(a)

0% 50% 100% methylated CpGs in fragment

signal

mass

16Da 16Da

NOME
1/2 METH
2/2 METH

(b)

peak	SNR
NOME	50.037
1/2 METH	47.883
2/2 METH	61.835

(c)

$$\text{MassCLEAVE} = \frac{(47.883 + 61.835)}{(50.037 + 47.883 + 61.835)} = 0.69$$

$$\text{ASF} = \frac{((0.5*47.883) + (1.0*61.835))}{(50.037 + 47.883 + 61.835)} = 0.54$$

Coolen_Supplementary_Figure_1