

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

