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Supplemental Data

miR-196a Ameliorates Phenotypes

of Huntington Disease in Cell, Transgenic Mouse,

and Induced Pluripotent Stem Cell Models

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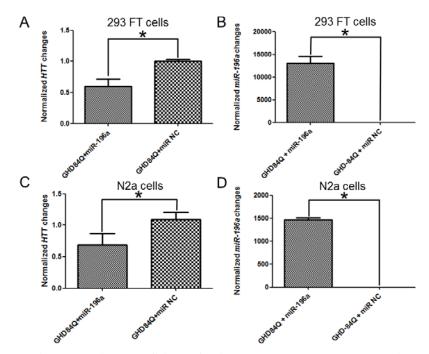


Figure S1. RNA expression profiling of miR-196a and mutant *HTT* in 293 FT and N2a cells after the treatments of miR-196a mimics. 293 FT (A and B) and N2a (C and D) cells were transfected with mutant *HTT* (GHD84Q), miR-196a mimics or miRNA unrelated control (miR NC), and then subjected for Q-RT-PCR (Applied Biosystems). (A and C) show the mRNA level of mutant *HTT* in 293 FT and N2a cells, respectively. (B and D) show the expression level of miR-196a in 293 FT and N2a cells, respectively. n=3, data represent mean \pm SD, and * represents significant difference between two groups.

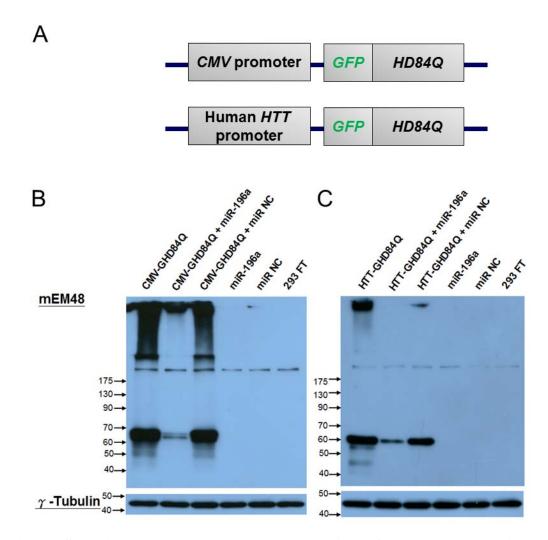


Figure S2. miR-196a suppressed the expression of mutant *HTT* **driven by different promoters** *in vitro*. (A) Top panel shows the mutant *HTT* construct containing the cytomegalovirus (CMV) promoter and mutant HTT with 84 CAG repeats (HD84Q) and GFP fusion protein. Bottom panel shows the mutant HTT construct containing the human endogenous HTT promoter, HD84Q and GFP fusion protein. (B) miR-196a mimics, unrelated controls (miR-NC) and mutant HTT driven by the CMV promoter (CMV-GHD84Q) were transfected into 293 FT cells, and then analyzed via Western blotting using mEM48 and γ-tubulin antibodies. Cells transfected with CMV-GHD84Q and miR-196a show lower expression level of mutant HTT compared to that of cells transfected with CMV-GHD84Q and miR-NC. (C) miR-196a mimics, unrelated controls (miR-NC) and mutant HTT driven by the human HTT promoter (HTT-GHD84Q) were used to perform the same experiment as described in (B). Cells transfected with HTT-GHD84Q and miR-196a also show lower expression level of mutant HTT-GHD84Q and miR-NC.

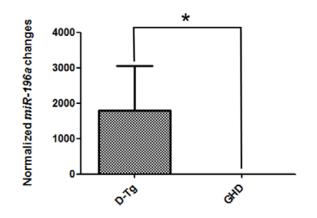


Figure S3. Expression of miR-196a in the brain of D-Tg and GHD transgenic mice. Brain tissues of different transgenic mice at one month of age (n=5-6 for each group) were subjected for Q-RT-PCR to detect the expression of miR-196a. Data represent mean \pm SD, * represents significant difference between two groups.

