Profiling brain morphology for autism spectrum disorder with two cross-culture large-scale consortia

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ABSTRACT

We explore neurodevelopmental heterogeneity in Autism Spectrum Disorder (ASD) through normative modeling of cross-
cultural cohorts. By leveraging large-scale datasets from Autism Brain Imaging Data Exchange (ABIDE) and China Autism
Brain Imaging Consortium (CABIC), our model identifies two ASD subgroups with distinct brain morphological abnormal-
ities: subgroup "L" is characterized by generally smaller brain region volumes and higher rates of abnormality, while sub-
group "H" exhibits larger volumes with less pronounced deviations in specific areas. Key areas, such as the isthmus cingu-
late and transverse temporal gyrus, were identified as critical for subgroup differentiation and ASD trait correlations. In sub-
group H, the regional volume of the isthmus cingulate cortex showed a direct correlation with individuals' autistic manner-
isms, potentially corresponding to its slower post-peak volumetric declines during development. These findings offer in-
sights into the biological mechanisms underlying ASD and support the advancement of subgroup-driven precision clinical
practices.

INTRODUCTION

Autism Spectrum Disorder (ASD), or autism, is a lifelong neurodevelopmental condition characterized by impairments in social com-
munication and the presence of repetitive, unusual sensorymotor behaviors [1,2]. The global prevalence of ASD is approximately 1%
in children [3], with different rates reported in specific regions, such as 2.8% in children aged 8 years in the United States [4] and 0.7%
in children aged 6 to 12 years in China [5]. Several factors, including improved survey methodologies, diagnostic practices, public
awareness and access to services, have contributed to this increase in prevalence [3,6]. Over time, understanding of ASD has devel-
oped from a categorical diagnosis to a dimensional perspective of neurodiversity [7]. This change redefined autism as a spectrum
that includes a wide range of characteristics within a unified framework [8]. However, the expanded diagnostic criteria may have too
low thresholds for diagnosis [9], and have introduced significant heterogeneity within ASD. This heterogeneity suggests that the term
"spectrum" encompasses multiple subgroups with distinct etiological phenotypes [10,11].

Recent neuroimaging studies increasingly highlight ASD's biological heterogeneity as a key barrier to identifying consistent brain-
behavior relationships. Traditional case-control neuroimaging studies, which assume ASD and typical developing groups as homo-
geneous entities, often fail to account for subgroup differences [12]. This has led to inconsistent findings across brain regions and par-
ticipants, further complicating efforts to identify reliable brain-behavior biomarkers. The decreasing effect sizes in group compari-
son studies over time [13] highlight the difficulty of constructing mechanistic models of ASD. This heterogeneity challenge extends
to intervention research, where differential treatment responses across ASD subgroups [14,15] suggest that precision approaches ac-
counting for neurobiological variation could enhance outcomes. Data-driven clustering techniques have emerged as a promising
approach to address this complexity by leveraging cognitive and behavioral profiles alongside patterns of brain morphology and
function. Various clustering methods [16–20] have been used to identify meaningful subgroups, in order to uncover the neurobiolog-
ical mechanisms of ASD and provide insights into subgroup-specific traits [8,21]. While despite decades of effort, inconsistencies in
sample selection, classification methods, and feature selection between studies remain significant challenges [21]. These issues have
limited the ability of clustering techniques to consistently identify robust and replicable subgroups.

Inconsistencies in ASD studies may be due to altered neurodevelopmental adaptations [22] and participant selection biases [23]. These
limitations highlight the need to group variables with strong biological relevance for the ASD subgroups [24]. At the same time, indi-

vidual differences in sex, intelligence, medication use, and comorbidities [25,26], along with methodological variability [27] in data ac-

quisition and analysis, complicate the interpretation of the results of neuroimaging studies. In response to these challenges, norma-

tive modeling [28] techniques offer a promising framework to capture the full range of neurobiological variation [12]. This approach en-

ables standardized assessments by comparing an individuals brain morphology to population-based references [29]. In previous ASD

studies, references were often built on internal or public datasets [18,20,30,31], but the relatively small sample size limits the general-

izability and reliability of the results. Recently, the Lifespan Brain Chart Consortium (LBCC, https://github.com/brainchart/lifespan)

provided neurodevelopmental variations throughout life from the most inclusive data available [32], providing a robust framework for

us to achieve percentile-based comparisons of ASD with considerable statistical power.

This study adjusted the LBCC normative models in two large-scale cross-cultural ASD consortia: the China Autism Brain Imaging

Consortium (CABIC) [33] and the Autism Brain Imaging Data Exchange (ABIDE) [34,35]. Focusing on childhood development, we used

the largest-scale brain charts [32] to explore neurodevelopmental heterogeneity in ASD before adolescence. We classified ASD into

subgroups using spectral clustering based on Out-of-Sample (OoS) centile scores, a biological measure which quantified brain mor-

phological deviations of ASD from normative growth. A Support Vector Machine (SVM) with Recursive Feature Elimination and Cross-

Validation (RFECV) identified key brain regions driving subgroup classification. The ABIDE-based classifier was then applied to CABIC

to identify similar subgroups. Brain-behavior analyses were performed separately for each dataset to identify reproducible subgroup-

specific correlations. From a perspective of brain morphology, this work disentangles the mechanisms of mixed neurosubtypes and

provides new insight into the biological complexity of ASD.

RESULTS

Brain Morphological Profiles Reveal Two Distinct Autism Subgroups

We first analyzed the ABIDE dataset. The distributions of the OoS centile scores across 34 bilateral Desikan-Killiany [36] cortical vol-

umes ranged from 0 to 1 (Figure S1a in the Supplementary Information). OoS scores estimate the morphological variations of each

participant in 34 brain regions compared to the median regional volumes of the population (50th centile, equivalent to a 0.5 OoS

score). Relative to 0.5, individuals with more atypical phenotypes have more extreme scores. A Shapiro-Wilk test on the 34 OoS

scores indicated that none followed a normal distribution (Table 1, column 2). Using spectral clustering on the OoS scores, we iden-

tified two distinct clusters (ASD subgroups) with the highest silhouette coefficient among cluster solutions ranging from two to ten

(Figure 1a). All p-values for between-subgroup comparisons (two-sample t-tests for the paracentral and pars orbitalis regions, and

rank-sum tests for all other regions) were < 0.001). One subgroup, referred to as "L", exhibited generally *Lower* OoS scores, while the

other referred to as "H", displayed *Higher* scores (Table 1, columns 5 and 7).

Certain regions of the brain showed significant differences in their OoS score distributions between the two subgroups (Figure 1g;

Figure S1b in the Supplementary Information. For CABIC results, please see Figure S2a and S2b). Subgroup H exhibited greater

variability in the occipital lobe, particularly in the lingual gyrus, pericalcarine cortex, and cuneus. In contrast, subgroup L showed

more pronounced reductions in these regions compared to the normative benchmark (0.5). Other regions, such as the pars oper-

cularis and superior temporal gyrus, also exhibited subgroup-specific changes. The results of the Shapiro-Wilk test for OoS scores

(Table 1, columns 4 and 6) indicated that more brain regions in subgroup H followed a normal distribution compared to subgroup

L. Broader variability was observed in regions such as the entorhinal cortex in subgroup L and the pericalcarine in subgroup H, high-

lighting further subgroup-specific clustering.

