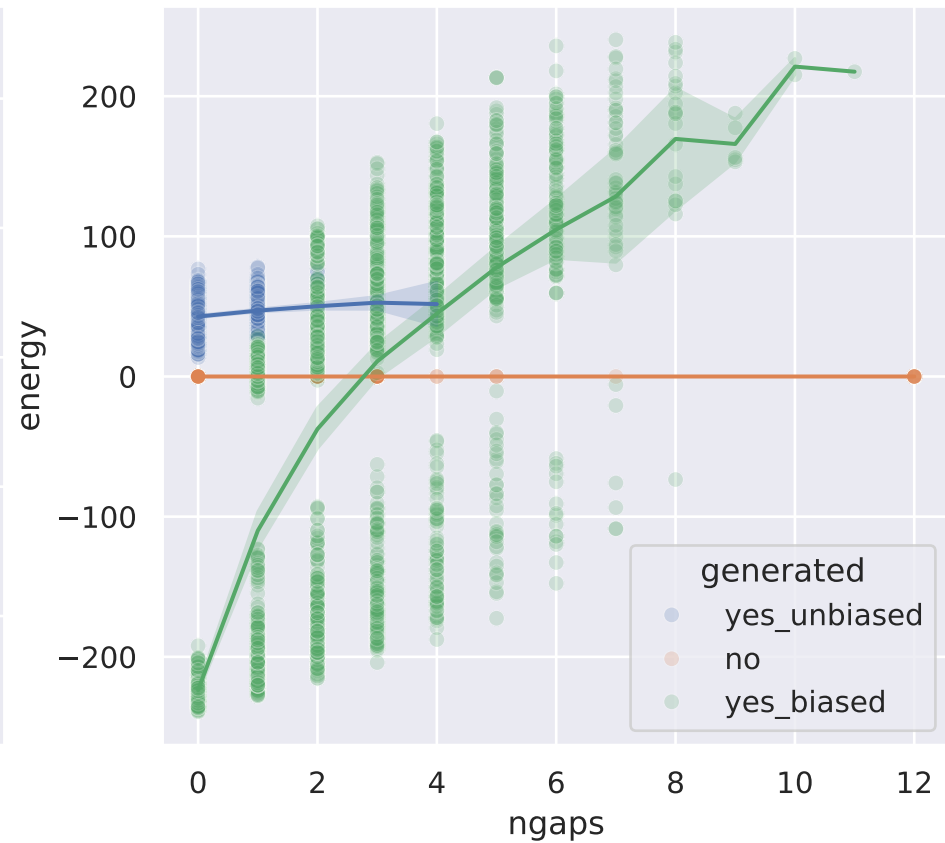
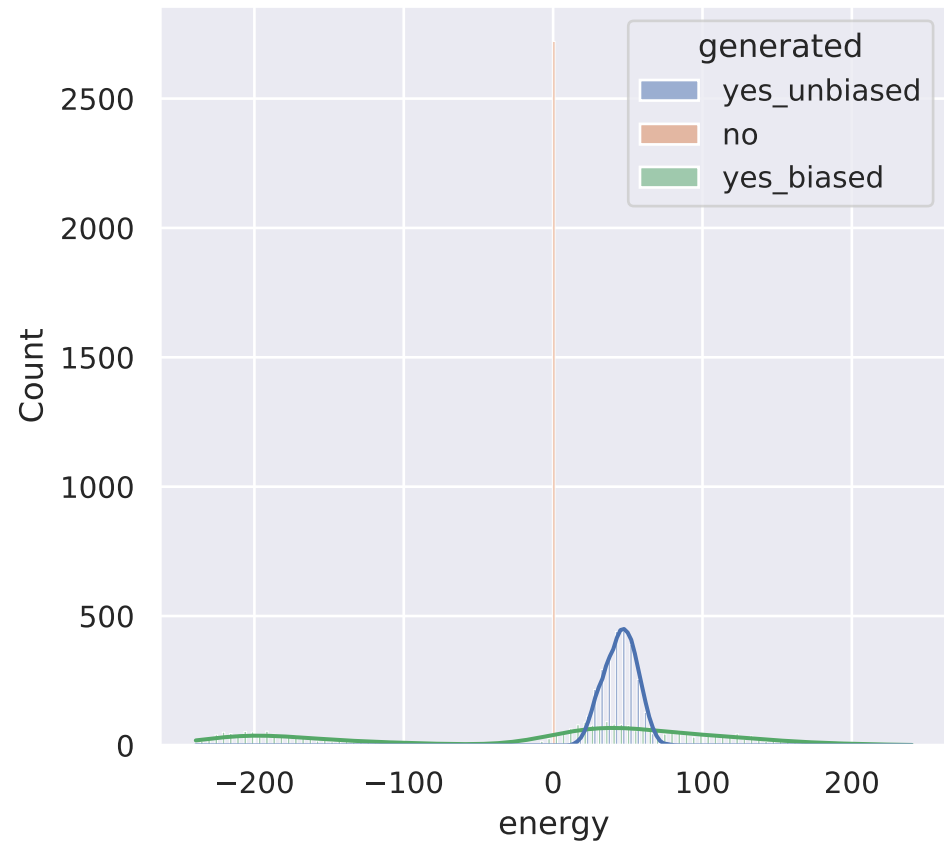
**Numeric Feature : D\_MFE**



