

Figure S1. The absolute immune score estimated by CIBERSORT-LM22 grouped by PAM50 subtypes in the GEO cohort.

Figure S2. Relative percentages of cell subsets estimated by CIBERSORT-LM7 (A, C, E, G) and CIBERSORT-LM22 (B, D, F, H) grouped by clinicalpathological features in GEO cohort. MoMaDC, macrophages, monocytes and DCs.

Figure S3. Univariable (A, C, E) and multivariable (B, D, F) Cox regression analysis of cell subsets estimated by CIBERSORT-LM7 or CIBERSORT-LM22 in GEO cohort.

Figure S4. Pearson's correlation coefficients between immune cell subsets with clinical significance in GEO cohort.

Figure S5. Multivariable survival analyses of immunorisk score in OS (A), RFS (B), DFS (C), DMFS (D) in GEO cohort. OS, overall survival; RFS, recurrence-free survival; DFS, disease-free survival; DMFS, distant metastasis-free survival; HR, hazard ratio; CI, confidence interval.

Figure S6. KEGG enrichment analysis based on the differential genes between immunotype A and immunotype B.

Figure S7. Protein-protein interaction network based on the differential genes between immunotype A and immunotype B.

Figure S8. PTGDS-related signalling pathways (A) and immune cell subsets (B) in GEO cohort. PTGDS, prostaglandin D2 synthase.

