

Huntingtin *HTT1a* is generated in a CAG repeat-length-dependent manner in human tissues

Franziska Hoschek¹, Julia Natan¹, Maximilian Wagner¹, Kirupa Sathasivam², Alshaimaa Abdelmoez^{1,3}, Björn von Einem¹, Gillian P. Bates², G. Bernhard Landwehrmeyer¹, Andreas Neueder^{1,*}

¹Department of Neurology, University Hospital Ulm, 89081 Ulm, Germany

²Huntington's Disease Centre, Department of Neurodegenerative Disease, Queen Square Institute of Neurology, University College London, London WC1N 3BG, United Kingdom

³Department of Pharmaceutical Organic Chemistry, Faculty of Pharmacy, Assiut University, Assiut, Egypt

***Correspondence**

Andreas Neueder

Department of Neurology, University Hospital Ulm, 89081 Ulm, Germany

P: +49 731 500 63117

E: andreas.neueder@uni-ulm.de

ORCID: [0000-0002-2389-5236](https://orcid.org/0000-0002-2389-5236)

Supporting Information

Supplementary Figures and Figure legends

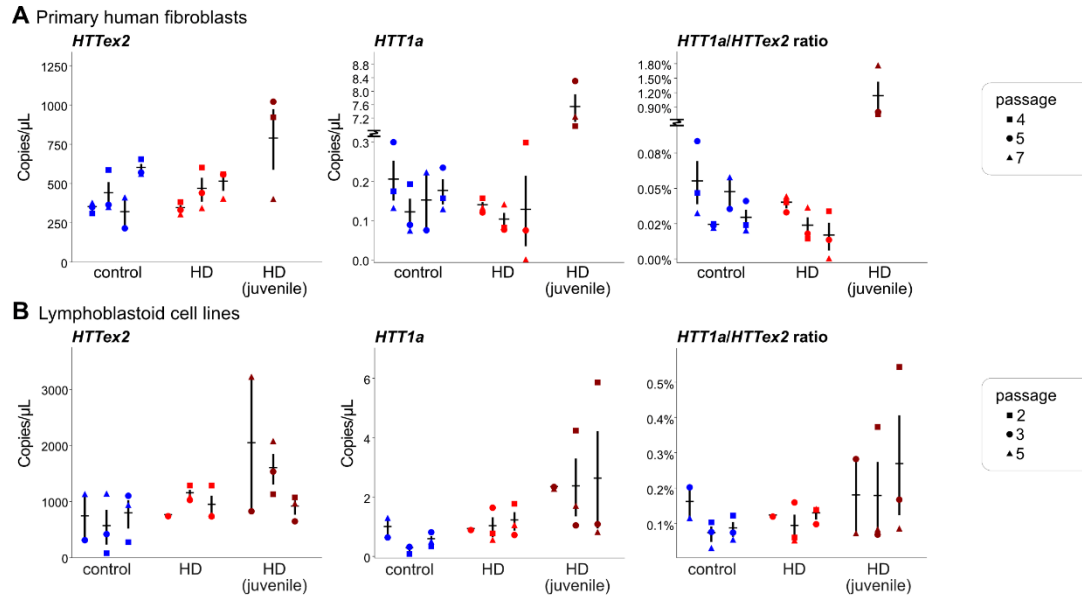


Figure S1. Time in culture has no major influence on *HTT1a* or *HTT* exon 2 expression in primary human fibroblasts and lymphoblastoid cell lines

HTT1a and *HTT* exon 2 (*HTTEx2*) expression in primary human fibroblast (A) and lymphoblastoid lines (B) was analysed in lines with a CAG repeat in the control (control), adult-onset (HD) or juvenile-onset range (HD juvenile). Each data point stack corresponds to one line with three passages as individual data points (squares, circles, triangles). CAG sizes and passage number were used as main effects in two-way ANOVA analyses and no significant differences were found.

