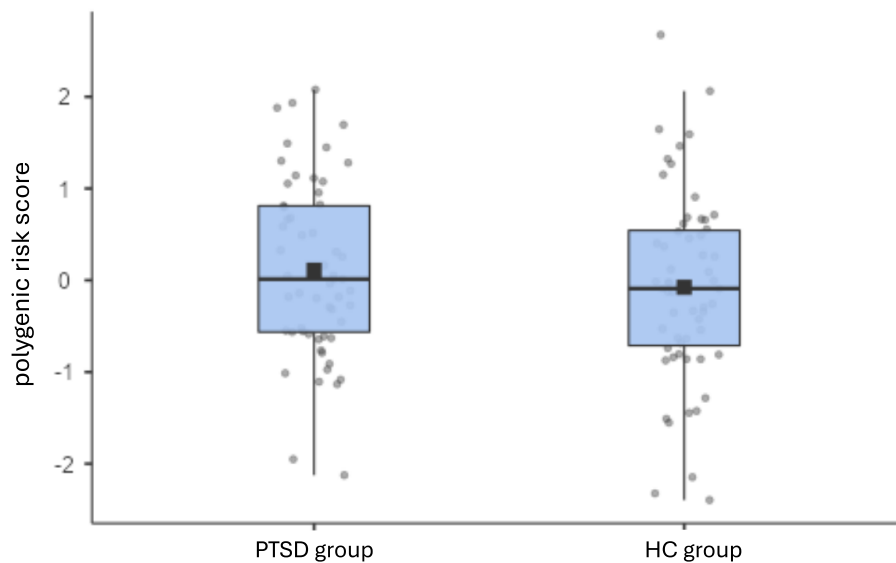
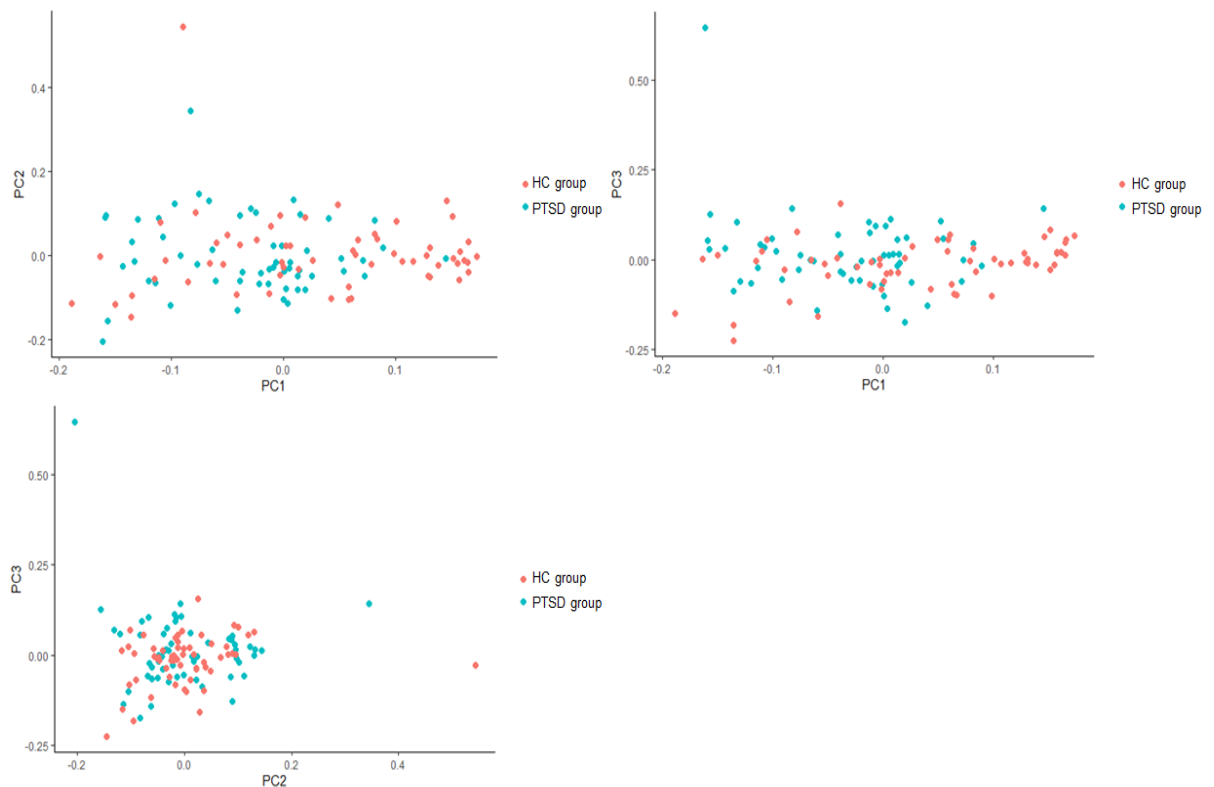


