

Supplementary Materials

Table S1. Regions with significant differences identified in all ASD vs. TD.

Brain regions	MNI Coordinates			<i>t</i> values	Cluster size (voxels)
	x	y	z		
ASD>TD					
Thalamus.R	19.5	-27	13.5	5.66	3753
Temporal.Sup.R	60	-4.5	0	5.42	6021
Lingual.L	-10.5	-31.5	-4.5	5.25	3412
Temporal.Sup.L	-60	-6	1.5	5.07	4145
Lingual.R	12	-73.5	0	4.30	172
Hippocampus.R	33	-12	-25.5	4.28	705
Fusiform.R	33	-54	-9	3.98	168
Precentral.R	33	-21	54	3.74	179
ASD<TD					
ParaHippocampal.R	24	4.5	-21	-3.94	209

Table S2. Regions with significant differences identified in two subtypes ASD vs. TD

Subtype	Brain regions	MNI Coordinates			<i>t</i> values	Cluster size (voxels)
		x	y	z		
Subtype 1						
<i>ASD < TD</i>						
	Insula.R	46.5	4.5	0	-8.28	30952
	Frontal.Sup.2.R	30	22.5	57	-6.82	638
	Temporal.Sup.R	69	-27	0	-6.53	515
	Angular.L	-52.5	-69	27	-6.30	715
	Angular.R	57	-61.5	27	-6.21	703
	ParaHippocampal.R	21	-34.5	-13.5	-6.19	176
	Frontal.Mid.2.L	-33	25.5	54	-6.15	283
	Occipital.Mid.R	37.5	-91.5	4.5	-6.15	157
	Precuneus.L	4.5	-55.5	7.5	-6.10	458
	Cingulate.Mid.L	-1.5	12	39	-5.96	202
	Thal.MDm.R	1.5	-19.5	4.5	-5.92	143
	Frontal.Inf.Tri.L	-49.5	39	10.5	-5.76	59
	ParaHippocampal.L	-21	-39	-13.5	-5.68	53
	Cingulate.Mid.R	1.5	10.5	37.5	-5.64	57
	Cerebellum.8.L	-39	-54	-58.5	-5.63	214
Subtype 2						
<i>ASD > TD</i>						
	Temporal.Sup.R	60	-4.5	0	11.42	8298
	Temporal.Sup.L	-51	-15	3	10.31	6751
	Thal.PuI.L	-12	-30	-3	8.72	1334
	Thal.PuM.R	10.5	-28.5	-4.5	8.35	1432
	Precuneus.L	-6	-64.5	27	7.05	1011
	Fusiform.L	31.5	-54	-10.5	6.55	141
	Fusiform.R	34.5	-31.5	-24	6.53	384
	Lingual.R	19.5	-64.5	-7.5	6.02	66
	Cingulate.Post.L	-6	-46.5	30	5.52	60

