Gene	**WT**	**R6/2**	**pValue**
ALKBH1	1 ± 0.08	1.27 ± 0.08	0.0027
ALKBH2	1 ± 0.2	1.4 ± 0.16	0.0237
ALKBH4	1 ± 0.63	2.73 ± 0.88	0.0213
ALKBH5	1 ± 0.2	1.42 ± 0.19	0.0217
ALKBH6	1 ± 0.08	1.05 ± 0.18	0.6349
CBLL1	1 ± 0.11	0.9 ± 0.15	0.3267
EIF3A	1 ± 0.07	1.18 ± 0.25	0.2382
FMRP	1 ± 0.05	1.02 ± 0.22	0.8489
FTO	1 ± 0.08	0.94 ± 0.11	0.4012
HNRG	1 ± 0.05	1.27 ± 0.14	0.024
HNRNPA	1 ± 0.06	1.18 ± 0.04	0.004
HNRNPC	1 ± 0.11	1.27 ± 0.21	0.072
IGF2BP1	1 ± 0.52	1.96 ± 0.79	0.0976
IGF2BP2	1 ± 0.38	1.23 ± 0.2	0.3408
IGF2BP3	1 ± 0.8	6.91 ± 1.29	0.0006
KIAA1429	1 ± 0.16	1.48 ± 0.16	0.0051
METTL1	1 ± 0.12	1.96 ± 0.46	0.021
METTL14	1 ± 1	0.75 ± 0.36	0.6657
METTL15	1 ± 0.05	1.42 ± 0.09	0.0007
METTL16	1 ± 0.09	1.49 ± 0.24	0.0194
METTL17	1 ± 0.19	0.96 ± 0.18	0.7415
METTL19	1 ± 0.14	1.27 ± 0.1	0.0237
METTL2	1 ± 0.1	1.61 ± 0.25	0.0101
METTL25	1 ± 0.17	1.2 ± 0.12	0.1042
METTL25B	1 ± 0.11	1.77 ± 0.27	0.0063
METTL26	1 ± 0.17	1.28 ± 0.11	0.0411
METTL27	1 ± 0.19	1.15 ± 0.08	0.2102
METTL3	1 ± 0.14	1.05 ± 0.19	0.6607
METTL4	1 ± 0.22	1.26 ± 0.18	0.1136
METTL5	1 ± 0.2	1.14 ± 0.22	0.3797
METTL6	1 ± 0.16	0.81 ± 0.03	0.097
METTL7A	1 ± 0.15	1.27 ± 0.15	0.0458
METTL8	1 ± 0.19	1.05 ± 0.07	0.6415
RBM15	1 ± 0.09	1.28 ± 0.13	0.0133
VIRMA	1 ± 0.13	1.09 ± 0.08	0.2946
WATP	1 ± 0.1	1.44 ± 0.23	0.0226
YTHDC1	1.14 ± 0.21	2.09 ± 0.15	0.0005
YTHDC2	1 ± 0.2	1.15 ± 0.14	0.2735
YTHDF1	1 ± 0.13	1 ± 0.13	>0.9999
YTHDF2	1 ± 0.08	1.4 ± 0.16	0.008

YTHDF3	1 ± 0.13	1.4 ± 0.23	0.0305
Z3CH	1 ± 0.2	1.13 ± 0.09	0.2973

Supplementary Table 1. Gene expression levels (mean ± SD) for Sec RNA modification regulatory genes, including writers, readers, and erasers, in WT and R6/2 Cortex. Statistical significance between wild-type (WT) and R6/2 groups was assessed using an unpaired *t*-test (N = 4 per group). Reported *p*-values indicate differences in expression between WT and R6/2

