

Supplementary Table 1. Association between expanded *NOTCH2NLC* repeat size and clinical/MRI features

	Expanded <i>NOTCH2NLC</i> total repeat number, mean \pm SD (range)		<i>P</i> value
	present	absent	
Clinical symptoms			
Cognitive decline	148.5 \pm 78.3 (97–361, n = 11)	111.0 \pm 20.7 (94–141, n = 4)	0.32
Hyporeflexia	151.7 \pm 80.9 (97–361, n = 10)	112.2 \pm 26.0 (94–361, n = 4)	0.12
Consciousness disturbance	145.0 \pm 84.9 (94–361, n = 9)	129.2 \pm 40.2 (97–198, n = 6)	0.98
Cerebellar ataxia	133.0 \pm 36.7 (97–198, n = 9)	146.8 \pm 105.2 (94–361, n = 6)	0.37
Dysarthria	124.3 \pm 29.7 (97–175, n = 8)	154.9 \pm 97.5 (94–361, n = 7)	0.89
Encephalitis episodes	145.3 \pm 90.9 (94–361, n = 8)	130.9 \pm 37.0 (97–198, n = 7)	0.67
Gait disturbance	132.0 \pm 39.1 (97–198, n = 8)	146.0 \pm 96.1 (94–361, n = 7)	0.59
Tremor	107.6 \pm 5.9 (101–117, n = 7)	165.6 \pm 87.8 (94–361, n = 8)	0.41
Urinary dysfunction	141.4 \pm 37.8 (97–198, n = 7)	136.0 \pm 91.1 (94–361, n = 8)	0.18
Psychiatric symptoms	162.9 \pm 94.6 (97–361, n = 7)	117.3 \pm 27.5 (94–175, n = 8)	0.27
MRI features			
Cerebellar atrophy	141.7 \pm 80.4 (94–361, n = 11)	129.8 \pm 24.0 (104–158, n = 4)	0.39
DWI high-intensity lesions in corpus callosum	147.7 \pm 82.4 (97–361, n = 10)	120.2 \pm 27.8 (94–158, n = 5)	0.53
DWI high-intensity lesions in posterior lobe	134.0 \pm 41.7 (101–198, n = 6)	141.6 \pm 85.1 (94–361, n = 9)	0.47
Paravermal lesions	104.0 \pm 7.7 (97–117, n = 5)	155.8 \pm 80.0 (94–361, n = 10)	0.07

