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Pathogenic Huntingtin Repeat Expansions in Patients with Frontotemporal Dementia and Amyotrophic Lateral Sclerosis

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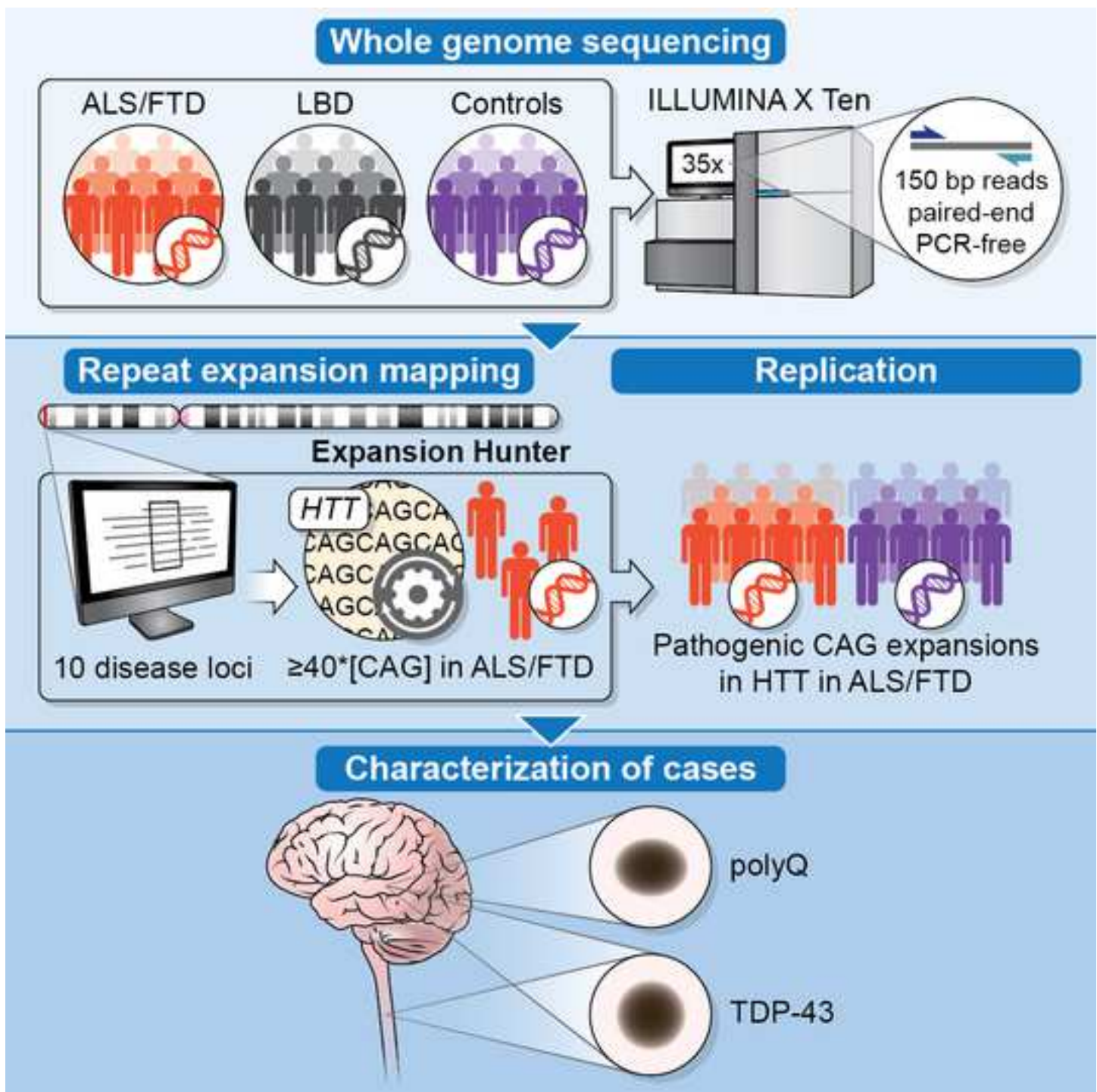
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Pathogenic Huntingtin Repeat Expansions in Patients with Frontotemporal Dementia and Amyotrophic Lateral Sclerosis

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SUMMARY

We examined the role of repeat expansions in the pathogenesis of frontotemporal dementia (FTD) and amyotrophic lateral sclerosis (ALS) by analyzing whole-genome sequence data from 2,442 FTD/ALS patients, 2,599 Lewy body dementia (LBD) patients, and 3,158 neurologically healthy subjects. Pathogenic expansions (range: 40 to 64 CAG repeats) in the huntingtin (*HTT*) gene were found in three (0.12%) patients diagnosed with pure FTD/ALS syndromes, but were not present in the LBD or healthy cohorts. We replicated our findings in an independent collection of 3,674 FTD/ALS patients. Postmortem evaluations of two patients revealed the classical TDP-43 pathology of FTD/ALS, as well as huntingtin-positive, ubiquitin-positive aggregates in the frontal cortex. The neostriatal atrophy that pathologically defines Huntington's disease was absent in both cases. Our findings reveal an etiological relationship between *HTT* repeat expansions and FTD/ALS syndromes, and indicate that genetic screening of FTD/ALS patients for *HTT* repeat expansions should be considered.

KEY WORDS: amyotrophic lateral sclerosis, frontotemporal dementia, Lewy body dementia, Huntington's disease, whole-genome sequencing, huntingtin, repeat expansions.

INTRODUCTION

Frontotemporal dementia (FTD, OMIM #600274) and amyotrophic lateral sclerosis (ALS, OMIM #105400) are progressive neurological disorders that are characterized clinically by cognitive deficits, language abnormalities, and muscle weakness (Neary et al., 2005; Rowland and Shneider, 2001). These aggressive illnesses typically occur between the ages of 40 and 70, leading to death within three to eight years of symptom onset (Chiò et al., 2013; Neary et al., 2005). Approximately 15,000 individuals die of FTD or ALS in the United States annually (Arthur et al., 2016), and there are no treatments that halt the degenerative process. Clinical, genetic, and neuropathologic data demonstrate that FTD and ALS are closely related conditions that exist along a spectrum of neurological disease (Lillo and Hodges, 2009).

Though progress has been made, much remains unclear about the genetic etiology of the FTD/ALS spectrum. Approximately 40% of FTD cases are familial, and causative mutations have been identified, most notably in *MAPT*, *GRN*, *C9orf72*, and *VCP* (Ferrari et al., 2019). In ALS, 10% of patients report a family history of the disease. The genetic etiology is known for two-thirds of these familial cases, whereas the underlying gene is recognized in 10% of sporadic cases (Chia et al., 2018; Renton et al., 2014). The intronic repeat expansion of the *C9orf72* gene is the most common cause of FTD and ALS (Majounie et al., 2012). Other repeat expansions have been implicated in neurological diseases. These include polyglutamine repeats observed in Huntington's disease (McDonald et al., 1993) and spinobulbar muscular atrophy (La Spada et al., 1991), and more complex expansions in the *RFC1* gene that were recently associated with autosomal recessive cerebellar ataxia (Cortese et al., 2019). Together, these data suggest that repeat expansions play a critical role in the pathogenesis of neurodegenerative diseases. This

type of mutation may be amenable to antisense oligonucleotide therapy, adding further incentive to their identification (Tabrizi et al., 2019).

The discovery of new genetic causes of FTD and ALS provides insights into the cellular mechanisms of neurodegeneration (Renton et al., 2014). From a clinical perspective, the molecular characterization of the genetic causes of disease in a patient helps to establish an accurate diagnosis and the genetic counseling of the patients and their families. It is also a necessary first step towards future precision medicine. To explore the genetic architecture of neurodegenerative disorders, we performed whole-genome sequencing in patients diagnosed with FTD/ALS, LBD, and neurologically healthy individuals and systematically assessed the role of previously identified, disease-causing repeat expansions.

RESULTS

Repeat analysis identifies FTD/ALS patients harboring *HTT* CAG repeat expansions

After quality control, whole-genome sequence data from 2,442 patients diagnosed with FTD/ALS, 2,599 LBD patients, and 3,158 neurologically healthy individuals were available for analysis. We used the ExpansionHunter – Targeted tool to assess ten repeat expansion motifs that have been previously associated with neurological disease and have been experimentally validated for this algorithm (Dolzhenko et al., 2019; Dolzhenko et al., 2017). The examined genes included *AR*, *ATN1*, *ATXN1*, *ATXN3*, *C9orf72*, *DMPK*, *FMRI*, *FXN*, *HTT*, and *PHOX2B* (**Table S1**). Consistent with the previous publications (Dolzhenko et al., 2019; Dolzhenko et al., 2017), we found excellent concordance between the identification of the known *C9orf72* repeat expansion using the ExpansionHunter – Targeted algorithm and a repeat-primed PCR assay for

C9orf72 (Majounie et al., 2012) among our samples (n = 7 (0.3%) discordance out of 2,147 samples with information for both assays, kappa = 0.974).

We identified three FTD/ALS patients who carried full-penetrance pathogenic repeat expansions (≥ 40) in the *HTT* gene, representing 0.12% of the patients diagnosed with FTD/ALS disorders. The sizes of the detected *HTT* expansions were 41, 40, and 40 repeats, which are deemed to be fully-penetrant (**Table 1**). In contrast, none of the LBD cases or healthy control subjects carried pathogenic *HTT* expansions. The lengths of the repeat expansions in these three FTD/ALS patients were confirmed by repeat-primed PCR and by cloning and Sanger sequencing (**Figure 1A** and **Figure S1**). We did not observe a higher rate of intermediate (27–35) or low-penetrance (36–39) *HTT* repeat expansions among patients diagnosed with FTD/ALS or LBD compared to control subjects (**Figure 1B**). Aside from *C9orf72* as a common cause of FTD and ALS, none of the other repeat expansions evaluated by the ExpansionHunter - Targeted algorithm displayed a similar pattern of being present in cases and absent in control subjects (see **Table S1**). For this reason, we focused our efforts on the *HTT* repeat expansion in FTD/ALS patients.

To replicate our findings, we assessed the *HTT* CAG repeat length in an independent cohort of 3,674 patients diagnosed with FTD/ALS spectrum disorders and 210 healthy control participants. We detected an additional five patients diagnosed with FTD/ALS that carried pathogenic *HTT* repeat expansions, representing 0.14% of this replication cohort (sizes 64, 40, 44, 40, 41 for Patients #4–8 in **Table 1**). We compared this to published data on the occurrence of *HTT* repeat expansions in the general population, which was only 0.03% (10 individuals had ≥ 40 repeats out of 31,463)(Gardiner et al., 2019; Peplow, 2016).

Overall, the carrier rate among patients diagnosed with FTD/ALS spectrum disorders in the discovery and replication cohorts was 4.4 times higher than that observed among healthy

individuals (Fisher's exact test p -value = 2.68×10^{-3} , odds ratio = 4.55, 95% confidence interval = 1.56–12.80, **Table 1**). None of the patients found to carry the *HTT* full-penetrance expansions had additional disease-causing mutations in fifty other genes implicated in FTD/ALS and other neurodegenerative diseases (see Methods for gene list). We performed a genome-wide association study (GWAS) on the FTD/ALS discovery cohort, and single-variant analysis similarly failed to identify loci that would account for our findings (**Figure S2**).

FTD/ALS patients with pathogenic *HTT* repeats have multiple haplotypes and exhibit somatic instability

The FTD/ALS patients carrying *HTT* full-penetrance repeat expansions harbored several different haplotypes that have previously been associated with this locus (**Figure S3**). The presence of multiple haplotypes indicated diverse ancestral sources among our samples, making it unlikely that another genetic variant outside of the expansion was causing disease in these patients. Furthermore, we did not detect interruptions within the *HTT* repeat expansion in any of the patients. We only encountered the loss of the CAA-CAG trailing sequence in a single individual (patient #8, **Figure 1D**).

Additionally, we examined somatic instability across multiple brain regions obtained from the postmortem tissues of two patients diagnosed with FTD/ALS (Patient #5, Patient #8), and from a Huntington's disease patient carrying 41 CAG repeats (**Figure 2**). We utilized repeat-primed PCR GeneMapper chromatograms to quantify CAG repeat length distributions, as recently published (Mouro Pinto et al., 2020) (**Figure S4**). The motor cortex and globus pallidus/putamen regions displayed the most instability in Patient #5 and Patient #8, whereas the spinal cord was among the most stable. A similar pattern was observed in the Huntington's disease patient. The

range of expansion indices (range = 0.042–0.985) observed in the FTD/ALS patients was also consistent with reports from Huntington’s disease patients carrying lower pathogenic-range *HTT* repeat expansions (Mouro Pinto et al., 2020).

Clinicopathologic analysis reveals huntingtin-positive aggregates predominantly in the frontal cortex

The clinical details of the eight patients carrying the *HTT* full-penetrance, pathogenic repeat expansions are summarized in **Table 2** and described in the supplemental information. None of the patients reported choreoathetosis. Four patients reported a family history of neurological disease. Patient #4 (**Table 2**) was an outlier among the cases we identified as carrying *HTT* pathogenic repeat expansions. She presented at 17 years of age with cognitive decline, supranuclear vertical gaze palsy, parkinsonism, postural instability, gait disturbance, spasticity, and hyperreflexia in the lower limbs. Treatment with levodopa did not yield a clinical improvement. Genetic screening of *HTT* performed at the time of presentation was incorrectly reported as normal, and she was initially diagnosed with FTD-PSP despite her young age. A repeat genetic panel conducted several years later to investigate possible causes of young-onset dementia correctly identified an expanded *HTT* repeat allele. Her diagnosis was updated to young-onset Huntington’s disease (Westphal variant). Her father had presented with a similar syndrome of cognitive decline, gait disorder, and dysarthria in his late twenties, and, post hoc after his daughter’s genetic diagnosis, was diagnosed with Huntington’s disease.

We examined postmortem brains obtained from two of our patients harboring *HTT* full-penetrance CAG repeats. The first patient was a woman carrying 40 *HTT* CAG repeats, who developed ALS symptoms at the age of 56 and died eleven years later of respiratory failure

following a typical course of motor neuron disease (**Table 2**, Patient #5). Postmortem examination showed mild atrophy of the precentral gyrus and thinning of the spinal cord anterior roots. Microscopic examination revealed classical neuropathological features of ALS: there was a loss of the motor neurons of the spinal cord and hypoglossal nuclei (**Figure 3A-B**). Staining with anti-TDP-43 antibodies showed rare neurons with nuclear to cytoplasmic TDP-43 translocation, and occasional neuropil skeins confined to the prefrontal cortex (Brodmann area 9, BA9; **Figure 3C**). Neither aberrant TDP-43 translocation nor ubiquitinated inclusions were detected in the dentate gyrus.

Interestingly, dual staining of the prefrontal cortex and striatum using anti-huntingtin/p62 antibodies showed nuclear and cytoplasmic aggregates of huntingtin and p62 with the highest density observed in the infragranular layers of the prefrontal cortex (**Figure 3D**). Ubiquitinated nuclear inclusions were found in the tail of the caudate nucleus (**Figure 3H**) and the frontal cortex (not shown). However, there was no atrophy, neuronal loss or active gliosis in the striatum (**Figures 3E-F, 3H-I**).

The second brain evaluated postmortem was that of a man carrying 41 CAG repeats in *HTT*, who presented with right foot weakness at age 61. He was diagnosed with ALS based on disease progression and electromyography, and he died from respiratory failure nine years after symptom onset following a typical course of motor neuron disease (Patient #8, **Table 2**).

Postmortem examination showed mild atrophy of the precentral gyrus and thinning of the anterior spinal roots. There was otherwise no cerebral cortical or striatal atrophy (**Figure 4A**), or evidence of neuronal loss or gliosis in the striatum on microscopic examination (**Figure 4B**). Staining for ubiquitin (**Figure 4C**) and polyglutamine showed scattered nuclear and cytoplasmic and neuropil aggregates within the striatum (**Figure 4D**) and motor cortex (**Figure 4E**).