Immune Score by PAM50 Intrinsic Subtypes

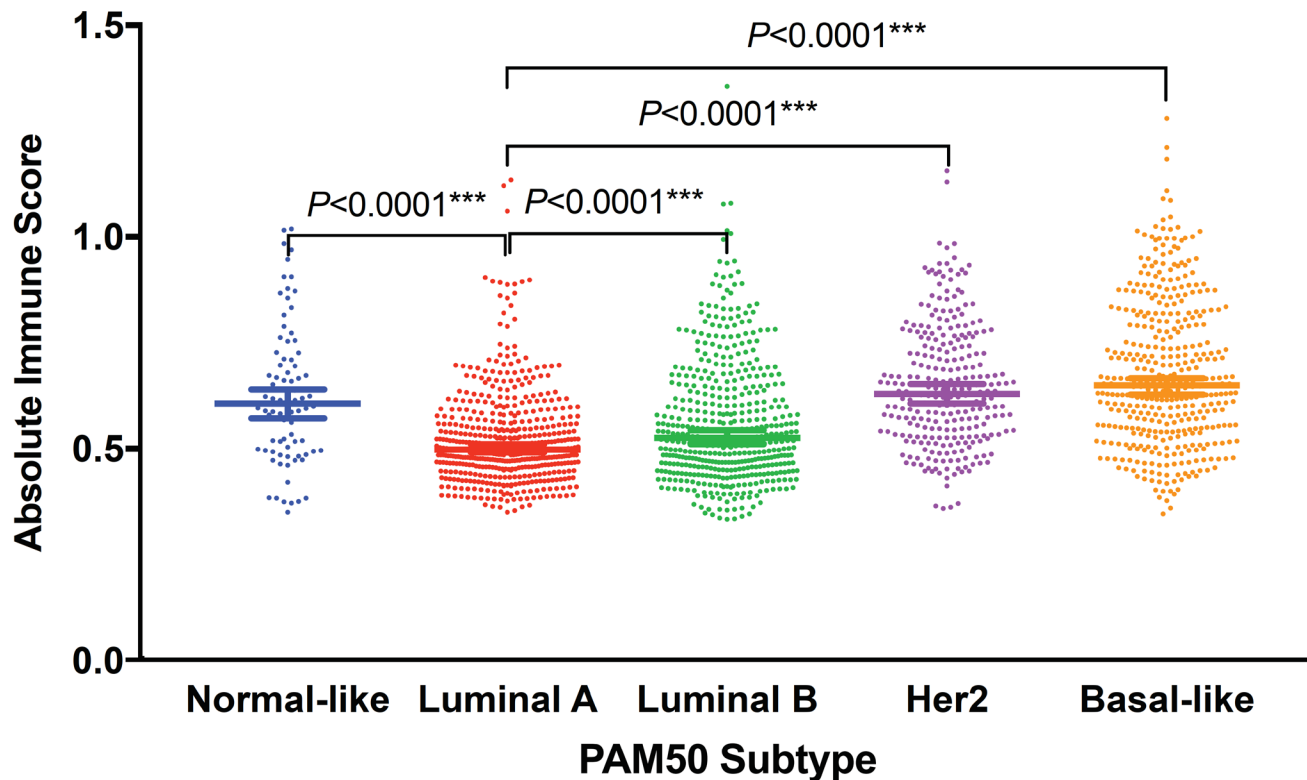


Figure S1

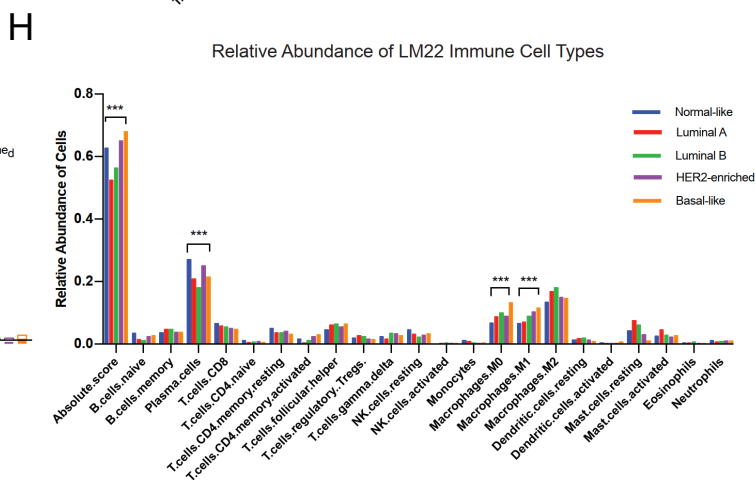
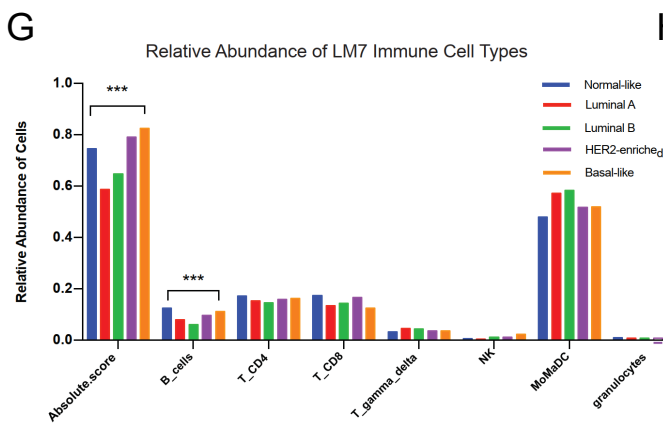
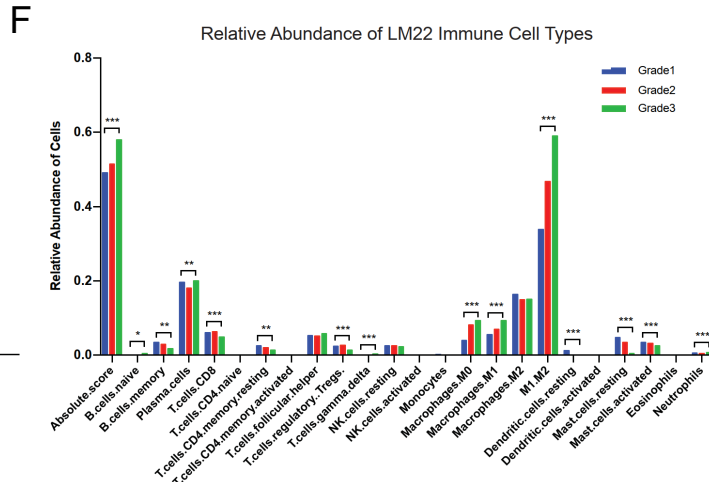
