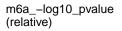
SLC10A1 + hsa-miR-29c-3p 3'UTR 2000 all\_chimeric\_reads - · allchim\_run1 - · allchim\_run2 allchim\_run3 allchim\_run4 allchim\_run5 allchim\_run6 allchim\_run7 allchim\_run8 6/6 seed match hsa-miR-29c-3p + SLC10A1 1000 (-1)\*SHAPE\_reactivity (-1)\*SHAPE\_reactivity 5/6 seed match hsa-miR-29c-3p + SLC10A1 RNAseq depth specific\_mir\_reads hsa-miR-29c-3p\_run1 hsa-miR-29c-3p\_run2 hsa-miR-29c-3p\_run3 hsa-miR-29c-3p\_run4 hsa-miR-29c-3p\_run5 hsa-miR-29c-3p\_run6 hsa-miR-29c-3p\_run7 hsa-miR-29c-3p\_run8 RNAseq\_read\_depth run2\_depth duplex\_dG -10 -15 -20



-1000

2000





1000 transcript position (all exons combined)

500

5'UTR

15

microRNA read pileup values

0

deltaG / m6a / SHAPE

-10

1500