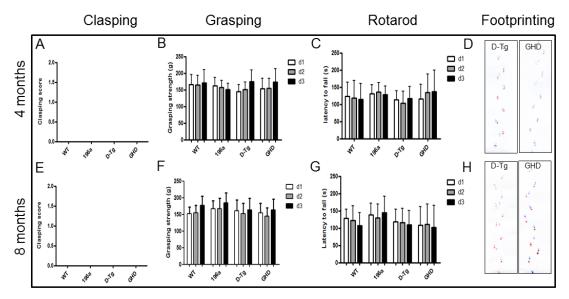


Figure S4. Behavioral phenotypes in four groups of mice at four and eight months of ages. Clasping (A, E), Grasping (B, F), Rotarod (C, G) and Footprinting (D, H) tests were performed at 4 (A-D) and 8 (E-H) months of age in four groups (n= 6-9 mice for each group). Data represent mean \pm SD.

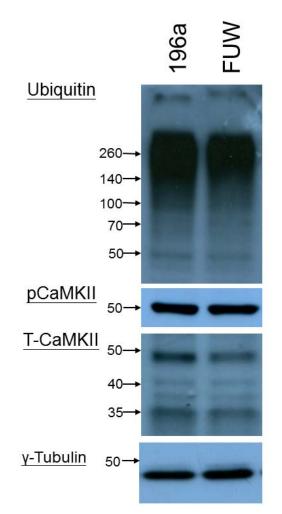


Figure S5. Expression of Ubiquitin and CaMKII in HD-iPSCs. Western blotting using the same membrane in Figure 4E immunoblotted with ubiquitin, pCaMKII and total CaMKII antibodies, showing stronger ubiquitin and total CaMKII in miR-196a infected HD-iPSCs, whereas similar signal of pCaMKII is observed between these two groups. γ -tubulin is used as an internal control.

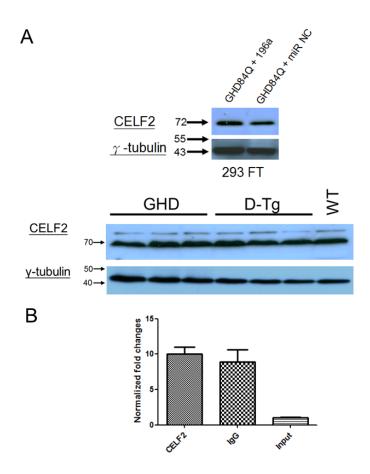


Figure S6. CELF2 does not involve in the mechanism of miR-196a on HD. (A) Top panel shows the Western blotting result revealing similar expression level of CELF2 between HD 293 FT cells transfected with miR-196a mimics and unrelated (NC) controls. Bottom panel is the Western blotting result revealing similar level of CELF2 in the brain samples of GHD and D-Tg transgenic mice. y-tubulin was used as the internal control. **(B)** Real-time **RT-PCR** performed after RNA immunoprecipitation using a CELF2 antibody in 293 FT cells showed similar binding ability of a CELF2 antibody compared to that of IgG control. Data represent mean \pm SD (n=3).

Table S1. Candidate genes involved in CaMKII-CREB, inflammatory response in brain and ubiquitin-dependent protein catabolic process pathways. miR-196a TargetScan genes and miR-196a microarray genes were imported into the MetaCore online software, and candidate genes related to three pathways are listed.

