Figure S1 OS results of immune cells are significantly different between groups (determined by the median value). OS, overall survival.
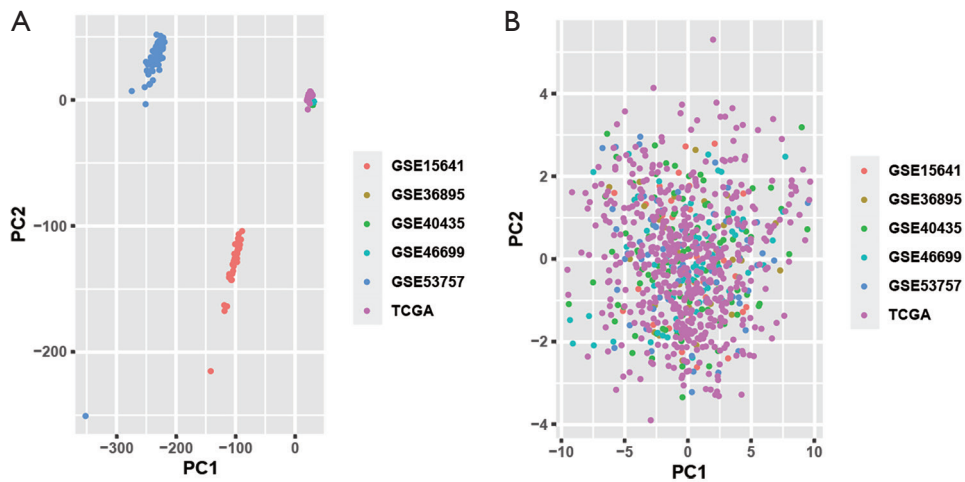

