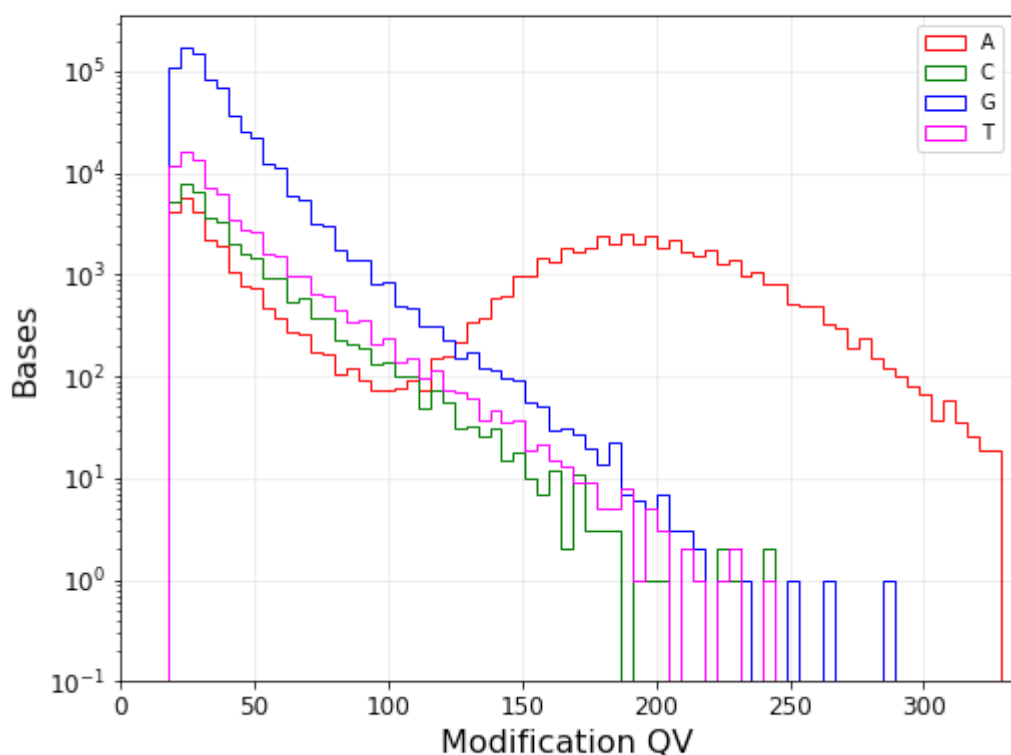


PacBio Sequel II CLR



PacBio RS II

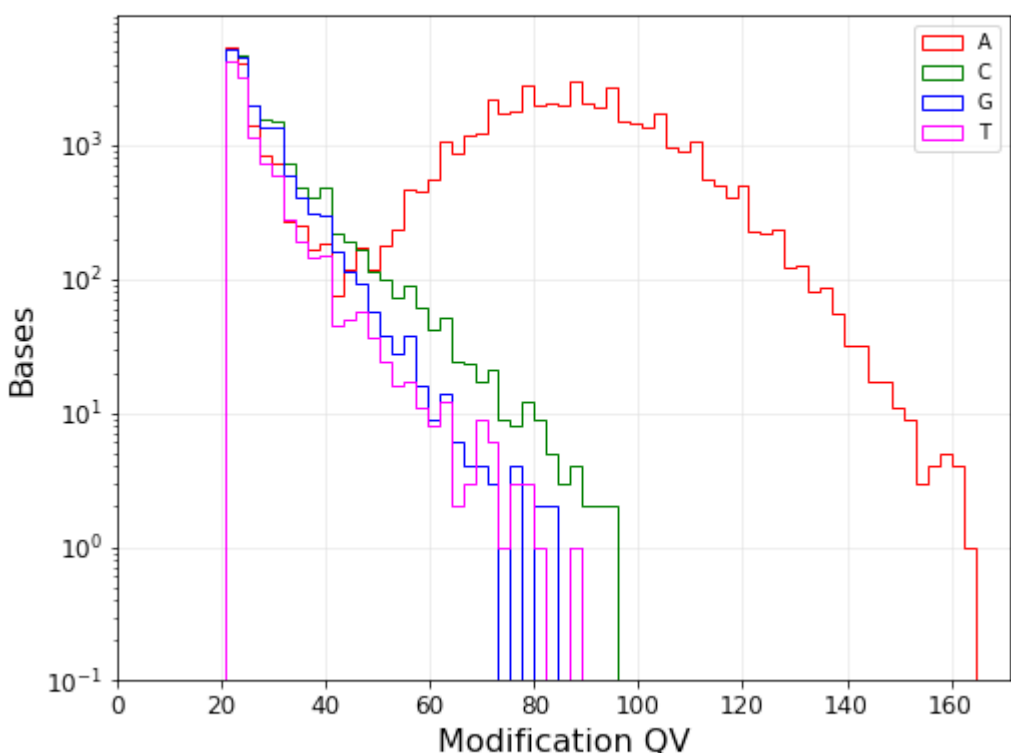


Figure S5. Distribution of modification QV values in *E. coli* PacBio libraries.

PacBio Sequel II CLR and RS II reads were processed by the SMRT Tools DNA modification pipeline, including read mapping and DNA modification detection using interpulse duration (IPD) values. Each methylated site is assigned a modification quality value (QV) score based on differences between observed and expected IPD values. Distributions of modification QV values are plotted for each of the four nucleotide bases.