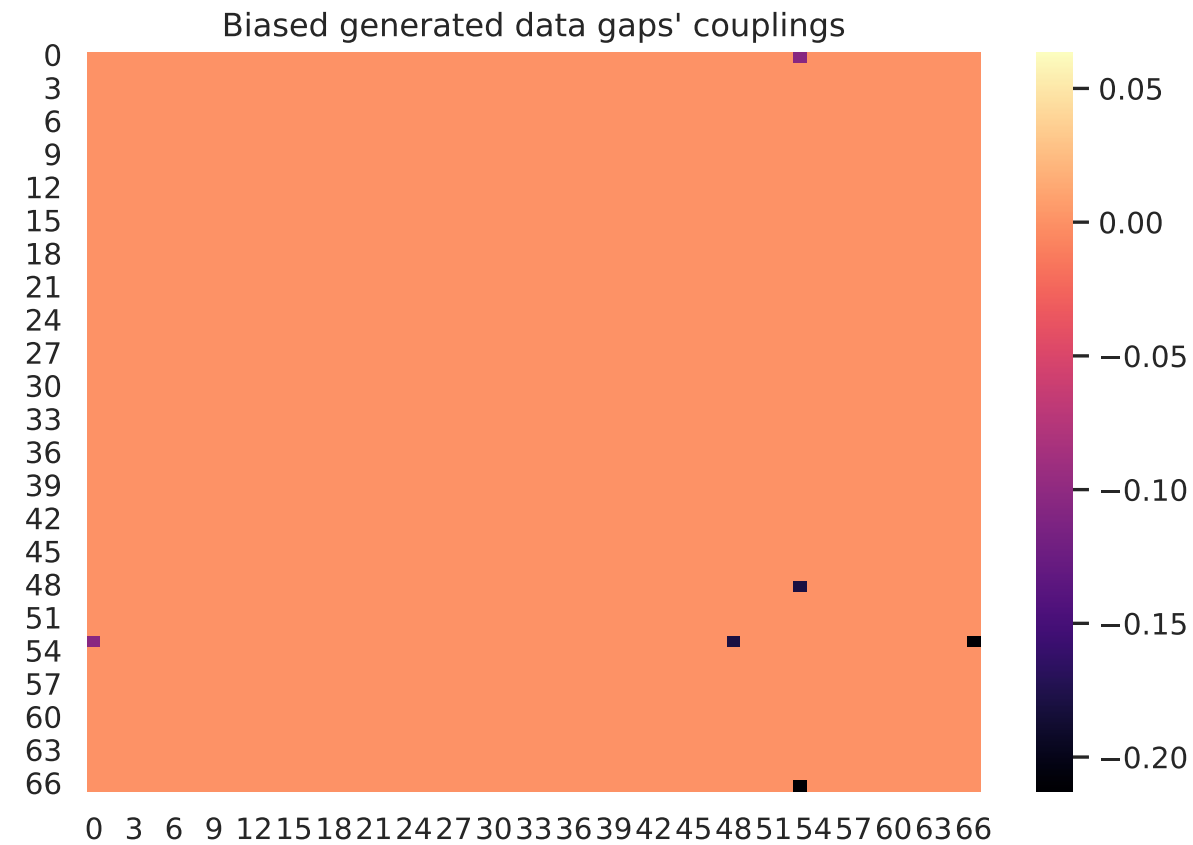
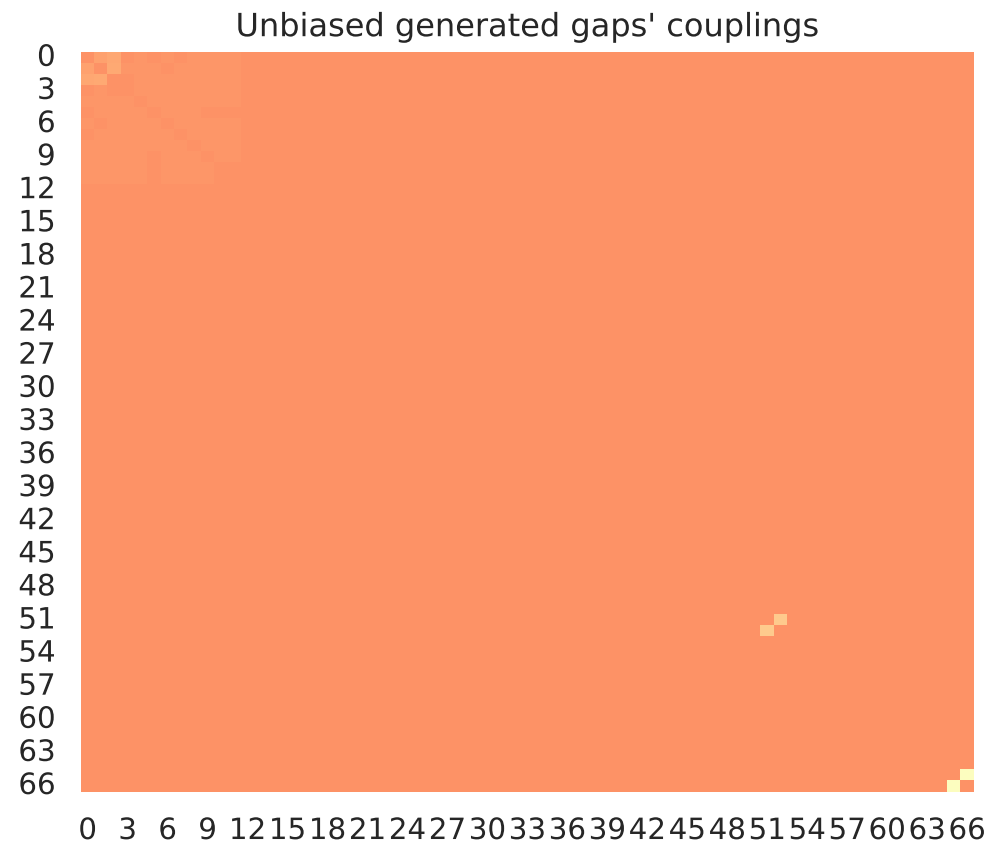
**Numeric Feature : ngaps**



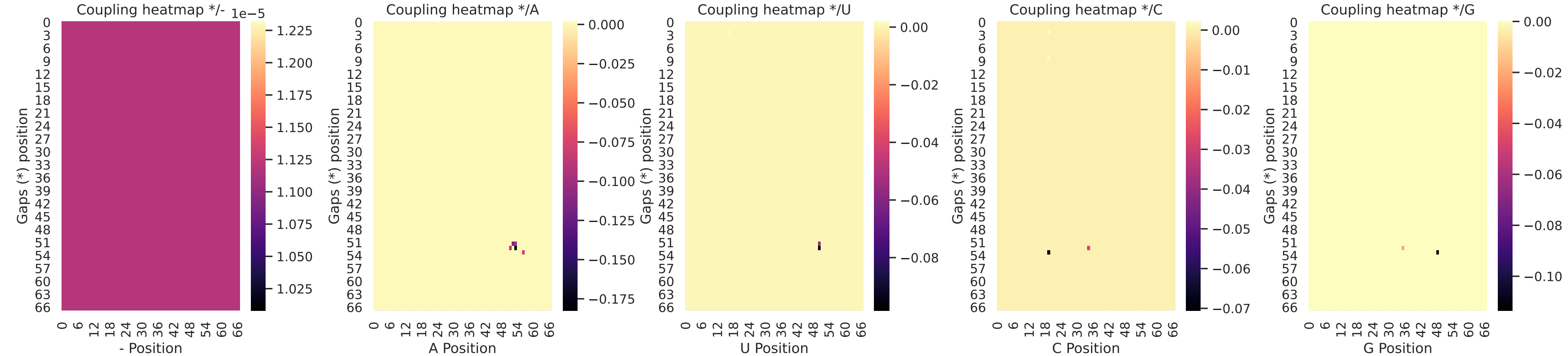
