# Appendix files

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## Appendix Figure S1.



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gmr::Gal4	
UAS::Httexon1-Q93	
UAS::fy-dsRNA <sup>KK100638</sup>	

Average no. of rhabdomeres per ommatidium 71 6-5-4-3-2-1. 0 gmr::Gal4 UAS::Httexon1-Q93 + + + + UAS::fy-dsRNA<sup>KK100638</sup> \_ +

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#### Appendix Figure S1. Data related to Figure 3.

(A) The expression of *Fuz* transcript was not affected while Fuz protein expression was abolished in *Fuz*<sup>-/-</sup> HEK293 cells. The *Fuz*<sup>-/-</sup> HEK293 cell line was generated through CRISPR/Cas9 technique. The parental HEK293 cells were used as control. n = 3.

(B) Fuz protein expression was reduced in rat primary cortical neurons upon Fuz-siRNA treatment. n = 3.

(C) Knockdown of *Fuz* expression reduced the Fuz protein expression in normal fibroblasts. n = 3.

(D) The expression level of *fuzzy* transcript was reduced in both *fuzzy*-knockdown (*fy-dsRNA*<sup>*KK100638*</sup>) and *fuzzy*-knockout (*fy*<sup>3</sup>) *Drosophila* lines. *fy*<sup>3</sup> is a null allele, it carries a 70 bp deletion in the *fy* coding region [1]. n = 3.

(E, F) (E) Neurodegenerative phenotype in SCA3 transgenic flies were suppressed in  $fy^3$  mutant background. The flies were of genotypes *w*; *gmr::Gal4 UAS::ATXN3fl-Q27/+; +/+*, *w*; *gmr::Gal4 UAS::ATXN3fl-Q27/fy<sup>3</sup>; +/+*, *w*; *gmr::Gal4/+; UAS::ATXN3fl-Q84/+* and *w*; *gmr::Gal4/fy<sup>3</sup>; UAS::ATXN3fl-Q27/fy<sup>3</sup>; +/+*, *w*; *gmr::Gal4/+; UAS::ATXN3fl-Q84/+* and *w*; *gmr::Gal4/fy<sup>3</sup>; UAS::ATXN3fl-Q84/+*. Scale bars: 5 µm. (F) is the quantification of (E). Error bars represent S.E.M., *n* = 3. For every control or experimental group, a total of 200 ommatidia collected from 20 fly eyes were examined in each replicate. Statistical analysis was performed using one-way ANOVA followed by post-hoc Tukey's test. \*\*\* *P* < 0.001. (G, H) (G) Knockdown of *fy* expression suppressed the neurodegeneration in HD transgenic flies. The flies were of genotypes *UAS::Httexon1-Q93; gmr::Gal4/+* and *UAS::Httexon1-Q93; gmr::Gal4/UAS::fy-dsRNA<sup>KK100638</sup>*. Scale bars: 5 µm. (H) is the quantification of (G). Error bars represent S.E.M., *n* = 3. For every control or experimental

group, a total of 200 ommatidia collected from 20 fly eyes were examined in each replicate. Statistical analysis was performed using two-tailed unpaired Student's *t*-test. \*\* P < 0.01. Data information: *beta-actin* or beta-tubulin was used as loading control. *n* represents the number of biological replicates. Only representative images, gels and blots are shown. Appendix Figure S2.



### Appendix Figure S2. Data related to Figure 7.

(A) Western blot analysis showing the overexpression of ATXN3tr-Q27/Q78, Httr-Q23/Q92,  $\alpha$ -synuclein and Tau proteins in rat primary cortical neurons. *n* = 3.

(B) Treatment of MPP+ induced capsase-3 cleavage in rat primary cortical neurons. n =3.

(C) Heat shock treatment increased the expression of heat shock protein 70 (Hsp70) in rat primary cortical neurons. n = 3.

(D)  $H_2O_2$  treatment increased the reactive oxygen species (ROS) production in rat primary cortical neurons. Scale bars: 50 µm. *n* = 3.

Data information: Beta-tubulin was used as loading control. *n* represents the number of biological replicates. Only representative images and blots are shown.

Appendix Table S1. Summary of the *Fuz* promoter methylation in different disease models.

Disease model	Fuz promoter	Fuz promoterMethylation	
	region change		restored by YY1
			overexpression
expanded polyQ	+117/+347CpG	hypomethylation	Yes
Αβ <sub>1-42</sub>	+117/+347CpG	hypomethylation	Yes
Tau	+117/+347CpG	hypomethylation	Yes
α-synuclein	-1962/-1861CpG	hypomethylation	No

Sample ID	Case ID	Dx	Age	Gender	PMI (minutes)	Brain Weight (grams)
SCA3-1	UMB1687	SCA3	50	Male	1,500	1,410
SCA3-2	UMB4626	SCA3	64	Male	720	1,550
SCA3-3	UMB5749	SCA3	45	Male	1,680	1,537
SCA3-4	UMB5777	SCA3	52	Male	1,320	n/a
SCA3-5	UMB5856	SCA3	61	Female	300	1,046
SCA3-6	T5147	SCA3	39	Female	1,265	1,000
CTL-1	T206	Control	49	Male	905	1,325
CTL-2	T274	Control	65	Female	1,422	1,066
CTL-3	Т99	Control	44	Male	2,955	1,817
CTL-4	T145	Control	57	Female	554	1,050
CTL-5	T343	Control	62	Male	496	1,301
CTL-6	T4812	Control	36	Male	517	1,225

Appendix Table S2. SCA3 patient and control brain sample description.

Dx: diagnosis, SCA3: spinocerebellar ataxia type 3, PMI: post-mortem interval, n/a: not available

Appendix Table S3. Clinical features of SCA3 cases and control individuals described in this study.

Variable	Control	SCA3
n	6	6
Age at death (years)	52.2 ± 11.1	51.8 ± 9.5
Male	4 (66.7%)	4 (66.7%)
Female	2 (33.3%)	2 (33.3%)
Brain Weight (grams)	1,297 ± 279	1,308 ± 266
Post Mortem Interval (minutes)	1,142 ± 957	1,131 ± 520

### Appendix Reference

1. Collier S, Gubb D (1997) Drosophila tissue polarity requires the cell-autonomous activity of the fuzzy gene, which encodes a novel transmembrane protein. *Development* **124:** 4029-4037