



Supplementary figure 2. Impact of 5' RACE reaction optimisation and NGS depth on detection sensitivity of novel 5' ends by RACE-Seq. Selection of gene-specific reverse transcription primer (a, b) or sequencing depth (c, d) results in differential novel 5' end detection sensitivity. Data is expressed as novel 5' end incidence read counts (numbers) and graphed as the frequency relative to the total novel 5' ends across the entire siRNA hybridisation site for siRNA19 (a, b) and siRNA 22 (c, d), to attract the reader's attention to the lack of Gaussian distribution without log transformation of read counts as compared to Fig. 4 in the manuscript.