Distinct Structural and Age Differences Between Subgroups

The median OoS scores before clustering (Figure 1b; Table 1, column 3) reveal a mixed pattern of deviations across regions. Most

regions exhibit reduced volumes, particularly in the occipital lobe. However, some regions, such as the precuneus, paracentral lob-

ule, transverse temporal gyrus, and insula, show slightly higher OoS scores. This combined pattern reflects overlapping structural

deviations from both subgroup H (Figure 1c, top) and L (Figure 1c, bottom), obscuring the distinct morphological differences that

become evident after clustering. For instance, although subgroup L shows smaller volumes in the insula and precuneus, the larger

volumes in subgroup H predominantly drive the combined pattern in the whole population. In contrast, smaller volumes of the lin-

Figure 1: Clustering-derived subgroups reveal distinct brain morphological patterns in ASD from ABIDE dataset.
a, Silhouette scores across different clustering solutions (2 to 10 clusters). The highest silhouette score indicates two distinct subgroups. **b,** Median OoS scores of 34 cortical regions before clustering. **c,** Median OoS scores of ASD subgroup H (top) and L (bottom). **d,** SHAP summary plot displaying the top 10 brain regions with the highest contributions to the SVM model's predictions. **e,** The mean SHAP values across the 29 selected cortical regions contributed to the classification. **f,** Prevalence maps depicting the proportion of participants with extreme (2.5% for subgroup L, 97.5% for subgroup H) structural anomalies. **g,** OoS scores across 34 cortical regions (top) and global measures (bottom) for subgroup H (orange) and L (green). TCV, total cortical volume; WMV, total white matter volume; GMV, total cortical gray matter volume; sGMV, total subcortical gray matter volume; CSF, total ventricular cerebrospinal fluid volume; mCT, mean cortical thickness; tSA, total surface area; Dots indicate the mean value of OoS scores, bars indicate the standard deviation. See Supplementary Information Figure S1b and Figure S1d for detailed density plots. Distribution of participant ages (**h**); IQ scales (**i**); ADI-R (**j**); PDD category (**k**, top left), MRI scanner model (**k**, top middle), manufacturer (**k**, top right), and data collection site (**k**, bottom); SRS (**l**); and ADOS (**m**) across the two subgroups, with subgroup L participants being significantly younger than those in subgroup H ($p = 0.02$). Note, the left hemispheres are plotted in **b**, **c**, **e**, and **f** just for visualization purposes. For plots **h**, **i**, **j**, **l**, and **m**, the center line shows the median; the box limits represent the 25th and 75th percentiles; the whiskers show the minimum and maximum values; and the dots represent potential outliers.

gual gyrus and the middle temporal gyrus in subgroup L have a stronger influence on the overall result. Some regions, such as the

pericalcarine cortex, are almost entirely influenced by subgroup L. Meanwhile, regions like the inferior and superior temporal gyrus

exhibit volumes close to the normative average because of the contrasting characteristics of both subgroups effectively canceling

each other out.

To identify the brain regions most associated with morphological abnormalities, we calculated the prevalence of abnormalities for

each region in the two subgroups. The prevalence represents the percentage of participants with OoS scores below 0.025 (2.5%

centile) for subgroup L, while above 0.975 (97.5% centile) for subgroup H. Subgroup L (Figure 1f, bottom; Table 1, column 8) exhib-

ited the highest prevalence of abnormalities in regions such as the middle and inferior temporal gyrus, pericalcarine cortex, frontal

pole, and medial orbital frontal gyrus. In contrast, subgroup H (Figure 1f, top; Table 1, column 9) generally exhibited less severe ab-

normalities, with a concentration in the insula, transverse temporal gyrus, and caudal anterior cingulate. Participants in subgroup

L were significantly younger than those in subgroup H (Figure 1h; $p = 0.02$, Table S1 in Supplementary Information). However, no

significant differences were observed in the category PDD ($p = 0.32$), the MRI scanner model ($p = 0.07$) and the manufacturer

($p = 0.86$), the data collection site ($p = 0.16$) (Figure 1k), IQ (Figure 1i, see Table S1 in Supplementary Information for details), or

scores from ADI-R (Figure 1j), SRS (Figure 1l), and ADOS-2 (Figure 1m). The corresponding results for CABIC are shown in Supple-

mentary Information Figure S3.

Machine Learning Reveals Subgroup Morphological Features

The optimized SVM model for the identification of subgroups demonstrated robust predictive performance. It used a polynomial

kernel with a regularization parameter $C = 0.1$ and a kernel coefficient $\gamma = 1$. The model achieved a high classification accuracy

$(0.95, p < 0.001)$ and a F1 score $(0.94, p < 0.001)$ in five cross-validation folds. Figure 1d shows the SHapley Additive exPlanations

(SHAP) summary plot for the top 10 selected features. Figure 1e and Table S2 in Supplementary Information summarize the mean

SHAP values for all 29 selected regions. SHAP values [37] quantify the contribution of individual brain regions to the predictions of

the model. Among the regions, the isthmus cingulate, entorhinal cortex, precuneus, and middle temporal gyrus emerged as the

most predictive features. Higher SHAP values for these regions were strongly associated with subgroup H, while lower values cor-

responded to subgroup L. These findings indicate different volumetric patterns in the cingulate, temporal, and parietal areas, effec-

tively distinguishing the two subgroups.

Distinct Structural Covariance Patterns Across Subgroups

Structural covariance analysis on OoS scores revealed significant correlations between brain regions, with distinct patterns observed

across ASD subgroups and control group (Figure 2c). These patterns were reproduced in both the ABIDE and CABIC datasets. In

subgroup H, enhanced covariation was identified between the isthmus cingulate and the caudal middle frontal region (ABIDE: $z =$

$2.88, p = 0.00$; CABIC: $z = 2.25, p = 0.02$). In subgroup L, the parahippocampal gyrus showed reduced covariation with the entorhinal

cortex (ABIDE: $z = -2.07, p = 0.04$; CABIC: $z = -3.25, p = 0.00$). Similarly, reduced covariation was observed between the posterior cin-

gulate and the entorhinal cortex (ABIDE: $z = -2.12, p = 0.03$; CABIC: $z = -2.64, p = 0.01$) and between the insula and the entorhinal

cortex (ABIDE: $z = -3.30, p = 0.00$; CABIC: $z = -2.18, p = 0.03$). An increased covariation was observed in subgroup L between the

parahippocampal gyrus and the lateral occipital cortex (ABIDE: $z = 1.97, p = 0.05$; CABIC: $z = 2.04, p = 0.04$).

Brain-Behavior Correlations in Subgroup H

We examined correlations between cortical region volumes (OoS scores) and clinical measures in the ABIDE and CABIC datasets,

identifying significant associations that were consistent between both datasets. All significant correlations were found within sub-

group H. The transverse temporal gyrus showed positive correlations with ADOS (ADOS-2 in ABIDE and ADOS in CABIC) Total and

Social Affect scores (Figure 2a). In the CABIC dataset, moderate correlations were observed for Total ($r(198) = 0.17, p = 0.02$) and So-

cial Affect ($r(191) = 0.21, p = 0.00$) score. Stronger correlations were identified in the ABIDE dataset for Total ($r(93) = 0.24, p = 0.01$)

and Social Affect ($r(93) = 0.20, p = 0.04$) score. The inferior temporal gyrus was positively correlated with RRB (restricted interests

and repetitive behaviors), with a slightly stronger correlation in ABIDE ($r(94) = 0.19, p = 0.05$) compared to CABIC ($r(189) = 0.17$,

$p = 0.02$). The volumetric centile of the isthmus cingulate is correlated with SRS Autistic Mannerisms, showing a higher correlation

Figure 2: Brain-behavior correlations and structural covariations of Out-of-Sample scores.
a, Reproducible correlations between brain region volumes, measured as Out-of-Sample (OoS) scores, and clinical measures across ABIDE and CABIC datasets (subgroup H only). **b,** Mediation models for significant brain-behavior associations identified in subgroup H (ABIDE cohort only). Black solid arrows represent significant effects, while gray arrows indicate non-significant ones. Top: transverse temporal; bottom left: inferior temporal; bottom right: isthmus cingulate. **c,** Significant structural covariations across ABIDE and CABIC datasets. Positive z-values (red lines) indicate stronger covariance in ASD participants compared to controls, while negative z-values (blue lines) reflect weaker covariance.

in ABIDE ($r(58) = 0.33, p = 0.01$) than in CABIC ($r(192) = 0.14, p = 0.04$). No significant correlations were identified between structural

covariance patterns and cognitive behavior outcomes.