FLAIR, fluid attenuated inversion recovery; DWI, diffusion weighted imaging

Supplementary Figure 1

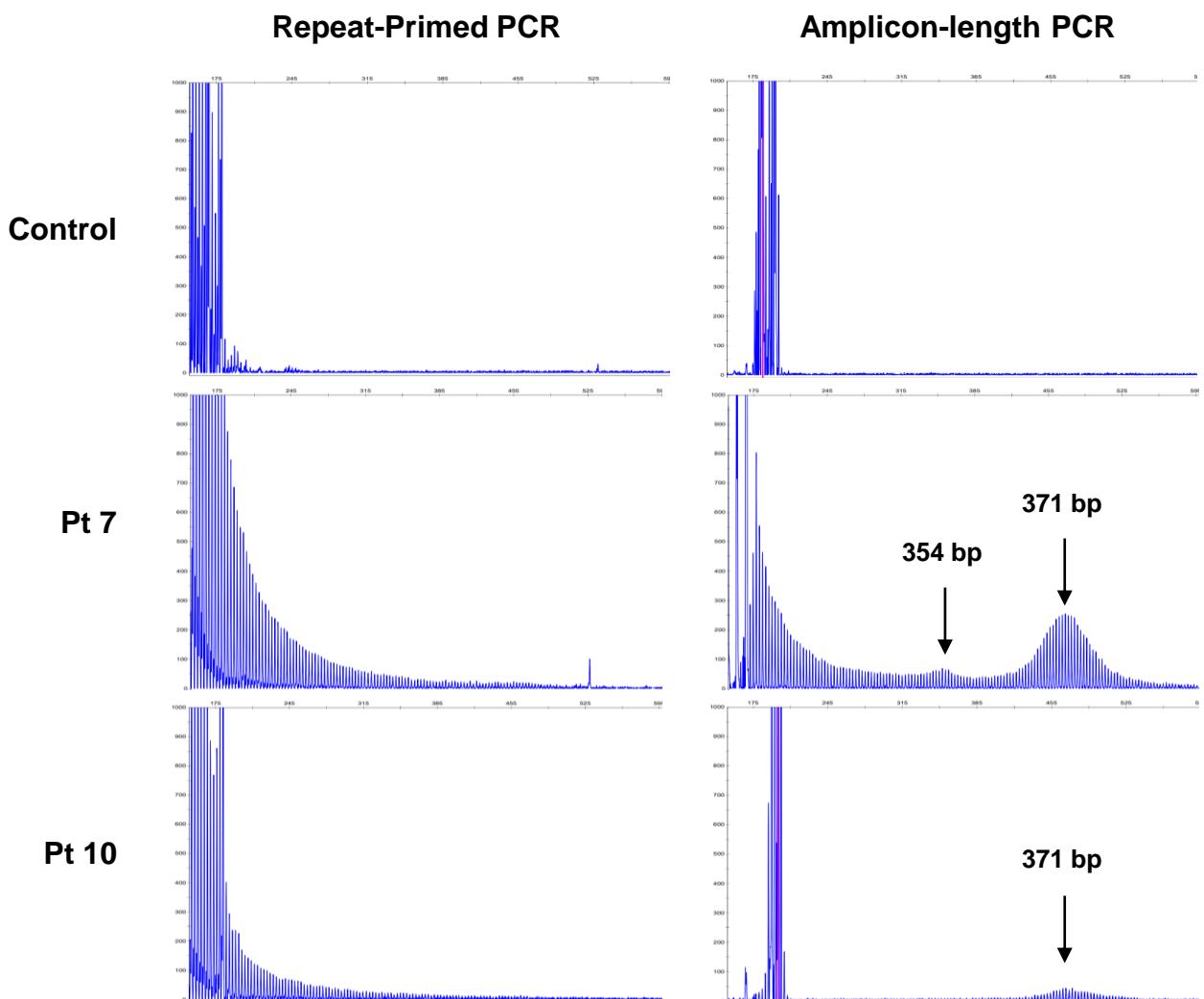


Figure Legend

Representative results of repeat-primed and amplicon-length PCR of *NOTCH2NLC*. In Pt 7 and 10, a sawtooth pattern was observed by repeat-primed PCR (*left*). In Pt 7, two peaks at 354 and 371 bp, corresponding to expanded alleles, were observed by amplicon-length PCR (*right*). In Pt 10, a single peak at 371 bp, corresponding to an expanded allele, was observed.

Supplementary Figure 2

Pt 1

Normal

Sequence logo for Pt 1 Normal sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by C (blue) at position 26, and G (green) again at positions 27-57.

Expansion

Sequence logo for Pt 1 Expansion sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by C (blue) at position 26, and G (green) again at positions 27-57. A small peak for A (yellow) is visible at position 58.

Pt 2

Normal

Sequence logo for Pt 2 Normal sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and G (green) again at positions 27-69.

Expansion

Sequence logo for Pt 2 Expansion sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and G (green) again at positions 27-69. A small peak for A (yellow) is visible at position 70.

Pt 3

Normal

Sequence logo for Pt 3 Normal sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-60.

Expansion

Sequence logo for Pt 3 Expansion sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-60. A small peak for A (yellow) is visible at position 61.

Pt 4

Normal

Sequence logo for Pt 4 Normal sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-75.

Expansion

Sequence logo for Pt 4 Expansion sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-75. A small peak for A (yellow) is visible at position 76.

Pt 5

Normal

Sequence logo for Pt 5 Normal sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-80.

Expansion

Sequence logo for Pt 5 Expansion sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-80. A small peak for A (yellow) is visible at position 81.

Pt 6

Normal

Sequence logo for Pt 6 Normal sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-60.

Expansion

Sequence logo for Pt 6 Expansion sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-60. A small peak for A (yellow) is visible at position 61.

Pt 8

Normal

Sequence logo for Pt 8 Normal sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-60.

Expansion

Sequence logo for Pt 8 Expansion sample. The logo shows a strong bias towards G (green) at positions 1-25, followed by G (green) at position 26, and C (blue) at positions 27-60. A small peak for A (yellow) is visible at position 61.

Supplementary Figure 2 (continued)

Pt 9

Normal

Pt 10

Normal

Pt 11

Normal

Pt 12

Normal

Pt 13

Normal

Pt 15

Normal

Figure Legend

Repeat sequences in *NOTCH2NLC* in patients with NIID were shown. Pt 2 carried a pure GGC repeat expansion. Other patients carried GGC repeat expansions with other trinucleotide sequences such as GGA, AGC, and GAC.