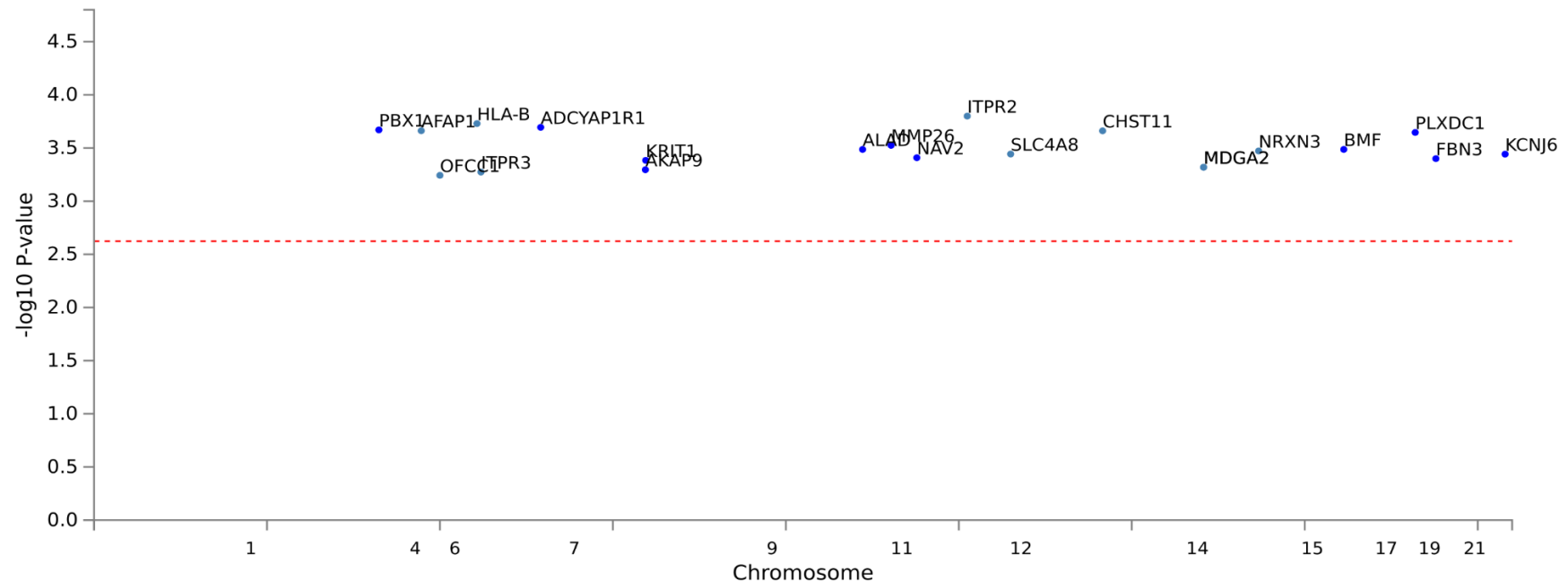
Supplementary Figure S1 Boxplot showing the distribution of standardized polygenic risk score for both groups

HC = healthy controls; PTSD = post-traumatic stress disorder.

