Table e-2: Modeling miRNAs reported to be differentially expressed in HD brain with ordinal categories of time-to-onset.

	Mean Expression	logFC	p-value	FDR q-value
miR-132-3p	4.57	0.13	1.66E-02	2.65E-01
miR-5695	4.10	0.13	4.99E-02	3.70E-01
miR-302a-5p	4.92	0.13	6.94E-02	3.70E-01
miR-138-2-3p	4.83	0.10	1.16E-01	4.57E-01
miR-10b-3p	5.31	0.09	1.77E-01	4.57E-01
miR-615-3p	4.81	0.06	1.83E-01	4.57E-01
miR-196a-5p	4.17	0.06	2.00E-01	4.57E-01
miR-490-5p	4.57	0.07	2.75E-01	5.51E-01
miR-196b-5p	4.52	0.06	3.11E-01	5.53E-01
miR-129-1-3p	4.06	0.04	4.04E-01	6.47E-01
miR-106a-5p	3.97	0.05	4.52E-01	6.58E-01
miR-363-3p	4.93	0.03	5.32E-01	7.10E-01
miR-302a-3p	7.20	0.03	6.68E-01	7.74E-01
miR-4449	4.43	0.03	6.78E-01	7.74E-01
miR-10b-5p	4.21	-0.02	7.26E-01	7.74E-01
miR-129-5p	5.05	-0.01	8.60E-01	8.60E-01

Table e-2: Results of univariate linear modeling of miRNAs expression versus ordinal categories of time-to-onset. Shown are 16 miRNAs reported to be highly and differentially expressed between HD and control brain by Hoss el al.[16].These p-values reflect the coefficient for ordinal group membership. 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 56 subjects. The logFC values represent the estimated change in miRNA expression between two adjacent ordinal groups.