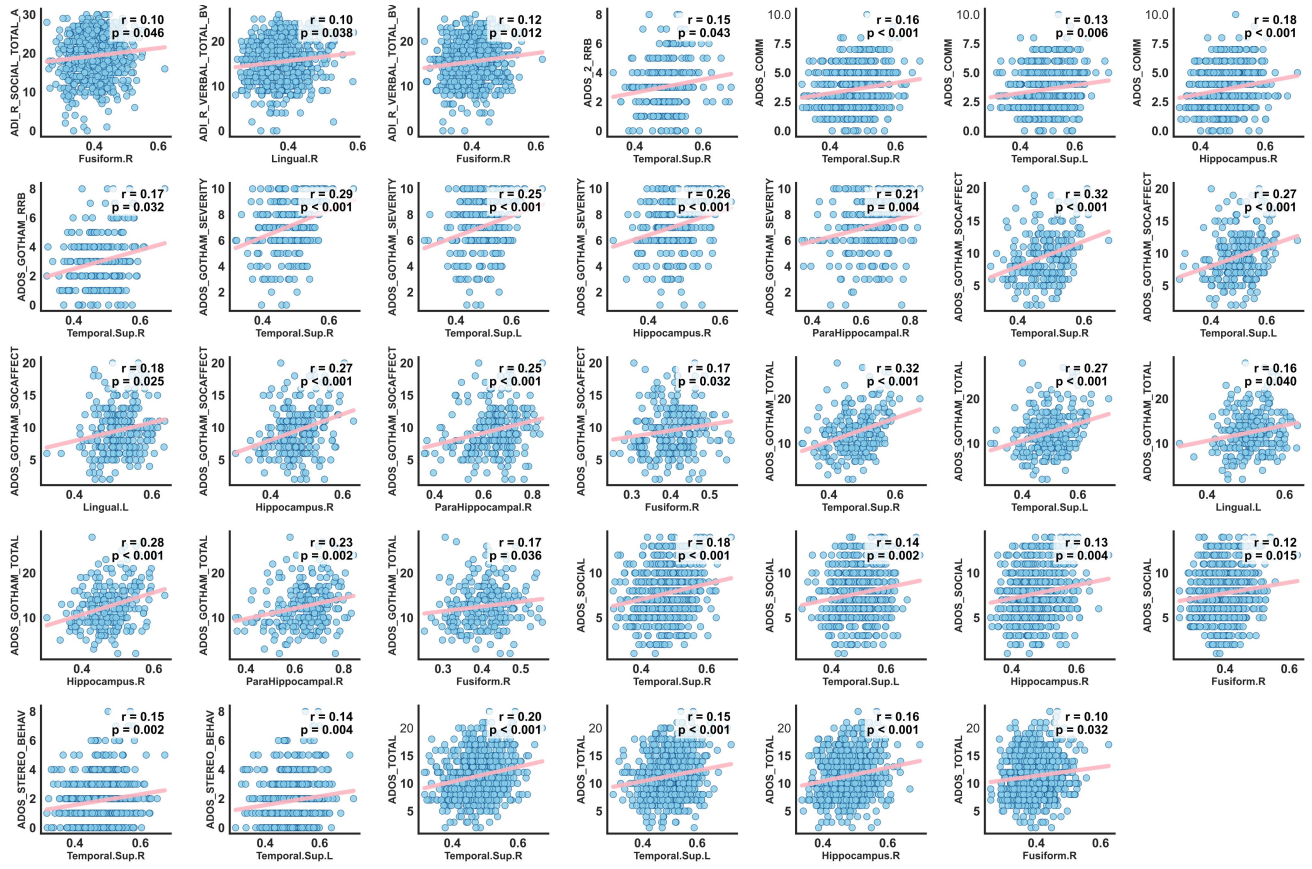


Fig. S1. The correlation analysis results between all clusters and scale scores ($p < 0.05$ with FDR correction).

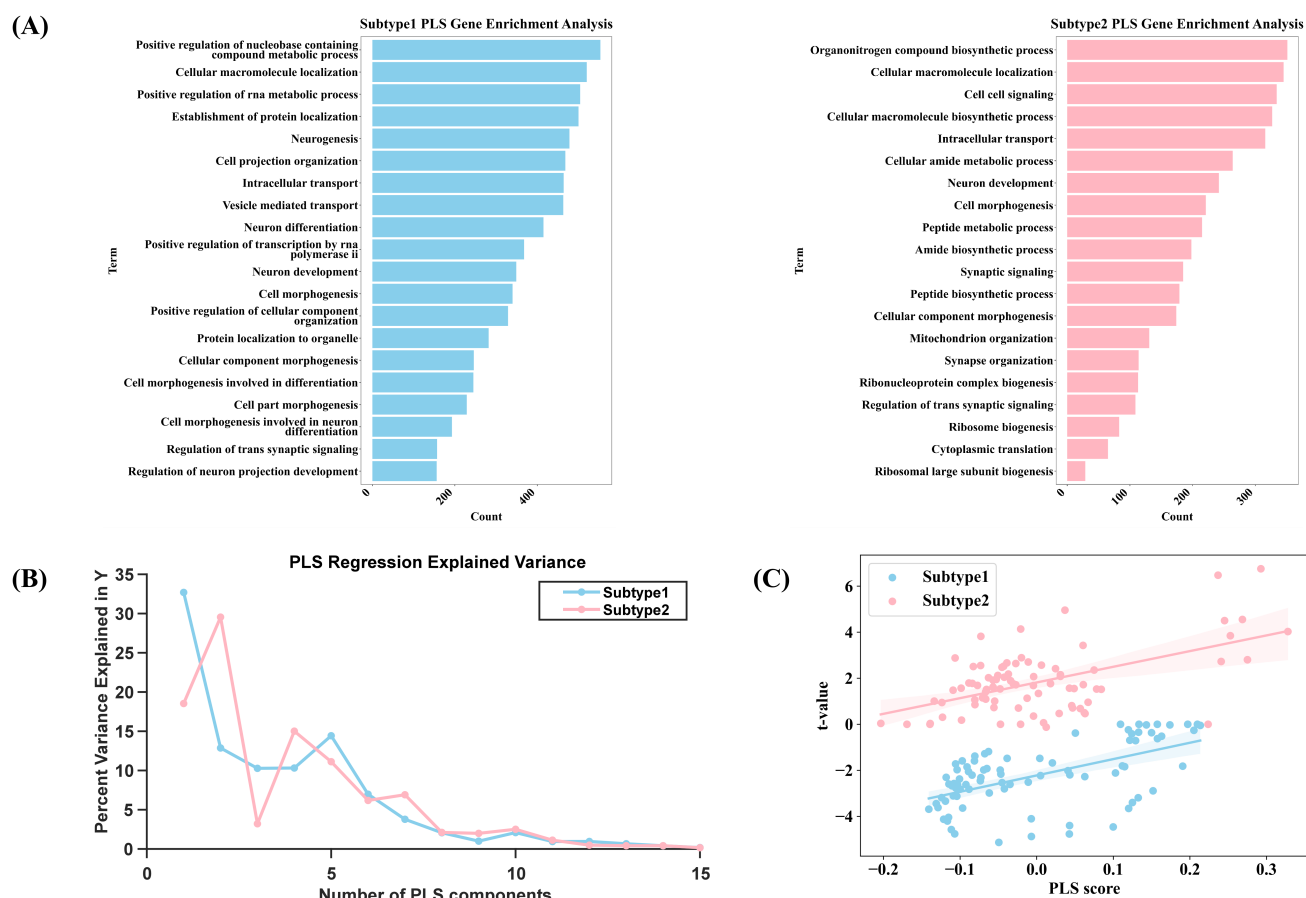


Fig. S2. Supplementary Neurobiological mechanism underlying the structural differences of the two distinct ASD subtypes. (A) Gene enrichment analyses were performed for genes associated with the structural alterations specific to each ASD subtype, with enrichment results ranked by gene count. (B) Variance explained by partial least squares (PLS) regression models. (C) Significant correlations between PLS scores and structural differences of the two ASD subtypes, with Subtype 1 and Subtype 2 plotted together in a single graph to enhance visual comparison.