**Numeric Feature : Sequences Energy and Nucleic acid average frequency**



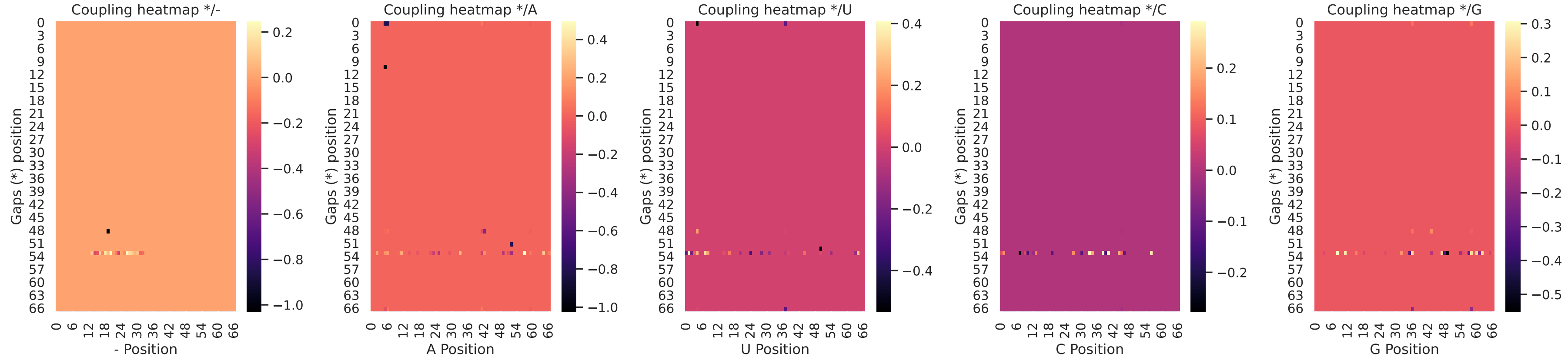