Figure S2 Two-dimensional plots are shown of principal components calculated PCA. (A) PCA of the expression matrix of six different datasets. (B) PCA of the immune cells enrichment scores of six different datasets. PCA, principal components analysis; TCGA, The Cancer Genome Atlas.
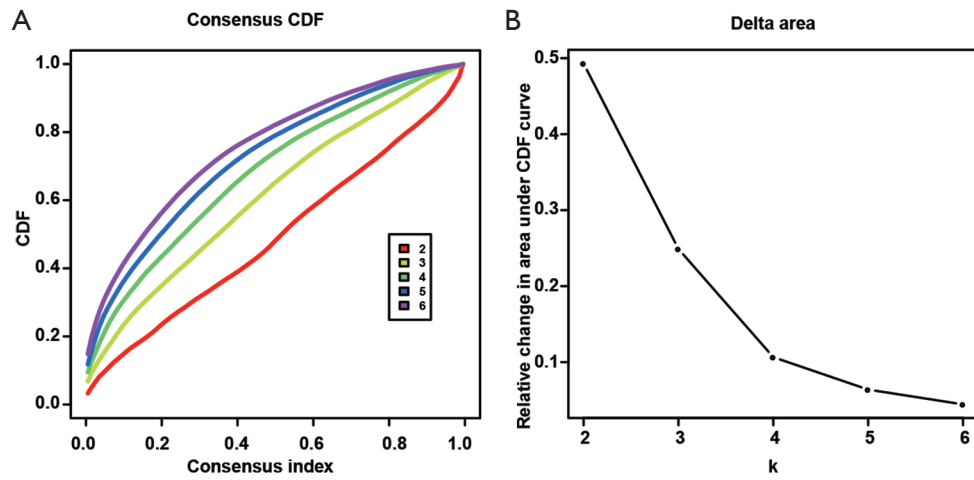
Figure S3 The selection of immune subtype numbers. (A) CC CDF for k=2 to 6. (B) Delta area curve of CC, indicating the relative change in area under CDF curve for each category number k compared with k–1. The horizontal axis represents the category number k, and the vertical axis represents the relative change in area under the CDF curve. CC, consensus clustering; CDF, cumulative distribution function.
