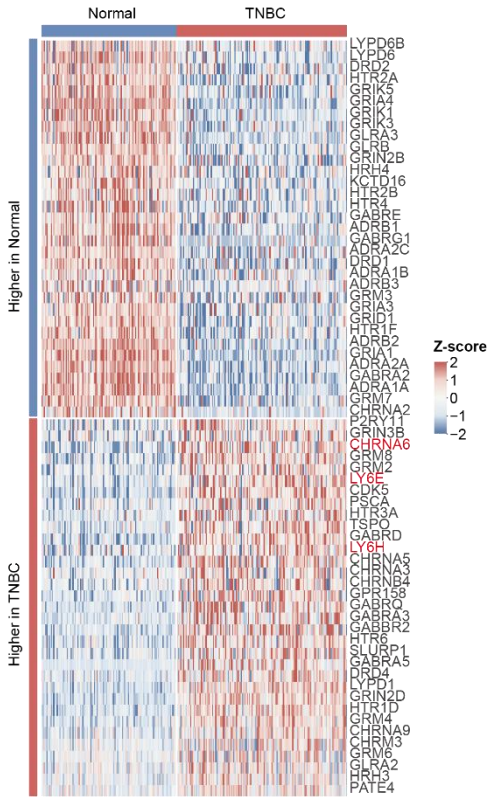
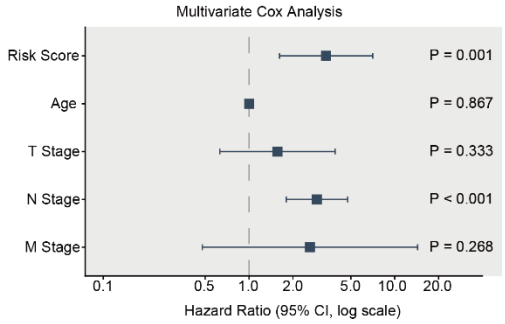
Supplementary Figure 1.



Supplementary Figure 1. Expression profiles of 66 neurotransmitter receptor-related genes in TNBC and normal breast tissues.

Heatmap depicting the expression patterns of the 66 neuroreceptor-related genes selected from the overlap between the DEGs (derived from TCGA TNBC vs. normal) and the neuroreceptor-related gene set. The expression levels were transformed by Z-score, with red and blue representing high and low expression, respectively.

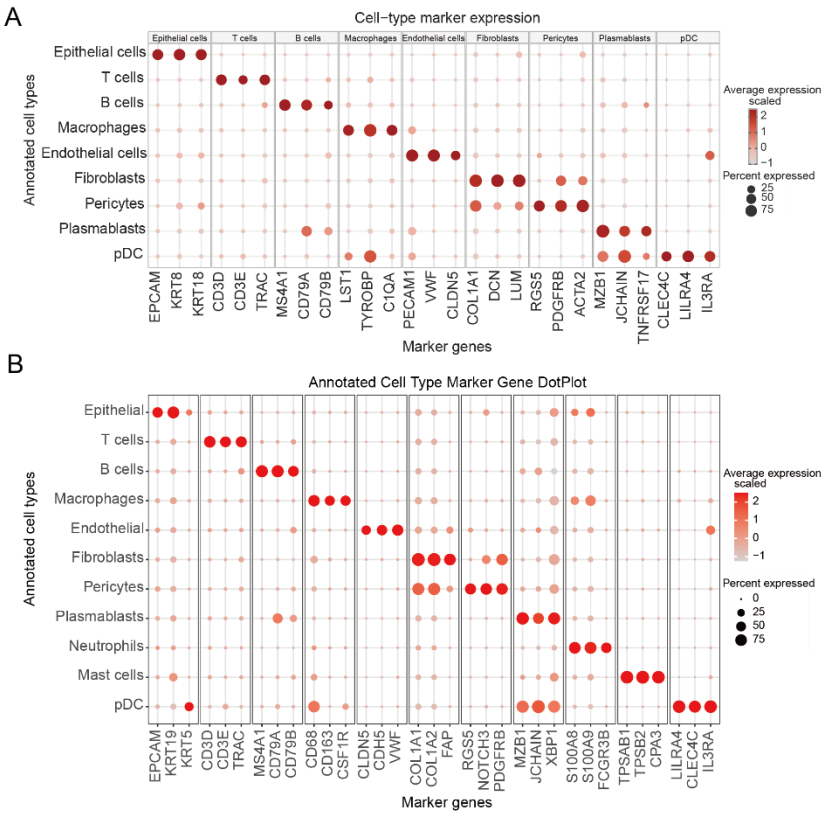
Supplementary Figure 2.