## Couplings heatmap for \*/\*



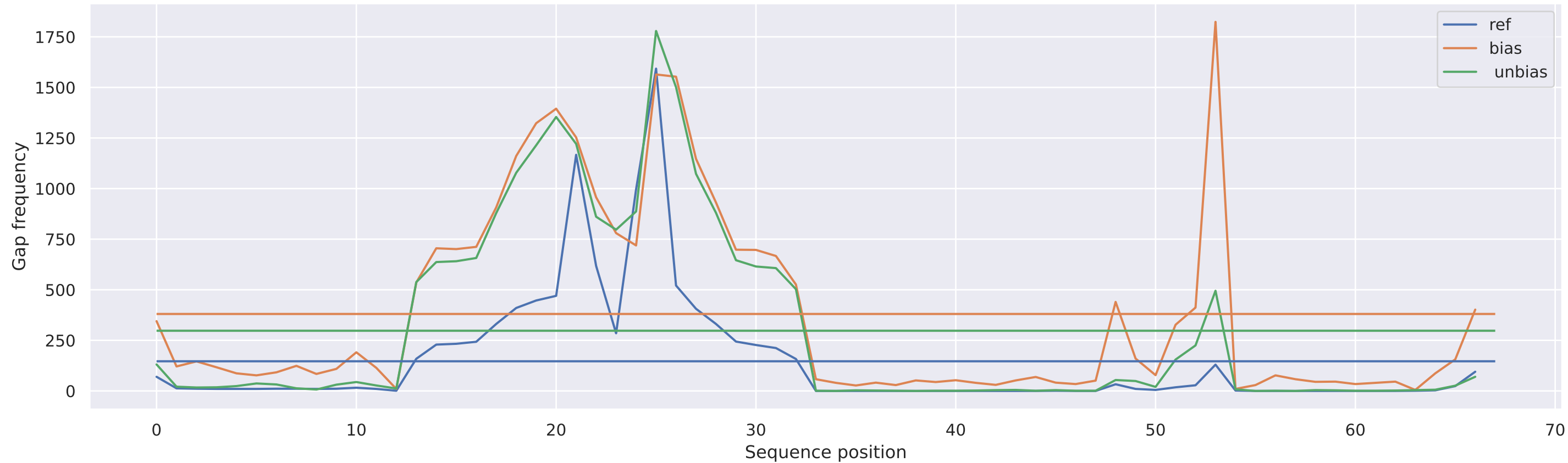
# Couplings heatmap for Unbiased

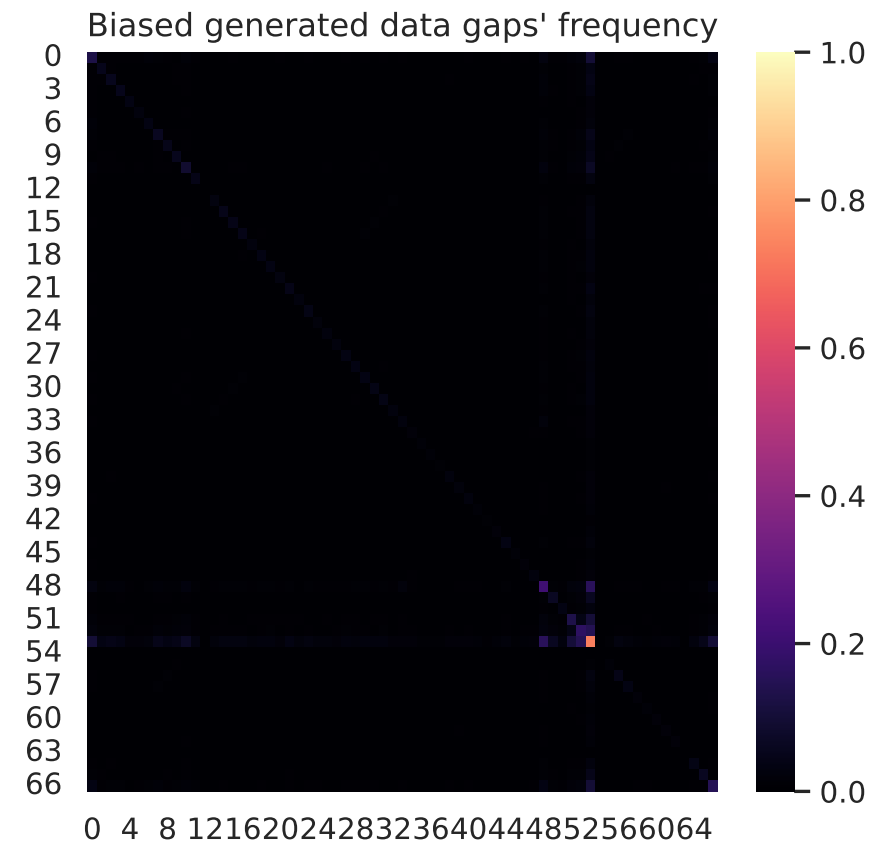