Gene	WT	R6/2	pValue
ALKBH1	1 ± 0.15	1.15 ± 0.18	0.2436
ALKBH2	1 ± 0.2	1.33 ± 0.19	0.054
ALKBH4	1 ± 0.39	0.83 ± 0.42	0.5646
ALKBH5	1 ± 0.14	1.16 ± 0.24	0.3084
ALKBH6	1 ± 0.18	1.21 ± 0.16	0.1434
CBLL1	1 ± 0.23	0.66 ± 0.09	0.0471
EIF3A	1 ± 0.31	0.98 ± 0.17	0.9109
FMRP	1 ± 0.22	0.66 ± 0.06	0.0475
FTO	1 ± 0.28	0.77 ± 0.09	0.2013
HNRG	1 ± 0.23	0.92 ± 0.22	0.6314
HNRNPA	1 ± 0.08	0.75 ± 0.07	0.0037
HNRNPC	1 ± 0.29	1.09 ± 0.25	0.6442
IGF2BP1	1 ± 0.41	0.96 ± 0.33	0.8933
IGF2BP2	1 ± 0.43	0.52 ± 0.09	0.1097
IGF2BP3	1 ± 0.56	16.27 ± 2.95	0.0015
KIAA1429	1 ± 0.13	0.75 ± 0.1	0.0245
METTL1	1 ± 0.18	1.63 ± 0.23	0.0061
METTL14	1 ± 0.65	0.46 ± 0.25	0.1967
METTL15	1 ± 0.09	1.34 ± 0.08	0.0012
METTL16	1 ± 0.29	1.35 ± 0.18	0.0963
METTL17	1 ± 0.14	0.88 ± 0.16	0.3073
METTL19	1 ± 0.15	1.11 ± 0.45	0.669
METTL2	1 ± 0.08	1.52 ± 0.22	0.0131
METTL25	1 ± 0.15	1.13 ± 0.14	0.2434
METTL25B	1 ± 0.2	1.52 ± 0.24	0.0173
METTL26	1 ± 0.14	1.75 ± 0.28	0.0072
METTL27	1 ± 0.19	1.21 ± 0.2	0.1741
METTL3	1 ± 0.19	0.99 ± 0.09	0.9346
METTL4	1 ± 0.19	1.01 ± 0.17	0.9266

METTL5	1 ± 0.08	1.19 ± 0.09	0.0222
METTL6	1 ± 0.19	0.8 ± 0.06	0.1217
METTL7A	1 ± 0.05	1.24 ± 0.1	0.0099
METTL7B	1 ± 0.14	1 ± 0.03	0.9713
RBM15	1 ± 0.17	1.2 ± 0.19	0.1655
VIRMA	1 ± 0.22	1.16 ± 0.15	0.2702
WTAP	1 ± 0.2	1.07 ± 0.1	0.5736
YTHDC1	1 ± 0.16	1.72 ± 0.2	0.0016
YTHDC2	1 ± 0.07	1.14 ± 0.13	0.1339
YTHDF1	1 ± 0.15	1.47 ± 0.22	0.0156
YTHDF2	1 ± 0.16	1.5 ± 0.22	0.012
YTHDF3	1 ± 0.15	1.71 ± 0.16	0.0007
Z3CH	1 ± 0.16	0.7 ± 0.09	0.0223

Supplementary Table 2. Gene expression levels (mean ± SD) for Sec RNA modification regulatory genes, including writers, readers, and erasers, in WT and R6/2 Striatum. Statistical significance between wild-type (WT) and R6/2 groups was assessed using an unpaired *t*-test (N = 4 per group). Reported *p*-values indicate differences in expression between WT and R6/2