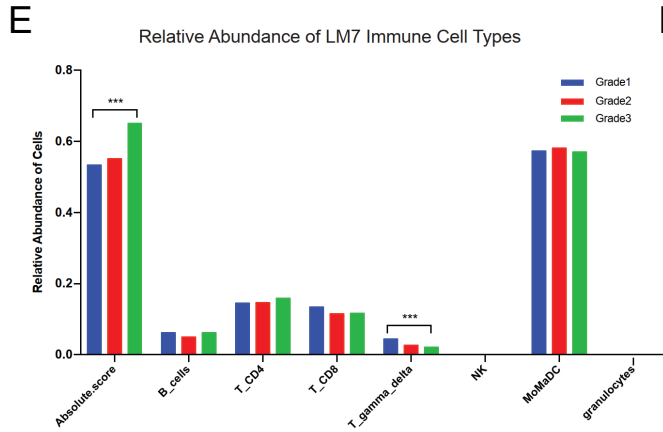
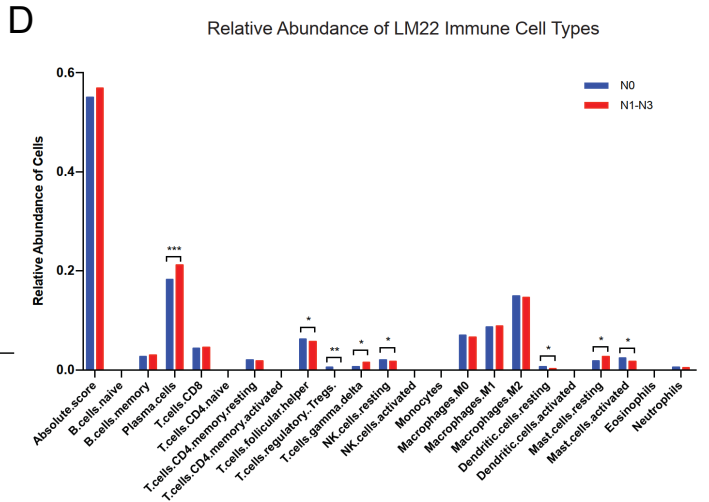
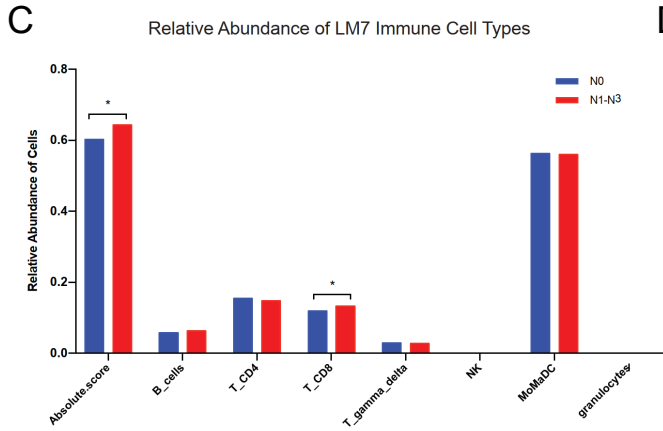
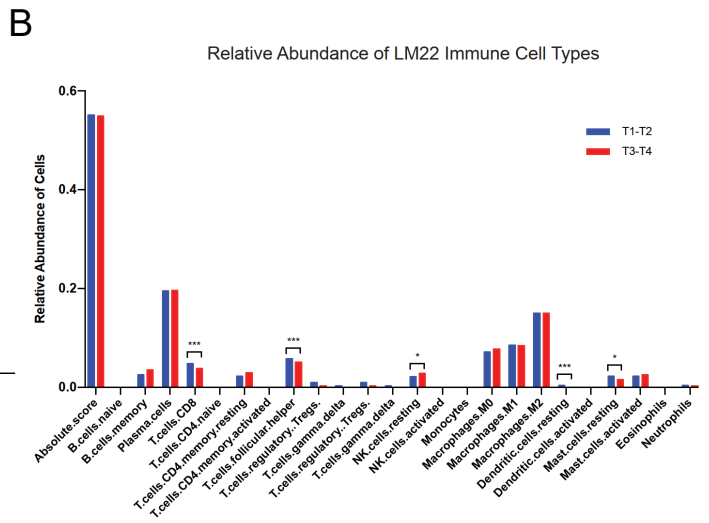
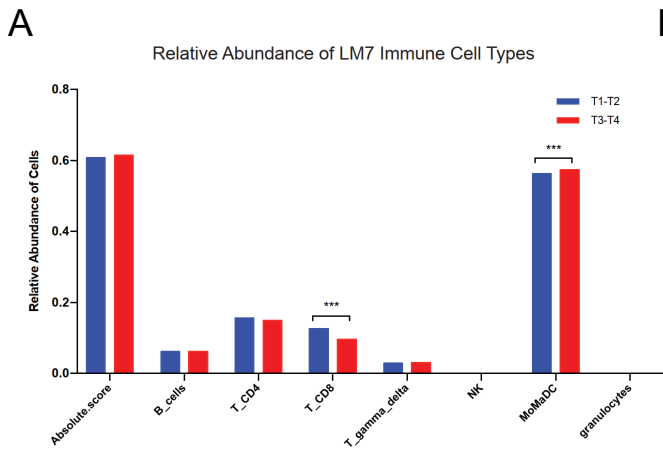
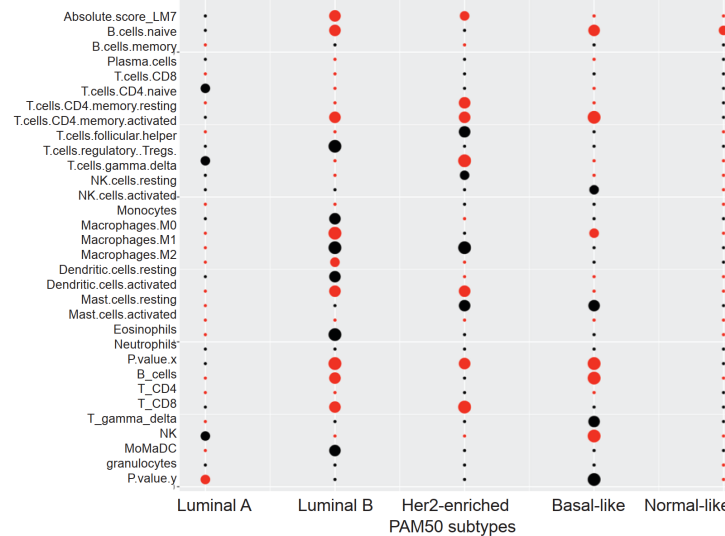


