

Supplementary Table 9: The 7 methylation stoichiometry hypermethylated 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_001025296	1.966109592	0.031204023	Dffa	GGACA;AGACA	1..916 gccctGGCTGTCGCTCTGAGCTGG <u>A</u> CA TAAGGAAGGCAGAG <u>A</u> CAGTCCAGCAGG CCTGCACCACgggagc 987..2467
NM_001025432	1.724472792	0.015923966	Crebbp	GGACA;GAACA	1..7345 accatGGCCAGCTCCATGGATCAGGG <u>A</u> CACCTGGGGAACCCTGA <u>A</u> CAGAGTGCAA TGCTCCCCCAgctga 7416..7507
NM_025862	1.792592057	0.020649672	Acad8	AGACA;GAACA	1..1420 tgagcTGTCAGCCACGCTGCTGGTTCTGAG <u>A</u> CAAGA <u>A</u> CAGAGTTCTTAGCAGAGC TAGAAGGGCTgctct 1491..2864
NM_001290484	1.686158604	0.030192482	Gtf3c5	GGACA;GGACA	1..1888 aggacATGCTGGCGAGTCATGATGG <u>A</u> CAGTTGGG <u>A</u> CAGGCTTGTGCCCCATCC AGGCAGTGAGatgag 1959..2823
NM_001358593	1.511629805	0.039840383	Lifr	AAACA	1..3931 caaggGAGAAAACCTTCCCAAGTCAA <u>A</u> CAGCGTTAATTTGCCTGACATTTACTGC GGTCTAGAGGagaac 4002..9876
NM_001363439	1.525933753	0.002115092	Sirt7	GAACA	1..1377 gaagaAAGTGGCATAGCCCGGAGTTGACAAA <u>A</u> CAGATTGGCACTTTGCAGATGG CTTGACCCTTgttca 1448..1870
NM_010444	1.966580515	0.006814971	Nr4a1	GGACA;GGACA	1..1877 ttggtACCCCCTCCACCTATTGTGG <u>A</u> CAAGATCTTTATGG <u>A</u> CACATTGTCTTTCTGA CCCCTGCCctgaa 1948..2476