Gene	WT	Zq175	pValue
ALKBH1	1 ± 0.64	1.5 ± 0.38	0.2382
ALKBH2	1 ± 0.58	0.91 ± 0.13	0.778
ALKBH3	1 ± 0.62	1.08 ± 0.47	0.8507
ALKBH4	1 ± 0.56	1.67 ± 0.62	0.1567
ALKBH5	1 ± 0.72	2.13 ± 0.17	0.0485
ALKBH6	1 ± 0.35	1.15 ± 0.25	0.5148
ALKBH7	1 ± 0.57	1 ± 0.16	0.9903
ALKBH8	1 ± 0.33	1.29 ± 0.22	0.2036
EIF3A	1 ± 0.17	0.82 ± 0.14	0.1563
FMRP	1 ± 0.12	0.8 ± 0.18	0.1316
FTO	1 ± 0.09	0.8 ± 0.13	0.0576
HNRNPA	1 ± 0.21	0.77 ± 0.13	0.1304
HNRNPC	1 ± 0.28	0.76 ± 0.16	0.2002
IGF2BP1	1 ± 0.41	0.66 ± 0.38	0.2706
IGF2BP2	1 ± 0.16	0.68 ± 0.21	0.0584
IGF2BP3	1 ± 0.36	2.45 ± 0.83	0.0308
KIAA1429	1 ± 0.09	0.83 ± 0.18	0.1525
METTL1	1 ± 0.19	0.97 ± 0.23	0.8267
METTL14	1 ± 0.48	1.02 ± 0.94	0.9689
METTL15	1 ± 0.08	1.16 ± 0.21	0.2246

METTL16	1 ± 0.53	1.82 ± 0.25	0.0468
METTL17	1 ± 0.26	1.54 ± 1.18	0.4294
METTL19	1 ± 0.07	0.92 ± 0.34	0.6794
METTL2	1 ± 0.24	0.96 ± 0.27	0.8196
METTL25	1 ± 0.34	0.83 ± 0.2	0.4184
METTL25B	1 ± 0.43	1.03 ± 0.14	0.9041
METTL26	1 ± 0.14	2.42 ± 1.32	0.1194
METTL27	1 ± 0.45	1.41 ± 0.6	0.3241
METTL3	1 ± 0.39	2.42 ± 0.49	0.0043
METTL4	1 ± 0.25	1.02 ± 0.32	0.9424
METTL5	1 ± 0.13	0.83 ± 0.16	0.1554
METTL6	1 ± 0.18	0.78 ± 0.21	0.1566
METTL7A	1 ± 0.68	1.25 ± 0.63	0.6122
METTL7B	1 ± 0.27	0.57 ± 0.35	0.1013
METTL8	1 ± 0.06	1.02 ± 0.31	0.893
VIRMA	1 ± 0.16	0.83 ± 0.1	0.1297
WTAP	1 ± 0.06	0.82 ± 0.09	0.0163
YTDHC2	1 ± 0.12	0.73 ± 0.1	0.0142
YTHDC1	1 ± 0.04	1.35 ± 0.39	0.1709
YTHDF1	1 ± 0.19	1.24 ± 0.25	0.183
YTHDF2	1 ± 0.3	1.42 ± 0.4	0.1463
YTHDF3	1 ± 0.22	0.89 ± 0.12	0.408
Z3CH	1 ± 0.21	0.58 ± 0.21	0.0267

Supplementary Table 3. Gene expression levels (mean ± SD) for Sec RNA modification regulatory genes, including writers, readers, and erasers, in WT and Zq175 Cortex. Statistical significance between wild-type (WT) and Zq175 groups was assessed using an unpaired *t*-test (N = 4 per group). Reported *p*-values indicate differences in expression between WT and Zq175.

Gene	WT	Zq175	pValue
ALKBH1	1 ± 0.43	1.14 ± 0.26	0.5957
ALKBH2	1 ± 0.56	0.73 ± 0.21	0.4249
ALKBH3	1 ± 0.45	1.08 ± 0.19	0.7734
ALKBH4	1 ± 0.36	4.5 ± 1.97	0.0355
ALKBH5	1 ± 0.53	0.76 ± 0.23	0.4429
ALKBH6	1 ± 0.48	0.78 ± 0.32	0.4797
ALKBH7	1 ± 0.46	1.3 ± 0.6	0.4597
ALKBH8	1 ± 0.54	1.05 ± 0.31	0.8765
EIF3A	1 ± 0.26	1.19 ± 0.12	0.2609
FMRP	1 ± 0.15	1.02 ± 0.08	0.8169