Supplementary Figure S2 Scatterplots showing the distribution of the first three PCs of the PTSD and HC groups

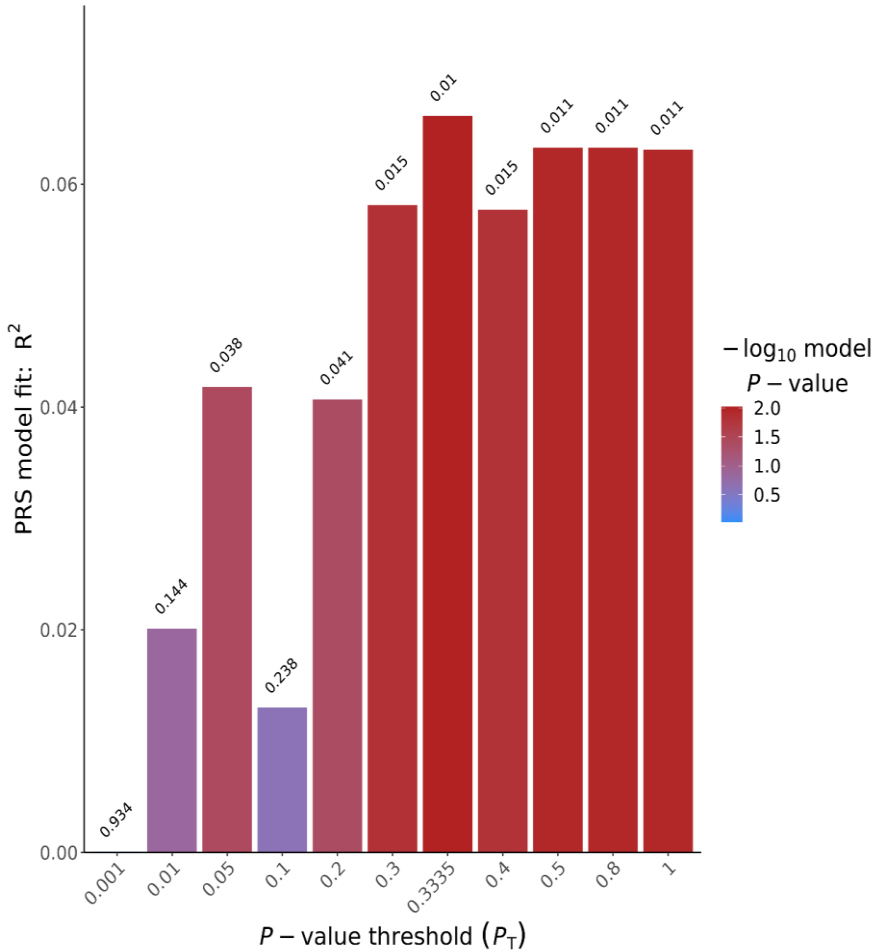
HC = healthy controls; PC = principal component; PTSD = post-traumatic stress disorder.

Supplementary Figure S3 Functional mapping and annotation of GWAS revealed that the SNVs mapped to 21 top protein-coding genes. Genome-wide significance (red dashed line) was defined at $P = 2.381 \times 10^{-3}$. *ITPR* and *HLA-B* were identified as the top significantly associated genes in the enrichment analysis, which are known to be involved in biological pathways related to PTSD



