

Supplementary Table 10: The top 10 methylation stoichiometry hypomethylated multi nucleotide m6A site between NPRA<sup>-/-</sup> vs NPRA<sup>+/+</sup>.

Trans ID	Fold change	P value	Gene Symbol	m6A motif Sequence	Transcript Sequence
NM_00117 7412	0.665938403	0.038683178	Usp35	GGACA;GAACA	1..2028 gggaaGGAGAAGGAGGTGGCAGAGGACAGGGAAGAGGAAGGAACAAGGGAAGA GGAGAAAGAAGAggggg 2099..3982
NM_03200 0	0.663517296	0.038668649	Trps1	AGACA	1..3879 tcaatCTGCCTCCTCATTCTCAGCTGTTGGATCAGACAATGACATTCCTCTAGATT TGGCGATCaagca 3950..10202
NM_00108 1117	0.663268282	0.04725004	Mki67	GAACA;GAACA	1..3791 gaattCATCAGGGAGTAAGAGAAGGTCACGAACATCTAAGAACAAGGCTCAGCCC CTAGAAGACCTggat 3862..10075
NM_00131 6753	0.66087263	0.048147267	Hmgxb4	AGACA;AGACA;AGACA	1..1421 acacGGGAGAAGAAAAAGAAAAGGGAAGACAAGACAGAGACAGAGAGAGGG GAGAAAAGCCGAaaaag 1492..4018
NM_02899 3	0.658784574	0.017666442	Mau2	GAACA	1..2091 tggccTAATCTGTGTCTGGGTGTCACCTGAGAAACAAGGGTGACAATGTGTGTA GGGGCATCATctgag 2162..5369
NM_02953 2	0.658685801	0.003899557	Snrnp35	GGACA;GGACA	1..772 gagggAGTTCAGGGAGGAGAGGGTCAAAAGCCGGACAAGAGGGACAGAAGTA AGTAGAGGCAGCagcag 843..1092
NM_15289 5	0.658017255	0.043819971	Kdm5b	GGACA;GGACA	1..4463 aagaaGAAAATCAAAGTCTGAGTCACCCCAAGGACATGGACAGTTTCAAGTTAGAAA GAGAGCGTAGctatg 4534..6300
NM_17892 3	0.657324708	0.031574943	Scaf4	GGACA;AGACA	1..3799 tggaaGAGAGAAGTAGACGCTCTAGTGGGCATCGGGACAGAGACAGGGATTCTA

					GAGATAGAGAGtcccg 3870..4448
NM_03239 3	0.656491231	0.023330276	Map1a	GAACA;GGACA;GAACA	1..4863 catcaGAAGGACGAGGCTCTAGATGAAGAGAA <u>CA</u> AGCCTGGAGG <u>CA</u> CAGCAGGAT AAGACTTCAG <u>A</u> acagaaag 4937..11823
NM_00104 5807	0.653115859	0.035249095	Rbm15	GGACA;GGACA	1..2047 ggatcGAAGGAGGGATGGCTGGTCACTGG <u>CA</u> GG <u>CA</u> GAGGTGATCGGGACTT GCCCAGCAGCAgggac 2118..3270