Polyglutamine aggregates were not detected in the spinal cord. There was a marked loss of spinal motor neurons (**Figure 4F**) and degeneration of the corticospinal tracts. Staining with anti-phospho-TDP-43 antibodies showed ALS-type TDP-43 cytoplasmic inclusions within some residual motor neurons (**Figure 4F, inset**).

To confirm the specificity of our pathological findings, we examined the prefrontal cortex (BA9) obtained from postmortems of individuals without Huntington's disease using the anti-huntingtin (2B4) immunostain previously used. These specimens consisted of four neurologically healthy individuals, three patients diagnosed with FTD/ALS, two patients with Alzheimer's disease, and one patient with diffuse LBD. All ten cases showed weak cytoplasmic immunostaining within neurons (**Figure S5A-B**) and did not show aggregation as seen in the two ALS cases with CAG expansions (**Figures 3–4**) or in Huntington's disease patients (**Figure S5C**). Microscopic examination of the spinal cords of nine patients diagnosed with typical Huntington's disease did not show spinal motor neuron loss.

DISCUSSION

Our data indicate that pathogenic CAG repeat expansions in *HTT* can give rise to FTD/ALS syndromes that are clinically distinct from the classical Huntington's disease syndrome. A careful review of the clinical features of the patients carrying pathogenic *HTT* expansions confirmed the diagnosis of FTD or ALS in seven out of the eight patients. None of the patients manifested choreoathetoid movements during their illness or reported a family history of Huntington's disease. Furthermore, the postmortem findings of two of our patients with *HTT* full-penetrance repeat expansions displayed the classical neuropathologic features of ALS, including loss of motor neurons of the anterior horns and hypoglossal nuclei, and the presence of

TDP-43-positive inclusions, thereby ruling out mimic syndromes as an explanation of our findings. However, the pathogenic repeat expansions' effects were corroborated by the occurrence of polyglutamine/huntingtin co-pathology within the frontal lobes. Finally, pathogenic *HTT* repeat expansions were specific to FTD/ALS cases, as they were not found in a similar-sized cohort of patients diagnosed with LBD.

It is possible that the patients carrying a *HTT* repeat expansion were simply misdiagnosed cases of atypical Huntington's disease or suffered from two different neurodegenerative diseases by chance, and they would have developed the classic Huntington's disease symptoms had they lived long enough. We believe that these are unlikely scenarios for several reasons. First, we identified multiple FTD/ALS patients in our discovery cohort following the same clinical pattern and found a similar occurrence rate in our replication cohort. In contrast, full-penetrance pathogenic *HTT* expansions were not present in our LBD or control whole-genome sequence data. Second, the apparently healthy striatum in both patients who underwent postmortem evaluation diminishes the likelihood of subclinical Huntington's disease as an explanation for their symptoms. The choreoathetoid movements observed in Huntington's disease originate from the striatum, and the lack of detectable neuronal loss on general surveys or reactive gliosis in this region of our FTD/ALS patients implies that the motor neuron disease was not masking these symptoms. Third, two of our eight patients lived at least nine years after symptom onset and did not manifest motor signs of Huntington's disease during this extended survival period. Fourth, the prevalence rates of FTD (22 per 100,000 population) (Onyike and Diehl-Schmid, 2013), ALS (6 per 100,000) (Chiò et al., 2013), and Huntington's disease (3 per 100,000) (Pringsheim et al., 2012) indicate that, by chance, there should only be three cases of disease co-occurrence in the entire United States population of 327 million. Instead, we identified eight patients among a

moderately-sized cohort of FTD/ALS cases (n = 6,116 patients). Finally, the age at onset among our patients overlapped with the predicted age at onset of Huntington's disease based on their CAG repeat length (**Figure 1C**).

Regardless of the semantic debate as to whether it is correct to designate *HTT* repeat expansions as a genetic cause of FTD/ALS spectrum disorders, our findings have direct implications for the clinical care of patients presenting with these neurological conditions and the neuropathologic staging of disease. Although there have been previous reports of the coexistence of FTD/ALS and Huntington's disease (Chhetri et al., 2014; Kanai et al., 2008; Nielsen et al., 2010; Papageorgiou et al., 2006; Phukan et al., 2010; Rubio et al., 1996; Sadeghian et al., 2011; Tada et al., 2012), pathogenic *HTT* mutations have not been described in cases of pure FTD and ALS. Even though these expansions account for less than 1% of FTD and ALS cases, clinical practice should be adapted to include regular screening of these patient populations for this mutation, particularly in light of the antisense oligonucleotide treatments targeting the *HTT* locus that are undergoing clinical trials (Tabrizi et al., 2019). The uncertainty and challenge in obtaining an early accurate diagnosis for patient #4 provide further support for the clinical utility of genetic testing for *HTT* in FTD/ALS syndromes.

Pathogenic *HTT* repeats tend to expand in length. This somatic instability increases with age and longer repeat expansion lengths, and varies from tissue to tissue. In particular, specific brain regions, such as the striatum and the cerebral cortex, have consistently demonstrated greater somatic instability, while the spinal cord is relatively stable (Mouro Pinto et al., 2020; Kennedy et al., 2003; Swami et al., 2009; Telenius et al., 1994; De Rooij et al., 1995). Our somatic instability analysis revealed similar tissue-specific profiles among our two patients. Interestingly, the motor cortex is a vulnerable area of pathology for FTD/ALS and displayed the maximum

level of somatic instability within our samples, a finding that is consistent with Huntington's disease patients. Given the higher levels of somatic instability observed in the motor cortex, the clinical presentation and pathological findings may arise from a tissue-specific instability (Mouro Pinto et al., 2020). Under this paradigm, the patients presenting with an FTD/ALS phenotype may have a distinct pattern of *HTT* CAG repeats across the different brain regions that leads to specific downstream pathology and clinical presentations.

From a neuropathologic perspective, we have identified a pathologic subtype that is distinct from the classical features observed in the brains of Huntington's disease patients (Vonsattel et al., 1985). This novel pattern is characterized by abundant huntingtin-positive, ubiquitin-positive inclusions in the frontal cortex and the absence of detectable neostriatal degeneration, with scarce TDP-43 positive co-pathology. The neuropathologic staging of Huntington's disease, as defined by Vonsattel and colleagues in 1985 (Vonsattel et al., 1985), rests on the progressive striatal degeneration. Based on our work, an addendum of the neuropathologic consensus criteria for diagnosing Huntington's disease should be considered to capture this subtype's precise frequency among the disease population.

Our study has several limitations. Whereas our cohorts focused on individuals of European ancestry, future studies should determine the importance of *HTT* expansions among non-European FTD/ALS spectrum disorders. Moreover, our research has limited power due to the rarity of these disorders. Based on the carrier rate observed in our study, we would require approximately 150,000 samples to achieve a genome-wide significance level of 5×10^{-8} based on a Bonferroni correction and 80% power. Such a conservative threshold is an implicit obstacle to identifying rare genetic causes of any rare disease. We hope that future studies and meta-analyses can meet these standards, and indeed we have made our data publicly available with

that goal in mind. In the meantime, researchers in the rare disease space must rely on objective collateral evidence to confirm the validity of their findings. In our example, the extra data pointing to *HTT* repeat expansions as a rare cause of FTD/ALS spectrum disorders include the similar mutation frequency across cohorts, the lack of similar findings in other neurological diseases, and the prior knowledge that similar-sized *HTT* repeat expansions cause neurodegeneration. Most convincingly, our autopsy data show a distinct pattern of huntingtin pathology in the frontal cortices in multiple patients that was not present in healthy individuals or patients with other neurological disorders.

There is an increasing consensus that molecularly-defined genetic causes of disease can present with heterogeneous neuropsychiatric syndromes. The polyglutamine expansion diseases spinocerebellar ataxia type 2 (SCA2) and 3 (SCA3) typically cause ataxia but can also cause levodopa-responsive parkinsonism (Simon-Sanchez et al., 2005). This consideration is particularly valid for frontal lobe diseases that can present with protean syndromes. For example, patients with *MAPT* mutations can present with behavioral variant FTD, nonfluent variant primary progressive aphasia, progressive supranuclear palsy, or corticobasal syndrome (van Swieten et al., 2000), and the pathogenic repeat expansion in the *C9orf72* gene has united two clinically disparate neurologic illnesses, FTD and ALS, into a single disease entity (Majounie et al., 2012). It may be worthwhile to screen patients presenting with psychiatric symptoms later in life or with other dementias to elucidate the entire phenotypic spectrum associated with pathogenic *HTT* repeat expansions.

We have made the individual-level genome sequence data for our patients and control subjects publicly available on the dbGaP web portal as a resource for other researchers. Our research highlights the power of performing whole-genome sequencing in large cohorts of patients with

complex neurodegenerative syndromes. We prioritized the screening of autopsy samples, as it allowed us to evaluate the neuropathologic changes associated with genetic variation quickly. As this technology's cost decreases, the size of cohorts that can undergo whole-genome sequencing will increase, enhancing our ability to detect rare, clinically actionable genetic mutations underlying neurologic diseases. The emergence of high-throughput, long-range sequencing will further strengthen our ability to identify novel repeat expansions driving neuropsychiatric disorders (Sedlazeck et al., 2018).

Our work leads to an increase in diagnostic accuracy and a refinement of the phenotype characteristics associated with pathogenic *HTT* repeat expansions. Although our discovery accounts for a small subset of FTD/ALS patients, clinicians should be aware of this unusual presentation associated with pathogenic *HTT* repeat expansions. They should consider instituting testing for their FTD and ALS patients, especially as it paves the way for disease-modifying therapies in this small patient subset.

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AUTHOR CONTRIBUTIONS

L.B., G.B., C.B.B., P.C., A.C., R.F., L.F., R.G., J.D.G., J.A.H., M.B.H., R.A.H., K.I., E.J., P.M.J., N.K., J.E.L., H.R.M., C.F.N., S.P., S.M.R., O.A.R., G.R., J.R., M.R., S.W.S., V.S.,

A.B.S., T.D.S., F.T., T.T., A.T., B.J.T., V.V., J.V., and M.L.W. collected and prepared the samples and performed the clinical evaluations. Y.A., S.A., R.C., A.C., C.L.D., R.D., J.D., R.F., J.G., M.B.H., R.A.H., P.K., J.E.L., H.R.M., M.K.P., M.S.S., T.D.S., Ar.T., V.V., C.V., J.V., and S. conducted the experiments and the data analysis. R.D., S.W.S., and B.J.T. wrote the manuscript.: A.C., R.F., L.F., J.G., J.A.H., M.B.H., J.E.L., H.R.M., A.B.S., S.W.S., and B.J.T. designed and supervised the experiments.

DECLARATION OF INTEREST

S.P-B, A.B.S., J.A.H., H.R.M, and B.J.T. hold US, EU, and Canadian patents on the clinical testing and therapeutic intervention for the hexanucleotide repeat expansion of C9orf72. S.W.S. serves on the Scientific Advisory Council of the Lewy Body Dementia Association and is an editorial board member for the Journal of Parkinson's Disease. B.J.T. is an editorial board member for JAMA Neurology, JNNP, and Neurobiology of Aging. V.S. is on the journal editorial boards of Amyotrophic Lateral Sclerosis, European Neurology, American Journal of Neurodegenerative Diseases, and Frontiers in Neurology. He has also received compensation for consulting services and speaking activities from AveXis, Cytokinetics, Italfarmaco, and Zambon. J.B.R is editor for Brain, and has received compensation for consulting services from Asceneuron, Biogen, UCB, Astex, and SV Health. J.E.L. is a member of the scientific advisory board for Cerevel Therapeutics, and a consultant and may provide expert testimony for Perkins Coie LLP.

MAIN FIGURE TITLES AND LEGENDS

Figure 1. Repeat sizing analysis identifies FTD/ALS patients harboring *HTT* CAG repeat expansions.

(A) An ideogram of chromosome 4 showing the *HTT* gene location at 4p16.3, the gene transcript (exon 1 in red), and representative repeat-primed PCR chromatograms depicting wild-type and *HTT* CAG repeat expansions. (B) The distributions of *HTT* CAG repeat expansions in the FTD/ALS (n = 2,442), LBD (n = 2,599), and control (n = 3,158) discovery cohorts. Insets are magnified views showing the number of cases carrying CAG repeat expansions ≥ 36 repeats. (C) Ages at symptom onset among FTD/ALS patients versus the size of their *HTT* repeat expansions. The curve represents the estimated onset age and corresponding standard deviation based on the number of CAG repeats (Langbehn et al., 2010). (D) The allelic structure of patients carrying *HTT* repeat expansions. The pathogenic repeat sequence is represented by $[\text{CAG}]_n$, where n corresponds to the number of repeats. The trailing CAG-CAA glutamine sequence, the CCG-CCA proline sequence, and the $[\text{CCT}]_n$ codons are also shown (Ciosi et al., 2019). See also Figures S1, S2, S3, and S6.

Figure 2. Quantitative analysis of somatic *HTT* mosaicism across brain regions in FTD/ALS and Huntington's disease patients.

(A-C) Measurements of somatic mosaicism across brain regions obtained at autopsy for Patient #5, Patient #8, and a Huntington's disease patient. (D) Heat map of the expansion indices aggregated for the three patients, with tissues displayed in order of mean expansion index. Grey boxes indicate regions that were not assessed. M Ctx, Motor Ctx = motor cortex; GP/Put = globus pallidus/putamen; Corp C, Corpus C = corpus callosum; P Ctx, Pariet Ctx = parietal cortex; F Ctx, Frontal Ctx = superior frontal cortex; Cd/Acb/Put = caudate/accumbens/putamen; Temp Pole = temporal pole; Cing Gyrus = cingulate gyrus; Hipp head = head of the hippocampus; Mb/SN = midbrain/substantia nigra; Hipp = hippocampal formation; L Pons = lower pons; Subthal N = subthalamic nucleus; U Pons = upper pons; SC Cerv = cervical spinal cord; Dent Gyrus = dentate gyrus; SC Lumb = lumbar spinal cord; SC Thor = thoracic spinal cord. See also Figure S4.

Figure 3. Neuropathologic changes observed in an ALS patient carrying a full-penetrance pathogenic *HTT* repeat expansion (Patient #5).

(A) A representative cervical cord section showing pallor of the lateral (*) and anterior corticospinal tracts (**) with ventral horn atrophy. (B) The loss of motor neurons of the anterior horns was severe. (C) Nucleocytoplasmic TDP-43 translocation (arrows) in the prefrontal cortex (BA9 area). (D) Frequent p62 (red arrow) and huntingtin (black arrow) dystrophic neurites (Insert), intranuclear huntingtin (black arrow), and p62 (red arrow) inclusions were noted within the prefrontal cortex. (E) The neostriatum was apparently normal, for example, at the level of the nucleus accumbens, and neither neuronal loss nor reactive gliosis was detectable. (F) & (G) Occasional huntingtin aggregates were seen within the neuropil of the nucleus accumbens. (H) The tail of the caudate nucleus was not atrophic, and the neuronal density was normal and without reactive gliosis. (I) & (J) Rare huntingtin aggregates involve the neuropil of the tail of the caudate nucleus (arrows). Scale bars: A: 1 mm, and C-D: 50 microns. See also Figure S5.

Figure 4. Neuropathologic changes observed in an ALS patient carrying a full-penetrance pathogenic *HTT* repeat expansion (Patient #8).

(A) A coronal section of the fresh brain showing that the caudate, putamen, and globus pallidus was intact with no evidence of atrophy. (B) Luxol fast blue/hematoxylin and eosin staining of the caudate nucleus showed no neuronal loss or gliosis. (C) Ubiquitin immunostaining of the caudate nucleus showed extranuclear aggregates (arrow) and rare intranuclear inclusions (arrowhead). (D-E) Immunohistochemistry for polyglutamine expansions showed occasional extranuclear inclusions within the caudate nucleus (D) and the peri-Rolandic cortex (E, arrows). (F) There was severe motor neuron loss within the anterior horn of the spinal cord (Luxol fast blue/hematoxylin and eosin). (Inset) A remaining motor neuron with a TDP-43 cytoplasmic inclusion. Scale bars: B: 50 microns, C-D: 20 microns, and F: 100 microns.

