

Supplementary Table 3: The 8 m6A site abundance hypomethylated m6A cluster between NPRA^{-/-} vs NPRA^{+/+}.

Trans ID	Fold change	P value	Peak Sequence	Gene Symbol	m6A motif Sequence
NM_0012 94279	0.402086081	0.001293019	1..4251 gcgcctcccagcatcccctcaccctcactcctcctgcctatcttggACTAAGAGAAAGAGCAGGGACTGT CTGAGGACAGCCGCGTTCTGTACCAA AA CAAGAGACAGAGACAGGAACAGAA CAAAACCACAAAAC T AAAACAACCCACAGGTGTATGTTGCTGCAAAA CCTTCAGACCCAGGGGTCTGGA ct gtgtactgtatatcttagtaaggaatagagaattggctctgtatg 4506..7609	Zfp827	GGACA
NM_0013 55499	0.57499309	0.04486493	1..1171 gattcctcgatcctatacaccacaacggagcatcccagccaacaaaACTGTCCACAACGTTGCCAGAGA TAGAATATCGAGAAAAAGGGAAAGAGAAGG CA AGGATGCCAAGAA C ACAA CCTTGGAATAAA T AACAACATTCTACAACCTGTAGACTCTAAGATACAAGA GATTGAGTATATGGAA AA ACCATATCAATAGTAAAAGATTAA CA ATGATCTTGT GGGAAGTACAGAAAATCTCTTAAAAGA GGA ctcatgcactgctcctcaaaaattacaaaatgccagt ggagttgtga 1485..4092	Maco1	GGACA;AAACA;TAACA; GGACA;AAACA;TAACA
NM_0013 57952	0.514332853	0.038567165	1..2865 gcagcaagatgggacaacggagacagcagcaaaagcactgagacaagtACTTTGAAAATATTGAATCCC CTCTCAATGAGAGGGGCTCTTCCACCTCTGTGGATAATCGAGA ACTTGA ACAGC ACATTCAGACTTCTGACCCAGAA ACTTTC AGTCTGAGGAACGCTCGGACTCAG ATGTGAATAA TG ACCGGAGTACAAGTTCGGTAGACA GTGATATTCTTAGCTCCA GTCACAGCAGTGACACTTTGTGCAATGCAGACAGCGCTCAGATTCTCTGGCCA ATGGACTTGACTCTCACAGTATCACAAGTAGTAGAAGAACTAAAGCAAACGAGG GGAAAAAGGAGACCTGG CA CAGCTGAAGAAGACTCTGGGA ct gacagtgaatatgacg agagtggaagagcagggggacatgcagtac 3299..5600	Usp47	GGACA

NM_0013 60003	0.536567779	0.016043736	1..3637 tccagactctgtttgaaatgtcgggtatcaaagtagaaggaaaaagagagACAGAAAAAGATCTCAGAAGAA AAAAAATAAGTCTTTGGACCCGAAGAAATCACCCAGGTTTCAGAGCGGACTGC TAATAATAATGTGTGTATTGATCGAGGAAAAAGTGC GGAGGGGGGAGGGGCGG TGTGAAAAATGGCAGAAGGACCAGAGCCTTGCAAGCCACAGActtggccactttactctgctt aagttctctggtcttgagtacgtggcatt 3911..4168	Ppp2r2c	AGACA
NM_0073 96	0.620338065	0.014993512	1..2126 cattactacagaggacattgtaacagtggtcacaatggtgacaaatgtgACTTTCCTCCCAAAGAATCTAGTC TATGATGGTGGCACCGTCTGTACACACTGAGGACTGGGACTCTGAACTGGAGCT GCTAAGCTAAGGAAAGTGCTTAGTTGATTTTCTGTGTGAAATGAGTAGGATGCCT CCAGGACATGTACGCAAGCAGCCCTTGTGGAAAGCATGGATCTGGGAGATGGA TCTGGGAACTTACTGCATCGTCTGCAGCACAGATATGAAGAGGAGTCTAAGGG AAAAGCTGCAACTGTAAAGAAActtctgaaaatgtactegaagaatgtggccctctccaatcaaggatctt 2490..5681	Acvr2a	GGACA
NM_0137 20	0.542535064	0.016826099	1..6591 tctaactcacaggcagaggccaagaaggattgtgaagattctctgggaaaggACAGTCTTAGAGAGAGATGGA GAAACACCTAAAGGGCCCTTAACTCAGAAGTACATTGGAATTCACAGAACT TTAACAAAGAGGCAAACGTTTCAGTTCTTTACAGAAATGAAGCCATGTCAAGAAA ATTCTGAACAAGGATATCTCTGAATTACTTGAAAAAGTGAAActttagagagtgtggagttc taaaaactgaggatggttctggagtggc 6865..13931	Mga	GGACA
NM_1770 77	0.463373718	0.002624413	1..4124 gaatacacaaaacttactagccagcagagagcccaggcctgtggaagagaagACAAGGAGATCTCTCGAAGCC CTCAGTCTGTGACCAGTGAGAAGTACTCCACAACCTGACTGACTGAGAAGGA AGGAAAGGCCCTTTCTTACCAGGGCTTGTACAGCCTTCAGTGTAGAGAGTGGGC TGTCAACACATTTGTCCTTTGGGGAActtttaatcactccatctgtgctgtctagtggccactctgtccc 4381..5440	Exoc6b	AGACA

NR_1564 45	0.321254734	0.000264501	1..530 aacatcaagaaccaaccaccaactgaagaaaggcagtcgtttggaaagACATTA <u>ACTCTGA</u> ACACAGAC TTTGTTTCATTAAGACAAGTTCCTATAAATATGATTTATATGAAAAAACTTTGA AGTACAATTCAGACTTACTTAGCAGTAGAACTGTGTAAGAAAGAAAGGAGACG GGTGTGGTGGATTTGGGGAACCACTTCTGTACCTGAAGCAAGAGAAACCCACG CTGGActggaatactcagaatataatggaacggaaggctctcagccataagga 822..1981	Zfp1	AGACA;GAACA
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