

Table e-1: Analysis of miRNAs reported to be differentially expressed in HD brain.

	Mean Expression	logFC	p-value	FDR q-value
miR-5695	3.92	0.85	1.95E-02	1.47E-01
miR-132-3p	3.26	0.65	2.62E-02	1.47E-01
miR-138-2-3p	4.58	0.60	2.75E-02	1.47E-01
miR-490-5p	4.17	0.56	3.77E-02	1.51E-01
miR-363-3p	4.90	0.49	6.12E-02	1.80E-01
miR-302a-5p	4.22	0.68	6.75E-02	1.80E-01
miR-129-1-3p	3.23	0.37	1.51E-01	3.40E-01
miR-106a-5p	3.89	0.48	1.82E-01	3.40E-01
miR-129-5p	3.82	-0.23	1.99E-01	3.40E-01
miR-10b-3p	3.12	0.44	2.13E-01	3.40E-01
miR-196a-5p	2.84	0.30	2.51E-01	3.65E-01
miR-196b-5p	4.38	0.25	4.40E-01	5.86E-01
miR-302a-3p	7.35	0.20	5.21E-01	6.17E-01
miR-615-3p	3.72	0.16	5.40E-01	6.17E-01
miR-10b-5p	3.25	0.12	6.29E-01	6.71E-01
miR-4449	4.48	-0.06	8.91E-01	8.91E-01

Table e-1: Results of differential expression of miRNAs between 14 Diagnosed HD and 14 Control subjects. Shown are 16 miRNAs reported to be highly and differentially expressed between HD and control brain by Hoss et al.¹⁶. These p-values reflect the coefficient for HD status, adjusted for subject age in a multivariate linear model. FDR q-values are calculated using the Benjamini-Hochberg procedure for the set of 16 candidate miRNAs. The mean expression values are calculated from the DESeq2/variance stabilized and batch corrected values across all 28 subjects.