MAIN TABLES AND LEGENDS

Table 1. Pathogenic *HTT* repeat expansions within the discovery and replication cohorts

	Discovery cohort		Replication cohort ^a	
	Number carriers/ number screened	Rate	Number carriers/ number screened	Rate
FTD/ALS ^b	3/2442	0.1%	5/3674	0.1%
LBD	0/2,599	0	-	-
Controls	0/3,158	0	10/31,583	0.03%

^a The replication control-cohort included 210 neurologically-healthy controls, 13,670 population controls from Gardiner et al., 2019 (Gardiner et al., 2019), and 17,703 neurologically-healthy individuals from the UK 100K Genomes Project. The replication case-cohort included 1,236 samples analyzed by repeat-primed PCR for *HTT* repeats and 2,648 samples analyzed by next-generation sequencing. All samples that whole-genome sequencing predicted to possess 40 or more CAG repeats were verified by repeat-primed PCR and by cloning and Sanger sequencing.

^b Within the FTD/ALS discovery cohort, 3/1,377 (0.2%) FTD patients and 0/1,065 ALS patients carried a pathogenic *HTT* repeat expansion. Within the FTD/ALS replication cohort, 2/1,009 (0.2%) FTD patients and 3/2,665 (0.1%) ALS patients carried a pathogenic *HTT* repeat expansion.

Table 2. Clinical details of the eight patients carrying a full-penetrance pathogenic *HTT* repeat expansion

Patient	Cohort	CAG repeats (A1/A2)	Clinical diagnosis	Age at onset (y)	Sex	Family history	Presenting symptoms
1	Discovery	41/21	PSP-FTD	68	M	No	-
2	Discovery	40/16	bvFTD	56	F	Yes	Behavioral changes
3	Discovery	40/17	nfvPPA	57	F	No	Language disturbance
4	Replication	64/17	PSP-FTD	17	F	Yes	Academic decline, dysarthria, bradykinesia, and gait disturbance
5	Replication	40/15	ALS	56	F	-	-
6	Replication	44/28	bvFTD	44	M	Yes	Personality changes and apathy
7	Replication	40/19	ALS	76	M	Yes	Lower limb weakness
8	Replication	41/17	ALS	61	M	No	Right foot weakness

Clinical diagnoses include progressive supranuclear palsy - frontotemporal dementia type (PSP-FTD), behavioral variant frontotemporal dementia (bvFTD), nonfluent variant primary progressive aphasia subtype of FTD (nfvPPA), and amyotrophic lateral sclerosis (ALS). Family history refers to a family history of neurological disease. A1, allele 1; A2, allele 2. DNA for Patient #5 and Patient #8 was extracted from frozen cerebellar tissue, and DNA for the other six patients was extracted from blood. See also Methods S1.

STAR METHODS

RESOURCE AVAILABILITY

Lead Contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Bryan Traynor (traynorb@mail.nih.gov).

Materials Availability

This study did not generate new unique reagents.

Data and Code Availability

The individual-level sequence data for the discovery genomes are available on dbGaP (accession number: phs001963.v1.p1 NIA DementiaSeq). The programming code used in this paper is available at https://github.com/dewanr2/Somatic_Instability.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Study cohorts

Discovery cohort

The study workflow is depicted in **Figure S6**. The discovery cohort included (i) 1,377 patients diagnosed with FTD spectrum disorders including the known subtypes of behavioral variant FTD, primary progressive aphasia, and progressive supranuclear palsy (PSP), (ii) 1,065 patients

diagnosed with ALS, (iii) 2,599 individuals diagnosed with Lewy body dementia (LBD), and (iv) 3,158 neurologically healthy participants. DNA was extracted from blood or frozen cerebellar tissue obtained at autopsy using standard methods [FTD-ALS cohort: 2,199 (90.0%) extracted from blood and 243 (10.0%) from brain tissue; LBD: 805 (31.0%) blood and 1,794 (69.0%) brains; Controls: 2,866 (90.8%) blood and 292 (9.2%) brains]. Patients with FTD were diagnosed according to the Neary criteria (Faber, 1999) or the Movement Disorders Society criteria for PSP (Höglinger et al., 2017). Patients with ALS were diagnosed according to the El Escorial criteria (Brooks, 1994), and the LBD cases were diagnosed with pathologically definite or clinically probable disease according to consensus criteria (Emre et al., 2007; McKeith et al., 2005). The LBD cases were included in this study as diseased control subjects. All participants included in the aged, healthy control cohort were free of neurological disease based on history and neurological examination (mean age = 77.0 years of age at collection, interquartile range = 69.0–86.0). All study participants were of European ancestry. **Table S2** lists the demographic characteristics of the cohorts.

Replication cohort

For replication, we used DNA obtained from 1,009 patients diagnosed with FTD, 2,665 patients diagnosed with ALS, and 210 neurologically healthy individuals. DNA for 2,837 (77.2%) of the FTD/ALS cases were extracted from blood. Of the remainder, 657 (17.9%) were extracted from frozen CNS tissue (cerebellum, cortex, pons, spinal cord), 140 (3.8%) were extracted from frozen organ tissue (adrenal gland, diaphragm, kidney, liver, muscle, thyroid), 31 (0.8%) from saliva, and 9 (0.3%) from iPS cell lines. DNA for 177 (84.3%) of the healthy subjects was extracted from blood. Of the remainder, 20 (9.5%) were extracted from frozen CNS tissue

(cerebellum, cortex, spinal cord, pons), 3 (1.4%) were extracted from frozen liver tissue, 4 (1.9%) from saliva, and 6 (2.9%) from iPS cell lines. The replication control cohort also included existing data for 13,670 population controls from Gardiner et al., 2019 (Gardiner et al., 2019), and 17,703 neurologically-healthy individuals from the UK 100K Genomes Project (Peplow, 2016). These *HTT* repeat expansion data were measured in DNA extracted from blood. The institutional review boards of participating institutions approved the study, and informed consent was obtained from all subjects or their surrogate decision-makers, according to the Declaration of Helsinki.

METHOD DETAILS

Data generation and pre-processing

Whole-genome sequencing

Genomic DNA was extracted from whole blood or cerebellar brain tissue using a Maxwell RSC Instrument (Promega Corp., Madison, WI, USA). Fluorometric quantitation of the genomic DNA samples was performed using the PicoGreen dsDNA assay (Thermo Fisher). PCR-free, paired-end, non-indexed libraries were constructed using the TruSeq PCR-free chemistry according to the manufacturer's instructions (Illumina Corp., San Diego, CA, USA). Sequencing was performed on an HiSeq X Ten sequencer (version 2.5 chemistry, Illumina) using 150 base pair (bp), paired-end cycles, applying a single sample to each lane.

Sequence alignment and variant calling

Raw genome data in FASTQ file format were transferred to Google Cloud Storage. Paired-end sequences were processed by following the pipeline standard developed by the Centers for Common Disease Genomics (CCDG; <https://www.genome.gov/27563570/>). This standard allows for whole-genome sequence data processed by different groups to generate ‘functionally equivalent’ results (DePristo et al., 2011; Li and Durbin, 2009; Poplin et al., 2018; Regier et al., 2018). The GRCh38DH reference genome was used for alignment, as specified in the CCDG standard. For whole-genome sequence alignments and processing, the Broad Institute’s implementation of the functional equivalence standardized pipeline was used. This pipeline, which incorporates the GATK (2016) Best Practices, was implemented in the workflow description language (WDL) for deployment and execution on the Google Cloud Platform (Regier et al., 2018). Single-nucleotide variants (SNV) and insertion-deletions (InDels) variants were called from the processed whole-genome sequence data following the GATK Best Practices using another Broad Institute workflow for joint discovery and Variant Quality Score Recalibration (VQSR). The Broad workflows for whole-genome sequence sample processing and joint discovery are publically available (<https://github.com/gatk-workflows/broad-prod-wgs-germline-snps-indels>). The average sequencing read-depth after filtering by alignment quality was 35x, and mean coverage per genome was 36.3 (95% confidence interval: 29.3–43.3). All of the whole-genome sequence data (discovery and replication cohorts) were processed using the same pipeline.

Known gene analysis

Whole-genome sequence data was analyzed for pathogenic mutations in fifty genes associated with neurodegenerative diseases, including *ALS2*, *APP*, *ATP13A2*, *ATXN2*, *BSN*, *C9orf72*, *CHCHD10*, *CHMP2B*, *CSF1R*, *DCTN1*, *DNAJC6*, *FBXO7*, *FIG4*, *FUS*, *GBA*, *GCH1*, *GRN*, *HNRNPA1*, *KIF5A*, *LRRK2*, *MAPT*, *MATR3*, *OPTN*, *PANK2*, *PARK2*, *PARK7*, *PFN1*, *PINK1*, *PLA2G6*, *POLG*, *PSEN1*, *PSEN2*, *RAB39B*, *SETX*, *SNCA*, *SOD1*, *SPG11*, *SPTLC1*, *SQSTM1*, *SYNJ1*, *TAF1*, *TARDBP*, *TBK1*, *TIA1*, *TUBA4A*, *UBQLN2*, *VAPB*, *VCP*, *VPS13C*, and *VPS35*.

The analysis was performed by subsetting gene regions from post-QC variant files using PLINK 2.0 and annotating variants in ANNOVAR (v. 2018-04/16).

Single-variant association analysis

We performed a GWAS in FTD/ALS (n = 2,451 cases and 4,029 controls) using generalized linear model association testing implemented in PLINK (version 2.0) with a minor allele frequency threshold of >5% based on the allele frequency estimates in the FTD case cohort. We used the step function in the R MASS package (version 7.3-53) to determine the minimum number of principal components (generated from common single nucleotide variants) required to correct for population substructure. Based on this analysis, we incorporated sex, age, and five principal components (PC1, PC2, PC3, PC5, PC8) as covariates in our model. Quantile-quantile plots revealed minimal residual population substructure, as estimated by the sample size-adjusted genome-wide inflation factor λ_{1000} of 1.005. The Bonferroni threshold for genome-wide significance was 5.0×10^{-8} .

Repeat expansion analysis

ExpansionHunter - Targeted software (version 3.0.1) was used to estimate repeat lengths of ten known, disease-causing expansions in samples that had undergone whole-genome sequencing (Dolzhenko et al., 2019). This algorithm has been validated using experimentally-confirmed samples carrying pathogenic expansions, including *HTT* (Dolzhenko et al., 2019). Fully-penetrant pathogenic alleles in the huntingtin (*HTT*) gene were defined as those containing 40 or more CAG repeats according to the American College of Medical Genetics diagnostic criteria (Bean and Bayrak-Toydemir, 2014). The number of repeats was validated using a repeat-primed PCR assay (Jama et al., 2013) and by cloning and Sanger sequencing for each sample reported by ExpansionHunter - Targeted algorithm to carry 40 or more *HTT* CAG repeats.

Repeat-primed PCR assay

The CAG trinucleotide repeat length in *HTT* was quantified using a previously validated repeat-primed PCR method (see **Table S3**) (Jama et al., 2013). The repeat-primed PCR assay to measure *HTT* CAG repeat length was performed using the Eppendorf Mastercycler pro thermal cycler (Fisher Scientific, Houston, TX, USA) in a final volume of 22 μ l containing 1X FailSafe Premix J (Epicenter, Madison, WI, USA), 1.0U Platinum *Taq* DNA polymerase (Invitrogen Corp., Carlsbad, CA, USA), 0.5 μ M Primer Mix containing 0.5 μ mol/l each of forward primer 5'-ATGAAGGCCTTCGAGTCCCTCAAGTCC-3', with a 5' 6FAM fluorescent tag, and reverse primer 5'-CGGTGGCGGCTGTTGCTGCTGCTGCTGCTG-3' (Eurofins Genomics LLC, Louisville, KY, USA), and 3 μ l of 25-50ng/ μ l genomic DNA. Cycling conditions were identical to those in Jama et al (Jama et al., 2013). The reverse primer 5'-end in this protocol contains a 15 bp sequence specific to the region between the *HTT* CAG and CCG trinucleotide repeats. This

primer binding region fully encapsulates the trailing CAA-CAG sequence to prevent against any changes in primer specificity due to loss of interruption (i.e., conversion to CAG-CAG).

The fragment length analysis was performed on an ABI 3730xl genetic analyzer (Applied Biosystems Inc., Foster City, CA, USA) using a mixture of 2µl of repeat-primed PCR products, 0.5µl GeneScan 500 LIZ size standard (Thermo Fisher Scientific, Cincinnati, OH, USA), and 7.5µl HiDi formamide (Applied Biosystems Inc.). The mixture was heated at 95°C for 3 minutes and then immediately cooled on ice for at least 5 minutes before loading for capillary electrophoresis. Data were analyzed using GeneMapper software (version 4, Applied Biosystems Inc.). Repeat expansions were quantifiable with a 3-bp periodicity. GeneMapper chromatograms were used to quantify somatic instability by calculating an expansion index for each sample (Mouro Pinto et al., 2020). All samples analyzed from Patient #5, Patient #8, and a Huntington's disease patient (for comparison) had the same modal allele length (CAG 40, 41, and 41 respectively).

Cloning and Sanger sequencing

The *HTT* region was PCR amplified using the forward (HD1F: 5' CCGCTCAGGTTCTGCTTTTA 3') and reverse (HD1FR 5' GGCTGAGGCAGCAGCGGCTG 3') primers with the following PCR components: 10ng genomic DNA, 2µl 10x PCR Buffer, 0.25µl Taq Polymerase, 0.4µl 10mM dNTP mix, 4µl Q Solution (Qiagen), 0.8µl 5uM forward primer, 0.8µl 5uM reverse primer, and water to a final reaction volume of 20µl. Thermocycling conditions are listed in **Table S3**. Amplified PCR products were assessed on 2% E-Gel EX Agarose Gels (Thermo Fisher) before cloning into the pCR4-TOPO TA vector supplied in the TOPO TA Cloning® Kits for Sequencing (Thermo Fisher). Cloning and the bacterial

transformation were performed according to the manufacturer's protocol. Colonies were picked, grown overnight, and plasmid was extracted using the QIAprep Spin Miniprep Kit (Qiagen). Plasmid with TA-cloned inserts were Sanger sequenced using the universal M13 forward primer.

Brain immunohistochemistry

Formalin-fixed, paraffin-embedded sections were prepared from postmortem brain and spinal cord regions and stained with Luxol fast blue counterstained with hematoxylin and eosin, and immunostained using polyclonal antibodies against huntingtin (clone 2B4), p62, and polyglutamine (clone 1c2) (see **Table S4** for primary antibody conditions). The 2B4 antibody targets the N'-end of the huntingtin protein and stains soluble huntingtin and insoluble aggregates. The huntingtin/p62 dual stains were developed using a 3,3'-diaminobenzidine (DAB) and alkaline phosphatase dual staining system on a Leica Bond autostainer with a hematoxylin counterstain. Primary antibodies and staining methods are listed in **Table S4**.

QUANTIFICATION AND STATISTICAL ANALYSIS

Genomes were excluded from analysis for the following reasons: (1) high contamination rate (> 5% based on VerifyBamID freemix metric) (Jun et al., 2012), (2) excessive heterozygosity rate (exceeding +/- 0.15 F-statistic), (3) low call rate (\leq 95%), (4) discordance between reported sex and genotypic sex, and (5) duplicate samples (determined by pi-hat statistic). Samples of non-European ancestry based on comparison of principal components with the HapMap 3 Genome Reference Panel were flagged, but not excluded (Altshuler et al., 2010; Chang et al., 2015).

