

Supplementary Table 4: The top 10 m6A site abundance hypermethylated multi nucleotide m6A site between NPRA^{-/-} vs NPRA^{+/+}.

Trans ID	Fold change	P value	Gene Symbol	m6A motif Sequence	transcript_Sequence
NM_001347445	2.849791118	0.001282253	Med13l	GGACA;GAACA	1..3840 gacttATGACCGTGTGCAGGCAGATAACAATGATTACTGGACAGAGT GCTTCAACGCATTGGAACagggga 3912..9322
NM_133218	2.182766399	0.007543886	Zfp704	AGACA;GAACA	1..7973 gaggcTTCCTTCCAGAGACTGTGTGCGCATTAGACACTTTAGAACA GCTGGAAAAGGACTGCAGatgtt 8044..13844
NM_001363439	2.165332147	5.24077E-05	Sirt7	GAACA	1..1377 gaagaAAGTGGCATAGCCCGGAGTTGACAAAAGACAGTTGGCACTTT GCAGATGGCTTGACCCTTgttca 1448..1870
NM_001081278	2.152381387	0.024453912	Tbc1d4	AGACA;GAACA	1..4318 ggaacAAGATAAAATGGCATATCAAAAAGACAGTGGAACAGATCCGG AAGCTGCTACCAGCAGATGcgctg 4389..6641
NM_001024926	2.108666634	0.043858803	Cyb5d2	TGACA;TGACA	1..1345 ggtaaTTGACTGAGCTCTTAACCTCTGACATTTGTGACATTTCTAAAA CCTCTACTCCAGGGCAAactga 1416..2376
NM_001081300	2.074368061	0.013428668	Tshz1	AGACA	1..4887 aacgaGCTATTATATGCAGGACTGGTTTGTGACAAGACATGCATGCA GCGGTTGGAGACGAAAGctgtc 4958..5717
NM_025862	1.998524368	0.011954037	Acad8	AGACA;GAACA	1..1420 tgageTGTCAGCCACGCTGCTGGTTCTGAGACAAGAACAGAGTTCTT AGCAGAGCTAGAAGGGCTgctct 1491..2864
NR_030711	1.98227468	0.019210282	Mir22hg	TAACA;AAACA	1..737 cagcaAATTCAAAAAGAGATTCAAATGTGTAACACTGTGGGAAAACA TATCTATGACTGGGGTTGtagct 808..1766

NM_027276	1.968573842	0.024412785	Cdc16	AGACA;AGACA	1..1734 ggattCGGAAGCTTATATCGGAGCAG <u>AC</u> ATTAAAG <u>ACA</u> AAATTAAGT GCTATGACTTCGATGTGCataca 1805..2334
NM_001081267	1.949281992	0.042492085	RsfI	GAACA;GGACA	1..1590 gtcagAAAGCAAGGTTAGAGGAGCCTGGGCTTCTGA <u>AC</u> ATGG <u>AC</u> ATG CCTCTCGAACCTTCTGAGaaagc 1661..11129