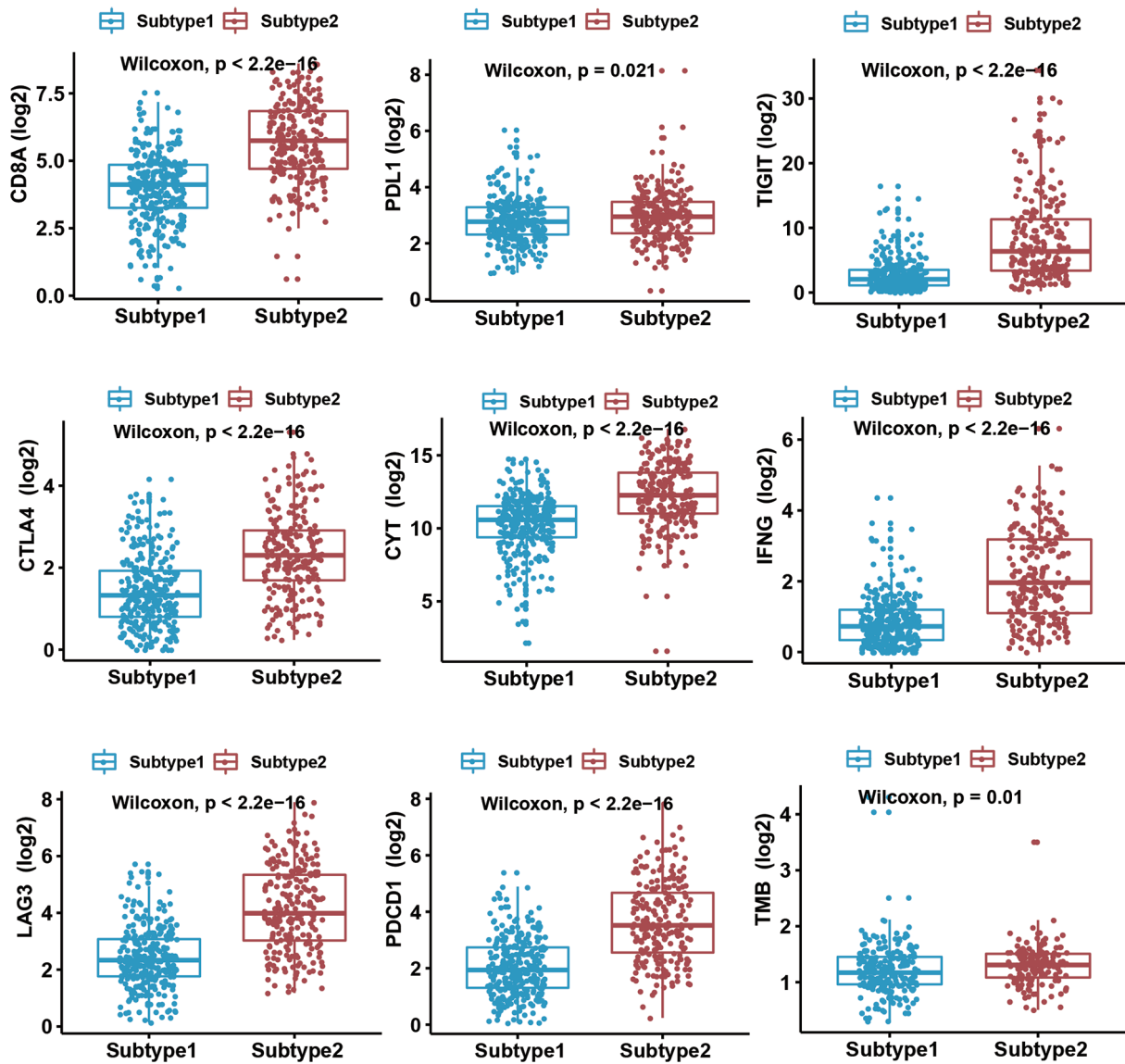
Figure S4 Comparison of the tumor immunotherapy indicators between the two immune subtypes in the TCGA dataset. Subtype2 tumors had significantly higher *CD8A*, *PDL1*, *TIGIT*, *CTLA4*, *CYT*, *IFNG*, *LAG3*, *PD1* (*PDCD1*) and *TMB* than subtype1 tumors (P<0.05). TCGA, The Cancer Genome Atlas; TMB, tumor mutational burden.
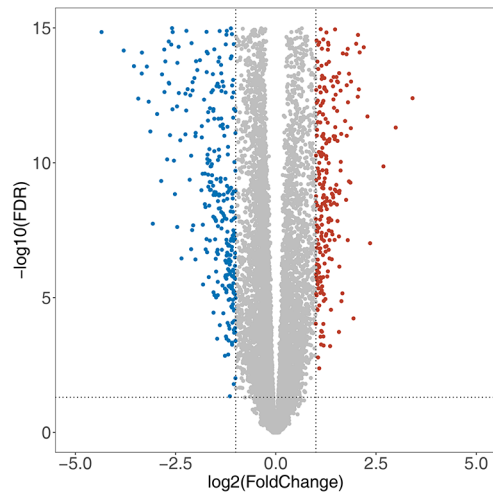
Figure S5 Volcano plot showing the gene expression differences between immune subtypes. Blue dots, down-regulated genes in subtype2. Red dots, upregulated genes in subtype2. FDR, false discovery rate.
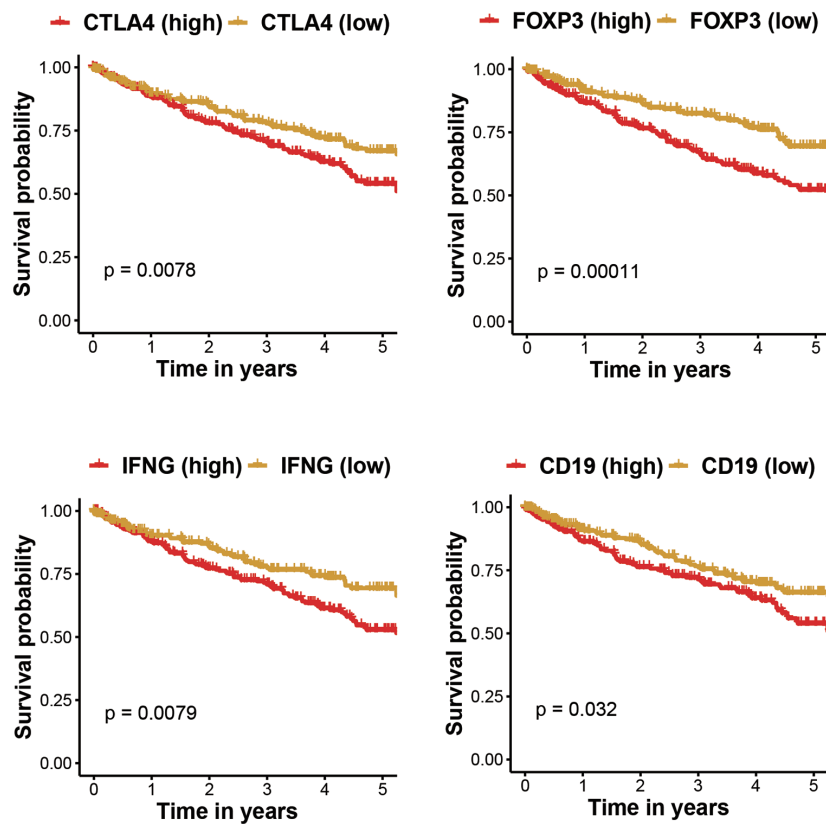