Trinucleotide repeat frequencies were compared between cohorts using Fisher's exact test with a Bonferroni-corrected significance threshold of 0.005 (0.05 divided by ten repeat expansions tested). Concordance between identifying the *C9orf72* repeat expansion using the ExpansionHunter – Targeted algorithm and a validated repeat-primed PCR assay for *C9orf72* (Majounie et al., 2021) was assessed using the R package *irr* (version 0.84.1). Genotype data defining the common haplotypes in the *HTT* locus (Chao et al., 2017) were extracted from the whole-genome sequence data using PLINK (version 2.0). The ExpansionHunter - Targeted output for the CAG repeat length was merged with the genotype information, and phasing was performed using Eagle (version 2.4).

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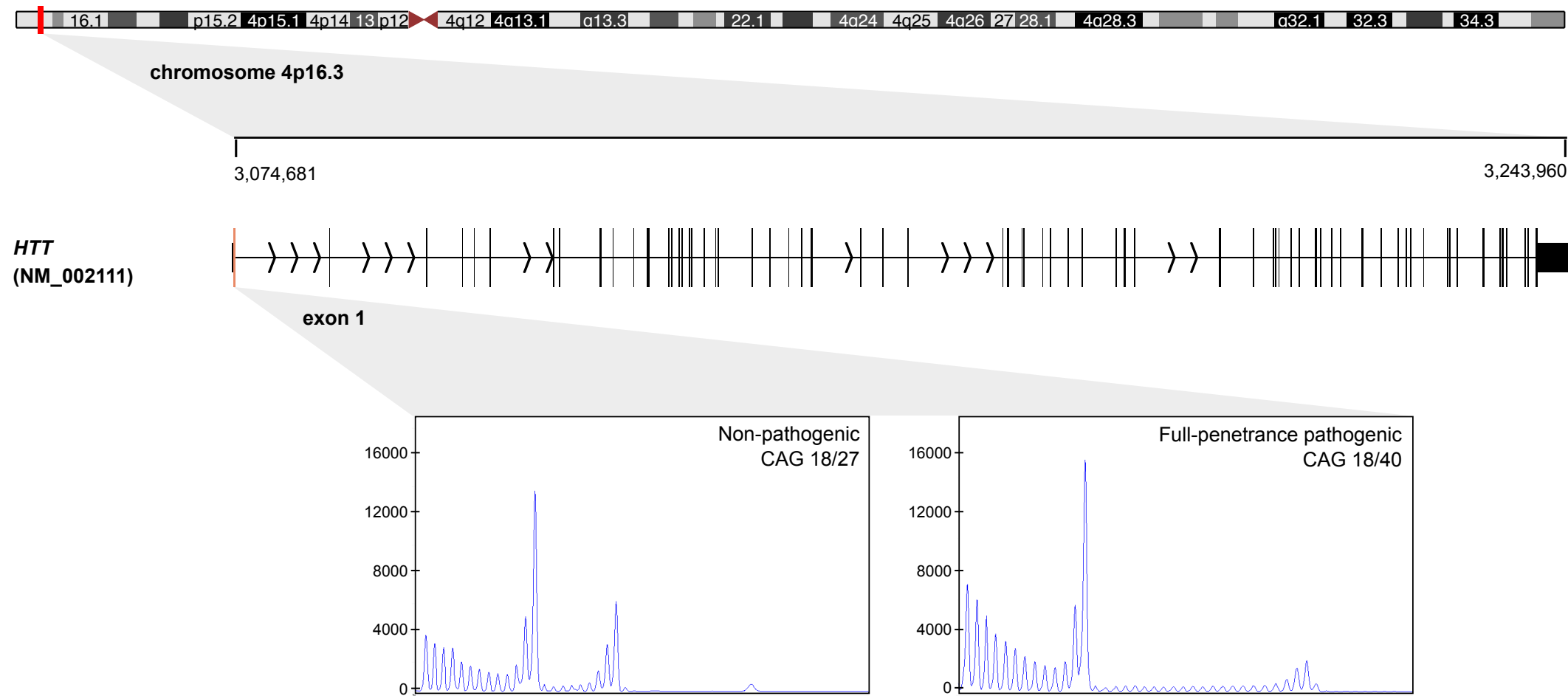
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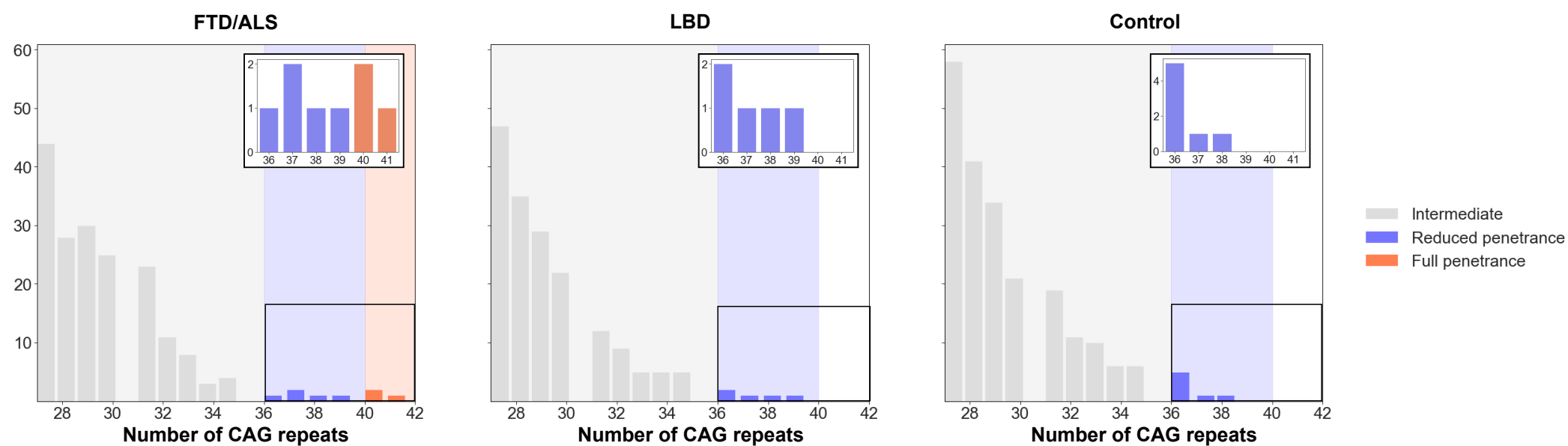
KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies		
Huntingtin/ p62 double stain	Millipore/ Abcam	MAB5492/ ab207305
Rabbit Anti-Ubiquitin	Dako	Z0458
Anti-polyglutamine-Expansion Diseases Marker Antibody, clone 5TF1-1C2	Millipore Sigma	MAB1574
Anti-phospho TDP-43 (pS409/410)	Cosmo Bio Co., Ltd	CAC-TIP-PTD-M01
Anti-TDP-43	Proteintech	10782-2-AP
Biological Samples		
Human cerebral brain tissue and/or whole blood	Comprehensive list of study sites listed in Acknowledgements of this paper	N/A
Chemicals, Peptides, and Recombinant Proteins		
1X FailSafe Premix J	Lucigen	FSP995J
Q Solution	Qiagen	201203
Critical Commercial Assays		
Maxwell RSC Tissue DNA Kit	Promega	AS1610
PicoGreen dsDNA assay	Thermo Fisher	P7589
TruSeq PCR-free Library Prep Kit	Illumina	20015963
HiSeq X Ten Reagent Kit	Illumina	FC-501-2501
2% E-Gel EX Agarose Gels	Thermo Fisher	G402002
TOPO TA Cloning® Kit	Thermo Fisher	K4575J10
QIAprep Spin Miniprep Kit	Qiagen	27106
Deposited Data		
Human reference genome NCBI build 38, GRCh38	Genome Reference Consortium	http://www.ncbi.nlm.nih.gov/projects/genome/assembly/grc/human/
Individual-level sequence data for the discovery genomes	This paper	dbGaP (phs001963.v1.p1)
ExpansionHunter – Targeted summary data for the discovery genomes	This paper	Table S4
Oligonucleotides		
<i>HTT</i> RP-PCR primer sequence, forward: 6FAM-ATGAAGGCCTTCGAGTCCCTCAAGTC	Jama et al., 2013	N/A
<i>HTT</i> RP-PCR primer sequence, reverse: ATGAAGGCCTTCGAGTCCCTCAAGTC	Jama et al., 2013	N/A
<i>HTT</i> PCR primer sequence, prior to cloning, forward: CCGCTCAGGTTCTGCTTTTA	Dabrowska et al., 2018	N/A
<i>HTT</i> PCR primer sequence, prior to cloning, reverse: GGCTGAGGCAGCAGCGGCTG	Dabrowska et al., 2018	N/A
Software and Algorithms		
ANNOVAR v. 2018-04/16	Wang et al., 2010	https://doc-openbio.readthedocs.io/projects/annovar/en/latest/
ExpansionHunter – Targeted v. 3.0.1	Dolzhenko et al., 2019	https://github.com/Illumina/ExpansionHunter

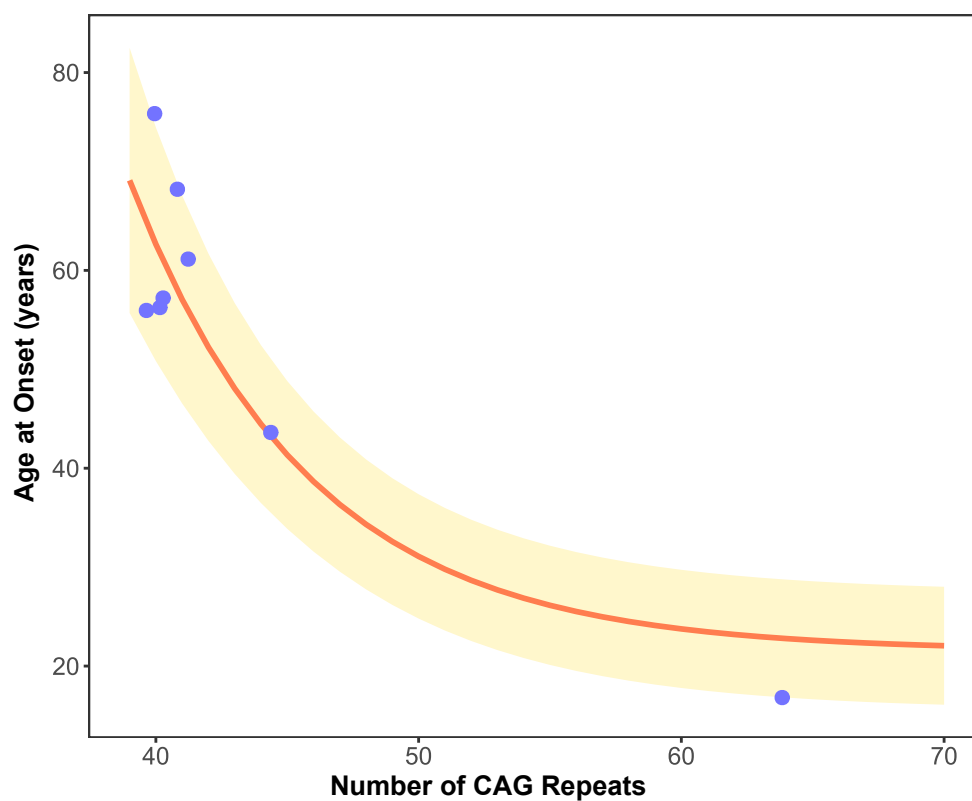
Eagle v. 2.4	Loh et al., 2016	https://data.broadinstitute.org/alkesgroup/Eagle/
GATK	Broad Institute	https://software.broadinstitute.org/gatk
Pipeline-Standardization	CCDG	https://github.com/CCDG/Pipeline-Standardization/blob/master/PipelineStandard.md
PLINK v. 2.0	Chang et al., 2015	https://www.cog-genomics.org/plink/2.0/
prod-wgs-germline-snps-indels	Broad Institute	https://github.com/gatk-workflows/broad-prod-wgs-germline-snps-indels
R	R Core Team	https://www.r-project.org
Samtools	Li et al., 2009	http://samtools.sourceforge.net/



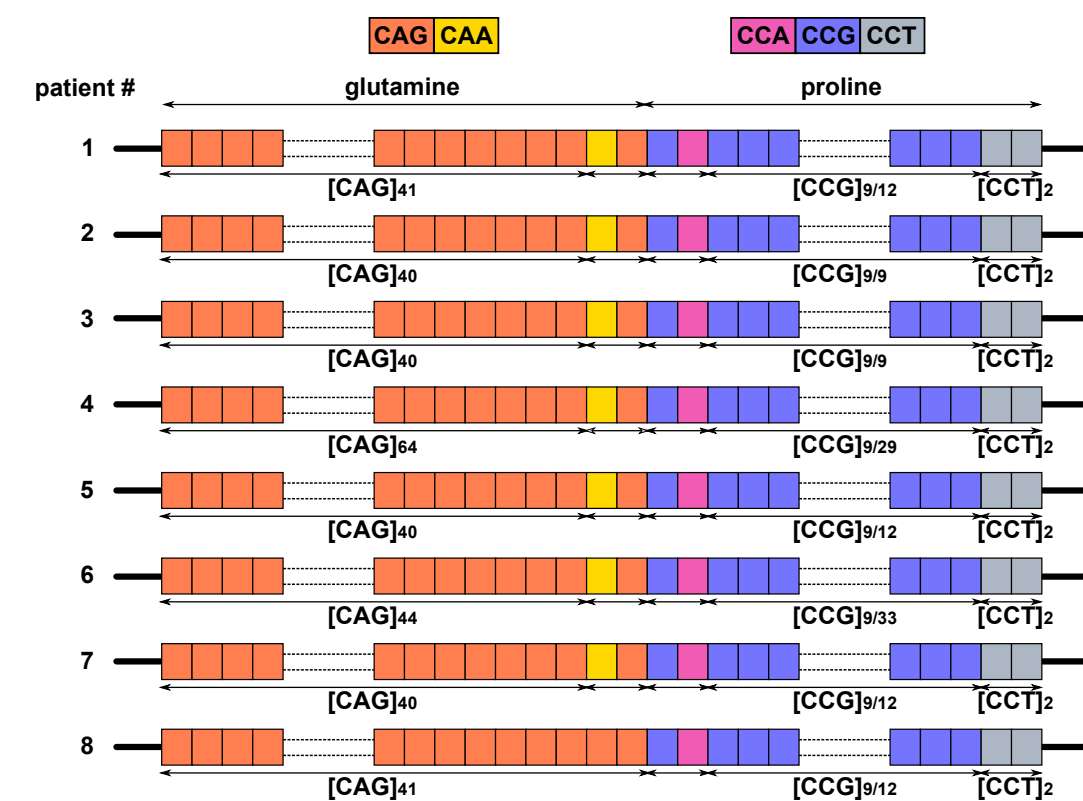
B Intermediate, reduced-penetrance, and full-penetrance repeat number distributions



