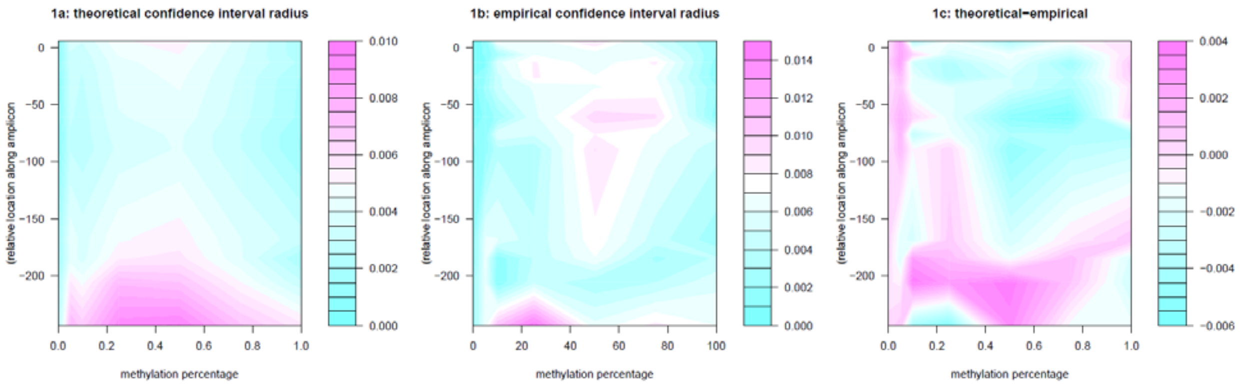

Supplemental Figure 3: Theoretical and empirical binomial model for methylation quantitation confidence interval radii of mouse methylation standards. Average empirical confidence interval radius is 0.0046, within the theoretical confidence interval radius. Average difference between the theoretical and empirical confidence interval was small, 0.00095. This model is based off the equation $\mu \pm 2\sqrt{\frac{\mu(1-\mu)}{n}}$ where μ is the methylation percentage and n is the sequencing depth.