As a common comorbidity of ASD, intellectual disability is closely associated with atypical brain morphological developmental pat-

terns that accompany individual differences in intellectual functioning. To examine whether Full-Scale Intelligence Quotient (FIQ)

mediates the relationships between brain morphology and cognitive behaviors within clusters, mediation analyses were conducted

on the significant correlations we found in subgroup H. Results revealed direct effects for specific cortical regions (Figure 2b). The

transverse temporal gyrus showed a direct effect on ADOS-2 Total ($C' = 0.21, p = 0.03$), while the isthmus cingulate exhibited a

direct effect on SRS Autistic Mannerisms ($C' = 0.32, p = 0.01$). As our analysis relied on cross-sectional data, the observed brain-

behavior relationships represent correlations rather than causal effects. Our mediation hypotheses regarding developmental brain-

behavior causality require validation through longitudinal studies. While no mediation effects through FIQ were observed, both

from brain → cognitive behaviors or in reverse (Figure S4). Neither direct nor indirect effects were significant for correlations to ADOS-

2 RRB or Social Affect.

DISCUSSION

This study used the ABIDE and CABIC datasets to discover distinct brain morphological subgroups of ASD within a young male co-

hort. We identified two subgroups characterized by significant differences in OoS scores in 34 cortical regions. Machine learning

models showed a high predictive accuracy in distinguishing these subgroups based on their brain morphology. Furthermore, struc-

tural covariance and brain behavior correlation analysis illustrated different patterns of morphological relationships and their associ-

ations with clinical measures, especially in subgroup H. The consistent correlations across both the ABIDE and CABIC datasets high-

light the robustness and reproducibility of our results across diverse cohorts. We will now discuss these findings from several neuro-

biological and neurodevelopmental perspectives to enhance our understanding of the distinct morphological patterns identified.

Two Subgroups Suggest Different Neurobiological Basis

Studies have reported extremely large or small head circumferences in individuals with ASD, possibly related to different subgroups. Early brain overgrowth is one of the most consistent findings in ASD research [38]. Abnormal increases in brain size during early development suggest that atypical cell proliferation significantly contributes to ASD symptoms [39]. Ultrasound studies have detected head enlargement during the second trimester in individuals later diagnosed with ASD [40]. iPSC-based studies reveal enlarged embryonic stage brain cortical organoids (BCOs) in babies with ASD, with larger BCOs associated with more severe social symptoms [41]. MRI scans of these individuals show overgrowth in primary auditory and somatosensory cortices, while undergrowth in the visual cortex [41]. This neuronal overproduction, caused by the acceleration of the cell cycle, results in impaired differentiation and ultimately disrupts neural functions [42].

Smaller brain volumes are also frequently reported in ASD. A meta-analysis [43] identified volumetric reductions in a large cluster of regions, including the parahippocampal gyrus and entorhinal cortex. Higher levels of autistic traits have been associated with a smaller total cortical volume (TCV), a lower cortical thickness, a smaller surface area and a lower gyrification [44,45]. One potential explanation for this global brain underdevelopment is impairment caused by insufficient blood circulation and oxygen saturation [46]. For example, children with complex congenital heart disease (CHD) also demonstrate cognitive difficulties similar to those observed in ASD and have an increased likelihood of developing ASD [47]. Similarly, head enlargement also coincide with greater increases in height often [45]. Therefore, brain overgrowth could be part of the broader physical growth dysregulation [48] too.

These evidences provide the distinct neurobiological basis for the subgroups identified in our study. The different underlying physiological mechanisms may explain the inconsistent effectiveness of commonly used pharmacological treatments. For example, unsupervised data-driven cluster analysis on ASD children revealed an optimum of two intranasal oxytocin intervention-sensitive subtypes [49]. Our discovery of two distinct ASD subtypes with divergent brain morphologies further supports the necessity for subtype-specific therapeutic strategies. Future research focusing on targeted pharmacological interventions for individual subtypes will not only explain how these treatments modulate brain function and ultimately translate into clinical benefits, but also advance personalized medicine in ASD. Specifically, by mapping neurobiological heterogeneity to differential therapeutic outcomes, this approach could reconcile previous inconsistencies in treatment efficacy while optimizing intervention protocols for mechanistically defined patient subgroups.

Hypothesis of Abnormal Brain Morphology Specific Functional Impairment Pathways

Abnormal neural migration and cortical laminar organization in ASD [50] suggest that structural abnormalities are unlikely to be localized. Postmortem studies have identified focal laminar disorganization and mis-migrated neurons in the prefrontal and temporal cortex, particularly in layers 2, 3, and 4 [50]. Layers 2 and 3 support information exchange between cortical regions, while layer 4 receives sensory inputs [51]. Disruptions in these layers can cause profound miscommunication between the sensory and higher-order cognitive regions. Key regions in our clustering analysis (such as the precuneus, isthmus cingulate, and entorhinal cortex; Figure 3a, a~c) are primarily involved in higher-order association networks (Figure 3a). As an idea for exploring hierarchical information flow of functional connectivity, Stepwise Functional Connectivity (SFC) analysis was introduced to disentangle brain functional networks, and has discovered the complex connectivity transitions from primary sensation to higher-order association regions of the brain [52,53]. These existing information flow suggest different pathways of impairment as the basis for the heterogeneity of ASD. Inconsistencies in information flow reported by previous ASD studies [21,54] may arise from two distinct structural impairment patterns identified in our study.

The regional volume abnormalities identified in our study involve distinct functional brain regions in the two subgroups. Subgroup L showed a notable prevalence in the middle temporal gyrus, inferior temporal gyrus, pericalcarine cortex and frontal pole (Figure 3a, d~g), while subgroup H in the caudal anterior cingulate, transverse temporal cortex, and insula (Figure 3a, h~j). Drawing on the spatial distributions [55] of 7 large-scale functional networks [56], we constructed a schematic (Figure 3b) of the latest 15 large-scale functional networks of the brain estimated from individuals [57] (Figure 3a). This perspective revealed different pathways of functional impairment in the regions with a high prevalence of abnormalities for each subgroup. Subgroup L exhibited an atypical morphol-

Figure 3: The theoretical brain functional network impairment model of two ASD subgroups.
a, A brain map combining the 34 Desikan regions[36] with the latest 15 large-scale brain functional networks estimated from individuals[57]. *a*, precuneus; *b*, isthmus cingulate; *c*, entorhinal; *d*, middle temporal; *e*, inferior temporal gyrus; *f*, pericalcarine; *g*, frontal pole; *h*, caudal anterior cingulate; *i*, transverse temporal; and *j*, insula. **b,** A schematic of the potential spatial distributions of distinct functional impairment networks inferred from 34 cortical regions with high abnormal prevalence for two subgroups. VIS, Visual (C, Central; P, Peripheral); SMOT, Somatomotor; AUD, Auditory; dATN, Dorsal Attention; PM-PPr, Premotor-Posterior Parietal Rostral; CG-OP, Cingulo-Opercular; SAL/PMN, Salience/Parietal Memory; FPN, Frontoparietal; LANG, Language; DN, Default networks.

ogy mainly affecting Visual – Dorsal Attention – Frontoparietal – Language and Default networks (Figure 3b, green path), while subgroup H affected the Auditory and Somatomotor – Cingulo-Opercular and Salience/Parietal Memory – Frontoparietal networks (Figure 3b, orange path), indicating disturbances in peculiar unimodal sensory integration and multimodal cortical functions. These networks are organized by three-order hierarchy that are agree well with myelination reference maps[57], showing that the cerebral cortex develops sequentially, radiating outward from motor and sensory cortex[58].

This phenomenon may hint at the presence of distinct abnormal brain functional circuits from first- to third-order networks in the subgroups. For example, in adults without ASD[59], increased gray matter volume in regions of the somatomotor network was associated with greater attention to detail, while changes in regions of the visual network were associated with poor imagination. These findings suggest potential cognitive patterns in two subgroups of ASD that have yet to be discovered. At the same time, these two subgroups we found may respond differently to biologically targeted therapies, emphasizing the need for more personalized approaches. For example, functional connectivity-guided continuous theta-burst stimulation (cTBS) on individual's dorsolateral prefrontal cortex target with the strongest connectivity to amygdala significantly improve social communication skills in minimally verbal ASD children[60]. As reduction in brain volume and improvements in behavior outcomes, this ASD subtype likely fit the characteristics of subgroup H in our study. Targeted modulation of subgroup specific impairment pathway may gain better therapeutic effects, therefore further refine treatment protocols for better translational outcomes. In this case, if observed social improvements stem from rebalancing the subgroup H pathway, future interventions could achieve enhanced treatment efficacy by employing personalized neuromodulation protocols that precisely target the most morphologically burdened brain regions within this circuitry.