C Age at onset for full-penetrance pathogenic *HTT* CAG repeat carriers



D Allelic structure at the *HTT* exon one CAG/CCG repeat expansion locus



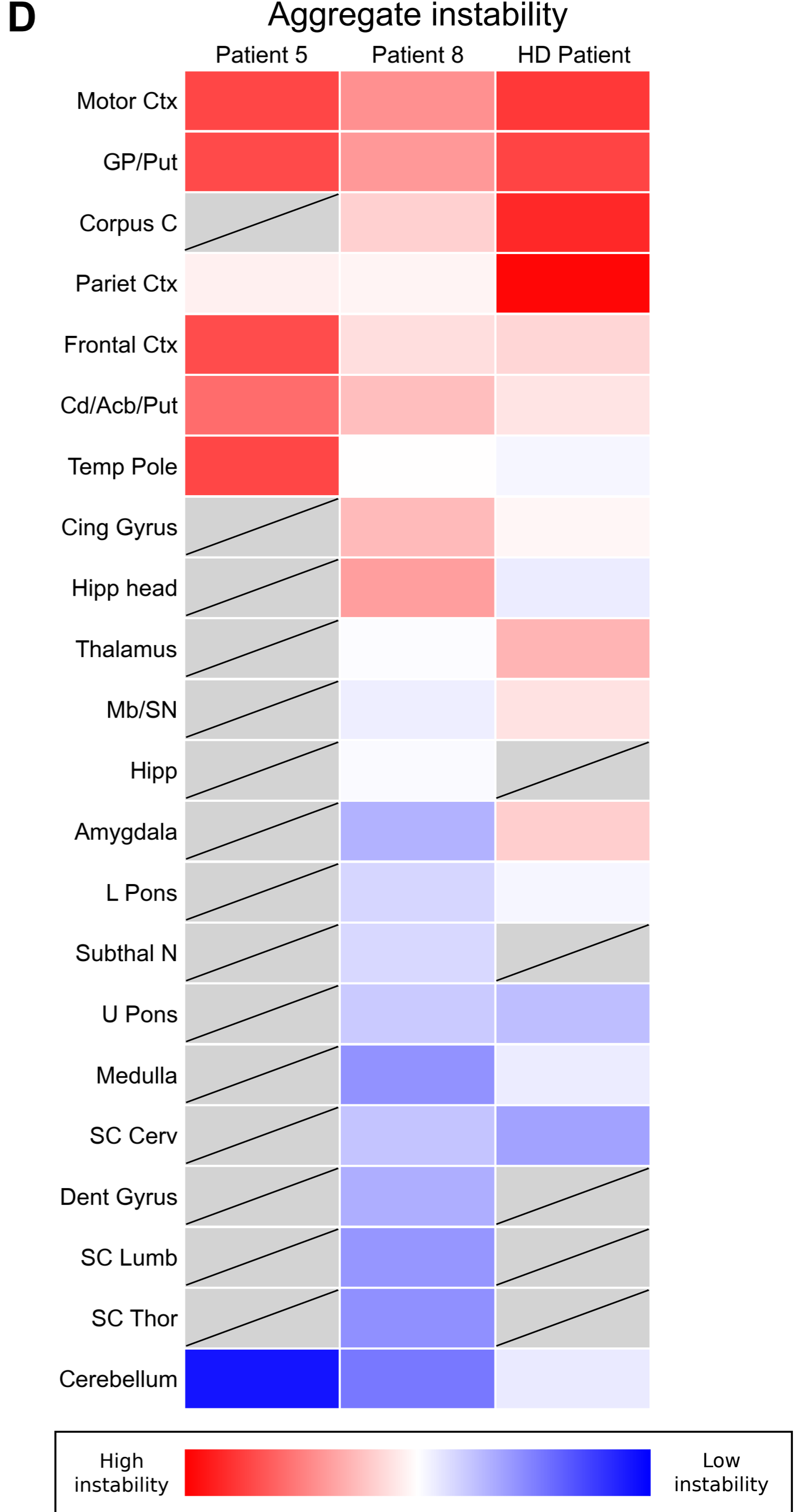
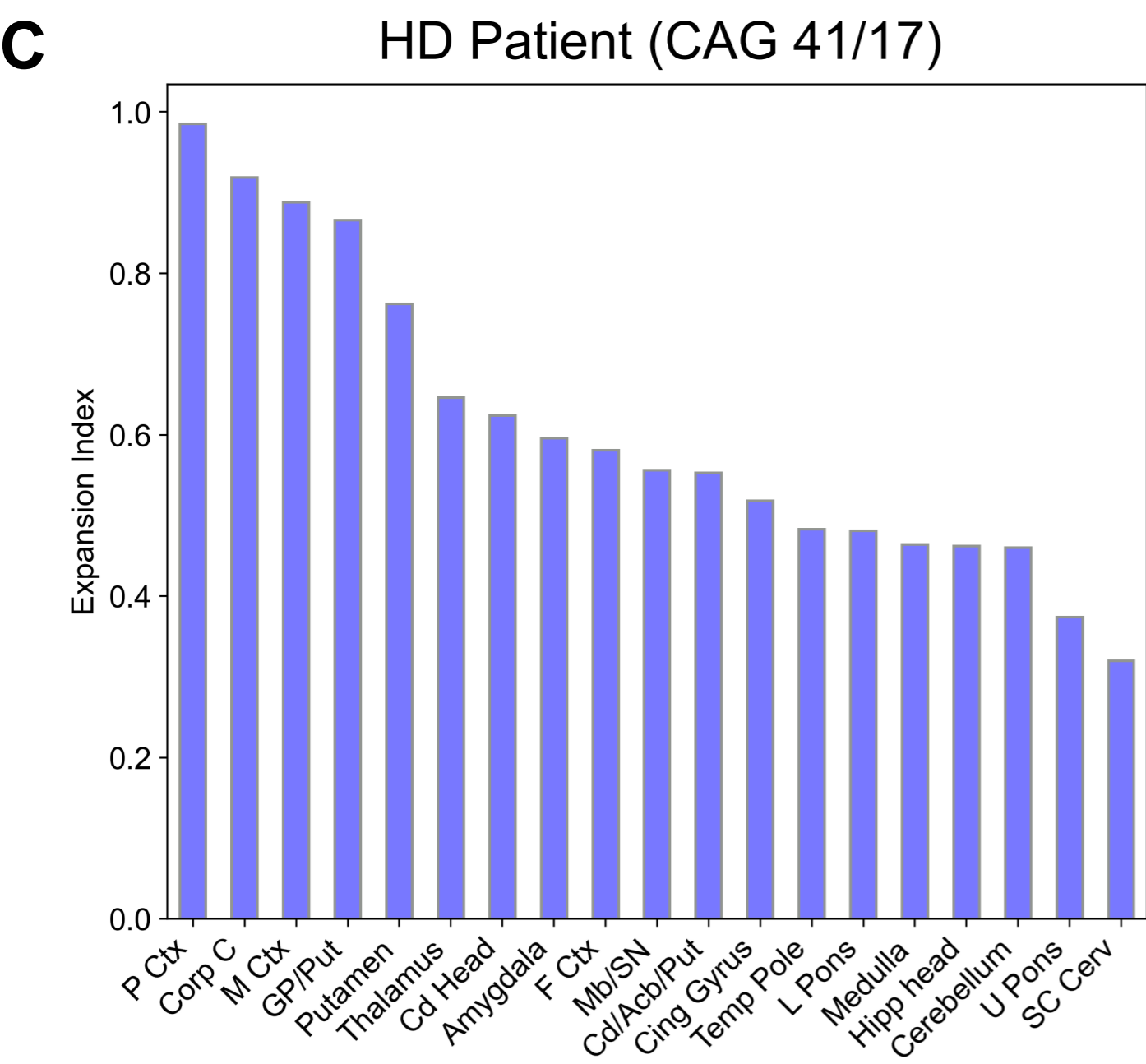
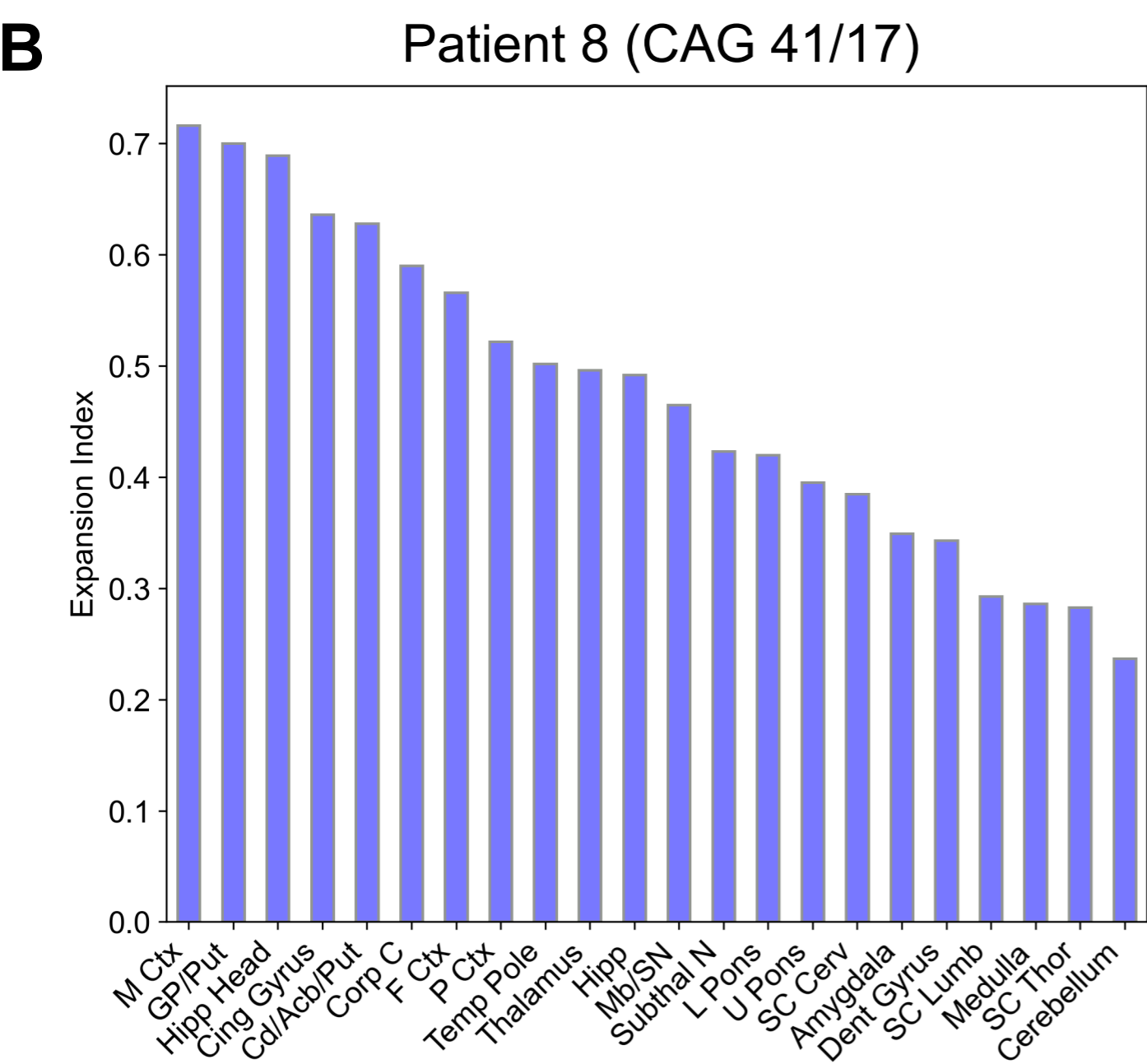
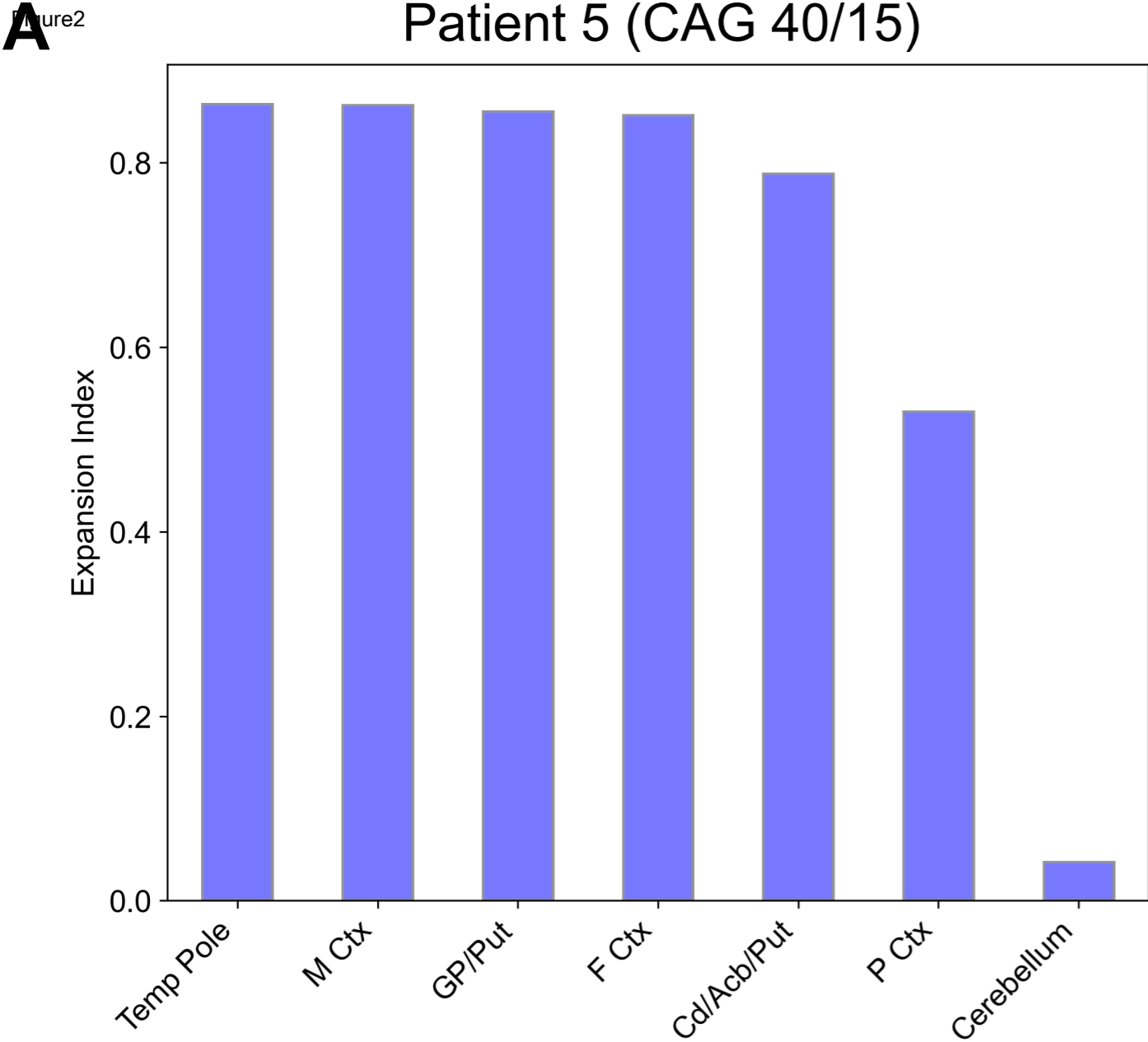