Supplementary Figure 2. Multivariable Cox regression analysis of the NRRS and clinicopathological factors.

Forest plot showing the multivariable Cox regression model incorporating the risk score and clinicopathological factors, including age, T stage, N stage, and M stage.

Supplementary Figure 3.

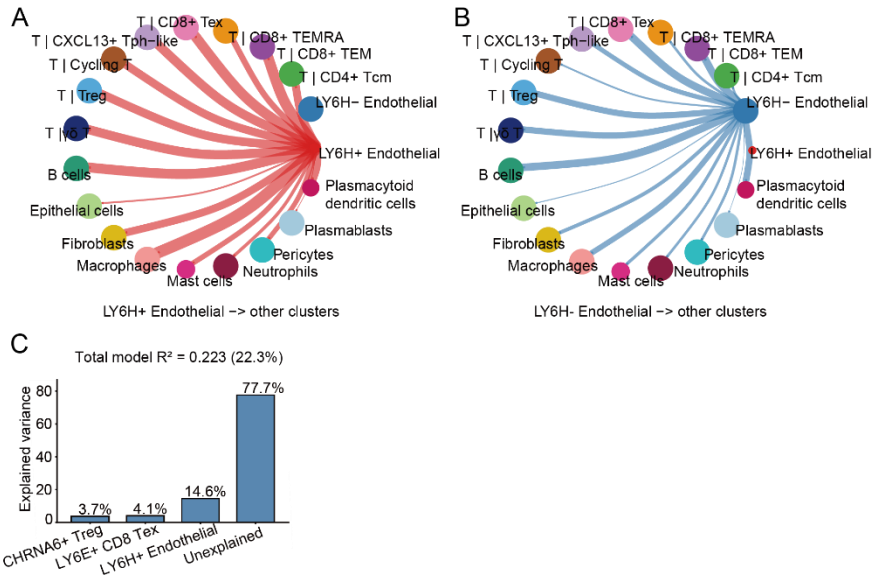


Supplementary Figure 3. Canonical marker gene expression across annotated cell clusters.

(A, B) Dot plots showing the expression profiles of canonical marker genes across annotated cell clusters in the GSE161529 (A) and GSE305078 (B) scRNA-seq cohorts. Dot color represents

average expression, and dot size denotes the percentage of cells expressing the respective gene.

Supplementary Figure 4.



Supplementary Figure 4. *LY6H*+ endothelial cell-mediated signaling networks and variance decomposition of the prognostic model.

(A, B) Outgoing signaling networks from LY6H+ (A) and LY6H- (B) endothelial cells to other major cell clusters. The width of the lines represents the inferred interaction strength. (C) Bar chart showing the variance decomposition of the prognostic model. The percentages denote the explained variance contributed by the CHRNA6+ Tregs, LY6E+ CD8 Tex, and LY6H+ endothelial signatures, alongside the unexplained proportion. The total model R^2 (22.3%) is annotated at the top.

Supplementary Table S1. List of 131 neurotransmitter receptor-related genes.

Gene symbol	Gene symbol	Gene symbol	Gene symbol	Gene symbol	Gene symbol	Gene symbol	Gene symbol
ADRA1A	*CHRM5*	*DRD1*	*GABRE*	*GRIA4*	*GRM3*	*HTR2C*	*LYPD6*
ADRA1B	*CHRNA1*	*DRD2*	*GABRG1*	*GRID1*	*GRM4*	*HTR3A*	*LYPD6B*
ADRA1D	*CHRNA10*	*DRD3*	*GABRG2*	*GRID2*	*GRM5*	*HTR3B*	*P2RY11*
ADRA2A	*CHRNA2*	*DRD4*	*GABRG3*	*GRIK1*	*GRM6*	*HTR3C*	*PATE1*
ADRA2B	*CHRNA3*	*DRD5*	*GABRP*	*GRIK2*	*GRM7*	*HTR3D*	*PATE4*
ADRA2C	*CHRNA4*	*GABBR1*	*GABRQ*	*GRIK3*	*GRM8*	*HTR3E*	*PSCA*
ADRB1	*CHRNA5*	*GABBR2*	*GABRR1*	*GRIK4*	*HRH1*	*HTR4*	*PTK2B*
ADRB2	*CHRNA6*	*GABRA1*	*GABRR2*	*GRIK5*	*HRH2*	*HTR5A*	*SLURP1*
ADRB3	*CHRNA7*	*GABRA2*	*GABRR3*	*GRIN1*	*HRH3*	*HTR6*	*SLURP2*
ANXA9	*CHRNA9*	*GABRA3*	*GLRA1*	*GRIN2A*	*HRH4*	*HTR7*	*SPDYE11*
APP	*CHRNB1*	*GABRA4*	*GLRA2*	*GRIN2B*	*HTR1A*	*KCTD16*	*TMEM35A*
CDK5	*CHRNB2*	*GABRA5*	*GLRA3*	*GRIN2C*	*HTR1B*	*LY6E*	*TSPO*
CHRFAM7A	*CHRNB3*	*GABRA6*	*GLRB*	*GRIN2D*	*HTR1D*	*LY6G6D*	
CHRM1	*CHRNB4*	*GABRB1*	*GPR158*	*GRIN3A*	*HTR1E*	*LY6H*	
CHRM2	*CHRND*	*GABRB2*	*GRIA1*	*GRIN3B*	*HTR1F*	*LY6S*	
CHRM3	*CHRNE*	*GABRB3*	*GRIA2*	*GRM1*	*HTR2A*	*LYNX1*	
CHRM4	*CHRNG*	*GABRD*	*GRIA3*	*GRM2*	*HTR2B*	*LYPD1*	