miR-196a targetscan genes		Camp IFCRED paulway			hrain			Cata	catabolic process	220	
	miR-196	miR-196a microarray	ay	miR-196a targetscan genes	miR-196	miR-196a microarray	rray	miR-196a taroetscan genes	miR-196	miR-196a microarray	ray
		2014		uugeessuu genes				ומו ארושים וואטוויש		50.01	
	Input IDs	rold change (D-Tg /GHD)	p-value	Input IDs	Input IDs	rold change (D-Tg /GHD)	p-value	Input IDs	Input IDs	rold change (D-Tg /GHD)	p-value
CALM3;CALM1 06	0610040J01Rik	-1.29	0.0131	EPHA3	Ahcy	-1.204	0.012	NEDD4L	Nedd4;Rpf1	-1.30	0.0369
	1700026L06Rik	-1.19	0.0087		Aimp1	-1.180	0.006	RNF5	Rnf5	-1.18	0.0254
HABP4 57	5730577103Rik	-1.15	0.0221		Akt1	-1.240	0.047	USP15	Usp15	-1.23	0.0256
	Adcy3	-1.21	0.0031		B4galt1	-1.169	0.003	CDC34	AI314180	-1.33	0.0115
	Aldh6a1	-1.23	0.0055		Bmp2	-1.198	0.023	ERLIN2	Amfr	-1.35	0.0415
	Atp2a2	-1.21	0.0443		Bťk	-1.069	0.031	MAP3K1	Anapc2	-1.15	0.0414
	Bag3	-1.25	0.0469		Ccl5	-3.236	0.021	RAD23B	Birc3	-1.21	0.0194
	Casp2	-1.23	0.0078		Cd24a	-1.295	0.001	SMURF1	Btrc	-1.36	0.0332
	Clcn3	-1.31	0.0336		Cebpa	-1.221	0.042	UBE2G2	Cd2ap	-1.47	0.0051
	Clta	-1.43	0.0444		Cela1	-1.512	0.040	USP31	Cul1	-1.27	0.0032
	Cnn1	-2.43	0.0420		Cnr2	-1.388	0.004	YOD1	Cul3	-1.41	0.0167
	Cnr2	-1.39	0.0040		Crcp	-1.166	0.029		Derl2	-1.21	0.0112
D2	D230025D16Rik	-1.26	0.0067		Csf1	-1.165	0.036		Dna jb9	-1.31	0.0014
	Dpysl2	-1.25	0.0500		Csf1r	-1.231	0.007		Edem3	-1.31	0.0263
	Gria1	-1.14	0.0340		Cyba	-1.185	0.002		Fbxw11	-1.28	0.0011
	Hcfc1r1	-1.19	0.0338		F12	-1.315	0.002		Herpud1	-1.22	0.0256
	Map3k7	-1.26	0.0069		F8	-1.126	0.008		Huwe1	-1.23	0.0404
	Mbd3I1	-1.26	0.0355		Fcer1g	-1.194	0.045		Itch	-1.19	0.0403
	Ncor2	-1.29	0.0105		Hifta	-1.382	0.031		Kctd10	-1.43	0.0140
	Nt5dc1	-1.25	0.0205		Lias	-1.326	0.011		Mdm2	-1.32	0.0182
	Rgs9	1.24	0.0325		Lipa	-1.317	0.018		Pcbp2	-1.46	0.0367
	Rnf146	-1.23	0.0013		Map2k3	-1.405	0.046		C6;Psma7	-1.34	0.0120
	Slc39a1	-1.34	0.0287		Mecom	-1.156	0.034		Psmc2	-1.27	0.0369
	Smad4	-1.32	0.0230		Myd88	-1.278	0.013		Psmc5	-1.16	0.0373
	Synpo	-1.35	0.0203		Naf1	-1.300	0.015		Rbbp6	-1.29	0.0074
	Synpo	-1.35	0.0203		Ncf1	-1.256	0.033		Rnf20	-1.18	0.0187
	Tpd52	-1.39	0.0393		Notch1	-1.398	0.040		Sirt2	-1.14	0.0005
	Ubxn7	-1.23	0.0057		Park7	-1.280	0.034		Tnfaip1	-1.32	0.0203
	Usp13	-1.27	0.0117		Pgd	-1.275	0.003		Trim13	-1.27	0.0227
	Xrcc1	-1.19	0.0132		PIscr1	-1.170	0.032		Trpc4ap	-1.25	0.0359
	Yipf2	-1.22	0.0481		Ptafr	-1.105	0.024		Ube 2d3	-1.21	0.0419
					Pxk	-1.148	0.036		Ube 2w	-1.26	0.0075
					Reg3a	-1.123	0.025		Ube 3a	-1.30	0.0284
					Scyl1	-1.354	0.024		Usp14	-1.39	0.0019
					Serpina3n	-1.428	0.040		Usp18	-2.05	0.0489
					Serpinb9	-1.237	0.049		Usp22	-1.32	0.0096
					Serpinf2	-1.113	0.036		Usp39	-1.26	0.0085
					Smad1	-1.324	0.047		Usp4	-1.17	0.0362
					Tfrc	-1.214	0.044				
					Thbs1	-1.638	0.037				
					TIr7	-1.255	0.035				
					Tnf	-1.459	0.020				
					Tnfrsf1a	-1.259	0.011				