Figure S6 OS results of four hub genes in the turquoise module are significantly different between groups (determined by the median value). OS, overall survival.
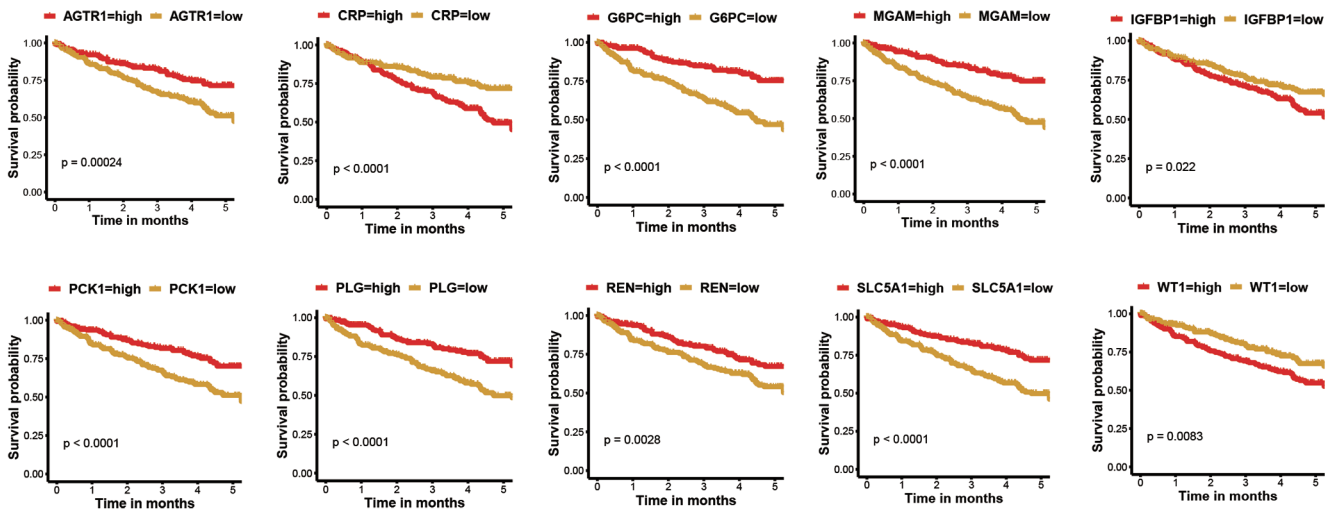
Figure S7 OS results of ten hub genes in the blue module are significantly different between groups (determined by the median value). OS, overall survival.
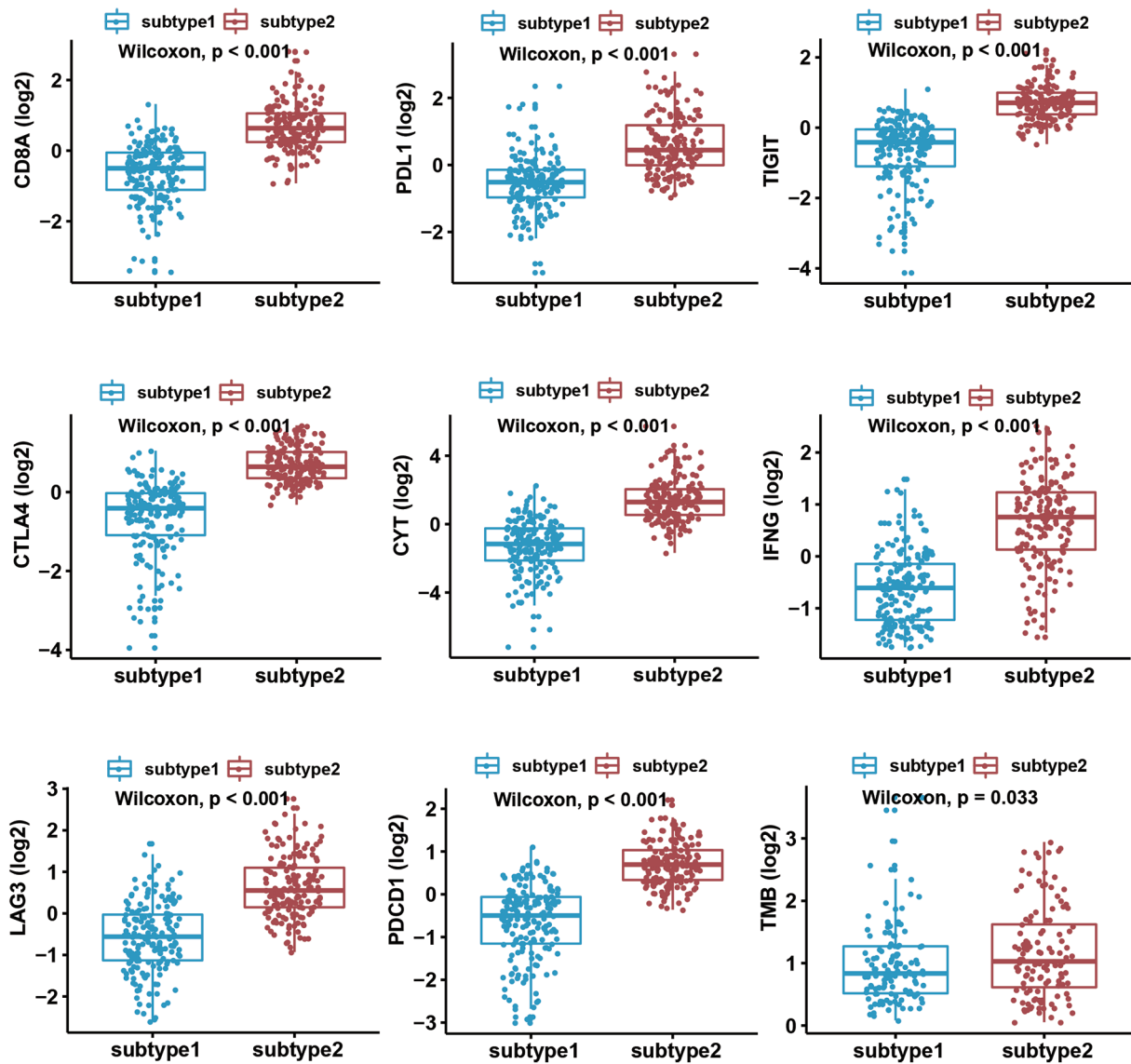
Figure S8 Comparison of the tumor immunotherapy indicators between the two immune subtypes in the IMvigor210 dataset. Subtype2 tumors had significantly higher *CD8A*, *PDL1*, *TIGIT*, *CTLA4*, *CYT*, *IFNG*, *LAG3*, *PD1* (*PDCD1*) and *TMB* than subtype1 tumors (P<0.05). TMB, tumor mutational burden.