FTO	1 ± 0.53	1.28 ± 0.84	0.5995
HNRG	1 ± 0.56	2.17 ± 1.06	0.1135
HNRNPA	1 ± 0.29	3.74 ± 1.14	0.0143
HNRNPC	1 ± 0.39	0.9 ± 0.27	0.6949
IGF2BP1	1 ± 0.37	1.09 ± 0.52	0.7793
IGF2BP2	1 ± 0.25	0.54 ± 0.23	0.0366
IGF2BP3	1 ± 0.31	4.5 ± 2.13	0.0448
KIAA1429	1 ± 0.53	0.49 ± 0.21	0.1492
METTL1	1 ± 0.4	2.56 ± 0.96	0.0398
METTL14	1 ± 0.49	6.8 ± 3.47	0.0428
METTL15	1 ± 0.51	1.78 ± 0.75	0.1429
METTL16	1 ± 0.47	1.83 ± 0.79	0.1344
METTL17	1 ± 0.26	3.87 ± 1.39	0.0239
METTL19	1 ± 0.4	2.39 ± 0.77	0.0271
METTL2	1 ± 0.42	1.23 ± 0.5	0.5042
METTL25	1 ± 0.33	2.07 ± 0.91	0.0949
METTL25B	1 ± 0.43	1.38 ± 0.53	0.3051
METTL26	1 ± 0.36	1.38 ± 0.51	0.2745
METTL27	1 ± 0.61	0.96 ± 0.37	0.9245
METTL3	1 ± 0.36	1.93 ± 0.53	0.0317
METTL4	1 ± 0.54	1.71 ± 0.73	0.1767
METTL5	1 ± 0.15	3.2 ± 1.38	0.0488
METTL6	1 ± 0.43	1.42 ± 0.61	0.305
METTL7A	1 ± 0.17	2.37 ± 1.12	0.0896
METTL8	1 ± 0.43	1.84 ± 0.67	0.0905
RBM15	1 ± 0.5	1.6 ± 0.48	0.132
VIRMA	1 ± 0.45	2.7 ± 1.1	0.0465
WTAP	1 ± 0.94	1.29 ± 1.05	0.6934
YTDHC2	1 ± 0.54	2.42 ± 1.17	0.0884
YTHDC1	1 ± 0.24	1.24 ± 0.36	0.3107
YTHDF1	1 ± 0.56	1.13 ± 0.26	0.6955
YTHDF2	1 ± 0.42	1.05 ± 0.38	0.8766
YTHDF3	1 ± 0.17	1.39 ± 0.14	0.0132
Z3CH	1 ± 0.72	2.47 ± 0.46	0.0184

Supplementary Table 4. Gene expression levels (mean ± SD) for Sec RNA modification regulatory genes, including writers, readers, and erasers, in WT and Zq175 Striatum. Statistical significance between wild-type (WT) and Zq175 groups was assessed using an unpaired *t*-test (N = 4 per group). Reported *p*-values indicate differences in expression between WT and Zq175.