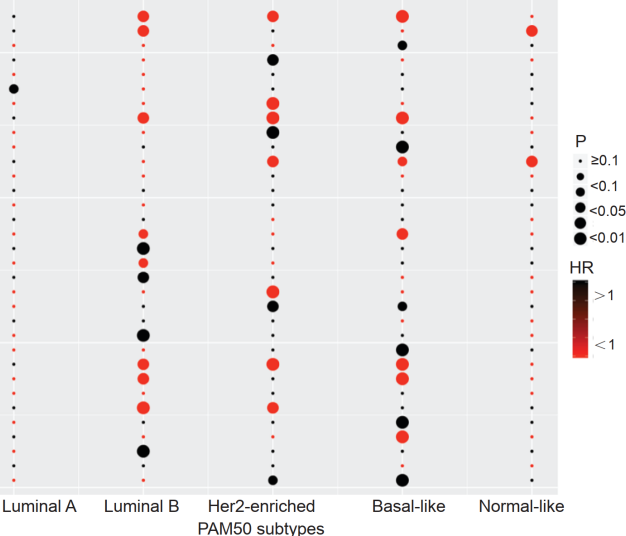
Figure S2

A

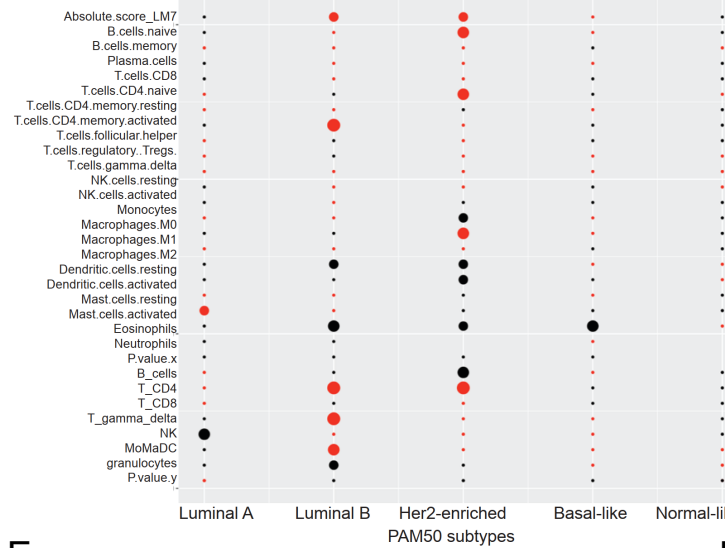
Univariable Survival Analysis of Immune Cell Subsets in GEO cohort

**B**

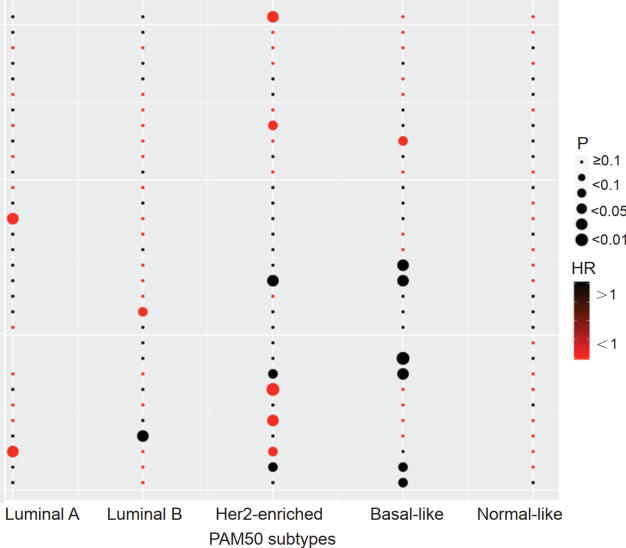
Multivariable Survival Analysis of Immune Cell Subsets in GEO cohort

**C**

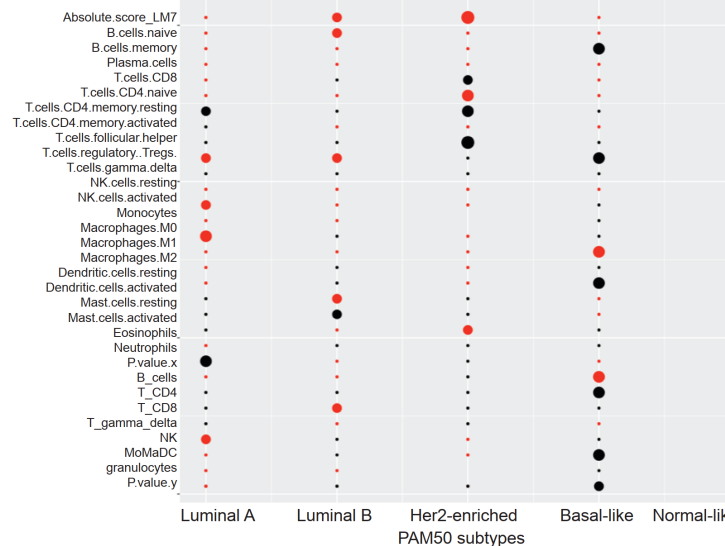
Univariable Survival Analysis of Immune Cell Subsets in METABRIC cohort

**D**

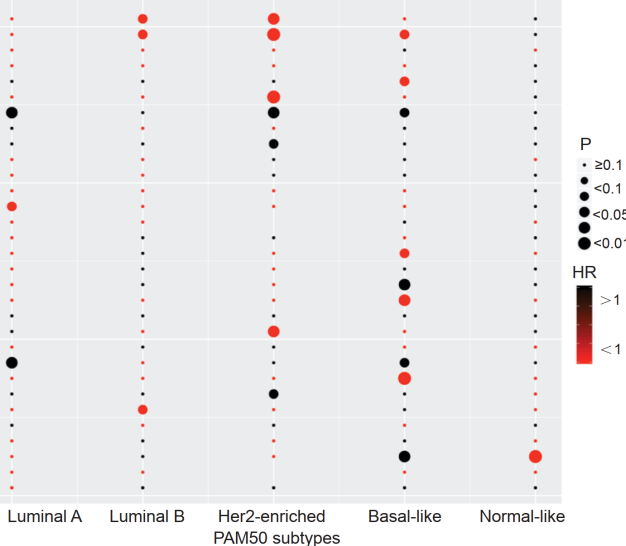
Multivariable Survival Analysis of Immune Cell Subsets in METABRIC cohort

