TABLE 1 | Features of trinucleotide expansion in humans

FROM THE FOLLOWING ARTICLE:
Mechanisms of trinucleotide repeat instability during human development
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Disease	Sequence	Location	Parent of origin of expansion	Repeat number (normal)	Repeat number (pre-mutation)	Repeat number (disease)	Somatic instability
Diseases with coding TNRs							
DRPLA	CAG	*ATN1* (exon 5)	P	6–35	35–48	49–88	Yes
HD	CAG	*HTT* (exon 1)	P	6–29	29–37	38–180	Yes
OPMD	GCN	*PABPN1* (exon 1)	P and M	10	12–17	>11	None found in tissue tested (hypothalamus)
SCA1	CAG	*ATXN1* (exon 8)	P	6–39	40	41–83	Yes
SCA2	CAG	*ATXN2* (exon 1)	P	<31	31–32	32–200	Unknown
SCA3 (Machado–Joseph disease)	CAG	*ATXN3* (exon 8)	P	12–40	41–85	52–86	Unknown
SCA6	CAG	*CACNA1A* (exon 47)	P	<18	19	20–33	None found
SCA7	CAG	*ATXN7* (exon 3)	P	4–17	28–33	>36 to >460	Yes
SCA17	CAG	*TBP* (exon 3)	P > M	25–42	43–48	45–66	Yes
SMBA	CAG	*AR* (exon 1)	P	13–31	32–39	40	None found
Diseases with non-coding TNRs							
DM1	CTG	*DMPK* (3′ UTR)	M	5–37	37–50	<50	Yes
DM2	CCTG	*CNBP* (intron 1)	Uncertain	<30	31–74	75–11,000	Yes
FRAX-E	GCC	*AFF2* (5′ UTR)	M	4–39	40–200	>200	Unknown
FRDA	GAA	*FXN* (intron 1)	Recessive	5–30	31–100	70–1,000	Yes
FXS	CGG	*FMR1* (5′ UTR)	M	6–50	55–200	200–4,000	Yes
HDL2	CTG	*JPH3* (exon 2A)	M	6–27	29–35	36–57	Unknown
SCA8	CTG	*ATXN8OS* (3′ UTR)	M	15–34	34–89	89–250	Unknown
SCA10	ATTCT	*ATXN10* (intron 9)	M and P (smaller changes with M)	10–29	29–400	400–4,500	Yes
SCA12	CAG	*PPP2R2B* (5′ UTR)	M and P (more unstable with P)	7–28	28–66	66–78	None found