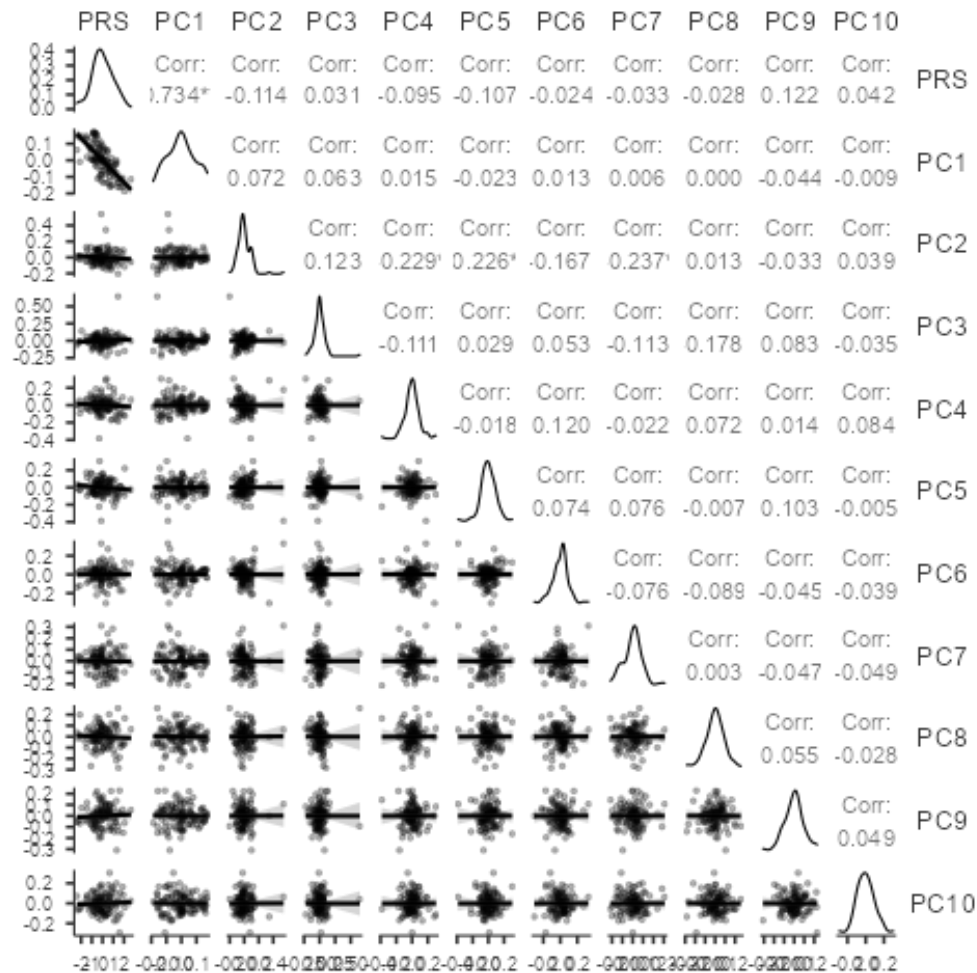
ADCYAP1R1 = adenylate cyclase activating polypeptide 1 receptor 1; *AFAP1* = Actin filament associated protein 1; *AKAP9* = A-kinase anchoring protein 9; *ALAD* = Aminolevulinate dehydratase; *BMF* = Bcl2 modifying factor; *CHST11* = carbohydrate sulfotransferase 11; *FBN3* = Fibrillin 3; GWAS = genome-wide association studies; *HLA-B* = Major histocompatibility complex, class 1, B; *ITPR2* = Inositol 1, 4, 5-trisphosphate receptor type 2; *ITPR3* = Inositol 1, 4, 5-trisphosphate receptor type 3; *KCNJ6* = Potassium inwardly rectifying channel subfamily J member 6; *KRIT1* = Krev interaction trapped protein 1; *MDGA2* = MAM domain containing glycosylphosphatidylinositol anchor 2; *MMP26* = Matrix metalloproteinase 26; *NAV2* = Neuron navigator 2; *NRXN3* = Neurexin 3-alpha; *OFCC1* = Orofacial cleft 1 candidate; *PBX1* = PBX Homeobox 1; *PLXDC1* = Plexin domain containing 1; PTSD = post-traumatic stress disorder; *SLC4A8* = Solute carrier family 4 member 8.

Supplementary Figure S4 Bar plot generated from PRSice 2.0 shows the predicted polygenic risk for PTSD



PTSD = post-traumatic stress disorder.
The x-axis represents a broad p-value threshold (PT), while the y-axis represents the explained variance (R^2) in our sample.