In typically developing children, the principal functional gradient[55] of the cortical organization reflects differentiation within unimodal sensory areas, progressing from the somatomotor and auditory cortex to the visual cortex. The transition from childhood to adolescence extends this organization to higher-order association cortices[61]. Brain maturation appears to involve a shift from local to distributed network architecture. The distinct morphological abnormalities in these two ASD subgroups, observed before this transition begins, raise a critical question: How do these "morphological foundations" disrupt their development from childhood to adolescence? These structural impairment pathways in childhood are likely to contribute further to heterogeneity in ASD during and after adolescence.

Understanding the Heterogeneity from a Developmental Perspective

Different network-based vulnerabilities suggest that interventions targeting specific impairments within each subgroup could be more effective. Interestingly, we found no significant differences in cognitive or behavioral measures between the subgroups. Although there distinct patterns of structural covariation between subgroups, but no significant correlations with autism-related behaviors. Structural covariance reflects long-term developmental changes. Reduced structural covariance may indicate disruptions in shared developmental pathways, while enhanced covariance could result from compensatory adaptations in response to atypical neurodevelopmental trajectories in ASD. This implies that morphological deficiencies may activate compensatory mechanisms during development, leading to similar cognitive and behavioral outcomes.

These neurodevelopmental compensation mechanisms raise questions about the stability of subgroup morphology distinctions across different developmental stages. To validate the robustness of our ASD clusters across different development stage, we implemented sliding 4-year age windows (with a predefined threshold of at least 80 participants to ensure statistical power). For each window, we applied the identical spectral clustering pipeline and evaluated the consistent cluster indices across each narrow age range and the full age range. All the narrow age range population yielded two distinct brain subtypes as similar as the characteristics in our main results. The assignment consistency were 90.48% (5~8.9 yrs, N = 84), 91.89% (6~9.9 yrs, N = 111), 98.67% (7~10.9 yrs, N = 150), 97.71% (8~11.9 yrs, N = 175) and 88.42% (9~12.9 yrs, N = 190). These remarkable consistency in subgroup classification suggests that the specific impairments on brain morphology are consistently maintained across development.

The observed age difference between subgroups, though minor, could have significant implications during sensitive developmental periods. Lifespan trajectories [32] of 34 brain regions show an early steep increase in volume, followed by a near-linear decline. The middle temporal gyrus peaks at 7.8 years, while the caudal anterior cingulate peaks at 9.2 years [32], possibly related to the result that subgroup L is generally younger than subgroup H. However, in the CABIC cohort, we observed an inverse age relationship across both classification methods (whether using the ABIDE-classifier or independent clustering), with the subgroup L being significantly older than the H (Figure S3a and S5i). The age difference subgroups needs future studies with larger sample sizes to validate. While here, we propose some possible reasons for the ABIDE cohort to understand that these distinct structural abnormalities likely reflect differences in the timing of atypical developmental processes.

The isthmus cingulate, a key region in subgroup clustering, typically peaks in volume at 3.8 years. The lack of age-related decline in cortical volume was consistently found in subgroup H in both the ABIDE and CABIC datasets (See Supplementary Analysis and Figure S1f). However, subgroup H aligns with normative references before age 5, while subgroup L shows smaller initial volumes (Figure S1e). In subgroup H, an increase in structural covariance between the caudal middle frontal cortex (peaking at 7.75 years) and the isthmus cingulate (Figure 2c) suggests synchronized developmental trajectories. This may reflect precocious caudal middle frontal development, delayed isthmus cingulate development, or both regions following similarly abnormal patterns [22]. Correlation analyses link larger isthmus cingulate volumes in subgroup H directly with more pronounced autistic mannerisms (Figure 2a). These evidence hint at delayed development of the isthmus cingulate in subgroup H. With a normal OoS distribution ($p = 0.06$; Table 1, column 6) in this subgroup, this morphological change appears to represent a homogeneous and quantifiable pattern. In subgroup L, the parahippocampal gyrus (peaking at 10.63 years) shows reduced covariance with the entorhinal cortex (peaking at 22.67 years) but increased covariance with the lateral occipital cortex (peaking at 5.21 years). This pattern suggests a precocious development of the parahippocampal gyrus and/or the delayed lateral occipital cortex in this subgroup. Enhanced structural covariances may also reflect compensatory adaptations to mitigate structural disadvantages inherent in abnormal developmental patterns.

Recent genome-wide association studies (GWAS) [62] reveal that cortical phenotypes exhibit distinct genetic architectures, with shared genetic variants influencing both normative brain size variation. Furthermore, significant genetic correlations between cortical expansion patterns and cognitive measures suggest multi-level mechanisms underlying neurodevelopment. These findings collectively motivate future study of ASD to build longitudinal cohorts to explore how genetically mediated cortical maturation trajectories influences different stages of development in ASD subgroups. Such approaches would bridge genotype-phenotype mapping to clinically biomarkers, advancing precision diagnostics and targeted interventions during sensitive neurodevelopmental windows.

Reproducibility across Datasets and Implications for Biomarker Development

One key contribution of this study is the reproducibility of brain-behavior associations across the ABIDE and CABIC datasets. In our analysis, we didn't apply on any multiple comparisons correction, three considerations may explain. First, the dual-dataset cross-validation design required consistent results across two independent cohorts (heterogeneous in culture/age), which substantially reduces false-positive risks through empirical replication. Second, as this is an exploratory target-discovery studies, overly conservative adjustments might obscure biologically meaningful results. Third, the cross-population reproducibility were prioritized in our study. We considered that uncorrected-but-replicated results had greater biological credibility than findings that were statistically corrected but failed to replicate. As the result, this cross-dataset validation confirms that the findings reflect stable neurobiological characteristics.

In subgroup H, an enlarged transverse temporal gyrus may impair precise auditory processing. This disruption can affect auditory responsiveness and the ability to integrate and understand information during social interactions. It may also damage early language perception and acquisition, particularly before a diagnosis of ASD is made. Research has found that when ASD is accompanied by cognitive learning needs, head enlargement becomes even more pronounced[45]. This suggests a shared mechanism linking brain overgrowth with impaired intellectual functioning. Alternatively, cognitive impairments might mediate the relationship between this overgrowth and ASD. Although intelligence moderates the relationship between ASD traits, transverse temporal gyrus abnormality remains a direct indicator (Figure 2b). This suggests impaired primary sensory perceptual function that is directly disrupted by abnormal sensory input. The inferior temporal gyrus (ITG) is also uniquely associated with restricted interests and repetitive behaviors, despite the low prevalence of structural abnormalities in subgroup H. This region plays a crucial role in object recognition[63]. Disruptions in these functions can lead to a tendency to focus repetitively on objects or details. While as the RRB scale in ADOS cannot depict all the dimensions of repetitive behaviors, related results need future studies focusing on more detailed investigations on RRB to validate.

We classified ASD subtypes solely based on brain morphology, assuming a causal relationship between brain structure and cognition. However, this relationship is inherently complex, thus interpreting the brain in regions goes against its interconnected nature. Although subgroup L exhibited a higher prevalence of structural abnormalities, suggesting more extensive morphological variations, we did not find reproducible brain-behavior associations between cohorts. Several factors may explain these findings. First, cognitive impairments related to structural abnormalities in subgroup L might be more sensitive to cultural differences. Second, the validity of ASD diagnoses in subgroup L might be questionable. The best predictor of a DSM-IV diagnosis has been found to be often the specific clinic attended, rather than any defining characteristic of the individual[64]. This indicates that current diagnostic tools may not capture the nuanced behaviors directly related to brain abnormalities in subgroup L. Considering global reduction in brain volume, which may result from cardiogenic etiological damage, our findings highlight the urgent need for new methods and paradigms to enable deep phenotyping and reduce the reliance on behavioral scales for differentiation. Third, heterogeneity within subgroups may also contribute to the limited reproducibility findings. Behavioral paradigms targeting brain regions with a normal distribution of OoS scores could better reveal subgroup-specific relationships between brain morphology and cognitive behavior.