Gene	Q7	Q111	pValue
ALKBH1	1.42 ± 0.37	4.95 ± 0.43	0.0005
ALKBH2	1.06 ± 0.08	1.12 ± 0.11	0.4968
ALKBH3	1.14 ± 0.14	2.01 ± 0.06	0.0033
ALKBH4	0.79 ± 0.21	2.98 ± 0.02	0.0026
ALKBH5	1.19 ± 0.18	2.41 ± 0.81	0.1149
ALKBH6	1.04 ± 0.05	2.87 ± 0.1	0.0002
ALKBH7	1.18 ± 0.16	1.39 ± 0.09	0.1301
ALKBH8	1.05 ± 0.09	2.23 ± 0.07	<0.0001
CBLL1	1.01 ± 0.1	0.9 ± 0.1	0.2541
EIF2A	1.25 ± 0.32	2.12 ± 0.05	0.0387
FMRP	0.89 ± 0.14	2.05 ± 0.13	0.0005
FTO	0.74 ± 0.24	6.3 ± 1.1	0.0099
HNRG	0.72 ± 0.24	1.34 ± 0.08	0.0366
HNRNPA	0.67 ± 0.3	1.11 ± 0.18	0.1075
HNRNPC	0.74 ± 0.23	1.1 ± 0.17	0.1037
IGF2BP1	0.76 ± 0.23	2.89 ± 0.29	0.0007
IGF2BP2	0.73 ± 0.24	1.91 ± 0.29	0.0061
IGF2BP3	0.71 ± 0.26	1.4 ± 0.2	0.0247
KIAA1429	0.79 ± 0.21	1.11 ± 0.17	0.111
METTL1	1.22 ± 0.26	2.63 ± 0.2	0.0022
METTL14	0.99 ± 0.01	1.48 ± 0.46	0.2108
METTL15	1.04 ± 0.05	1.93 ± 0.04	<0.0001
METTL16	1.06 ± 0.07	2.63 ± 0.07	<0.0001
METTL17	1.03 ± 0.08	3.37 ± 0.28	0.0027
METTL19	0.91 ± 0.12	3.32 ± 0.73	0.0271
METTL2	1.12 ± 0.12	2.36 ± 0.23	0.0035
METTL25	0.87 ± 0.2	0.86 ± 0.1	0.9557
METTL25B	1.37 ± 0.32	3.18 ± 0.4	0.004
METTL26	1.4 ± 0.52	2.77 ± 0.35	0.0243
METTL27	1.11 ± 0.1	2.04 ± 0.09	0.0003
METTL3	1.05 ± 0.04	2.54 ± 0.14	0.0014
METTL4	1.03 ± 0.04	2.53 ± 0.01	<0.0001
METTL5	1.1 ± 0.12	3.6 ± 0.27	0.001
METTL6	1.1 ± 0.1	2.1 ± 0.01	0.003
METTL7A	1.05 ± 0.06	10.7 ± 1	0.0035
METTL7B	0.91 ± 0.57	4.04 ± 0.7	0.0045
METTL8	1.02 ± 0.04	1.83 ± 0.03	<0.0001
RBM15	0.85 ± 0.13	1.46 ± 0.15	0.0058
VIRMA	0.71 ± 0.25	1.32 ± 0.13	0.034
WTAP	0.77 ± 0.23	1.43 ± 0.18	0.0205

YTHDC1	0.73 ± 0.25	1.84 ± 0.14	0.0054
YTHDC2	0.71 ± 0.26	1.16 ± 0.06	0.0857
YTHDF1	0.97 ± 0.03	1.6 ± 0.05	0.0002
YTHDF2	0.76 ± 0.21	1.36 ± 0.23	0.0284
YTHDF3	0.76 ± 0.22	1.04 ± 0.7	0.0016

Supplementary Table 5. Gene expression levels (mean ± SD) for Sec RNA modification regulatory genes, including writers, readers, and erasers, in Q7 and Q111 cells grown at 33°C in serum free media for 24 hours. Statistical significance between Q7 and Q111 cells was assessed using an unpaired *t*-test (N = 3 per group). Reported *p*-values indicate differences in expression between Q7 and Q111 cells.