Table S1 The enriched pathways in immune subtype1

Pathway	Padj	NES	Size
PPAR signaling pathway	<0.05	−2.076462405	69
Oxidative phosphorylation	<0.05	−2.075496402	116
Vibrio cholerae infection	<0.05	−2.01780083	52
Fatty acid metabolism	<0.05	−1.99482005	42
Retinol metabolism	<0.05	−1.927153616	63
Tyrosine metabolism	<0.05	−1.908248892	41
Drug metabolism cytochrome P450	<0.05	−1.829246779	70
Glycolysis gluconeogenesis	<0.05	−1.793530881	61
Propanoate metabolism	<0.05	−1.779770488	32
Epithelial cell signaling in *Helicobacter pylori* infection	<0.05	−1.773782491	67

A negative NES means that genes over-represented in the gene set are upregulated in immune subtype1. Padj, adjusted P values (the FDR); FDR, false discovery rate; NES, normalized enrichment score.

Table S2 The enriched pathways in immune subtype2

Pathway	Padj	NES	Size
Natural killer cell mediated cytotoxicity	<0.05	2.101136753	130
Leishmania infections	<0.05	2.112326976	69
Asthma	<0.05	2.147862606	28
T cell receptor signaling pathway	<0.05	2.203600853	106
Chemokine signaling pathway	<0.05	2.213683506	184
Allograft rejection	<0.05	2.244700522	35
Graft versus host disease	<0.05	2.25556481	37
Primary immunodeficiency	<0.05	2.271887799	35
Cytokine-cytokine receptor interaction	<0.05	2.28028487	257
Intestinal immune network for IgA production	<0.05	2.310500831	46
Antigen processing and presentation	<0.05	2.363167045	79

A positive NES means that genes over-represented in the gene set are upregulated in immune subtype2. Padj, adjusted P values (the FDR); FDR, false discovery rate; NES, normalized enrichment score.

Table S3 Baseline characteristics of patients in the IMvigor210 cohort

Clinical type	Sample [%]
Immunotherapy outcome	
CR/PR	68 [19]
SD/PD	230 [66]
NA	50 [15]
Gender	
Male	272 [78]
Female	76 [22]
Tobacco history	
Previous	197 [57]
Never	116 [33]
Current	35 [10]
Received platinum	
Yes	272 [78]
No	76 [22]

CR, complete response; PR, partial response; SD, stable disease; PD, progressive disease; NA, data is not available.