Figure 3

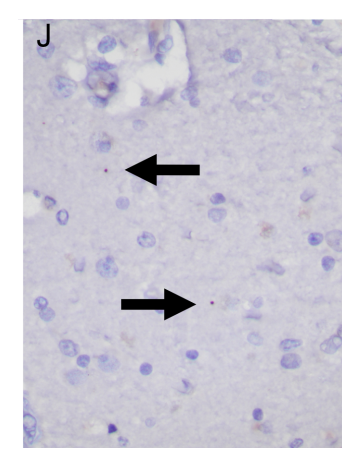
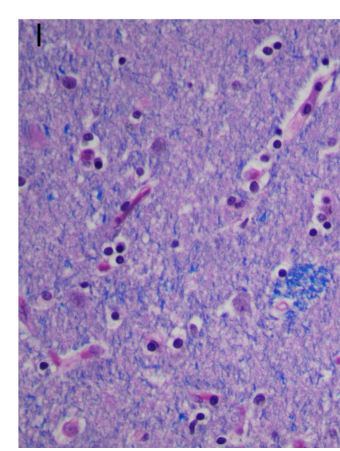
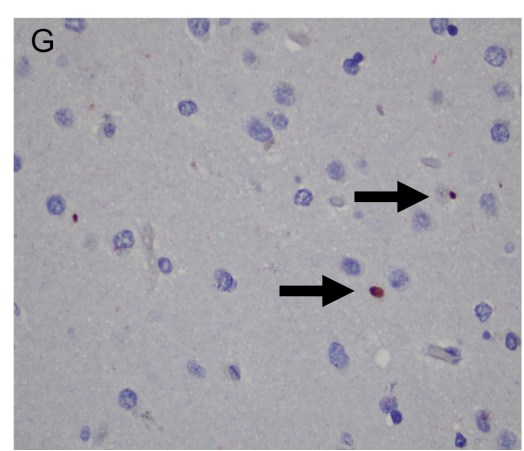
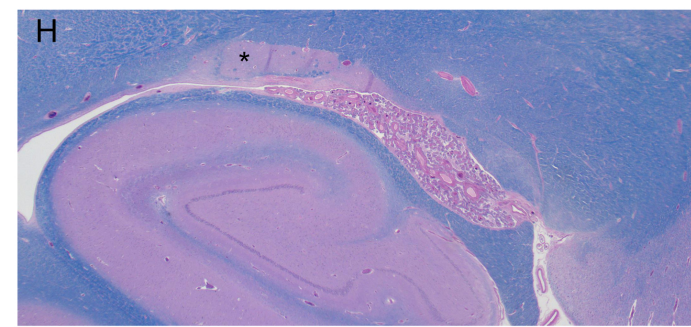
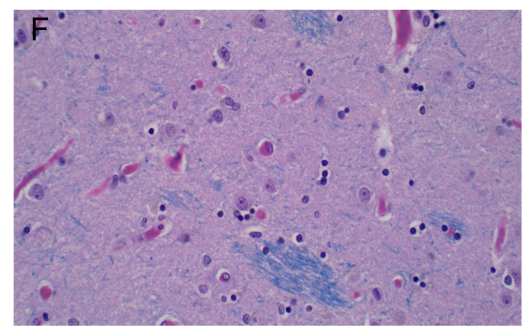
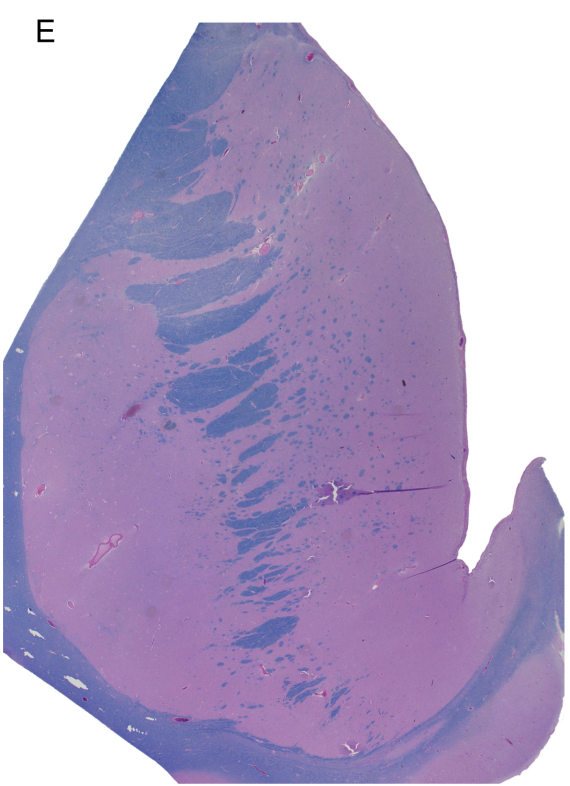
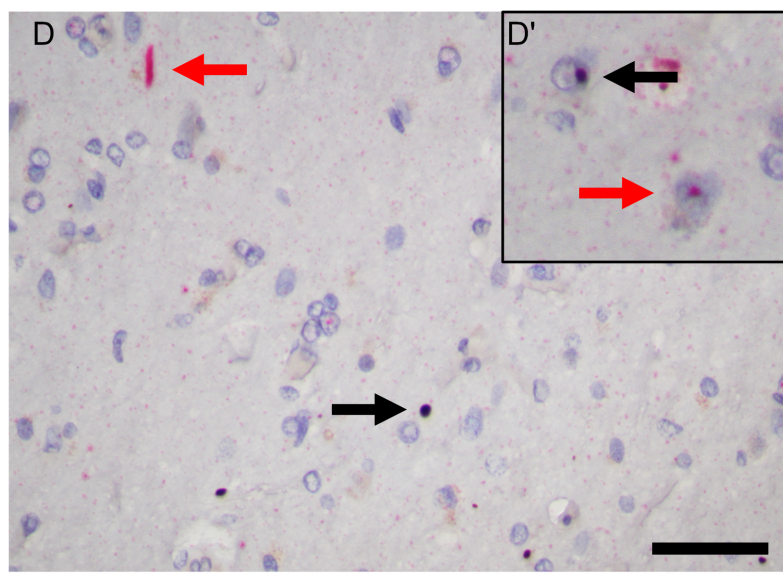
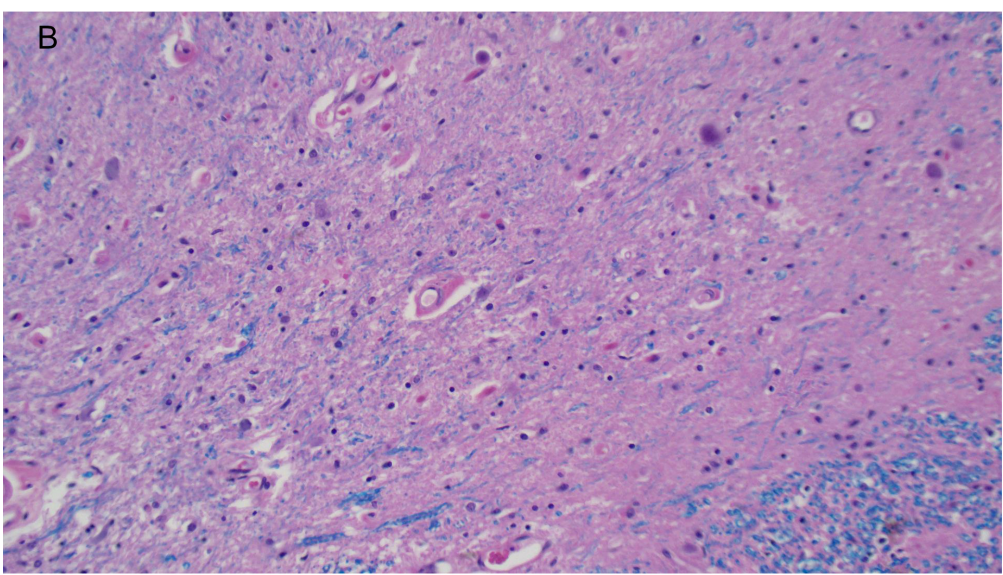
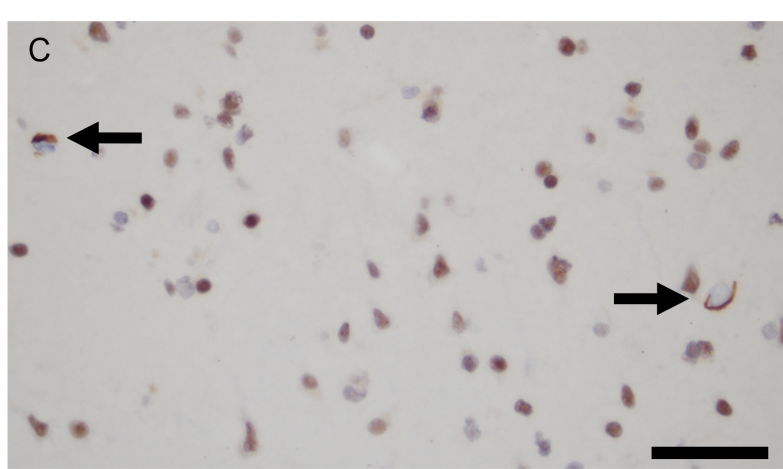
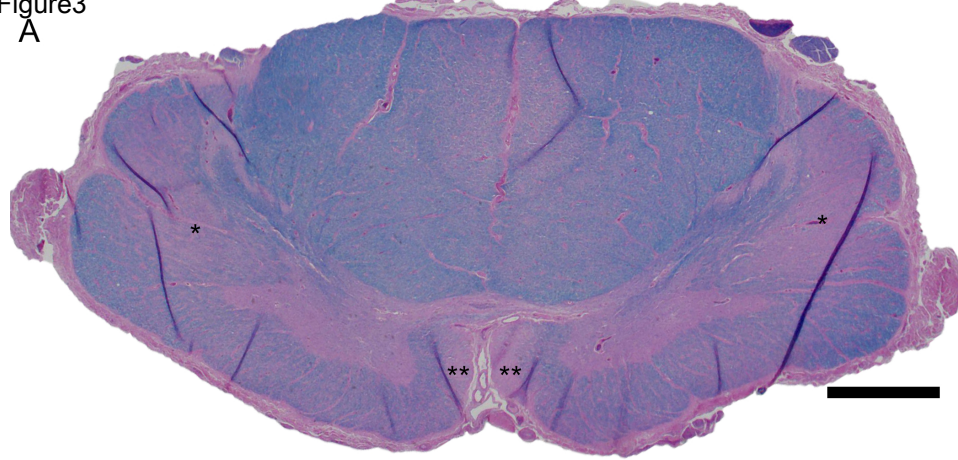
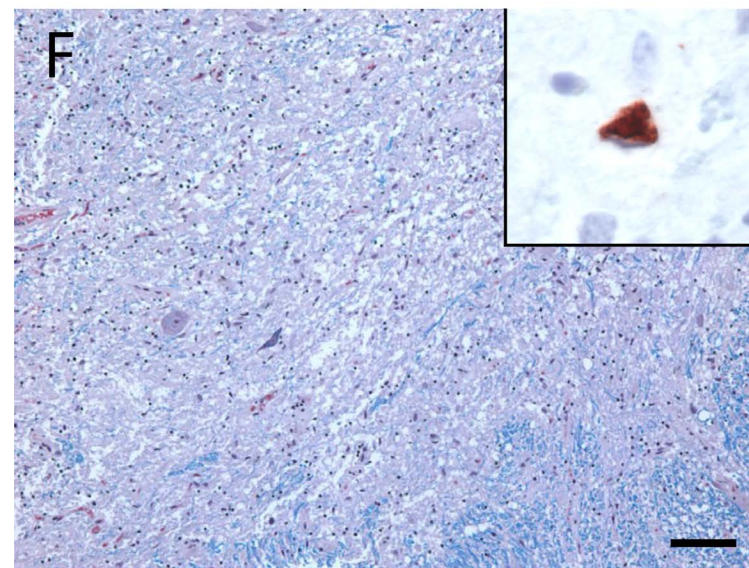
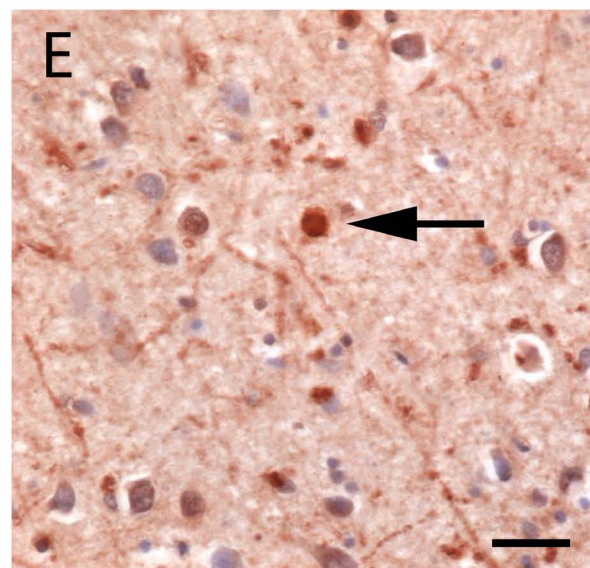
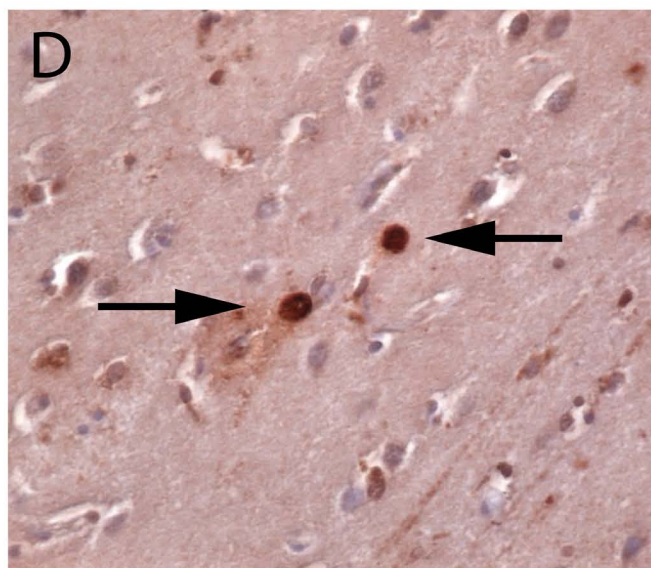
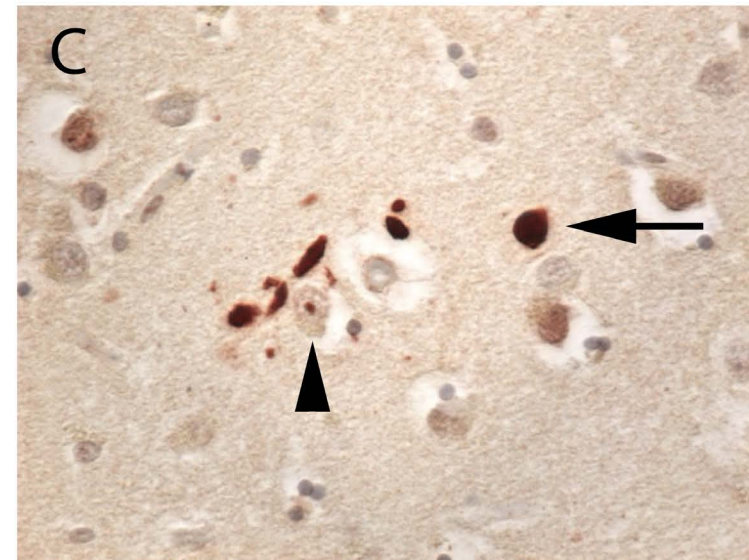
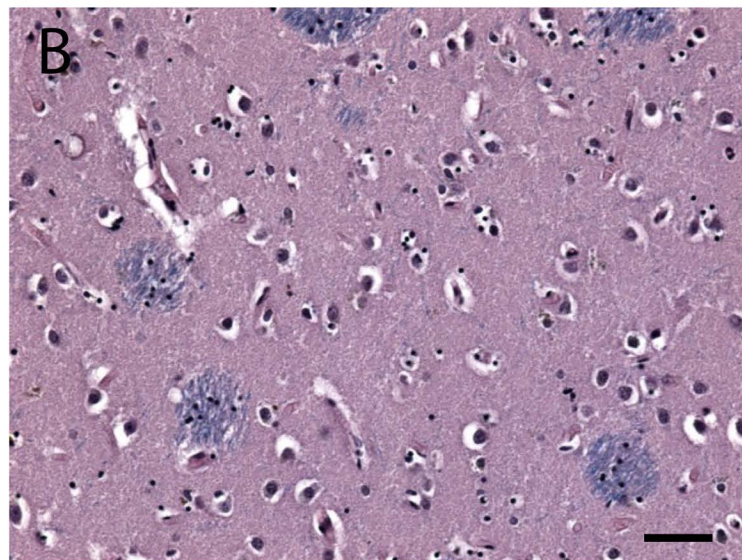
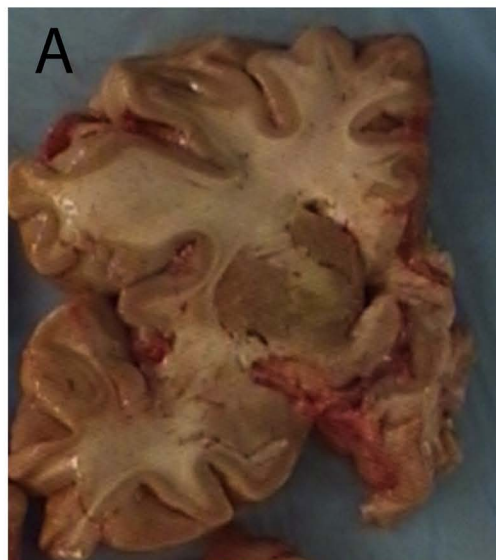


Figure 4



Supplemental Information

Supplemental Materials and Methods

Methods S1. Description of clinical cases carrying pathogenic *HTT* repeat expansions. Related to Table 2.

