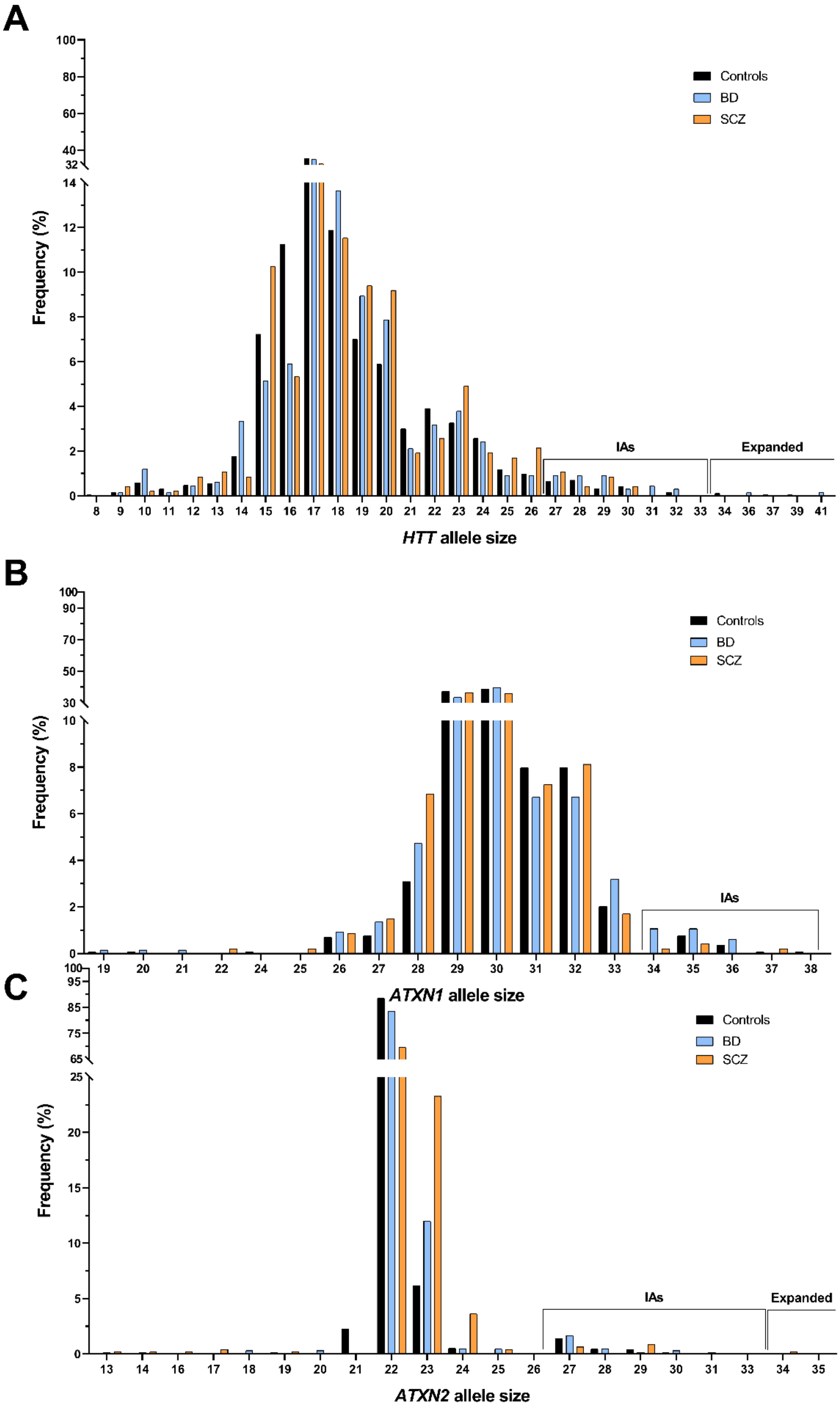
Supplementary Information



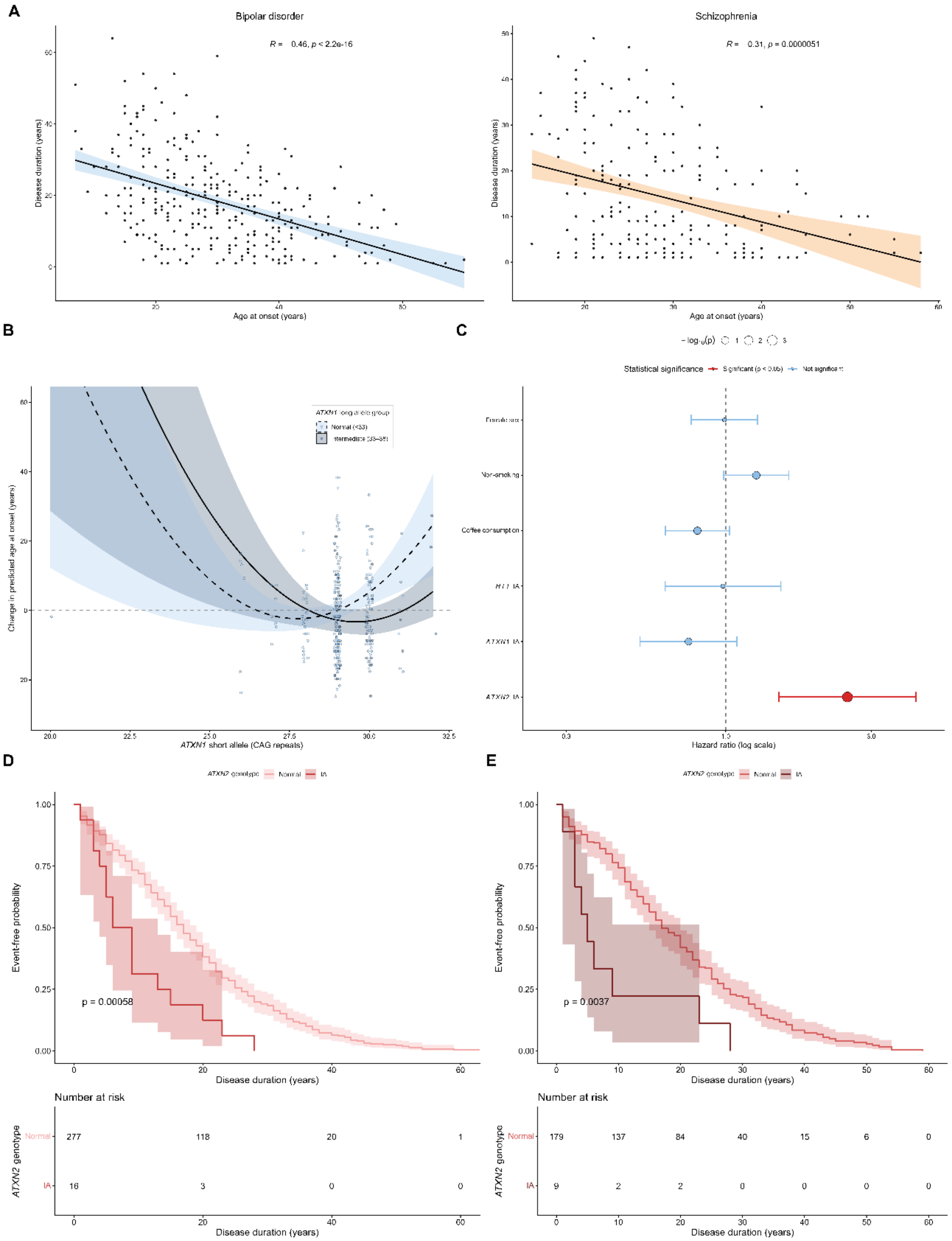
Supplementary Figure 1. CAG repeat size frequencies of *HTT*, *ATXN1* and *ATXN2* in the studied cohorts.

(A) *HTT* CAG repeat size distribution across all observed alleles (allele 1 and 2) in all cohorts. The most frequent allele sizes were 17 and 18 CAG repeats in all groups. Intermediate-length alleles (27–35 CAGs) were present in all cohorts. Expanded alleles (≥36 CAGs) were detected in controls and BD.

(B) *ATXN1* CAG repeat size distribution across all observed alleles (allele 1 and 2) in all cohorts. The most frequent allele sizes were 29 and 30 CAG repeats in all groups. Intermediate alleles (33–38 repeats) were present in all cohorts. No expanded alleles (>38 CAGs) were observed in any group.

(C) *ATXN2* CAG repeat size distribution. The most common alleles were 22 and 23 CAGs across the three cohorts. Intermediate alleles (27–32 CAGs) were present in all cohorts. Expanded alleles (≥33 CAGs) were detected only in schizophrenia (SCZ) patients.

CAG repeat size categories were defined as follows: *HTT*: normal <27, intermediate 27–35, expanded ≥36; *ATXN1*: normal <33, intermediate 33–38, expanded >38; *ATXN2*: normal <27, intermediate 27–32, expanded ≥33. Frequencies are expressed as percentages of all alleles per cohort and include both alleles per individual. Colors represent diagnostic groups: black for controls, blue for BD, and orange for SCZ.



Supplementary Figure 2. Age at onset and disease duration analyses in bipolar disorder and Schizophrenia.

(A) Correlation between age at onset and disease duration in bipolar disorder (BD) and Schizophrenia (SCZ), assessed using Spearman's rank correlation. Each point represents an individual; solid lines indicate fitted trends with 95% confidence intervals.