In our analysis, we have rigorously controlled for site effects to minimize their impact on the results. To validate our approach, we performed independent spectral cluster analysis using only NYU site data from ABIDE. The assignment consistency compare with the main analysis reached 90.48%, demonstrating both the robustness of our clustering framework to site-specific variability and the biological validity of the identified subtypes. This high concordance further supports the clinical translatability of our neurosubtyping scheme, as it exists even when derived from diverse data sources, therefore providing a solid foundation for future multi-site biomarker development targeting subtype-specific mechanisms.

Limitations & Future Direction

Some limitations in this study should be noted. First, previous research highlights atypical structural connectome asymmetry in ASD[65], while we could not fully evaluate hemispheric differences within subgroups using LBCC trajectories. Second, the cross-sectional nature of the data limits causal inferences about how these abnormalities of the brain morphology arise and their relationships

with ASD symptoms. Future research should thoroughly investigate brain function and cognitive differences between these sub-
groups while exploring how demographic, environmental, and developmental factors shape brain-based subtypes. Combining lon-
gitudinal data *invivo* and *invitro* [42] could expand cohort diversity and provide deeper insights into the neurobiological and molec-
ular mechanisms underlying different subtypes. When designing research cohorts to study further, focus on more representative
ASD prototypes [66] could help reduce heterogeneity within subgroups. Third, we should note that the use of ADOS rather than ADOS-
2 in the CABIC cohort represents a methodological limitation that future studies with larger datasets should address.

More attention should be paid on people with more severe ASDs, such as minimally verbal autism, who remain underrepresented
in brain imaging studies [67], partly due to the challenges of collecting neuroimaging data, especially in young children. Our research
strategy uses structural magnetic resonance imaging, feasible in natural sleep or sedation, with significant clinical potential. How-
ever, multimodal approaches with higher ecological validity are essential to identify neurosubtypes that include these samples. Im-
portantly, all current findings are derived from male ASD cohorts, any clinical translations should be cautiously limited to male pop-
ulations until validated in females. Therefore, future studies should expand ASD cohorts with more female representation to enable
comprehensive study of sex-specific brain morphological heterogeneity.

At the same time, replication with different clustering algorithms is required to confirm the stability of these findings. For exam-
ple, we employed Gaussian mixture modeling (GMM) as a validation framework to assess consistency with our main clustering re-
sults. GMM assumes the observed data are generated from a mixture of multiple distinct Gaussian distributions [68]. As the high clus-
ter indices consistency (83.58%) across both methods, the brain morphology and cognitive behavior have the similar characteris-
tics as spectral clustering analysis (Figure S6). Participants in subgroup L were also significantly younger than those in subgroup
H ($p = 0.03$). No significant differences were observed in other comparisons between two subgroups. These replication with GMM
demonstrates that our ASD neurosubtyping is not method-dependent. While more nuanced clustering approaches and strategies
should be explored in the future, as disease variations may exist within the range of normal variation [69], and multiple subpopula-
tions may also exist in typically developing populations [70]. Finally, translational studies using animal models are essential for under-
standing the mechanisms underlying these different subtypes. Such studies can provide critical information on how abnormalities
in brain morphology develop [71].

Conclusion

Linking specific brain morphology abnormalities to cognitive or behavioral impairments in ASD is challenging. Different biological
mechanisms can lead to similar behavioral outcomes, complicating the identification of neural correlates. This overlap may explain
the difficulty in replicating neuroimaging findings between studies or cohorts. Using the largest brain normative datasets and two
large-scale cross-cultural consortiums, we applied normative modeling to disentangle the heterogeneity of brain morphology in
ASD. By breaking the ASD population into smaller and more morphologically homogeneous subgroups, we identified two subtypes
of morphological abnormalities. We identified significant correlations between cortical regions and autistic traits across both con-
sortia, with particular emphasis on the isthmus cingulate cortex, as well as the transverse and inferior temporal gyri. Based on the
abnormal prevalence of regional volumes, we found two structural impairment pathways that could disrupt sensory to higher cog-
nitive functions. These findings highlight the importance of untangling mixed biological mechanisms and offer insight to develop
effective subgroup-driven individualized interventions. In conclusion, our study provides a reference for elucidating the etiological
mechanisms of neurodevelopmental disorders and advancing future subgroup-driven precision clinical practice.

MATERIALS AND METHODS

Participants and Data Preprocessing

334 Participants were selected from the Autism Brain Imaging Data Exchange (ABIDE) cohort [34,35]. The original dataset includes 1,833
335 autistic and 1,838 non-autistic individuals aged 2~64 years from 56 sites. All diagnoses were based on the DSM-IV or DSM-V cri-
336 teria. We used T1-weighted MRI data from the ABIDE (I and II) cohort. The acquisition parameters are publicly available at ABIDE
337 website. Data quality was assessed through manual visual inspection aided by visualization outputs from (MRIQC) [72] (version 22.0.6).
338 We visually rated the quality of 2,451 images using a 3-class framework [73], with "0" denoting images that suffered from gross arte-

facts and were considered unusable, "1" with some artefacts, but that were still considered usable, and "2" free from visible arte-

facts. Images with an "0" score (for example, with severe motion artifacts, segmentation errors, or structural abnormalities) were ex-

cluded. A total of 1907 (77.8%) images passed the quality control.

Due to the limited samples of female ASD participants, and the consideration that sex-specific developmental trajectories[32] and

autism-related neuroanatomical differences[74,75] may confound data-driven population clustering, our study focuses only on male

participants under 13 years old. This age range reflects our interest in brain development during childhood and early adolescence.

This yielded 274 participants for downstream analyses. The participant ID list is provided in the Supplementary Materials.

Pre-processing performed through the Connectome Computation System (CCS) pipeline[76,77]. FreeSurfer (toolbox: version 6.0.0)

was used for skull removal, cortical reconstruction, segmentation, and registration in the Montreal Neurological Institute (MNI) tem-

plate. Each T1-weighted image was segmented into gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF).

The total cortical volume (TCV) was calculated as the sum of the GM and WM volumes, following the LBCC method[32]. The mean

cortical thickness (CT) was calculated as a weighted average of the thicknesses of the left and right hemispheres. The total surface

area (SA) was determined by summing the surface areas of white matter of both hemispheres. Regional brain volumes for 34 bilat-

erally averaged cortical regions were evaluated using Desikan-Killiany parcellation[36]. To reduce site-related variability, we applied

ComBat harmonization[78]. This process was implemented using (*neuroCombat*) R package.

Normative Scoring and Clustering Analysis

To assess how the brain morphology of each participant aligned with age-standardized normative trajectories, we used the out-of-

sample (OoS) centile score[32]. First, all non-ASD individuals from the site-harmonized ABIDE data set were employed to estimate

cohort-specific statistical offsets. The centile scores of each brain measurement were then estimated for all individuals with ASD

compared to the offset trajectory (see *Methods: Centile scoring of new MRI data* in the original LBCC work[32]). This approach takes

advantage of the generalized additive models for location, scale, and shape (GAMLSS)[79] framework to estimate statistical offsets

such as mean, variance, and skewness. These offsets capture individual deviations from typical brain development. OoS scores are

comparable between age and cohort. The scoring process was conducted with the publicly available code from Lifespan Charts

website.

Using OoS scores from 34 brain regions as classification features, we applied spectral clustering[80] among individuals with ASD in

the ABIDE cohort. Spectral clustering was selected for its ability to detect nonlinear data structures, which are common in brain

imaging datasets. Unlike k-means clustering, which relies on centroid-based optimization, spectral clustering transforms the data

into a lower-dimensional space using the eigenvalues of a similarity matrix. Before clustering, the Jarque-Bera test was performed

to determine whether OoS scores follow a normal distribution.

Clustering analysis was implemented using the *kernlab* package R. We tested clusters of 2 to 10 to identify the optimal solution.