Patient #1

The patient developed asymmetric, transiently levodopa-responsive tremor at age 68, followed by the development of progressive postural and oculomotor problems within three years from symptom onset. He fulfilled the MDS clinical criteria for probable PSP. MRI showed atrophy of the mesencephalon (Colibri sign) and reduced dopamine transporter uptake on SPECT. The clinical course was very slowly progressive. Examination twelve years after symptom onset revealed mild dementia, characterized by psychomotor slowing, reduced verbal fluency, attention, and episodic memory, with a mini-mental status examination of 24/30. There was no family history of neurological disease. The patient passed away at age 83. An autopsy was not performed.

Patient #2

The patient developed behavioral changes at the age of 56, and she was diagnosed with behavioral variant FTD. By report, her elderly mother had been diagnosed with Alzheimer's disease.

Patient #3

The patient was a woman who developed language disturbances at the age of 57. She was subsequently diagnosed as having nonfluent primary progressive aphasia FTD subtype. There was no family history of neurological disease.

Patient #4

The patient was a 19-year-old woman who had presented with a two-year history of progressive academic performance decline, dysarthria, bradykinesia, and gait disturbance. Her speech had become progressively slurred and soft, and her handwriting had deteriorated. She did not report any falls, but she did have several episodes of syncope that were initially diagnosed as seizures. Cranial nerve examination revealed supranuclear vertical gaze palsy, masked facies, and dysarthria. She also had bradykinesia with cogwheeling in her upper limbs, and spasticity and hyperreflexia in the lower limbs. Brain MRI showed basal ganglia iron deposition. She was

started on carbidopa/levodopa but did not improve. An initial genetic screen of *HTT* was reported as normal. The patient's father was said to have a similar neurological syndrome consisting of cognitive decline, gait disorder, and dysarthria that started in his late twenties. The genetic screening was repeated at a later stage in her illness to investigate early-onset, familial dementia. This testing correctly identified an expanded *HTT* repeat allele, and her diagnosis was updated to young-onset Huntington's disease (Westphal syndrome).

Patient #5

The patient developed symptoms of ALS at the age of 56 and died eleven years later of respiratory failure after a typical course of motor neuron disease. An MRI of the brain performed approximately ten years prior to death did not show significant cerebral or striatal atrophy.

Patient #6

The patient presented at the age of 44 with personality changes (short temper) and decreased initiative (apathy). His memory was intact, and neuropsychological evaluation was consistent with FTD. His father had speech loss and gait disturbance at the age of 40 and died from his illness at the age of 52.

Patient #7

This right-handed man presented with lower limb weakness at the age of 76. His sibling had been diagnosed with ALS. Neurological examination at the age of 84 revealed an ALS Functional Rating Scale of 17 (maximum score of the ALSFRS-R = 40). He had upper and lower motor neuron signs in the bulbar region, the upper limbs, and the lower limbs. Additionally, he was diagnosed with FTD. He was placed on non-invasive positive pressure ventilation for respiratory failure.

Patient #8

This patient was a man who developed a right foot drop at the age of 62. He was initially diagnosed with primary lateral sclerosis and had a baclofen pump implanted for treating spasticity. His symptoms progressed, and the diagnosis was changed to ALS based on neurophysiological testing. Before death, he was unable to ambulate, used a motorized wheelchair, had limited hand movements, wore a cervical collar to correct head tilt, and used an eye gaze system to communicate. He died at the age of 70 due to respiratory failure.

Supplemental Figures

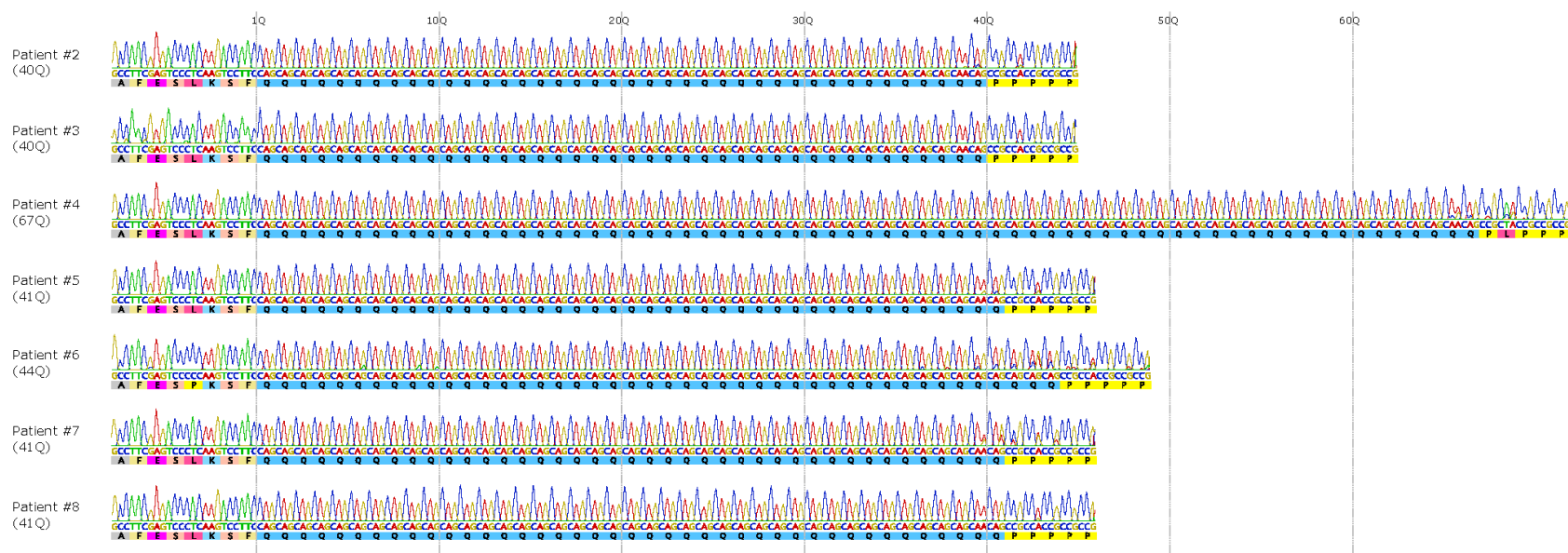


Figure S1. Sanger sequencing chromatograms of the *HTT* CAG repeat expansion. Related to Figure 1.

HTT CAG repeat length was assessed by cloning followed by Sanger sequencing for seven of the eight FTD/ALS patients carrying full-penetrance pathogenic repeat expansions (≥ 40 CAG repeats). DNA was not available for the eighth patient (Patient #1).

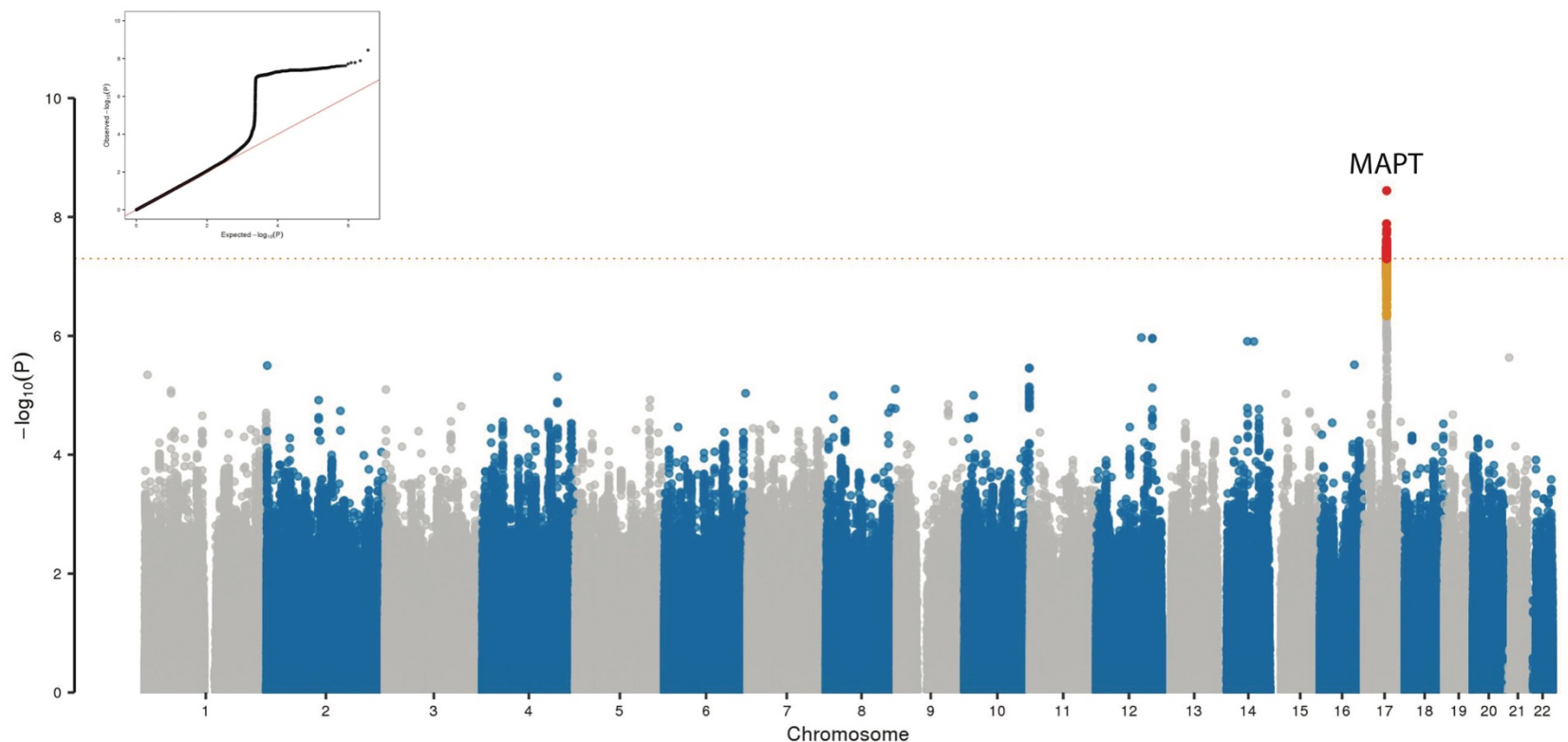


Figure S2. Genome-wide association study of the FTD/ALS discovery cohort. Related to Figure 1.

Manhattan plot depicting GWAS results (MAF >5%) based on 2,451 cases and 4,029 controls that passed filtering metrics for the FTD/ALS patient cohort. Chromosomal positions (build hg38) are depicted on the x-axis, and association p -values are indicated on the y-axis using a $-\log_{10}$ scale. Genome-wide significant signals are shown by red dots, and orange dots indicate suggestive variants. The name The horizontal dashed line indicates the Bonferroni threshold for genome-wide significance. The gene with the closest proximity to the top variant at the significant locus on chromosome 17 is shown. The insert figure shows the quartile-quartile plot ($\lambda = 1.016$, $\lambda_{1000} = 1.005$).

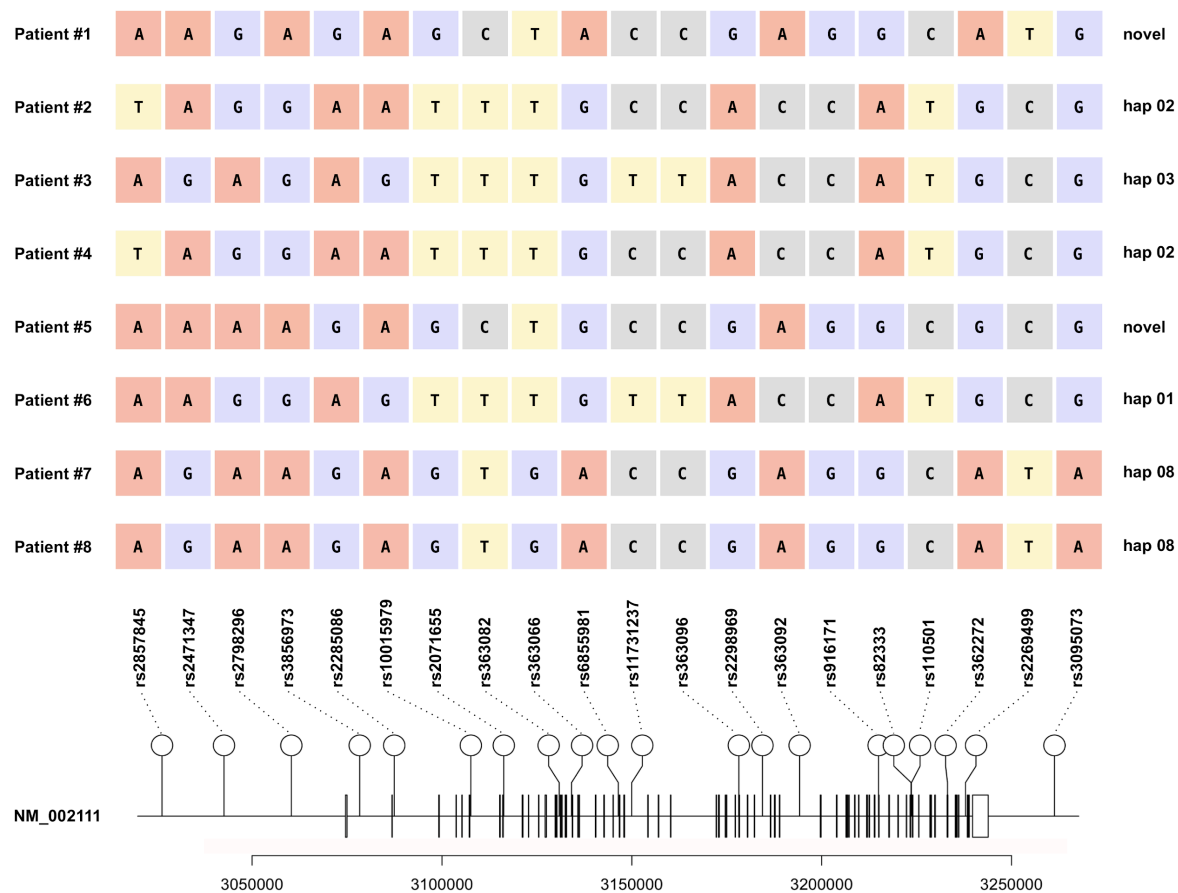


Figure S3. The occurrence of known haplotypes across the *HTT* locus. Related to Figure 1.

Haplotypes across the *HTT* locus are shown for the eight FTD/ALS patients carrying full penetrance repeat expansions. Numbered haplotypes correspond to known haplotypes associated with Huntington’s disease, as defined by Chao and colleagues (Chao et al., 2017). Haplotypes not previously associated with Huntington’s disease are marked as “novel.” Individual SNPs used to define the haplotypes are shown below, along with their locations along the *HTT* gene (NM_002111).