Supplementary Figure S5 Spearman's correlations between PRS and the 10 principal components revealed that only the first principal component (PC1) was correlated with PRS (Rho = -0.734; $p = < 0.01$).



Supplementary Table S1 Descriptive analysis of trauma variables (childhood trauma and childhood trauma domains) for the low and high risk groups

Variable	Low risk (n=29)	High risk (n=29)	p-value	Statistical test
Emotional neglect				
Mean (SD)	7.85 (2.66)	9.46 (4.22)	0.199	Mann-Whitney
Median (min-max)	7 (5-14)	8 (5-21)		
Physical neglect				
Mean (SD)	5.38 (0.63)	6.43 (1.62)	0.007	Mann-Whitney
Median (min-max)	5 (5-7)	6 (5-11)		
Emotional abuse				
Mean (SD)	7.62 (2.26)	9.96 (4.64)	0.089	Mann-Whitney
Median (min-max)	8 (5-12)	8.50 (5-21)		
Physical abuse				
Mean (SD)	5.50 (0.99)	6.68 (2.44)	0.008	Mann-Whitney
Median (min-max)	5 (5-9)	6 (5-16)		
Sexual abuse				
Mean (SD)	5.35 (0.84)	6.68 (4.42)	0.475	Mann-Whitney
Median (min-max)	5 (5-8)	5 (5-25)		
Childhood trauma				
Mean (SD)	31.70 (4.97)	39.20 (12)	0.031	Mann-Whitney
Median (min-max)	31.50 (25-41)	32.50 (25-71)		

Supplementary Table S2 Frequency of cases (PTSD group) and HCs (HC group) in the low risk and high risk groups

PRS/group	Counts (N)	% of total
High risk		
HC group	12	20.7 %
PTSD group	17	29.3 %
Low risk		
HC group	18	31.0 %
PTSD group	11	19.0 %

HC = healthy controls; PTSD = post-traumatic stress disorder.

Supplementary Table S3 Summary statistics display the p-values and association data for the top 10 SNVs identified in the GWAS

CHR	SNV	BP	A1	OR	STAT	p
12	rs10878292	65898179	G	0.1313	-4.419	9,93E-03
11	rs4910407	11700694	C	4.737	4.074	4,62E-02
6	rs464367	33244641	G	5.401	3.978	6,96E-02
1	rs10921042	191869962	G	0.05942	-3.962	7,43E-02
14	rs10137605	60309485	A	0.1314	-3.914	9,07E-02
18	rs35219613	56999477	G	0.1151	-3.871	0.0001082
4	rs6828518	185751763	A	0.1477	-3.859	0.0001139
16	rs1559451	86676242	G	0.2048	-3.852	0.000117
2	rs60076148	151767049	C	4.899	3.852	0.0001174
3	rs2555239	37604095	A	0.2219	-3.845	0.0001204

A1 = reference allele; BP = base pair positions; CHR = chromosome; GWAS = genome-wide association studies; OR = odds ratio; SNV = single nucleotide variants; STAT = statistical test value.

Supplementary Table S4 Logistic regression model (PTSD diagnosis ~ PRS + LEC + CTQ + PRS × LEC × CTQ + age + per capita income + educational level + PC1-PC10). The results indicated an inverse relationship, with the PTSD group showing lower PRS than the HC Group (adjusted p = 0.007; OR = 0.035)

Predictors	Adjusted p	OR	95%CI
PRS	0.007	0.035	0.005-0.237
LEC	0.765	1.049	0.765-1.439
Total CTQ	0.142	1.096	0.9696-1.240
PRS × LEC × Total CTQ	0.049	1.015	1.004-1.027

× = interactions between predictors; CTQ = Childhood Trauma Questionnaire; LEC = Life Events Checklist (corresponding to traumatic life events); OR = odds ratio; PRS = polygenic risk score.

The dependent variable was the diagnosis, which included post-traumatic stress disorder and healthy control groups.