Supplemental Table: Main findings of each arm of the study.

Arm of Study	Main Findings
Unrelated cohort (N=781)	• 424 (77.7%) FECD cases were CTG18.1exp+ • 18 (7.7%) controls were CTG18.1exp+ • A diagnosis of FECD associated with CTG18.1 expansion status ($p=2.48x10^{-44}$) and $CTG18.1_L$ ($p=3.38x10^{-46}$) • CTG18.1exp+ status associated with FECD severity ($p=5.62x10^{-7}$) • FECD severity associated with $CTG18.1_L$ among FECD cases ($p=8.8x10^{-4}$)
Family cohort (N=112 families; 331 subjects)	• 146 (67.0%) FECD cases were CTG18.1exp+ • 27 (23.9%) controls were CTG18.1exp+ • A diagnosis of FECD associated with CTG18.1 expansion status ($p=6.23x10^{-13}$) and $\log_{10}$ ($CTG18.1_L$) ($p=8.0x10^{-6}$) • Penetrance of FECD associated with CTG18.1exp+ was 85.4%
CTG18.1exp+ families (N=87 families; 249 subjects)	• Penetrance of FECD increased by age quartile (range: 44.4-86.2%) • No sex difference in penetrance of FECD (p=0.08)
Parent-offspring relationships from CTG18.1exp+ families (N=62 families; 106 offspring)	• CTG18.1 expansion transmitted to offspring in 62 (58.5%) parent-offspring relationships • 41 (66.1%) CTG18.1exp+ offspring exhibited the FECD phenotype • No significant difference in transmission of the expanded repeat by parental sex (p=0.62) • 8 (18.2%) offspring who did not inherit the CTG18.1 expansion exhibited the FECD phenotype
Intergenerational instability among CTG18.1exp+ offspring (N=62)	• 8 (12.9%) had change in $CTG18.1_L$ $\geq$50 repeats • 3 (4.8%) expansions of 1,900 repeats • 5 (8.1%) contractions (range: -900 to -1,900 repeats)