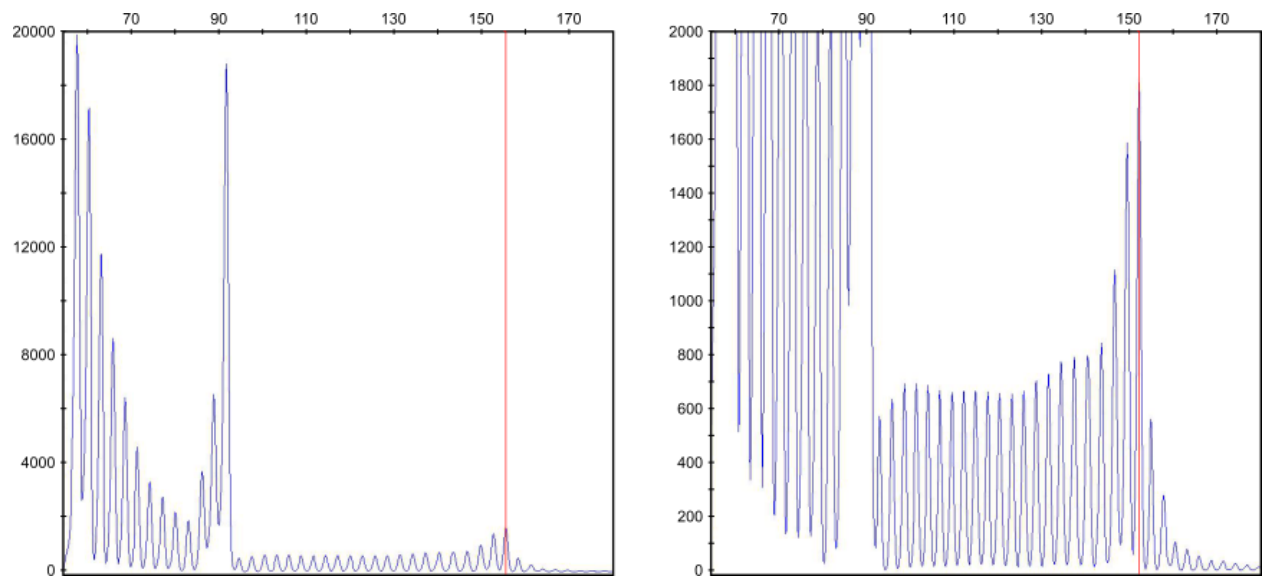


Figure S4. A representative chromatogram from the repeat-primed PCR assay used to quantify somatic mosaicism of the *HTT* CAG repeat expansion. Related to Figure 2.

The left panel shows the maximum view chromatogram, and the right panel shows a magnified view of the expanded allele. The red line indicates the modal peak, and expansion peaks can be visualized to the right of this peak.

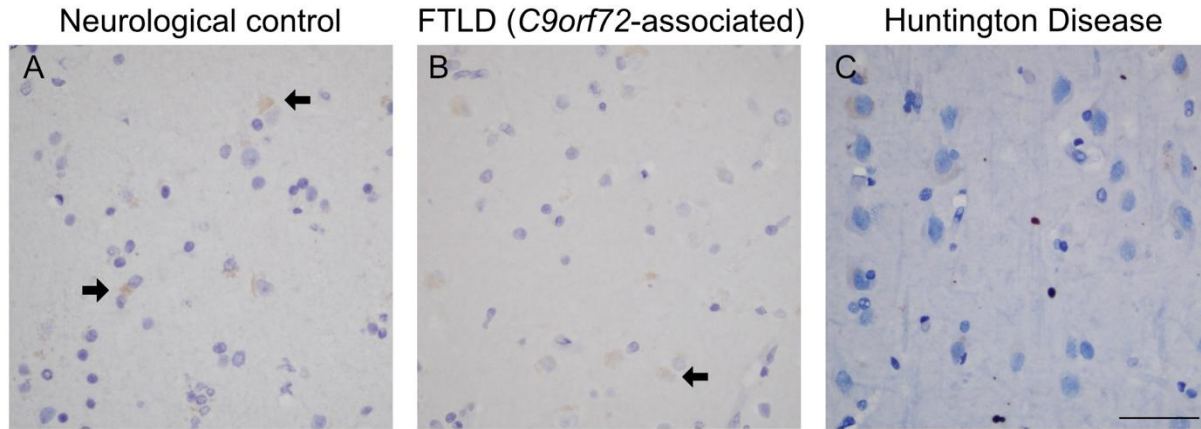


Figure S5. Photomicrographs of layer V of the prefrontal cortex (BA9) immunostained against huntingtin. Related to Figure 3.

(A-B) A 91-year-old woman without antemortem neurological impairment and a 71-year-old man with *C9orf72* FTD. Weak, diffuse, cytoplasmic staining of huntingtin was seen within the neurons (indicated by arrows) in these two brains, and no huntingtin aggregates were found. (C) A 75-year-old woman with Huntington's disease (CAG: 42/15) demonstrating extra-nuclear Huntingtin aggregates and faint cytoplasmic staining in a subset of neurons. Scale bar: 50 μ m

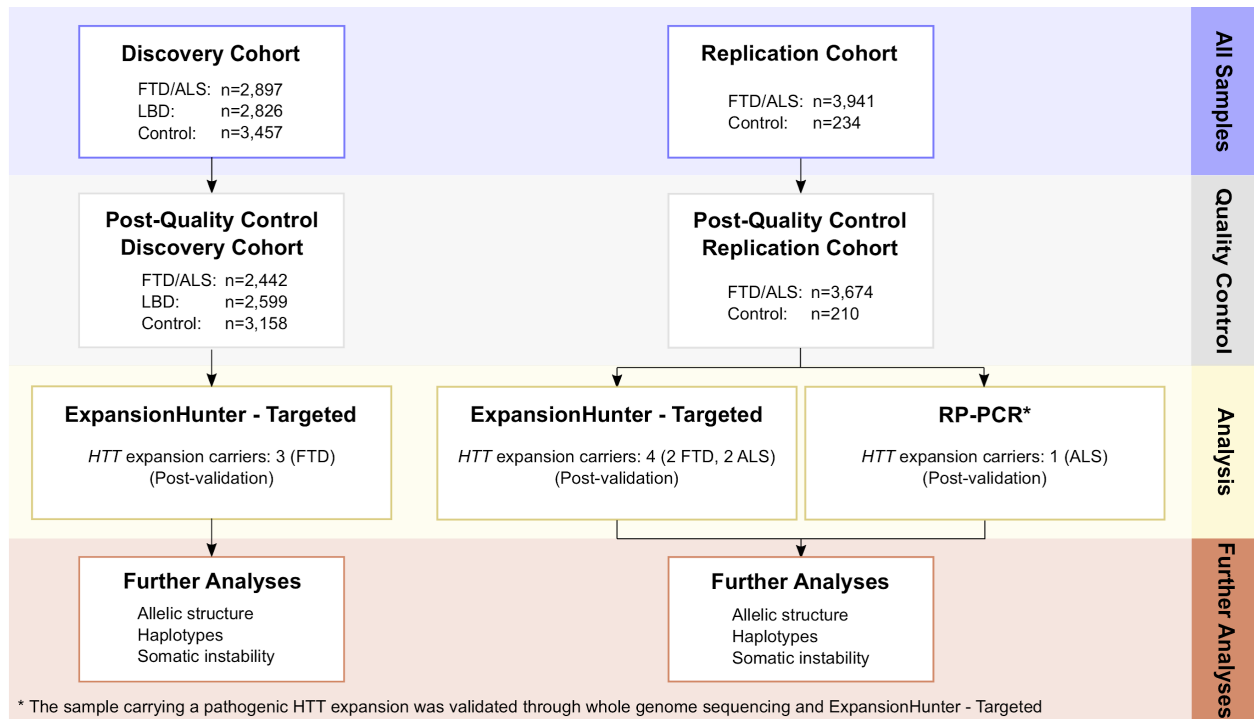


Figure S6. Flow chart outlining the study. Related to Figure 1.

Supplementary Tables

Table S1. Results of ExpansionHunter – Targeted applied to whole-genome sequence data for ten disease-causing repeat expansions. Related to STAR Methods.

Gene	Chr	Inheritance*	Lower Bound	Control Pathogenic / Total	Control Pathogenic Freq	FTD Pathogenic / Total	FTD Pathogenic Freq	ALS Pathogenic / Total	ALS Pathogenic Freq	LBD Pathogenic / Total	LBD Pathogenic Freq
AR	X	XL	37	10/3157	0.003168	3/1377	0.002179	3/1065	0.002817	6/2599	0.002309
AR Female	X	XL	37	2/1665	0.001201	1/634	0.001577	1/490	0.002041	2/903	0.002215
AR Male	X	XL	37	8/1454	0.005502	2/743	0.002692	2/575	0.003478	4/1603	0.002495
ATN1	12	AD	48	0/3158	0	0/1377	0	0/1065	0	0/2598	0
ATXN1	6	AD	39	14/3158	0.004433	6/1377	0.004357	4/1065	0.003756	16/2599	0.006156
ATXN3	14	AD	52	0/3158	0	0/1377	0	0/1065	0	0/2599	0
C9orf72	9	AD	30	5/3158	0.001583	59/1377	0.042847	108/1065	0.101408	6/2599	0.002309
DMPK	19	AD	50	4/3158	0.001267	2/1377	0.001452	1/1065	0.000939	2/2599	0.00077
FMR1	X	XL	200	0/3158	0	0/1377	0	0/1065	0	0/2599	0
FMR1 Female	X	XL	200	0/1665	0	0/634	0	0/490	0	0/903	0
FMR1 Male	X	XL	200	0/1455	0	0/743	0	0/575	0	0/1603	0
FXN (hom)	9	AR	66	0/3158	0	0/1377	0	0/1065	0	0/2599	0
HTT (CAG)	4	AD	40	0/3158	0	3/1377	0.002179	0/1065	0	0/2599	0
PHOX2B	4	AD	25	776/3158	0.245725	296/1377	0.21496	251/1065	0.235681	542/2599	0.208542

* Modes of inheritance: x-linked (XL), autosomal dominant (AD), autosomal recessive (AR); homozygous (hom) refers to biallelic expansion in genes with autosomal recessive. All ten disease-causing repeat expansions have been previously experimentally validated (Dolzhenko et al.; 2017, Dolzhenko et al., 2019).

Table S2. Demographic and clinical features of samples included in the analysis. Related to Table 1.

	FTD (n = 1,476)	ALS (n = 1,065)	LBD (n = 2,599)	Control (n = 3,158)
Female (%)	678 (46.0%)	490 (46.0%)	1,649 (63.4%)	1,483 (47.0%)
Age (IQR)	65.2 (58.0–71.0)	65.6 (59.0–73.0)	74.7 (68.0–82.0)	77.0 (69.0–86.0)
Site of onset				
Cognitive (%)	1,476 (100%)	2 (0.2%)	2,599 (100.0%)	-
Bulbar (%)	-	322 (30.2%)	-	-
Spinal (%)	-	603 (56.6%)	-	-
Family history (%)	67 (4.5%)	111 (10.4%)	240 (9.2%)	-
<i>C9orf72</i> carrier	50 (3.4%)	104 (9.8%)	-	-

FTD, frontotemporal dementia; ALS, amyotrophic lateral sclerosis; LBD, Lewy body dementia; IQR, interquartile range; *C9orf72* carrier status is based on repeat-primed PCR and ExpansionHunter – Targeted; Site of onset is missing for 138 ALS cases. *C9orf72* status is missing for 6 ALS and 22 FTD cases. The contributing study sites and consortia for these samples were: Pitie-Salpetriere Hospital (Paris), University of Thessalia (Volos), Dublin Brain Bank (Dublin), University of Torino (Torino), University Hospital of Cagliari (Cagliari), University of Bari (Bari), University of Luxembourg (Luxembourg City), Hospital de Sant Pau (Barcelona), University Hospital Mutua de Terrassa (Barcelona), Biobanc-Hospital Clinic - IDIBAPS (Barcelona), Hospital Universitario "Marques de Valdecilla" (Santander), King's College London (London), University College London (London), Imperial College London (London), University of Bristol Brain Bank (Bristol), Newcastle University (Newcastle upon Tyne), The University of Manchester (Manchester), McGill University (Montreal), University of Toronto (Toronto), Virginia Commonwealth University (Richmond, VA), Banner Sun Health Research Institute (Phoenix, AZ), Rush Alzheimer's Disease Center (Chicago, IL), Northwestern University (Evanston, IL), Parkinson's Disease Biomarker Program, Fox Investigation for New Discovery of Biomarkers Program, Indiana University School of Medicine (Indianapolis, IN), National Institutes of Health (Bethesda, MD), New York University Langone Medical Center (New York, NY), Icahn School of Medicine at Mount Sinai (New York, NY), National Cell Repository for Alzheimer's Disease (Indianapolis, IN), University of California San Diego (San Diego, CA), University of California (Irvine, CA), North American Brain Expression Consortium, NINDS Biorepository at Coriell Institute (Camden, NJ), University of Maryland Brain Bank (Baltimore, MD), University of Kansas Medical Center (Kansas City, KS), University of Michigan Brain Bank (Ann Arbor, MI), Mayo Clinic (Jacksonville, FL), Mayo Clinic (Rochester, MN), Brigham & Women's Hospital (Boston, MA), Scripps Translational Science Institute (La Jolla, CA), Johns Hopkins University (Baltimore, MD), Oregon Health & Science University Brain Bank (Portland, OR), and Baltimore Longitudinal Study on Aging (Baltimore, MD).

Table S3. Primer sequences and conditions used for the repeat-primed PCR and for cloning and Sanger sequencing. Related to STAR Methods.

Primers	Sequence
Forward_RPPCR	6FAM-ATGAAGGCCTTCGAGTCCCTCAAGTC
Reverse_RPPCR	ATGAAGGCCTTCGAGTCCCTCAAGTC
HD1F	CCGCTCAGGTTCTGCTTTTA
HD1FR	GGCTGAGGCAGCAGCGGCTG

Thermocycling conditions for the repeat-primed PCR (RPPCR) were as per Jama et al., 2013. HD1F and HD1FR refer to the forward and reverse primers respectively used for PCR amplification prior to cloning. Thermocycling conditions for the Sanger sequencing were as follows: 95°C for 5 minutes, then (94°C for 20 seconds, 70°C for 30 seconds, 72°C for 30 seconds) x 2 cycles, (94°C for 20 seconds, 68°C for 30 seconds, 72°C for 30 seconds) x 3 cycles, (94°C for 20 seconds, 66°C for 30 seconds, 72°C for 30 seconds) x 4 cycles, (94°C for 20 seconds, 64°C for 30 seconds, 72°C for 30 seconds) x 5 cycles, (94°C for 20 seconds, 62°C for 30 seconds, 72°C for 30 seconds) x 6 cycles, (94°C for 20 seconds, 60°C for 30 seconds, 72°C for 30 seconds) x 8 cycles, (94°C for 20 seconds, 58°C for 30 seconds, 72°C for 30 seconds) x 12 cycles, followed by a final extension stage of 72°C for 10 minutes.

Table S4. Conditions used for immunohistochemistry staining of brain and spinal cord tissue. Related to STAR Methods.

Antibody	Company	Catalogue number	Dilution	Primary antibody incubation time (minutes)	Protocol and dilution	Platform
Huntingtin/p62 double stain	Millipore/Abcam	MAB5492/ab207305	1:2000	32/24	64 min (CC1)	Roche Ventana Instrument
Huntingtin single stain	Millipore	MAB5492	1:2000	32	64 min (CC1)	Roche Ventana Instrument
Rabbit Anti-Ubiquitin	Dako	Z0458	1:2000	21 hrs	--	Manual
Anti-polyglutamine-Expansion Diseases Marker Antibody, clone 5TF1-1C2	Millipore Sigma	MAB1574	1:500	21 hrs	--	Manual
Anti-phospho TDP-43 (pS409/410)	Cosmo Bio Co., Ltd	CAC-TIP-PTD-M01	1:2000	21 hrs	pretreat 10min boil citrate buffer, pH 6.0	Manual
Anti-TDP-43	Proteintech	10782-2-AP	1:2000	32	64 min (CC1)	Leica Bond Platform

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