**E**

Univariable Survival Analysis of Immune Cell Subsets in TCGA cohort

**F**

Multivariable Survival Analysis of Immune Cell Subsets in TCGA cohort

**Figure S3**

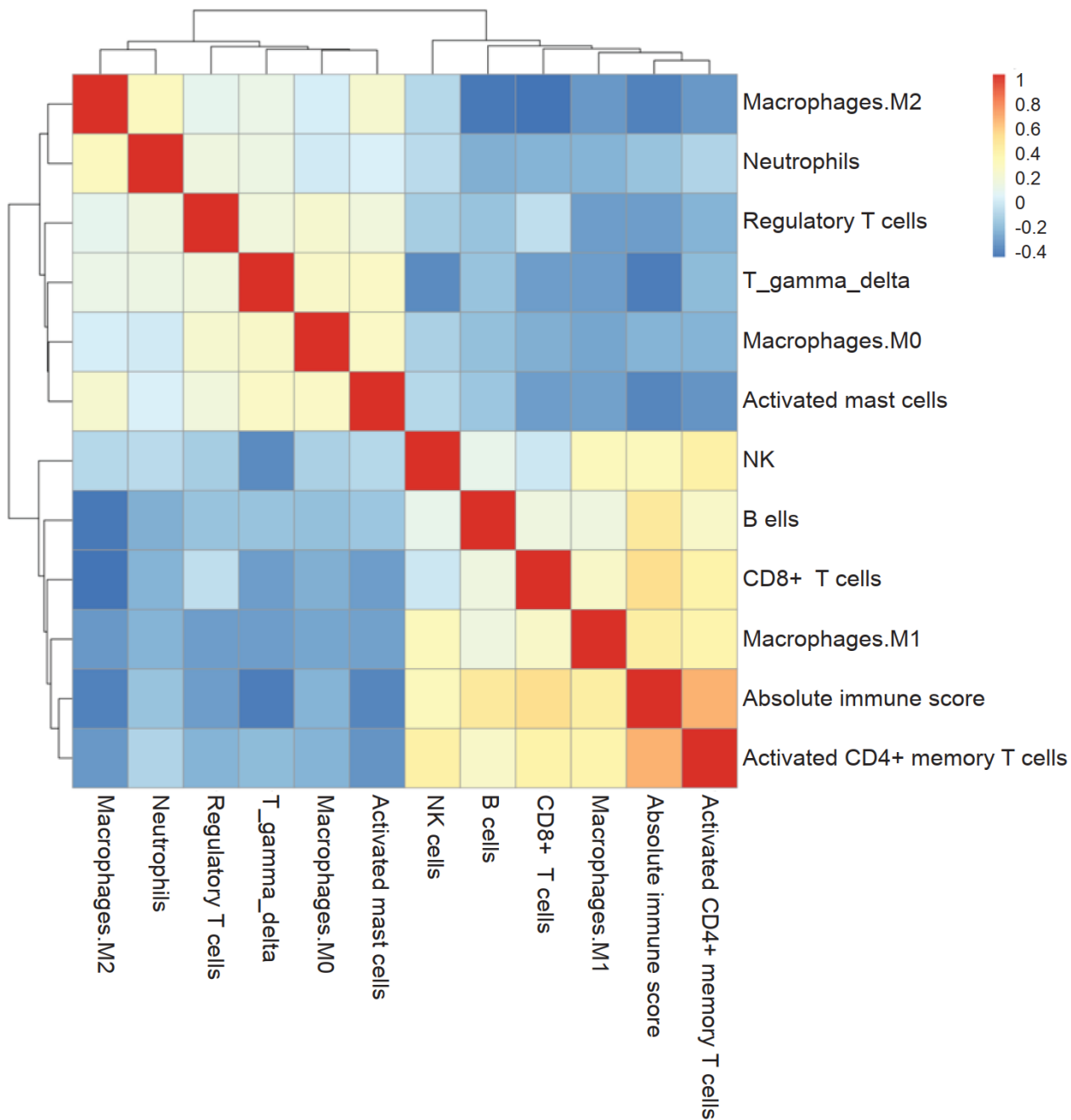
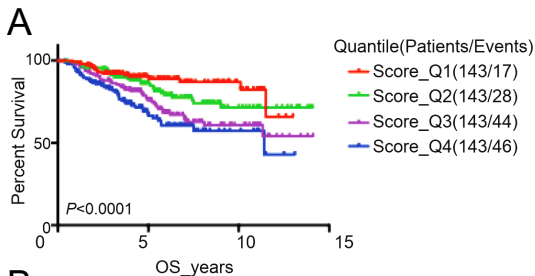
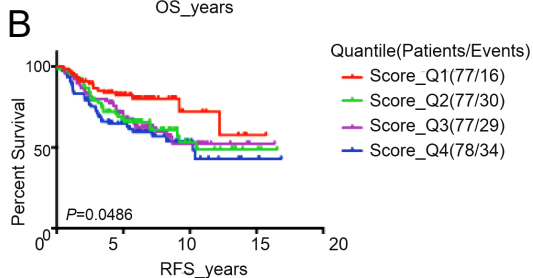


Figure S4



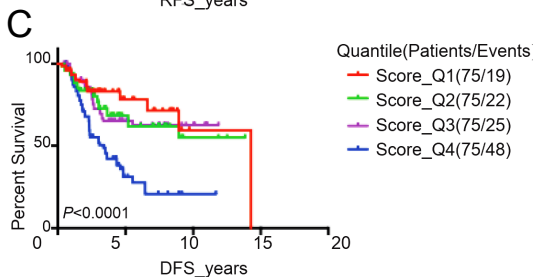
Multivariable survival analyses in non-LuminalA population(N=342, OS events=92)