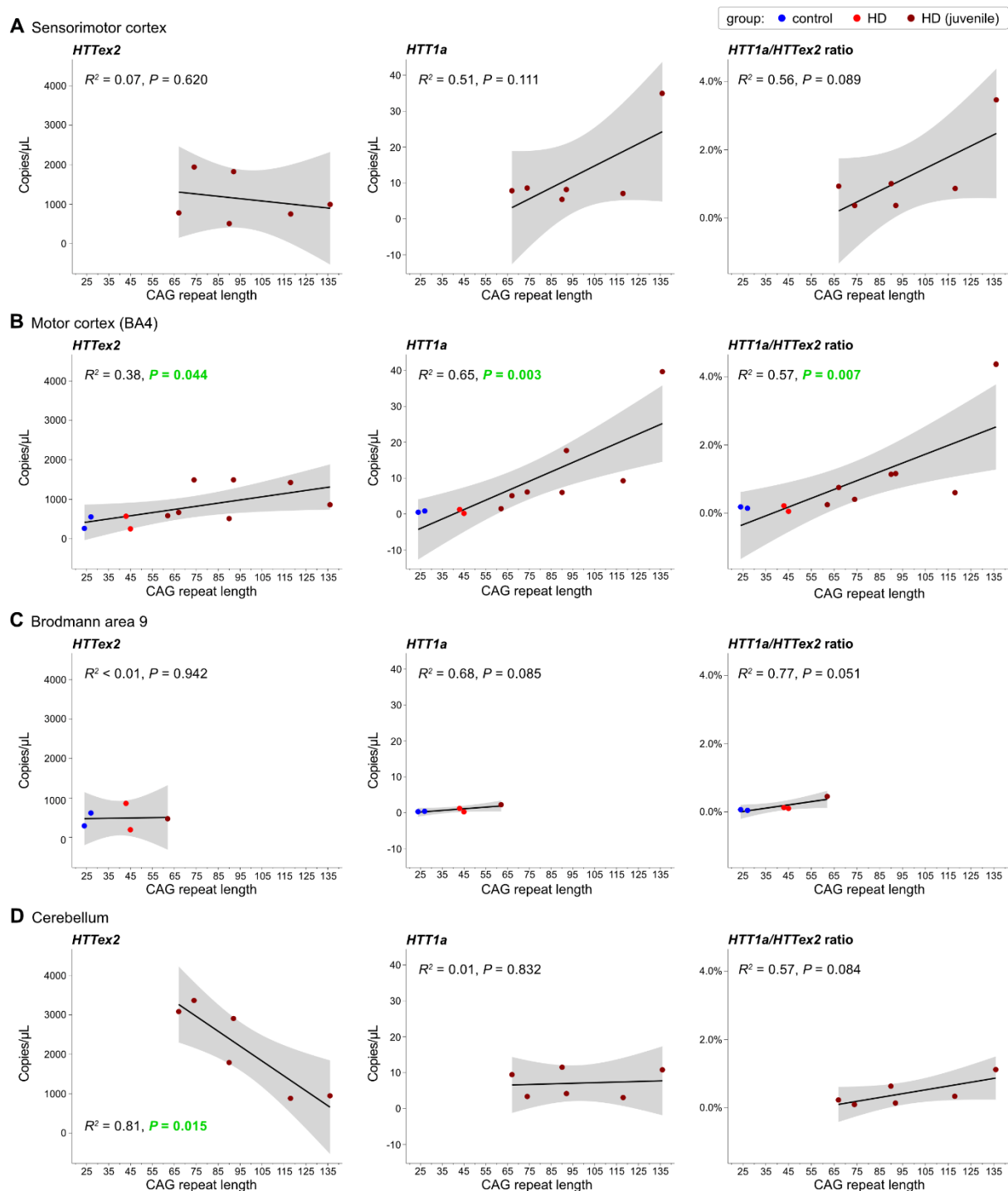


Figure S2. *HTT1a* is generated in a CAG repeat-length-dependent manner in *post mortem* motor cortex

HTT1a and *HTT* exon 2 (*HTTEx2*) expression levels in sensorimotor cortex (A), motor cortex (BA4) (B), BA9 cortex (C) and cerebellum (D) were analysed from *HTT* mutation carriers with adult-onset CAG repeat lengths (HD) or juvenile-onset CAG repeat lengths (HD juvenile) and control individuals (control), respectively. The black line represents the linear model of expression level with CAG repeat length. R^2 (coefficient of determination) and P value for the fit of the linear modelling are shown. Grey areas represent the standard error of the regression model.

