

Supplementary Table 7: The top 10 m6A site abundance hypomethylated single 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_001347491	0.665489941	0.006871362	Zscan26	AGACA	1..974 gttctGTTGCTGCTGACCATCAGGAAATCTCTAAAG <u>ACA</u> AAAGGTCATCCCTGC CAAGAGTGTGGGaaagt 1045..4362
NM_001355075	0.664545856	0.036500643	Ext2	GGACA	1..2565 actctGTGAAAATGCCAAAGGAAGGAAGCCTCAGGG <u>AC</u> AGGCTGCAACTTG GAGCCCAGCGCATCactct 2636..2943
NM_024452	0.664243345	0.044640765	Luzp1	GAACA	1..3177 atgttCAGAAGACCCCCGACTGGAATAGGTAGGA <u>ACA</u> TGGAAGCTACTAAC GCCTATACGCAGAggcc 3248..7529
NM_175331	0.663609178	0.033183306	Nt5dc3	GGACA	1..2023 gagacCTCTTGATGGCTGCCTGTGTTCCGTAGGTGGAGAGTGG <u>ACA</u> CTTCTT GATTCTGTGAGACattc 2094..5952
NM_133978	0.663125176	0.012930618	Cmtm7	AGACA	1..883 gcacaGTAGAGAGACTTGTGGATCTGCCTGCATAG <u>ACA</u> CGCCTTCTTCATA CCCTCAGGACCGAgacca 954..1137
NM_172739	0.663121888	0.019265021	Arhgap35	GGACA	1..4274 aagaaAGAGGAGGACCAGGCATCCCAAGGTTATAAAGGG <u>ACA</u> ATGCTGTC ATTCCATATGAAACagatg 4345..8393
NM_033320	0.663011245	0.045900854	Glee	TAACA	1..3817 gacgtGAGGGAGGATGCCTCTGTGTCCTGGGGGTA <u>ACA</u> AAATGAGACTCTG GGTGTGCAGGAATtctgc 3888..4625
NM_001364556	0.662351757	0.036141824	C87436	GAACA	1..546 cataaCAGACCTTGTCTCAAAAAGAAAAG <u>ACA</u> AACTGGGCTGCCAAGAGC TCTACCTAGAGGAGttgga 617..3004

NM_001168525	0.662341543	0.029579154	Sgms1	GAACA	1..1090 caaggAGGGATAGTGTCTGCCCTGTACGAACAAGTGACTGCTGACGTCTGAG AGCAAGCTGGGGGtactg 1161..4039
NM_001346801	0.661750593	0.025409269	Pprc1	AGACA	1..2247 tcagcGAAGGCAGCAACGGCAAACGGAAGCAGAGAACAAGGAATTCTCAGCC CCCAGTTGTTGGCAagtgg 2318..5250