

Supplementary Table 5: The top 10 m6A site abundance hypomethylated multi nucleotide m6A site between NPRA^{-/-} vs NPRA^{+/+}.

Trans ID	Fold change	P value	Gene Symbol	m6A motif Sequence	Transcript Sequence
NM_011567	0.663165532	0.040496124	Tead4	GGACA;GGACA	1..1850 tgagaGACTTGGAGAGCAATGGTAGGGGGG <u>G</u> CAAGTCCAGG <u>A</u> CATGGGGACCTGGGAGGGGACCTtcagg 1921..3076
NM_178065	0.66161237	0.040059418	Are11	GGACA	1..3081 cctgcTTGGCTCCCAAGCTCTCTAGAGCATCTGG <u>A</u> CACATGTTAACAAGCATAGCCACTGACCTTaaacca 3152..5404
NM_001160400	0.660570376	0.036890548	Megf8	GGACA	1..7604 tgtttGGCGTCCAACCCAAGTTCACCAATGTGG <u>A</u> CATTTCGCCTGACACTAGACGTGACCTTCGGCgctgt 7675..10040
NM_009621	0.658691095	0.032453887	Adamts1	AGACA;GGACA	1..3019 tcaggTTGGCAGAGAAGAGTAGTGCACTGCAGAG <u>A</u> CATTAACGG <u>A</u> CACCCTGCTTCCGAATGTGCaagg 3090..4883
NM_026183	0.65132725	0.021203393	Slc47a1	AGACA;AAACA	1..1915 tctctCTTTGGGTGTGTGTTTGGAGAGAGACAGAGAGAGGGAG <u>A</u> CACCCCCCAAGAGATATAAA <u>A</u> Cagaaag 1987..2634
NM_001048250	0.649230673	0.034245272	Smim15	AAACA;AAACA	1..325 agccaGAGAGAAGGAGCAAAAGAAGAA <u>A</u> CAAAACGGCAAGAAA <u>A</u> CATCGCAAAAGCTAAACGACtaaag 396..1864
NM_011997	0.648794555	0.04380147	Casp8ap2	GGACA;AGACA	1..2410 tctgaAGATGCCAGCCAAGAATTGG <u>A</u> CACCAAAAG <u>A</u> CACGATGGTATAAATGCTTGCTATTTTcgaag 2481..6813
NM_001168253	0.647342273	0.045259656	Fam83h	AGACA;GGACA	1..1768 gggccAGCGTTTTCCATGCCAAGCAACCTTGAG <u>A</u> CAAGGCCTGG <u>A</u> CACCGCTTCGAGGCAGAACctgag 1839..4535

NM_010518	0.646602254	0.047226865	Igfbp5	GGACA;GGACA	1..3745 gcacaGAAAGGGATGCCTCCTGTTGCCTGGACAGGACAGTTGGCTGGGAA GGAAAGAGAAAATTGatctt 3816..5854
NM_001033173	0.642819	0.038690112	Usp31	AGACA	1..3428 ccggaGCTTGAGTAGAGAAGGCTCCAGACAAGCTTAGGCTCTGACAGAG CCAGCGTCACCTCCAacctcc 3499..10198