Supplementary Tables

Table S1. Sample Information

Tissue	Sample ID	HD status	CAG repeat length	Tissue	Sample ID	HD status	CAG repeat length
Post mortem brain ¹	FR_13	control	24	Skeletal muscle ⁴	MTMHD_35	control	19
	FR_14	control	27		MTMHD_21	control	18
	UB_03	adult	45		MTMHD_26	control	20
	UB_11	adult	43		MTMHD_23	control	16
	UB_10	juvenile	62		MTMHD_24	control	19
	B5817	juvenile	67		MTMHD_53	control	16
	B5345	juvenile	74		MTMHD_50	control	24
	B5928	juvenile	90		MTMHD_20	adult	45
	B4522	juvenile	92		MTMHD_27	adult	48
	B4383	juvenile	118		MTMHD_38	adult	45
	B5504	juvenile	136		MTMHD_42	adult	45
Primary human fibroblasts ²	MTMHD_53	control	16		MTMHD_41	adult	43
	MTMHD_13	control	16		MTMHD_65	adult	50
	MTMHD_23	control	16		MTMHD_52	adult	46
	GM02155	control	17	Lymphoblastoid cells ⁵	EN-110915-20195	control	17
	MTMHD_07	control	18		EN-271015-00367	control	18
	MTMHD_06	adult	44		EN-241215-05520	control	23
	MTMHD_62	adult	44		EN-120915-09734	adult	42
	MTMHD_16	adult	44		EN-110915-03607	adult	41
	GM03621	juvenile	61		EN-120915-16051	adult	43
	GM04737	juvenile	64		EN-120915-37418	juvenile	67
	GM04723	juvenile	70		EN-110915-21894	juvenile	62
	GM04281	juvenile	72		EN-120915-20923	juvenile	60
	GM05539	juvenile	98		EN-120915-43070	juvenile	60
	GM09197	juvenile	177		HR-300915-21905	juvenile	66
PBMCs ³	MTMHD_45	control	27				
	MTMHD_26	control	20				
	MTMHD_40	control	18				
	MTMHD_68	control	15				
	MTMHD_56	control	18				
	MTMHD_42	adult	45				
	MTMHD_41	adult	43				
	MTMHD_05	adult	43				
	MTMHD_67	adult	46				
	MTMHD_63	adult	42				
	MTMHD_08	adult	45				

CAG sizes for *post mortem* brains¹ (BXXXX) and primary fibroblasts² (GMOXXXX) samples have been partly published in [1]. CAG sizes for PBMCs³ and skeletal muscle⁴ samples (MTMHD_XX) have been published in [2]. CAG sizes of lymphoblastoid cells⁵ (EN-X...) were and all other repeat sizes were determined by the authors. Consistency between the published and newly defined CAG sizes was ensured by reanalysis of several samples.

Supplementary references

1. Neueder, A., C. Landles, R. Ghosh, D. Howland, R.H. Myers, R.L.M. Faull, S.J. Tabrizi, and G.P. Bates, *The pathogenic exon 1 HTT protein is produced by incomplete splicing in Huntington's disease patients*. Sci Rep, 2017. 7(1): p. 1307. DOI: 10.1038/s41598-017-01510-z
2. Neueder, A., K. Kojer, T. Hering, D.J. Lavery, J. Chen, N. Birth, J. Hallitsch, S. Trautmann, J. Parker, M. Flower, et al., *Abnormal molecular signatures of inflammation, energy metabolism, and vesicle biology in human Huntington disease peripheral tissues*. Genome Biol, 2022. 23(1): p. 189. DOI: 10.1186/s13059-022-02752-5