(B) Interaction between ATXN1 CAG repeat length and age at onset in BD. Lines represent model-based predictions from the linear regression including quadratic and interaction terms, centered to the predicted age at onset of a reference individual with median short and long alleles. Shaded areas indicate 95% confidence intervals. Points show individual observations, jittered for visualization.

(C) Forest plot summarizing hazard ratios (HRs) from Cox proportional hazards models evaluating the association between genetic variables and disease duration in BD. Points indicate HR estimates and horizontal bars represent 95% confidence intervals; color denotes statistical significance (red: $p<0.05$; blue: not significant).

(D) Time-to-event curves of disease duration in BD stratified by ATXN2 genotype (normal vs intermediate alleles). The y-axis represents the event-free probability, defined as the probability of not yet reaching the end of follow-up. Shaded areas indicate 95% confidence intervals, and the table shows the number of individuals at risk over time. Group differences were assessed using log-rank tests.

(E) Time-to-event curves of disease duration in BD patients with cognitive impairment, stratified by ATXN2 genotype and displayed as in panel D.

BD, bipolar disorder; SCZ, Schizophrenia; CAG, cytosine–adenine–guanine trinucleotide repeat; HR, hazard ratio; IA, Intermediate Allele.

Supplementary Table 1. HTT, ATXN1, ATXN2 CAG repeat sizes across cohorts.

Group	**Short allele size**						**Long allele size**					
	HTT	**p (effect)**	***ATXN1***	**p (effect)**	***ATXN2***	**p (effect)**	***HTT***	**p (effect)**	***ATXN1***	**p (effect)**	***ATXN2***	**p (effect)**
Control	16.69±2.04	-	29.18±1.09	-	21.95±0.49	-	19.68±3.36	-	30.56±1.41	-	22.40±1.23	-
BD	16.76±2.24	ns	29.12±1.21	ns	21.95±0.81	**p<0.001* (0.20) vs SCZ**	20.07±3.61	0.16 (0.05)	30.63±1.56	ns	22.57±1.38	**p<0.001* (0.14) vs control and SCZ**
SCZ	16.78±2.19	ns	29.04±1.00	ns	22.00±1.09	**p<0.001* (0.22)**	20.07±3.36	0.12 (0.06)	30.40±1.32	ns	22.71±1.39	**p<0.001* (0.24)**
BD subtype												
BD-I	16.68±2.22	ns	29.02±1.30	ns	21.91±0.89	ns	20.25±3.70	ns	30.50±1.49	ns	22.57±1.40	**p<0.001* (0.11)**
BD-other	16.92±2.04	ns	29.23±0.88	ns	22.01±0.69	ns	19.81±3.43	ns	30.79±1.54	ns	22.64±1.42	**p<0.001* (0.12)**
CD diagnosis in BD												
BD with CD	17.03±2.19	**p=0.014* (0.08)**	29.11±1.14	ns	21.98±0.74	**p=0.035* (0.08)**	20.26±3.52	**p=0.049* (0.07)**	30.58±1.59	ns	22.55±1.31	**p<0.001* (0.11)**
BD without CD	16.23±2.21	p=0.72 (0.01)	29.21±0.76	ns	21.87±1.00	p=0.79 (0.008)	19.94±3.76	p=0.63 (0.02)	30.68±1.43	ns	22.50±1.24	**p=0.023 (0.08)**
SCZ subtype												
SCZ-paranoid	16.80±2.19	ns	29.01±1.00	ns	21.98±1.16	**p<0.001* (0.21)**	20.19±3.41	ns	30.37±1.32	ns	22.69±1.37	**p<0.001* (0.22)**
SCZ-other	16.86±2.16	ns	29.29±0.98	ns	22.14±0.45	**p=0.02* (0.10)**	19.46±2.91	ns	30.64±1.28	ns	22.93±1.61	**p<0.001* (0.14)**
CD diagnosis in SCZ												
SCZ with CD	16.88±2.09	ns	29.02±1.07	ns	22.01±0.99	**p<0.001* (0.20)**	19.98±3.30	ns	30.44±1.41	ns	22.70±1.38	**p<0.001* (0.23)**
SCZ without CD	16.09±2.23	ns	29.18±0.67	ns	21.97±1.64	**p<0.001* (0.17)**	20.41±3.84	ns	30.29±0.97	ns	22.85±1.35	**p<0.001* (0.16)**

*: Wilcoxon or Dunn tests with Holm-corrected p < 0.05; ns: non-significant; Kruskall-Wallis is performed before dunn post-hoc; wilcox-effect size is performed. Effect size magnitudes were interpreted as follows: 0.10–<0.30 (small), 0.30–<0.50 (moderate), and ≥0.50 (large).