Gene	Q7 37C	Q111 37C	pValue 37
ALKBH1	1.87 ± 0.03	10.11 ± 5.47	0.121
ALKBH2	1.04 ± 0	1.13 ± 0.2	0.5297
ALKBH3	1.26 ± 0.01	2.86 ± 1.04	0.116
ALKBH4	0.83 ± 0.05	5.41 ± 1.06	0.0173
ALKBH5	1.72 ± 0.04	3.59 ± 0.47	0.0201
ALKBH6	1.42 ± 0.16	4.11 ± 0.11	<0.0001
ALKBH7	2.21 ± 0.15	4.12 ± 1.89	0.2226
ALKBH8	1.55 ± 0.1	3.07 ± 0.38	0.0155
CBLL1	0.77 ± 0.03	1.01 ± 0.25	0.2375
EIF2A	1.7 ± 0.01	2.71 ± 0.37	0.0411
FMRP	0.73 ± 0.02	3.8 ± 1.12	0.0415
FTO	0.97 ± 0.23	8.4 ± 1.68	0.0152
HNRG	0.73 ± 0.15	1.52 ± 0.48	0.0923
HNRNPA	0.83 ± 0.19	0.98 ± 0.27	0.2114
HNRNPC	1.12 ± 0.05	1.8 ± 0.65	0.2114
IGF2BP1	1.57 ± 0.21	3.25 ± 1.22	0.1367
IGF2BP2	1.22 ± 0.44	2.72 ± 0.37	0.0115
IGF2BP3	1.01 ± 0.2	2.31 ± 0.32	0.0066
KIAA1429	1.08 ± 0.08	1.43 ± 0.45	0.313
METTL1	1.09 ± 0.1	4.35 ± 1.11	0.0355
METTL14	1.18 ± 0.25	1.67 ± 0.29	0.092
METTL15	1.49 ± 0.29	3.56 ± 0.12	0.0024
METTL16	1.99 ± 0.18	4.59 ± 0.24	0.0002
METTL17	1.76 ± 0.22	9.14 ± 0.14	<0.0001
METTL19	1.21 ± 0.07	4.94 ± 0.64	0.0091
METTL2	1.6 ± 0.08	3.88 ± 0.1	<0.0001
METTL25	0.62 ± 0.02	1.21 ± 0.09	0.0062
METTL25B	1.9 ± 0.17	5.94 ± 1.53	0.043

METTL26	3.14 ± 0.08	2.63 ± 1.21	0.5479
METTL27	1.67 ± 0.01	4.07 ± 1.7	0.1342
METTL3	1.44 ± 0.01	4.64 ± 0.11	0.0003
METTL4	1.93 ± 0.11	4.3 ± 0.21	0.0004
METTL5	1.76 ± 0.12	4.58 ± 0.1	<0.0001
METTL6	1.53 ± 0.18	4.58 ± 0.58	0.0076
METTL7A	1.33 ± 0.49	13.91 ± 0.64	<0.0001
METTL7B	0.28 ± 0.02	3.93 ± 0.72	0.0126
METTL8	0.82 ± 0.06	2.07 ± 0.09	0.0001
RBM15	0.88 ± 0.18	2.41 ± 0.56	0.0326
VIRMA	1.19 ± 0.31	1.59 ± 0.36	0.2206
WTAP	1.01 ± 0.22	1.57 ± 0.53	0.2003
YTHDC1	1.14 ± 0.22	3.04 ± 0.23	0.0005
YTHDC2	0.72 ± 0.23	1.29 ± 0.4	0.1143
YTHDF1	1.09 ± 0.03	2.48 ± 0.2	0.0063
YTHDF2	0.79 ± 0.09	1.17 ± 0.42	0.261
YTHDF3	1.18 ± 0.23	2.09 ± 0.57	0.0915

Supplementary Table 6. Gene expression levels (mean ± SD) for Sec RNA modification regulatory genes, including writers, readers, and erasers, in Q7 and Q111 cells grown at 37°C in serum free media for 24 hours. Statistical significance between Q7 and Q111 cells was assessed using an unpaired *t*-test (N = 3 per group). Reported *p*-values indicate differences in expression between Q7 and Q111 cells.