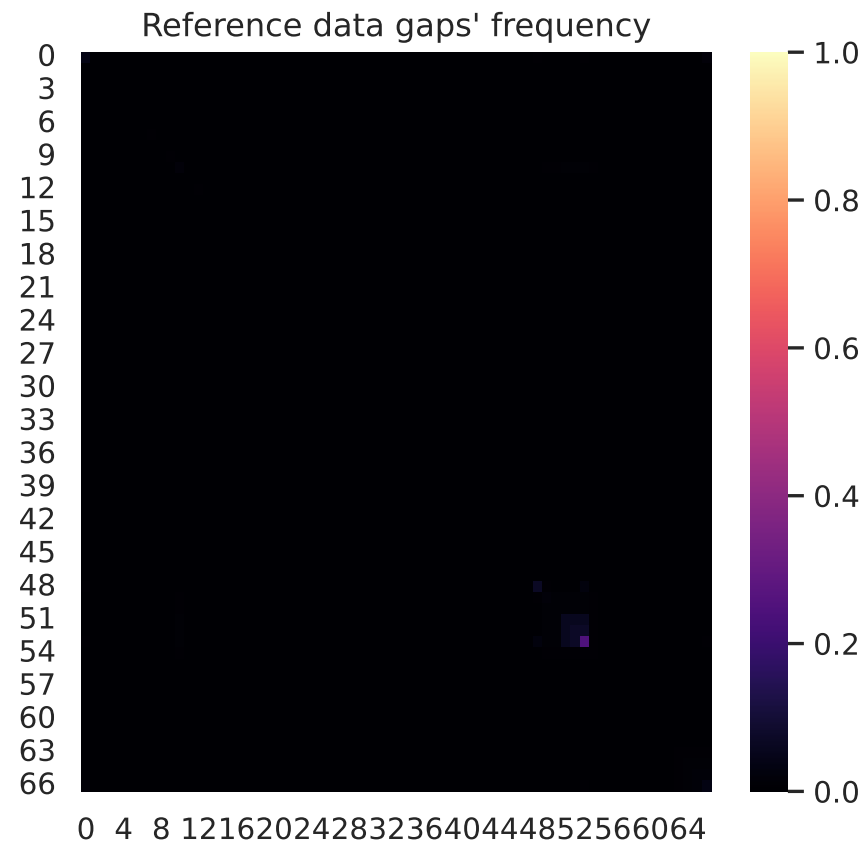
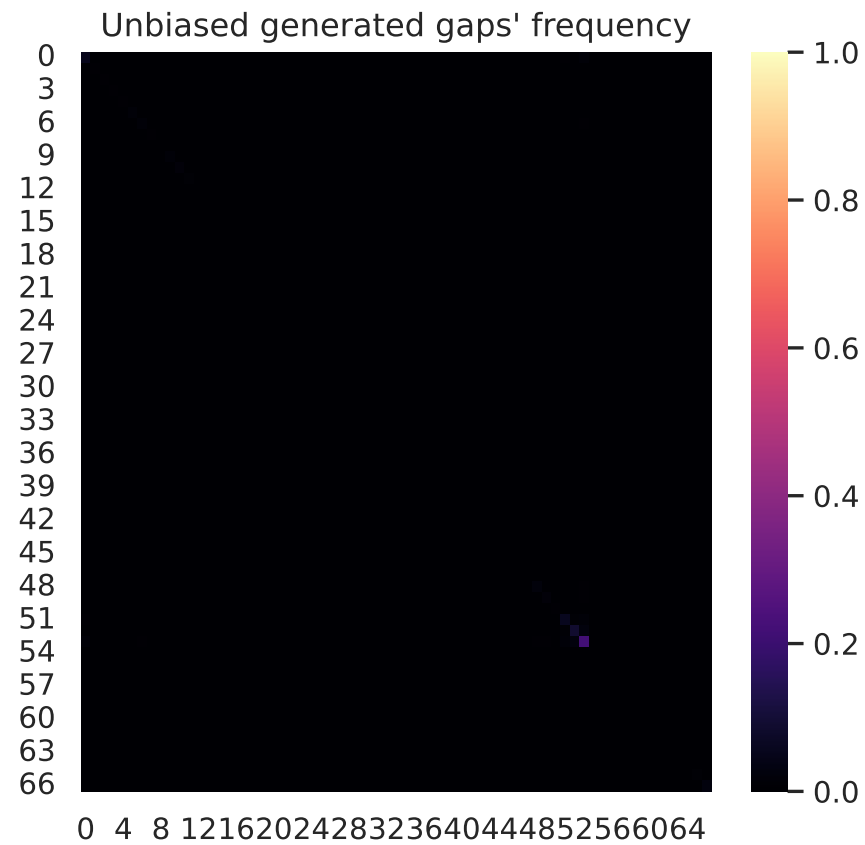


# Couplings heatmap for