	HR	95%CI		P
diagnosed age	1.010	0.992	1.028	0.9164
T_stage	1.414	1.009	1.980	0.0144
N_class	2.899	1.721	4.882	0.3877
pam50	1.554	1.202	2.009	0.0333
Score	2.212	1.436	3.406	0.0734



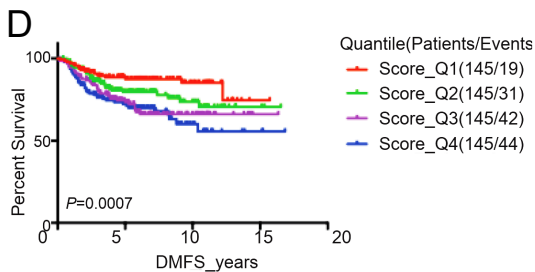
Multivariable survival analyses in non-LumA population(N=202, RFS events=66)

	HR	95%CI		P
diagnosed age	1.010	0.992	1.028	0.2851
T_stage	1.414	1.009	1.980	0.2829
N_class	2.899	1.721	4.882	0.0005
pam50	1.554	1.202	2.009	8.8e-07
Score	2.212	1.436	3.406	0.0049



Multivariable survival analyses in non-LumA population(N=145, DFS events=55)

	HR	95%CI		P
diagnosed age	0.994	0.973	1.016	0.6090
T_stage	1.330	0.908	1.945	0.1440
N_class	1.590	0.895	2.811	0.1140
pam50	1.160	0.846	1.582	0.3600
Score	6.120	2.79	13.405	5.9e-06



Multivariable survival analyses in non-LumA population(N=342, DMFS events=92)

	HR	95%CI		P
diagnosed age	0.998	0.981	1.015	0.7923
T_stage	1.690	1.204	2.360	0.0024
N_class	2.320	1.436	3.750	0.0006
pam50	1.070	0.819	1.387	0.6364
Score	3.350	2.057	5.463	1.21e-06

