

Supplementary Table 8: The 9 methylation stoichiometry hypomethylated m6A cluster between NPRA^{-/-} vs NPRA^{+/+}.

Trans ID	Fold change	P value	Peak Sequence	Gene Symbol	m6A motif Sequence
NM_001167885	0.650388735	0.025836871	1..3101 caagcgggatgaggagagcagggggccatgtgcagaggcctgcacgagaACGGGGTGTGCTGCAGCGACCC CCTCTCCCTGCTCGAGTCCCAGATGGAGGTGGACGACTACAGTCAATATGAGGAG GACAGCACAGATGAATCCTCATCTTCTGAGGGGGAGGAGGAGGAGGAGGACTGC GAGGATGACTTCGATGATGACTTCATTCCTTCTCCTCCGGCAAAGCGGCTGAGGCT AATTGTTGGTAAAGACTCCATAGATATTGACATTTCTTCAAGGAGAAGAGAAGAT CAGTCTCTAAGACTGAACGCATGAGCGCTCACTCATTGTTCTGGAGAActaaaaagtaaaa atcccgccacagctcttggcacagcacttctgtggt 3492..6131	Kmt5b	TGACA
NM_001294279	0.404397682	0.001820777	1..4251 g'gcctcccagcatcccctcaccacaactccttgcctatcttggACTAAGAGAAAGAGCAGGGACTGTC TGAGGACAGCCCGCTTCTGTACCAAACCAAGAGACAGAGACAGGAACAGACA AAAACCACAAAACCTTAAACACAACCCACAGCAGGTGTATGTTGCTGCAAAACCT TCAGACCCAGGGTCTGGAccatgtgtactgtatatcttagtaaggaatagagaattggctctgtatg 4506..7609	Zfp827	GGACA
NM_001355499	0.370126275	0.004301819	1..1171 gattcctcgatccttatacaccacaacggaggcatcccagccaacaaaACTGTCCACAACGTTGCCAGAGAT AGAATATCGAGAAAAAGGGAAAGAGAAGGACAAGGATGCCAAGAAACACAACCT TGGAATAAAATAACAACATTCTACAACCTGTAGACTCTAAGATACAAGAGATT GAGTATATGGAACCATATCAATAGTAAAAGATTAAACAATGATCTTGTGGAA GTACAGAAAATCTCTTAAAGAGGActcatgctgcttctcaaaaaattacaaaaatgccagtggagttgtga 1485..4092	Maco1	GGACA;AA ACA;TAAC A;GGACA; AAACA;TA ACA
NM_001357952	0.519187126	0.01448799	1..2865 gcagcaagatggggacaacggagacagcagcaaaagcactgagacaagtACTTTGAAAATATTGAATCCCCCT	Usp47	GGACA

			CTCAATGAGAGGGGCTCTCCACCTCTGTGGATAATCGAGAACTTGAACAGCACA TTCAGACTTCTGACCCAGAAAACCTTCAGTCTGAGGAACGCTCGGACTCAGATGTG AATAATGACCGGAGTACAAGTTCGGTAGACAGTGATATTCTTAGCTCCAGTCACA GCAGTGACACTTTGTGCAATGCAGACAGCGCTCAGATTCTCTGGCCAATGGACTT GACTCTCACAGTATCACAAAGTAGTAGAAGAACTAAAGCAAACGAGGGGAAAAAG GAGACCTGGACACAGCTGAAGAAGACTCTGGActgacagtgaatatgacgagagtggcaagagca ggggggacatgcagtac 3299..5600		
NM_001360886	0.498890549	0.015777075	1..2279 cagcatcagcgaattcatacgggagagaagccttataagtgcagtgaatgtACAATGCTTTACCGGGAGCGTG CACCTGACTGAACA TCGGAGTACTCACACTGGAGAGAAACC TTACA ACTCTGAGT GCCACAGACTTTCAGCCAGAGCACATACTCAGCATCAGAAGATTCATTCA GGAGAGAAGCTTTTGGGGTGTGAGGActgtgaaaaagcctccagtgtcactctgctctcaccacaccagag at 2542..2847	Zfp184	TGACA
NM_007396	0.581639801	0.003036387	1..2126 cattactacagggacattgtaacagtggtcacaatgggacaaatgtACTTTCCTCCCAAAGAATCTAGTCTA TGATGGTGGCACCGTCTGTACACACTGAGGACTGGGACTCTGAACTGGAGCTGCT AAGCTAAGGAAAGTGCTTAGTTGATTTTCTGTGTGAAATGAGTAGGATGCCTCCAG GACTGTACGCAAGCAGCCCCTTGTGGAAAGCATGGATCTGGGAGATGGATCTGG GAACTTACTGCATCGTCTGCAGCACAGATATGAAGAGGAGTCTAAGGGAAAAGC TGCAAACTGTAAAGAActctgaaaatgtactgaagaatgtggccctctcaaatcaaggatctt 2490..5681	Acvr2a	GGACA
NM_013720	0.472459284	0.003682577	1..6591 tctaactcacaggcagagccaagaagattgtgaagattctctggggaaggACTCTTAGAGAGAGATGGAG AAAACA CTTAAAGGGCCCTTAACTCAGAAGTACATTGGAATTTACAGAACTT AACAAAGAGGCAAACGTTTCAGTTCTTTACAGAAATGAAGCCATGTCAAGAAAATT CTGAACAGGATATCTCTGAATTACTTGAAAAAGTGGAAActattgagagtggagggttctaaaaa ctgaggatggttctggagtggc 6865..13931	Mga	GGACA

NM_019825	0.612947074	0.015636855	1..5565 tctgccaatcgtcgaagcccagtcctccagtaagggcaaaggaaaagtggACA AA ATTGGCCAGATTTTGCTG ACCAAGGCTTGTAAAGAAAGTTACAGGCTCTCTGGAGAAAGGGGAAGAACAATATG GTGCAGATGGAGAGACTGAAGGCCAGGGCTAGAGATCACAACCTCTGGGCTAAT GGGAACAGAGCAGTGCTCCACAGAGCTGGA ca gtaaaacccaacacccctcagcaccactctactaaaa atgaccteta 5831..6872	Ncoa6	GGACA;GA ACA
NR_156445	0.535503518	0.008561465	1..530 aacatcaagaaccaaccaccaactgaagaaagaggcagtcgttttgaaagACATTA ACTCTGA ACACAGACTT TGTTTCATTAAGACAAGTTCCTATAAATATGATTTATATGAAA AACTTTGA AGT ACAATTCAGACTTACTTAGCAGTAGAACTGTGTAAGAAAGAAAGGAGACGGGTG TGGTGGATTTGGGGA ACC ACTTCTGTACCTGAAGCAAGAGAA ACC CCACGCTGGA ctggaatactcagaatataatggaaacggaagggtctcagccataagga 822..1981	Zfp1	AGACA;GA ACA