The quality of clustering was evaluated using the Silhouette Coefficient (SC)[81], which assesses both within-cluster cohesion and

between-cluster separation. SC values range from -1 to 1, with higher scores indicating better defined clusters. The optimal num-

ber of clusters was decided by the highest SC score.

Key Brain Regions for Subgroup Classification

We developed a predictive model using machine learning with individual OoS scores from 34 regions of the brain as input charac-

teristics. We trained a Support Vector Machine (SVM) classifier[82] with Recursive Feature Elimination and Cross-Validation (RFECV).

This was implemented using the *scikit-learn* library in Python. Combining recursive feature elimination (RFE)[83] with cross-validation

allows the model to iteratively identify the most informative features while maintaining generalizability and robustness. The data

set was divided into 80% training sets and 20% testing sets. Using a linear SVM as the base estimator, RFECV removed less impor-

tant features in a stepwise manner, with performance monitored through 5-fold cross-validation. This process ensured that the final

feature set balanced predictive power and reduced over-fitting.

Following feature selection, we fine-tuned the SVM model by performing a grid search to optimize key hyperparameters, includ-

ing regularization strength (C) and kernel coefficients (γ). The model was evaluated across different kernel functions, such as linear,

382 polynomial, and radial basis functions, to determine the best configuration. Once optimized, the model was trained on the selected

383 features to achieve optimal classification performance. SHapley Additive exPlanations (SHAP) [37] were applied to quantify the contri-

384 bution of each brain region to the model predictions.

Structural Covariance Network Analysis

386 To investigate morphological relationships of a specific cluster, we constructed structural covariance analysis [84] on OoS scores of

387 each two regions. Pearson's correlation analysis was performed on residuals obtained from linear regression models that controlled

388 for site effects and TCV OoS scores. To enable statistical comparison, correlation coefficients were normalized using Fishers r-to-z

389 transformation, defined as:

$$Z = \frac{1}{2} \log_e \left(\frac{1+r}{1-r} \right), \tag{1}$$

390 where r represents the Pearson correlation coefficient between two regions. The difference (cluster i/ii vs. normal control) in trans-

391 formed correlation coefficients was calculated using:

$$z = \frac{Z_1 - Z_2}{\sqrt{\frac{1}{n_1 - 3} + \frac{1}{n_2 - 3}}}, \tag{2}$$

392 where n_1 and n_2 are the two sample sizes being compared. The resulting z-values were converted to p-values using the cumulative

393 distribution function of the standard normal distribution.

Cluster Differences and Brain-Behavior Analysis

We investigated differences between clusters and demographic, technical and clinical variables. For categorical variables, such as

subtypes of perinatal developmental disorders (PDD), scanner models, and manufacturers, Chi-square tests were employed. For

data collection sites, Fishers exact test was used with Monte Carlo simulations to approximate p values. To ensure robust analysis,

sites with fewer than 10 participants were excluded. For other continuous variables, statistical methods were selected based on

data distribution: the Wilcoxon rank sum test was used for nonnormally distributed data, and the two-sample t-test for data shows

normal distribution. The effect sizes were calculated using Cramér's V for categorical variables and Cohens d for continuous vari-

ables. Statistical significance was set at $p < 0.05$.

To further explore brain-behavior relationships within clusters, we performed correlation analyses using Full-Scale Intelligence Quo-

tient (FIQ), ADOS-2 (Social Affect and Restricted and Repetitive Behaviors, RRB), ADI-R (Social Interaction and RRB), and SRS sub-

scales. Pearson's correlation was applied to most measures, while Spearman's correlation was used for ADOS-2 RRB scores due to

their limited range. In these analyzes, the effects of the site and the OoS scores of TCV were controlled. Statistical significance was

set at $p < 0.05$, and no correction for multiple comparisons was applied.

For each group, we also examined partial correlations to investigate structural covariance between 34 brain regions and their asso-

ciation with cognitive behaviors. For each participant, the partial covariance scores of two regions were calculated as

$$\text{partial\_p} = \text{residual}_{region1} \times \text{residual}_{region2},$$

The resulting partial covariance scores were then correlated with the same measurements with the same correlated methods.

Finally, we performed mediation analyzes to examine whether FIQ mediates the relationships between brain morphology and cog-

nitive behaviors within clusters. Linear models were used to estimate direct and indirect effects, with adjustments for site and OoS

scores of TCV. All brain morphology and cognitive behavior variables were standardized to ensure comparability among participants.

The significance of indirect effects was assessed using the Sobel test. As the brain abnormalities are detectable in the early develop-

ment [40] before the emergence of autistic behaviors [85], we built a mediation model to examine the brain's effect on cognitive be-

haviors. To provide a more comprehensive account, we also analyzed the reverse mediation model.

Detection of Reproducible Results Between Datasets

We applied the ABIDE-based classifier to an independent dataset from the China Autism Brain Imaging Consortium (CABIC)[33], which is a multicenter collaboration among clinical and research institutions in China. It is designed to collect neuroimaging, demographic, and behavioral data on children and adolescents with ASD. Diagnoses in the CABIC cohort were based on DSM-IV, DSM-V, or ICD-11 criteria and validated using ADOS and ADI-R. The dataset includes 2,656 participants, including 1,503 ASD individuals and 1,153 typically developing children. Detailed MRI acquisition parameters are publicly accessible at CABIC Site. There were in total 968 ASD males (4.56 ± 1.69) and 526 (7.37 ± 2.73) typically controls included into analysis.

CABIC participants, aged 1 to 13 years, tend to exhibit more severe ASD symptoms, resulting in lower variability within clusters. Although this homogeneity is clinically valuable, it poses challenges in detecting subtle brain-behavior relationships. In contrast, the ABIDE cohort provides greater behavioral differences, enhancing the ability to identify nuanced patterns in brain structure. By leveraging these complementary datasets, our goal was to identify results that are reproducible across both cohorts. We repeated the statistical, structural covariance, and correlation analyses on CABIC cohort. However, the limited FIQ data in CABIC restricted the replication of mediation analysis with sufficient statistical power. Therefore, mediation analysis was conducted on the ABIDE cohort only.

In this study, we applied a SVM classifier trained on the ABIDE cohort on the CABIC cohort. To evaluate the consistency between this transfer approach and independent clustering approach, we replicated the identical analytical process directly on ASD participants from CABIC cohort (See details in the Supplementary Information). Optimal cluster solutions was also two (Figure S5a). Among 968 participants, 929 (95.97%) exhibited consistent cluster indices across both methods. This high concordance highlights the robustness of our spectral clustering framework across heterogeneous datasets.

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AUTHOR CONTRIBUTIONS

Conception and Design: X.-R.F., X.-N.Z. Data Analysis: X.-R.F. MRI Data Preprocessing: Y.H., CABIC. Initial Drafting of the Manuscript: X.-R.F. Critical Review and Editing of the Manuscript: All authors contributed to the critical review and editing of the manuscript.

AUTHOR COMPETING INTERESTS

Competing interests

The authors declare no competing interests.

DATA AVAILABILITY

The datasets analyzed in this study are publicly available. The ABIDE dataset can be accessed from the Autism Brain Imaging Data Exchange repository at http://fcon_1000.projects.nitrc.org/indi/abide. The CABIC dataset is available upon request through the CABIC Data Sharing Initiative at https://php.bdnilab.com. The key data we used in this study are the OoS centile scores we calculated for each participant with ABIDE and CABIC. To foster researcher on replication and extended exploration, we shared these data through the *Chinese Color Nest Data Community: Fostering Lifespan Development of Brain-Mind Health*. Data have been deposited into CSV files[86] at https://doi.org/10.57760/sciencedb.24587, and they are accessible upon the requests according to the instructions described on this page.

CODE AVAILABILITY

All code used in the analyses is available at https://github.com/XueruFan/ASD-Project. For detailed information on how to use these codes and replicate this study step-by-step, please see the explanation in the README.md file.

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TABLES

Table 1: Group comparisons of regions morphology between overall and two ASD subgroups.