Figure S5

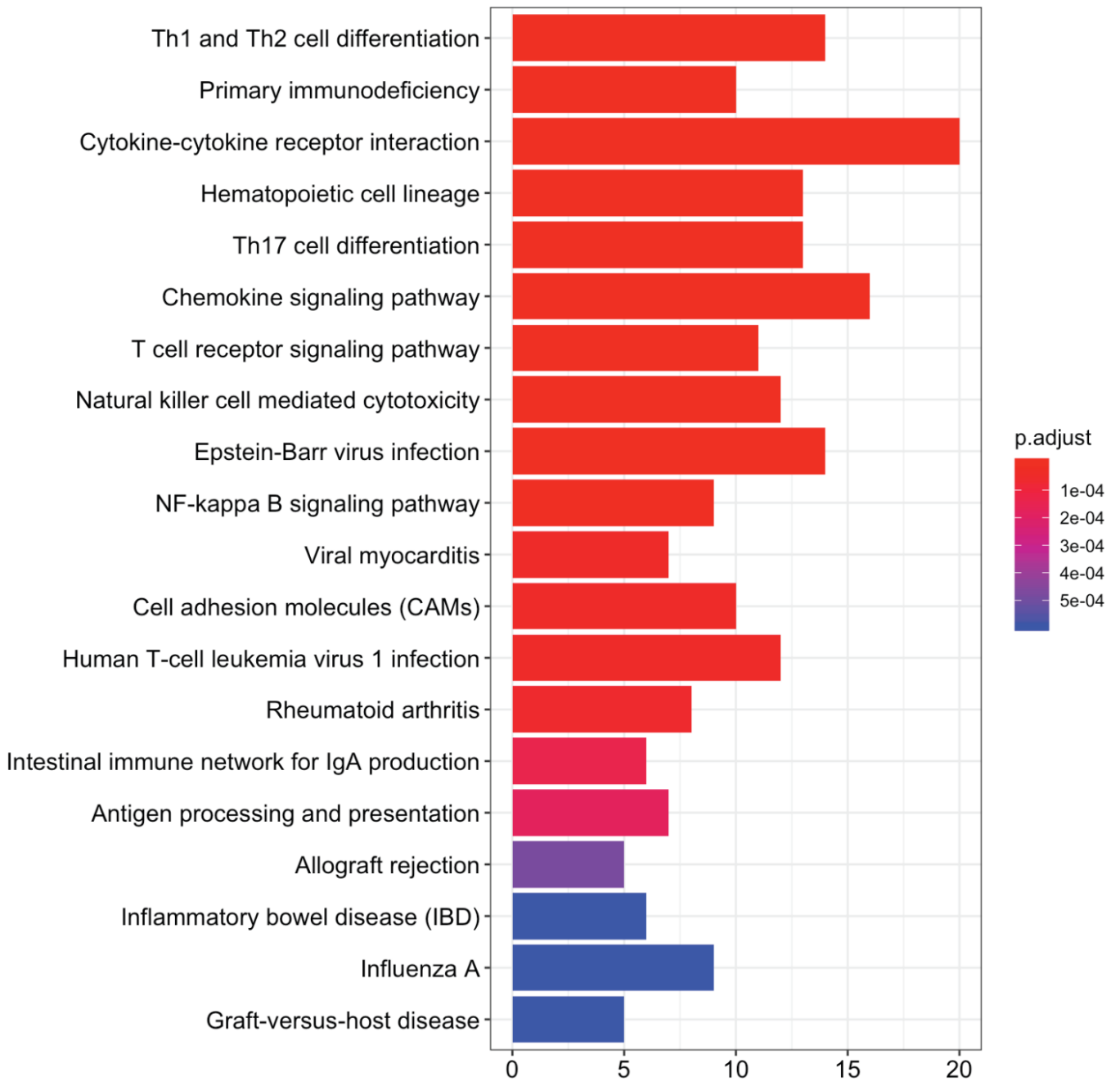
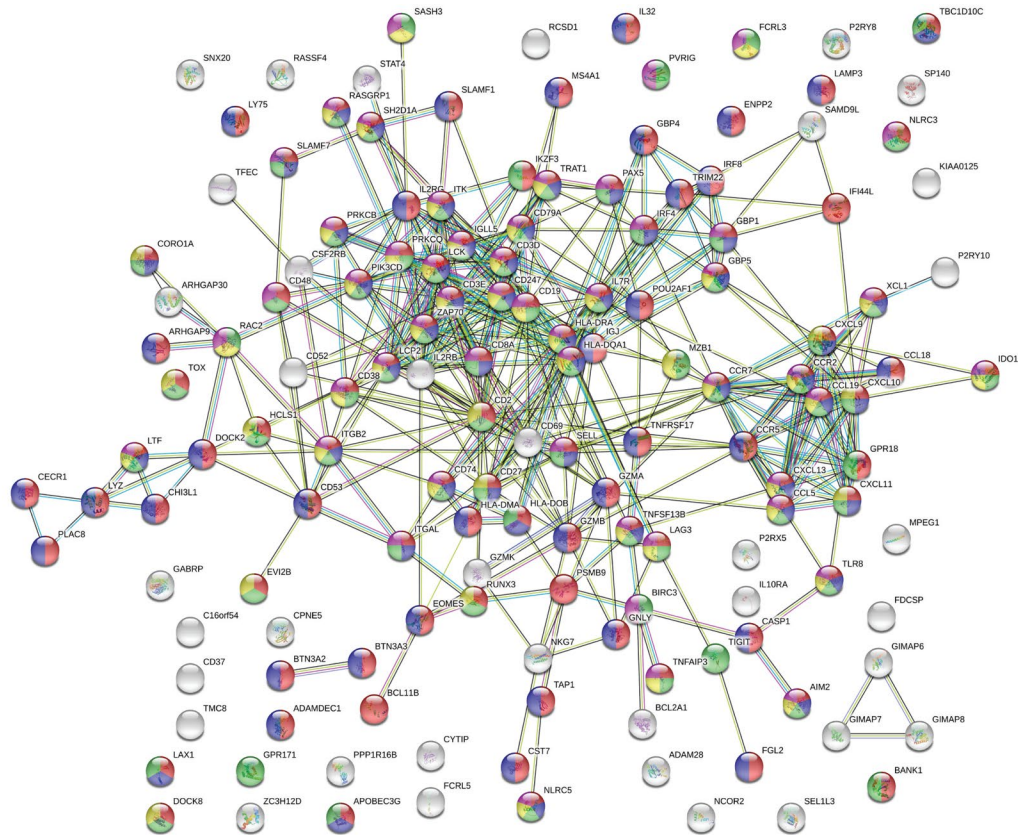


Figure S6

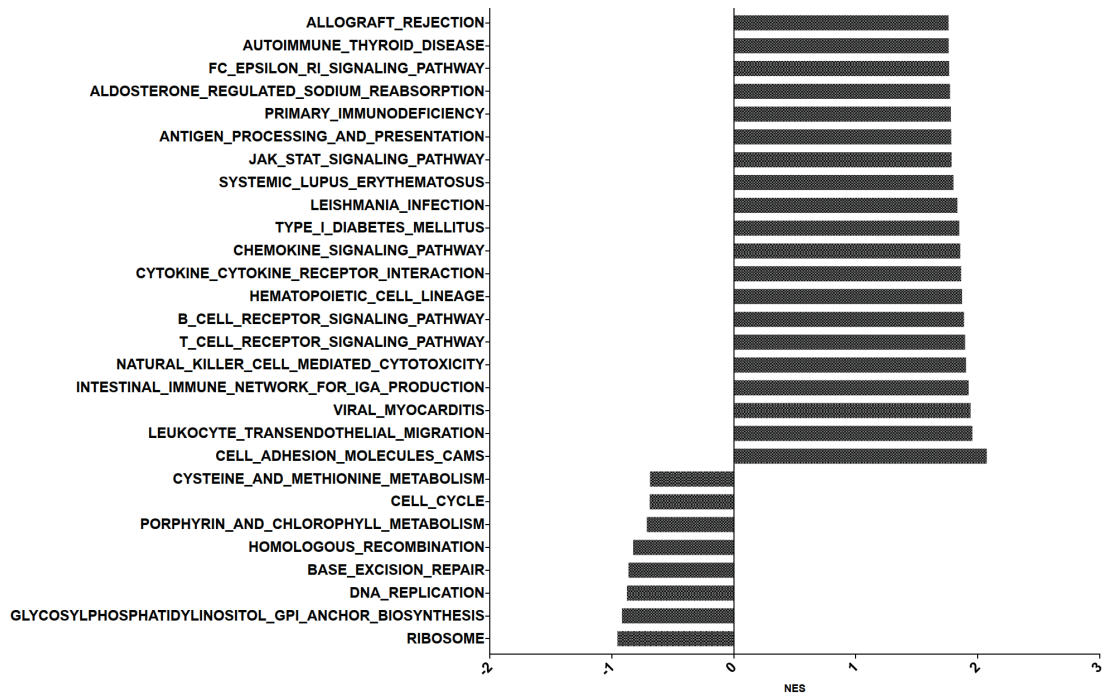


- Biological process**
- Immune system process
 - Immune response
 - Regulation of immune system process
 - Positive regulation of immune system process
 - Regulation of immune response