Gene	Primer	Sequence 5’-3’
METTL1	FP	AGCTGCATGAGTGGATGTG
	RP	AGCTGCATGAGTGGATGTG
METTL2	FP	CTTCTATGTGAGAGGTGATGGC
	RP	AGCTGTTTCCCTCGATTCAC
METTL3	FP	ATCCAGGCCCATAAGAAACAG
	RP	CTATCACTACGGAAGGTTGGG
METTL4	FP	CTATATCCTTCGTGGTCTGTGG
	RP	CTCTCCCCAGTACAAGACATTC
METTL5	FP	GGATTCGAAAAGCCCAAGTTAC
	RP	CTAAGTACTCCACAGCCACATC
METTL6	FP	GAGTCTGTGGATGCCGTTAC
	RP	GATCATTCAGCCCGTAGTCAC
METTL8	FP	GAATACTAGAGGTTGGCTGTGG
	RP	CTGTAGGACTTGTGGGACTTTAC
METTL14	FP	AGACGCCTTCATCTCTTTGAG
	RP	CTCTGTACATCCGGTCAAGTATG
METTL15	FP	TGAAGAGAAAGAGTTGGAAGCC
	RP	AGAATGGCTCTTGTATGTCCTC
METTL16	FP	CTAATTCCCACAGTCCCCTTG
	RP	GGTTGCTCCAAGTAAGGGATAG
METTL19	FP	CAGAGCAGGAAGACACAGTAC
	RP	GGCGGGTATGTTCTGGATTTC
METTL25B	FP	CCCGACTAACAGCTCCTTTTC
	RP	AGCCCACATCCACAACTTG
KIAA1429	FP	TTCCATCTTGAAGGTTCCGG
	RP	CCACAATTTTCGGGTGTTGAG

RBM15	FP	TTCATGCCTTCCCACCTTG
	RP	ATCTTCATCCGCTGTTCACC
ZC3H13	FP	CAAGAGATGGGAAGGACAGAG
	RP	CTGAATAGATGACCCTGACTGTG
FTO	FP	TCACAGCCTCGGTTTAGTTC
	RP	GCAGGATCAAAGGATTTCAACG
WTAP	FP	TTTGGAGGGAAAGTACACAGATC
	RP	TCCTGCTCTTTGGTTGCTAG
YTHDF1	FP	CCCCAGAGAACAAAAGGACAAG
	RP	GACAGGTAAGGATCACTCATCG
YTHDF2	FP	ACTATGAGAAACGCCAAGAGG
	RP	TTAGGATAAGGAGATGCAACCG
YTHDF3	FP	TGCACATTATGAAAAGCGTCAAG
	RP	GGCATTTCCAGAGTCTACATCA
IGF2BP1	FP	GAGCAGGAGATGGTACAAGTG
	RP	TTGGAGTCAGGTGTTTCTGG
IGF2BP2	FP	CAATCCATGCTACCCCAGAAG
	RP	TGCCAATCAGTCTTCCAACG
IGF2BP3	FP	ATCTGTTTATTCCCGCCCTG
	RP	TCACCATCCGCACTTTAGC
HNRNPC	FP	GCTTTGCCTTTGTCCAGTATG
	RP	CGTTTCACACCTGCTTTTCC
HNRNPA2B1	FP	CAAAGTTCTAGGAGTGGAAGAGG
	RP	CCCATTATAGCCATCCCCAAA
YTHDC1	FP	TTTTCAGGAGTTCGCCGAG
	RP	GTAAGGATGGTGTGGAGGTTG
YTHDC2	FP	TTACTGTCCTGGTGTTCTGTG
	RP	CTGTCTTCCATCTCACTGTCAC