Region	OoS Scores						AbP[1] (%)	
	All		L		H		L	H
	p	Median	*p*	Median	*p*	Median		
Superior frontal	0.01	0.48	0.02	0.28	0.37	0.62	5.56	2.70
Rostral middle frontal	0.01	0.46	0.02	0.25	0.32	0.60	7.94	0.68
Caudal middle frontal	0.00	0.42	0.00	0.26	0.05	0.60	6.35	2.70
Pars opercularis	0.00	0.47	0.00	0.23	0.07	0.61	6.35	4.73
Pars triangularis	0.00	0.45	0.02	0.28	0.02	0.60	6.35	1.35
Pars orbitalis	0.01	0.46	0.06	0.33	0.11	0.56	5.56	0.68
Frontal pole	0.00	0.48	0.02	0.34	0.03	0.60	11.90	2.03
Lateral orbital frontal	0.00	0.46	0.01	0.26	0.06	0.63	7.94	2.03
Medial orbital frontal	0.00	0.42	0.00	0.26	0.04	0.61	10.32	2.70
Rostral anterior cingulate	0.00	0.45	0.00	0.25	0.04	0.65	4.76	2.70
Caudal anterior cingulate	0.00	0.47	0.01	0.30	0.00	0.68	3.97	6.76
Precentral	0.00	0.45	0.01	0.26	0.17	0.60	6.35	3.38
Paracentral	0.01	0.52	0.05	0.34	0.10	0.62	4.76	5.41
Postcentral	0.00	0.48	0.01	0.29	0.05	0.64	7.14	4.05
Supramarginal	0.00	0.49	0.01	0.31	0.04	0.65	7.94	3.38
Posterior cingulate	0.00	0.46	0.02	0.29	0.04	0.64	7.94	5.41
Isthmus cingulate	0.00	0.47	0.00	0.27	0.06	0.64	3.97	4.05
Precuneus	0.00	0.52	0.04	0.29	0.02	0.70	5.56	4.73
Superior parietal	0.00	0.44	0.00	0.27	0.08	0.60	7.94	2.70
Inferior parietal	0.00	0.45	0.07	0.30	0.02	0.63	7.94	2.03
Transverse temporal	0.00	0.52	0.02	0.32	0.03	0.68	7.94	6.08
Banks superior temporal	0.00	0.44	0.00	0.26	0.02	0.59	3.97	5.41
Superior temporal	0.00	0.49	0.00	0.26	0.04	0.67	6.35	4.05
Middle temporal	0.00	0.44	0.02	0.24	0.06	0.61	17.46	2.70
Inferior temporal	0.00	0.49	0.05	0.30	0.04	0.62	11.90	0.68
Fusiform	0.00	0.45	0.01	0.26	0.09	0.59	10.32	1.35
Parahippocampal	0.00	0.49	0.02	0.33	0.01	0.63	3.17	2.70
Entorhinal	0.01	0.51	0.05	0.40	0.04	0.62	6.35	0.68
Temporal pole	0.00	0.44	0.03	0.36	0.02	0.58	10.32	1.35
Lateral occipital	0.00	0.46	0.01	0.28	0.02	0.63	9.52	2.70
Lingual	0.00	0.40	0.00	0.24	0.01	0.58	7.94	2.70
Pericalcarine	0.00	0.36	0.00	0.23	0.01	0.53	11.90	2.70
Cuneus	0.00	0.46	0.01	0.25	0.03	0.55	6.35	1.35
Insula	0.00	0.53	0.02	0.31	0.02	0.69	3.17	6.08

[1] AbP: Prevalence of abnormalities.

SUPPLEMENTARY INFORMATION

Supplementary Analysis

Brain Growth Charts and Age-Related Changes in OoS Scores for ASD Subgroup

To investigate potential developmental trajectories in ASD subgroups, here we illustrated the normative growth trajectories for volumes of the bilaterally averaged cortical regions with ABIDE dataset. The analysis focused on three brain regionstransverse temporal, inferior temporal, and isthmus cingulatethat exhibited reproducible correlations across both datasets. The subgroup-specific brain charts (Figure S1e) were upgraded from the LBCC charts and adjusted by leveraging all the samples from the ABIDE. Then, we applied Generalized Additive Mixed Models (GAMM) using the *gamm4* R package to explore the relationship between OoS scores and age within subgroup H across the CABIC and ABIDE datasets.

$$\text{OoS score} \sim s(\text{Age}, \text{bs} = \text{"tp"}, \text{k} = 4) + \text{TCV}$$

Although OoS scores are adjusted for age-related effects, examining residual variability allows us to gain additional insights into brain-cognition relationships within specific subgroups.

In the transverse temporal region (Figure S1f, left), CABIC presented a non-significant positive trend with age ($R^2 = 0.07, p = 0.56, F = 0.57$), while ABIDE displayed a marginally significant trend ($R^2 = 0.06, p = 0.04, F = 4.10$). For the inferior temporal region (Figure S1f, middle), CABIC showed a moderate but non-significant trend ($R^2 = 0.20, p = 0.22, F = 1.49$), while ABIDE exhibited a flat, non-significant pattern ($R^2 = 0.07, p = 0.46, F = 0.56$). The most robust findings were observed in the isthmus cingulate (Figure S1f, right). CABIC demonstrated a significant positive association between OoS scores and age ($R^2 = 0.13, p < 0.001, F = 72.69$), suggesting meaningful developmental changes in this region. ABIDE also showed a positive trend, albeit with a smaller effect size ($R^2 = 0.12, p = 0.02, F = 5.51$).

Spectral Clustering Independently on CABIC Cohort

To evaluate the differences between applying the ABIDE-classifier on CABIC and independently clustering analysis on CABIC, we replicated the identical analytical process directly on ASD participants from CABIC cohort. There were two distinct clusters (ASD subgroups) with the highest silhouette coefficient among cluster solutions ranging from two to ten (Figure S5a). The optimized SVM model also used a polynomial kernel with a regularization parameter $C = 0.1$ and a kernel coefficient $\gamma = 0.1$. The model achieved a high classification accuracy ($0.97, p < 0.001$) and a F1 score ($0.97, p < 0.001$) in five cross-validation folds. As the high cluster indices consistency (95.97%) across both methods, the brain morphology and cognitive behavior have the similar characteristics as the main analysis (Figure S5 b~f, i~m). Participants in subgroup L were significantly older than those in subgroup H ($p < 0.001$,). No significant differences were observed in other comparisons between two subgroups.

Significant correlations were found within two subgroups. For subgroup H, the same correlations were found as the main analysis (Figure S5g). The transverse temporal gyrus showed positive correlations with ADOS Total ($r(201) = 0.16, p = 0.03$) and Social Affect ($r(193) = 0.21, p = 0.00$) score. The inferior temporal gyrus was positively correlated with RRB ($r(191) = 0.17, p = 0.02$). The volumetric centile of the isthmus cingulate is correlated with SRS Autistic Mannerisms ($r(199) = 0.15, p = 0.03$). For subgroup L (Figure S5h), the volumetric centile of pars triangularis was positive correlations with ADOS RRB ($r(72) = 0.24, p = 0.04$). As for subgroup L from ABIDE cohort, $r(86) = 0.23, p = 0.02$.

Supplementary Figures

Figure S1

a, Distributions of ABIDE Out-of-Sample (OoS) scores across 34 cortical regions before clustering. **b,** Distributions of ABIDE OoS scores across 34 cortical regions after clustering. **c,** Distributions of ABIDE OoS scores across global measures before clustering. **d,** Distributions of OoS scores across global measures after clustering. **e,** ABIDE Subgroup-specific brain charts of cortical regional volumes of transverse temporal (left), inferior temporal (middle), and isthmus cingulate (right). **f,** The developmental effects of OoS scores in individuals from subgroup H were modeled using GAMM across the ABIDE and CABIC datasets. In plots **b**, **d**, and **e**, orange for subgroup H and green for subgroup L. TCV, total cortical volume; WMV, total white matter volume; GMV, total cortical gray matter volume; sGMV, total subcortical gray matter volume; CSF, total ventricular cerebrospinal fluid volume; mCT, mean cortical thickness; tSA, total surface area.