- KEGG Pathways**
- Cytokine-cytokine receptor interaction
 - Th1 and Th2 cell differentiation
 - Primary immunodeficiency
 - Chemokine signaling pathway
 - Hematopoietic cell lineage

Figure S7

A



B

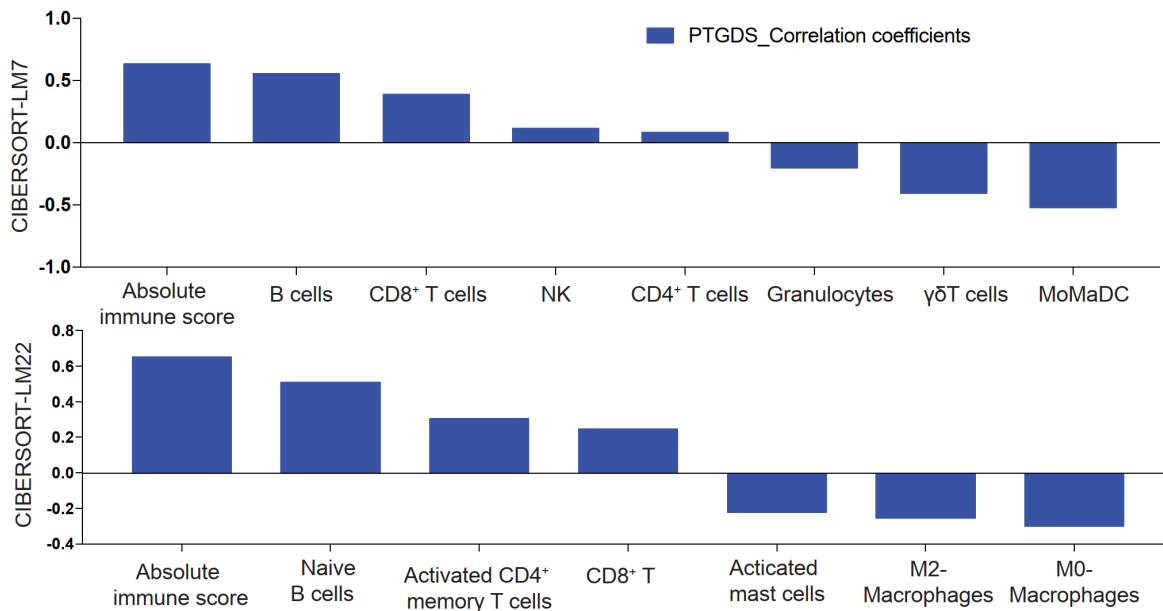


Figure S8

Supplementary Tables

Table S1. GEO-GPL570 databases screened for analysis

Author	Year	Country	Sample	Source Accession	PMID
Loi S et al.	2007	Canada	87	GSE6532	17401012
Loi S et al.	2008	Canada	77	GSE9195	18498629
Desmedt C et al.	2010	Canada	120	GSE16446	21422418
Sircoulomb F et al.	2009	France	51	GSE17907	20932292
Li Y et al.	2010	USA	115	GSE19615	20098429
Kao KJ et al.	2011	Taiwan, China	327	GSE20685	21501481
Dedeurwaerder S et al.	2011	Canada	88	GSE20713	21910250
Gendrin C et al.	2010	USA	266	GSE21563	25561709
Sabatier R et al.	2011	France	353	GSE31448	22110708
Clarke C et al.	2013	Ireland	104	GSE42568	23740839
Huang C et al.	2014	Taiwan, China	81	GSE48390	24098497
Fumagalli D et al.	2016	Belgium	94	GSE58984	N/A

Table S2. Harrell's concordance indexes of the IRS, TNM stage, and nomogram in GEO, TCGA and METABRIC cohorts

Cohort	Harrell's concordance indexes (95% CI)		
	IRS	TNM stage	Nomogram
GEO	0.63 (0.58–0.68)	0.66 (0.59–0.73)	0.71 (0.64–0.78)
TCGA	0.56 (0.49–0.63)	0.73 (0.66–0.80)	0.77 (0.70–0.84)
METABRIC	0.52 (0.50–0.54)	0.60 (0.58–0.62)	0.62 (0.59–0.65)

IRS, immunorisk score; HR, hazard ratio; CI, confidence interval.

Table S3. Univariable Cox regression analysis of PTGDS with overall survival in GEO, TCGA and METABRIC cohorts

Cohort	HR	95% CI	P-value
GEO	0.67	0.55-0.83	0.0001***
TCGA-BRCA	0.84	0.58-0.98	0.016*
METABRIC	0.93	0.88-0.99	0.027*

HR, hazard ratio; CI, confidence interval; * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.