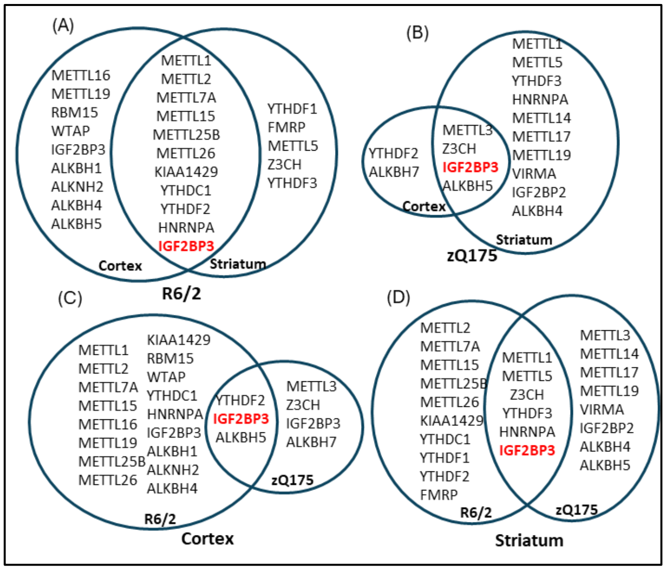
VIRMA	FP	ACCTCATACAATGACCCAACC
	RP	ATCGACAGAAGCAAGGTGAC
CBLL1	FP	CTGACTTCCGTTCCCACTG
	RP	CTTTGCTGGCTTGTTTGGAG
HNRNPG	FP	TCAAGCAGAGATTACCCAAGC
	RP	ATCACGGGAACTGGAATGAC
EIF3A	FP	TGGGAATCATACAGGCAGTG
	RP	AGTTGTCACATAGCTTGCGG
FMRP	FP	AGAGGGTGTTAGTGGTTTCATC
	RP	AGAACAGTGGCATTAGCGATG
ALKBH1	FP	TTCATTCCAAACCCCTTCCTC
	RP	TTAGTCATGTGCTTGTCCAGG
ALKBH2	FP	TCTTACCCTGACACCAAAGC
	RP	GCTCGTCATCTCTGTGCTC
ALKBH3	FP	ACGGGACCTTGCTAATCATG
	RP	CTCTTGGGTCTGGATAAACGG
ALKBH4	FP	CTCCAAGTTGCTTTAGTTCCAAG
	RP	TTAACTTTAGGGCCATAGTCCTG
ALKBH5	FP	AGTTCCAGTTCAAGCCCATC
	RP	GGCGTTCCTTAATGTCCTGAG
ALKBH6	FP	GAAGACGCTGTAGACGGAC
	RP	CTTGGAGATGAAGTCAGGGAC
ALKBH7	FP	CAAGTGTTATGAAGCTGGTGC
	RP	CATGGGAGAAGTCATATCGGG
ALKBH8	FP	GCCCATATTGACACGCATTC
	RP	ATCACCAGCAAACTCCGAC
METTL7A	FP	GTGACCGATGGCTCTGTG
	RP	GTAGACCGTTCATCTGCCAC

METTL7B	FP	CCCTGGTGCTATGTTCTGTG
	RP	AGGCTCTAAAACTCGCTGC
METTL17	FP	CAGGAACTCAGCTACAGTGAAG
	RP	ACCCAAAGTCCATCAACGTC
METTL25	FP	GATGTGCTAACGAAAACTGGG
	RP	AAGAGTGATTCAGTAGGCAGC
METTL26	FP	GACACCTGCTCAAAACCAAG
	RP	CAGAAGGACTGTGTCACGAAG
METTL27	FP	CTGATCCTCTGTGTATGGTCTC
	RP	GGAGTCTTTTCAGTCCCTTTGG

Supplementary Table 7. Primer sequence of m^{6}A regulatory genes used in the study. FP: Forward Primer, RP: Reverse Primer

Target	Vendor	Dilution	Catalog
METTL3	Proteintech	1:1000	
YTHDC1	Cell Signaling Technology	1:2000	
YTHDC2	Cell Signaling Technology	1:2000	
IGF2BP2	Proteintech	1:5000	
IGF2BP3	Proteintech	1:5000	
METTl14	Proteintech	1:1000	
Caspase 3	Proteintech	1:1000	
Caspase 9	Proteintech	1:1000	
m^{6}A	Proteintech	1:1000	
β-Actin	Proteintech	1:5000	
IC2	Abcam	1:5000	

Supplementary Table 8. Antibody information used in the study. This table lists all primary antibodies used in the study, their dilution, catalog numbers and vendors.



Supplementary Figure 1. Venn analysis of differentially expressed genes in the cortex and striatum of Huntington's disease mouse models. (A) Venn diagram showing overlap of differentially expressed genes between the cortex and striatum in the R6/2 mouse model. (B) Venn diagram showing overlap of differentially expressed genes between the cortex and striatum in the zQ175 mouse model. (C) Venn diagram comparing differentially expressed genes in the cortex between R6/2 and zQ175 mouse models. (D) Venn diagram comparing differentially expressed genes in the striatum between R6/2 and zQ175 mouse models. Differential expression was defined as $p < 0.05$.