Supplementary figure 3

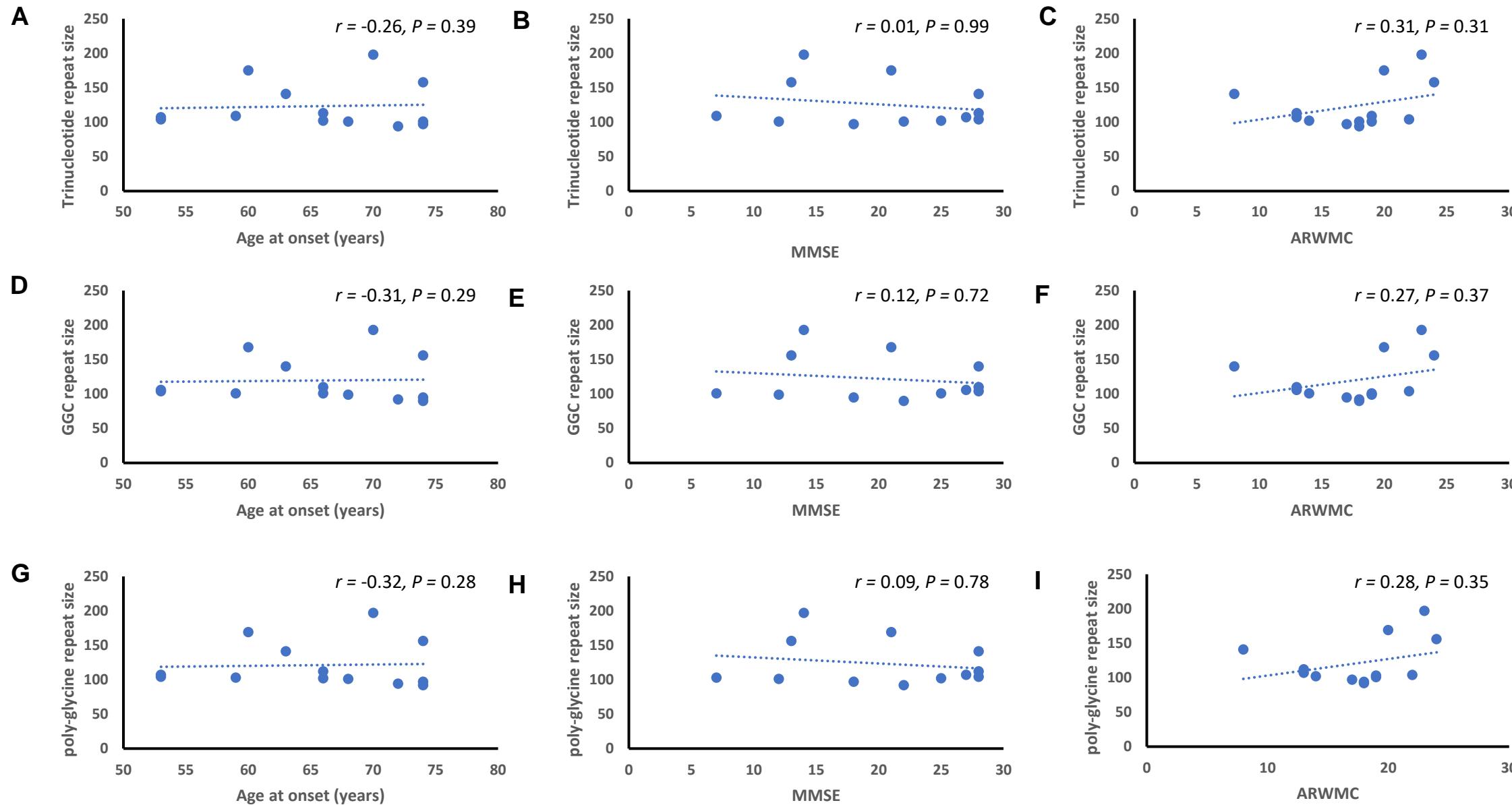


Figure legend

Correlation between trinucleotide repeat length and age at onset (**A**), MMSE (**B**), and ARWMC (**C**) were shown. Correlations of these parameters were analyzed based on cumulative GGC repeat length (**D-F**) or poly-glycine repeat length (**G-I**).