

defining the UTRs (tan boxes)

RNA-seq (light grey)

mir-eCLIP (different colors)

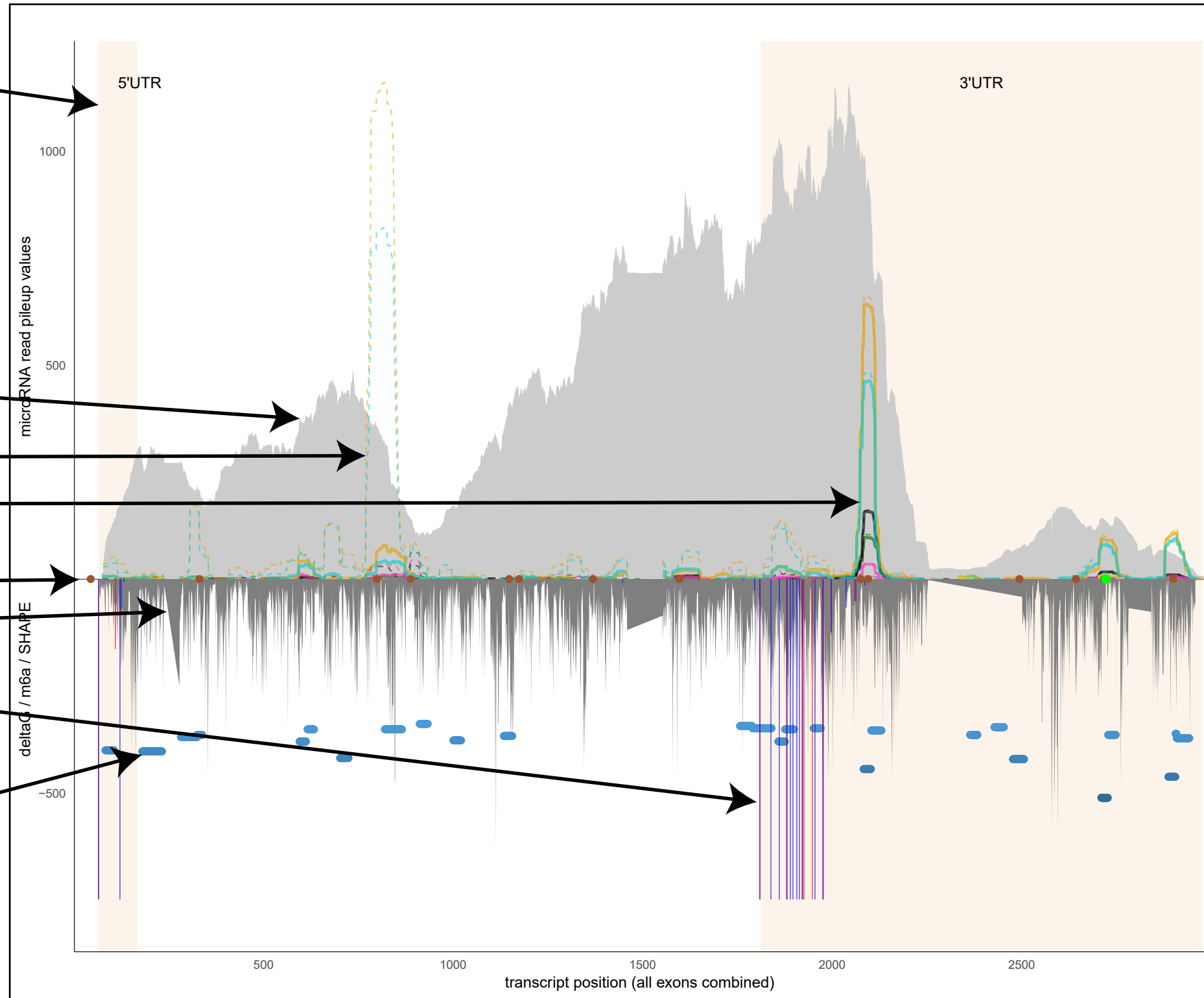
- dashed = all microRNA reads
- solid = specific microRNA reads corresponding to the selected microRNA indicated in the key

seed matching (maroon and green dots)

SHAPE (dark grey)

m6a (red and blue)

in silico folding / complementarity (blue dots)



all_chimeric_reads

- allchim_run1
- allchim_run2
- allchim_run3
- allchim_run4
- allchim_run5
- allchim_run6
- allchim_run7
- allchim_run8

(-1)*SHAPE_reactivity

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specific_mir_reads

- hsa-miR-122-5p_run1
- hsa-miR-122-5p_run2
- hsa-miR-122-5p_run3
- hsa-miR-122-5p_run4
- hsa-miR-122-5p_run5
- hsa-miR-122-5p_run6
- hsa-miR-122-5p_run7
- hsa-miR-122-5p_run8

RNAseq_read_depth

- run2_depth

6/6 seed match

- hsa-miR-122-5p + CYP3A4

duplex_dG

- -10
- -15
- -20
- -25
- -30

m6a_-log10_pvalue (relative)

- p_m6a_rep1
- p_m6a_rep2

5/6 seed match

- hsa-miR-122-5p + CYP3A4