

Difference in joint trimming and ligation probabilities  
(model with MH - model without MH)

0.15  
0.10  
0.05  
0.00

0 1 2 3 4 5 6 7 8 9 10 11 12 13

Number of MH nucleotides within  
trimming and ligation configuration

count

1e+00 1e+02 1e+04 1e+06