biased



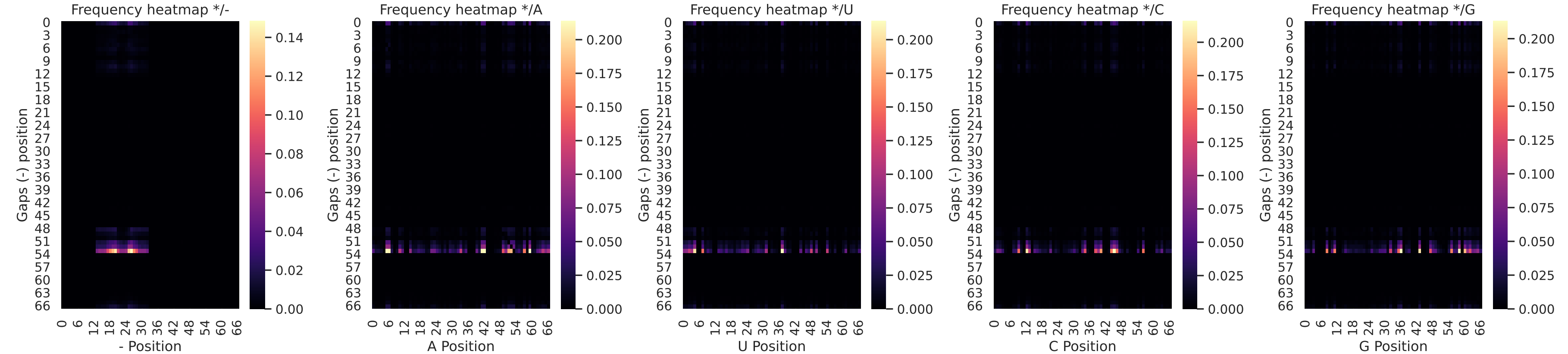
Gaps' frequency depending on position in the MSA's sequences



