SLCO1B1 + hsa-miR-22-3p 5'UTR 3'UTR all_chimeric_reads - · allchim_run1 - - allchim run2 allchim_run3 allchim_run4 allchim_run5 allchim_run6 allchim_run7 microRNA read pileup values allchim_run8 (-1)*SHAPE_reactivity 1000 (-1)*SHAPE_reactivity 5/6 seed match • hsa-miR-22-3p + SLCO1B1 6/6 seed match • hsa-miR-22-3p + SLCO1B1 RNAseq depth RNAseq_read_depth run2_depth duplex_dG -10 -15 0 -20 -25 deltaG / m6a / SHAPE -30 specific_mir_reads hsa-miR-22-3p_run1 hsa-miR-22-3p_run2 hsa-miR-22-3p_run3 hsa-miR-22-3p_run4 hsa-miR-22-3p_run5 hsa-miR-22-3p_run6 hsa-miR-22-3p_run7 hsa-miR-22-3p_run8 m6a_-log10_pvalue (relative) -5 -1000p_m6a_rep1 p_m6a_rep2 1500 500 1000 2000 2500 transcript position (all exons combined)