Supplementary Table S2. Gene lists for the CHRNA6^{+} Treg, LY6E^{+} CD8^{+} Tex, and LY6H^{+} endothelial cell signatures.

CHRNA6+ Treg vs CHRNA6- Treg				
Gene	**avg_log2FC**	**pct.1**	**pct.2**	**p_val_adj**
LGALS9	0.565529842	0.385	0.193	0.000104
TNFRSF25	0.554955302	0.451	0.256	0.002487
TOX2	0.518713485	0.323	0.171	0.016484
CCR8	0.56994595	0.205	0.091	0.009006
HAVCR2	0.55845236	0.236	0.111	0.013984
BTLA	0.90257893	0.123	0.046	0.026546
EMC10	0.688894227	0.39	0.185	1.42E-06
SMIM15	0.737556839	0.308	0.132	2.21E-06
CYB5B	0.785532879	0.318	0.153	5.54E-05
NCDN	1.464942462	0.123	0.037	4.82E-05
RTF2	0.614204131	0.421	0.228	0.000633
GTSF1L	1.824202591	0.067	0.014	0.000153
UROS	0.746885352	0.256	0.117	0.000853
COPS7B	1.05842749	0.138	0.048	0.000464
SHKBP1	0.636841245	0.282	0.136	0.002737
LY6H+ Endothelial vs LY6H- Endothelial				
Gene	**avg_log2FC**	**pct.1**	**pct.2**	**p_val_adj**
CLDN5	1.867923841	0.863	0.432	1.79E-22
GPIHBP1	2.894204184	0.526	0.08	4.42E-43
APLN	2.964021198	0.358	0.106	5.39E-11
PLXDC1	3.101149278	0.189	0.018	2.13E-21
PALD1	2.223877463	0.516	0.143	5.01E-20
ARHGAP18	2.05940333	0.789	0.271	2.07E-28
PGF	3.235100795	0.726	0.151	2.60E-49
WNT5A	4.112098966	0.2	0.01	7.03E-39
EGLN3	2.359974158	0.242	0.055	3.66E-09
LOX	2.88646105	0.474	0.084	2.12E-32
CD276	1.524909841	0.516	0.196	7.47E-10
VSIR	1.282741149	0.547	0.217	5.98E-10
LGALS1	1.538046892	0.937	0.592	1.08E-15
AOC3	1.129723742	0.442	0.211	0.001579
CXCR4	0.647296491	0.432	0.202	0.011567
LY6E Top25% Tex vs LY6E bottom25% Tex				
Gene	**avg_log2FC**	**pct.1**	**pct.2**	**p_val_adj**
LGALS9	1.491482399	0.303	0.087	1.14E-55
CD38	1.182163198	0.327	0.134	3.64E-39

LAG3	0.614314813	0.739	0.514	1.09E-35
CXCL13	0.916237145	0.647	0.494	1.08E-23
CTLA4	0.392140139	0.545	0.399	2.02E-11
PDCD1	0.309189928	0.375	0.246	9.02E-09
HAVCR2	0.257469341	0.463	0.342	1.42E-05
IFI35	1.597171972	0.499	0.178	9.30E-93
MT2A	1.155063938	0.754	0.472	1.55E-83
OASL	1.100361456	0.578	0.291	1.12E-67
CTSC	0.772913152	0.69	0.438	4.59E-47
SIT1	0.907208259	0.365	0.175	3.91E-32
CORO1A	0.61461737	0.833	0.656	7.82E-42
CCDC85B	0.599131636	0.572	0.357	7.70E-30
CLIC1	0.427380021	0.857	0.685	1.29E-34