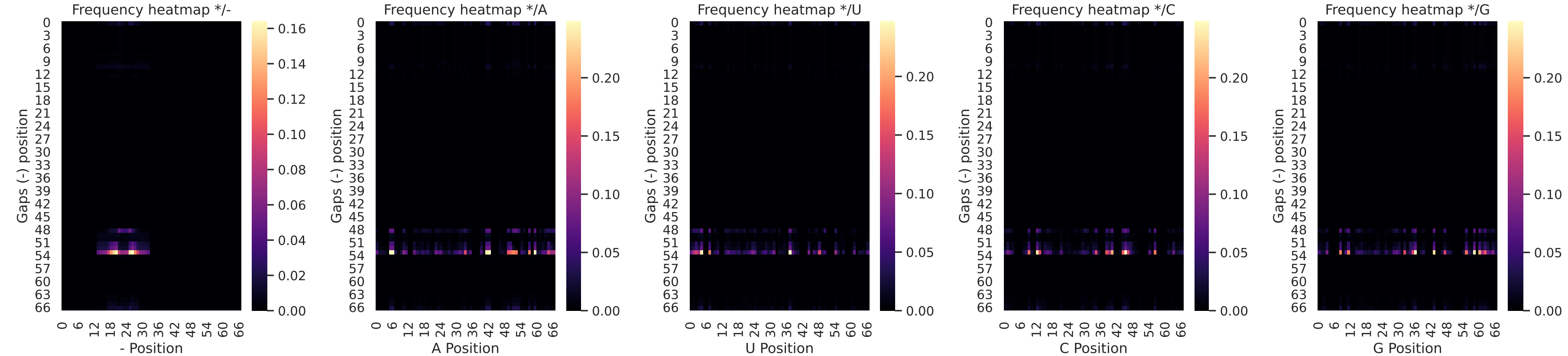




# Frequency heatmap for Unbiased



## Frequency heatmap for ref



# Frequency heatmap for biased