Figure S2

Brain morphology of two CABIC subgroups. a, Distributions of Out-of-Sample (OoS) scores across 34 cortical regions after clustering. **b,** Distributions of OoS scores across global measures after clustering. TCV, total cortical volume; WMV, total white matter volume; GMV, total cortical gray matter volume; sGMV, total subcortical gray matter volume; CSF, total ventricular cerebrospinal fluid volume; mCT, mean cortical thickness; tSA, total surface area. **c,** Median OoS scores of 34 before cortical regions before clustering. **d,** Median OoS scores of ASD subgroup H (top) and L (bottom). **e,** Prevalence maps depicting the proportion of participants with extreme (top, 97.5% for subgroup H; bottom, 2.5% for subgroup L) structural anomalies. Note, the left hemispheres are plotted in **c**, and **d** just for visualization purposes.

Figure S3

Differences between two CABIC subgroups. Distribution of participant ages (**a**); FIQ scales (**b**); data collection site (**c**); ADOS (**d**); and SRS (**e**) across the two subgroups of CABIC. Only significant difference of age ($p < 0.001$) between subgroups. For plots **a** to **e**, the center line shows the median; the box limits represent the 25th and 75th percentiles; the whiskers show the minimum and maximum values; and the dots represent potential outliers.

Figure S4

Mediation models (for significant brain-behavior associations identified in ABIDE subgroup H) to examine the cognitive behaviors' effect on brain morphology. Black solid arrows represent significant effects, while gray arrows indicate non-significant ones. Top: transverse temporal; bottom left: inferior temporal; bottom right: isthmus cingulate.

Figure S5

Independent spectral clustering analysis of CABIC applying the same analytical pipeline used for ABIDE. a, Silhouette scores across different clustering solutions (2 to 10 clusters). The highest silhouette score indicates two distinct subgroups. **b,** Median OoS scores of 34 cortical regions before clustering. **c,** Median OoS scores of ASD subgroup H (top) and L (bottom). **d,** OoS scores across global measures for subgroup H (orange) and L (green). TCV, total cortical volume; WMV, total white matter volume; GMV, total cortical gray matter volume; sGMV, total subcortical gray matter volume; CSF, total ventricular cerebrospinal fluid volume; mCT, mean cortical thickness; tSA, total surface area. **e,** Prevalence maps depicting the proportion of participants with extreme (2.5% for subgroup L, 97.5% for subgroup H) structural anomalies. **f,** OoS scores across 34 cortical regions for subgroup H (orange) and L (green). Reproducible correlations (**g**, subgroup H; **h**, subgroup L) between brain region volumes, measured as Out-of-Sample (OoS) scores, and clinical measures across ABIDE and CABIC datasets. Distribution of participant ages (**i**); data collection site (**j**); FIQ (**k**); ADOS (**l**); and SRS (**m**) across the two subgroups, with subgroup L participants being significantly older than those in subgroup H ($p < 0.001$). Note, the left hemispheres are plotted in **b**, **c**, and **e** just for visualization purposes. For plots **i**, **k**, **l**, and **m**, the center line shows the median; the box limits represent the 25th and 75th percentiles; the whiskers show the minimum and maximum values; and the dots represent potential outliers.

Results of GMM clustering analysis on ABIDE cohort. a, Silhouette scores across different clustering solutions (2 to 10 clusters). The highest silhouette score indicates two distinct subgroups. **b,** SHAP summary plot displaying the top 10 brain regions with the highest contributions to the SVM model's predictions. **c,** Median OoS scores of ASD subgroup H (top) and L (bottom). **e,** Prevalence maps depicting the proportion of participants with extreme (top, 97.5% for subgroup H; bottom, 2.5% for subgroup L) structural anomalies. Note, the left hemispheres are plotted in **c**, and **d** just for visualization purposes.

Figure S1

Figure S2

Figure S3

FIQ

A = -0.24, p = 0.02   B = 0.01, p = 0.93

A×B = -0.00
z = -0.09, p = 0.93

ADOS-2
Total

C' = 0.25, p = 0.03

FIQ

A = -0.30, p = 0.00   B = 0.01, p = 0.92

A×B = -0.00
z = -0.09, p = 0.92

ADOS-2
Social Affect

C' = 0.22, p = 0.07

FIQ

A = 0.02, p = 0.84   B = -0.11, p = 0.29

A×B = -0.00
z = -0.19, p = 0.85

ADOS-2
RRB

C' = 0.14, p = 0.14

FIQ

A = -0.02, p = 0.86   B = -0.05, p = 0.71

A×B = 0.00
z = 0.16, p = 0.87

SRS
Mannerisms

C' = 0.33, p = 0.01

Figure S4

Figure S5

Figure S6

Supplementary Tables

Table S1. Statistical comparison between two clustering ASD groups for different measures.

Phenotype		Group(N)	Median	Mean	SD	Shapiro-Wilk Test	Rank-Sum Test	Two-sample t-Test	Cohen's d
Age		H (148)	10.51	10.25	1.87	0.00	0.02		-0.30
		L(126)	9.94	9.65	2.09	0.00			
IQ	PIQ	H (115)	109	109.43	18.05	0.77		0.11	-0.21
		L(111)	104	105.76	16.21	0.19			
	VIQ	H (116)	110	109.51	17.23	0.70		0.16	-0.19
		L(106)	106	106.29	16.94	0.45			
	FIQ	H (139)	110	108.66	18.39	0.26		0.09	-0.21
		L(117)	104	105.02	15.83	0.28			
ADOS-2	RRB	H (108)	3	3.06	1.84	0.00	0.94		0.02
		L(100)	3	3.09	1.85	0.00			
	Social Affect	H (107)	9	9.36	3.44	0.00	0.11		-0.18
		L(100)	8	8.73	3.76	0.00			
	Total	H (108)	12	11.62	4.75	0.00	0.15		-0.14
		L(100)	11	11.84	4.75	0.00			
	Severity	H (107)	7	7.16	1.78	0.00	0.18		-0.23
		L(100)	7	6.71	2.14	0.00			
ADI-R	RRB	H (120)	5	5.56	2.66	0.01	0.14		0.16
		L(103)	6	5.96	2.38	0.02			
	Nonverbal	H (120)	8	8.12	2.96	0.15	0.14		0.29
		L(28)	9.5	9.07	3.40	0.00			
	Verbal	H (120)	15	15.35	4.33	0.01	0.44		0.09
		L(103)	16	15.75	4.35	0.07			
	Social	H (119)	19	18.84	5.52	0.04	0.77		0.04
		L(103)	19	19.07	5.68	0.07			
SRS	Autistic Mannersims	H (67)	16	16.49	6.96	0.53	0.15		0.22
		L(69)	19	18.10	7.54	0.04			
	Motivation	H (67)	13	13.73	6.38	0.18		0.68	0.07
		L(69)	14	14.17	6.38	0.52			
	Communication	H (67)	29	30.43	10.48	0.89		0.93	-0.01
		L(69)	31	30.28	11.67	0.38			
	Cognition	H (67)	17	16.57	6.60	0.74		0.39	0.15
		L(69)	17	16.57	6.60	0.42			
	Awareness	H (67)	12	12.25	3.84	0.12		0.62	-0.09
		L(69)	11	11.93	3.73	0.39			

Table S2. Mean SHAP values for all 29 selected regions.

Region	Mean SHAP value
Isthmus cingulate	0.05
Entorhinal	0.04
Precuneus	0.04
Middle temporal	0.04
Fusiform	0.03
Transverse temporal	0.03
Rostral middle frontal	0.03
Postcentral	0.03
Inferior temporal	0.03
Rostral anterior cingulate	0.03
Supramarginal	0.02
Insula	0.02
Pericalcarine	0.02
Frontal pole	0.02
Lateral occipital	0.02
Posterior cingulate	0.02
Superior parietal	0.02
Pars opercularis	0.02
Caudal anterior cingulate	0.02
Medial orbital frontal	0.02
Lateral orbital frontal	0.02
Superior frontal	0.02
Inferior parietal	0.02
Caudal middle frontal	0.02
Cuneus	0.01
Pars orbitalis	0.01
Temporal pole	0.01
Precentral	0.01
Lingual	0.01

Supplementary Materials

ABIDE_ClusterID.csv
CABIC_ClusterID.csv

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