

1 **Figure S1. The expression of m6A related genes in CESC and HNSC and their**  
2 **location.**

3 (A) Venn of differentially expressed m6A regulators in tumor tissue and normal tissue  
4 in CESC and HNSC. (B) Expression levels of the 17 shared differentially expressed  
5 m6A regulators. (C-D) The location of DEGs in HNSC and CESC on chromosomes.

6 **Figure S2. Expression levels of m6A regulators in HPV-positive and negative**  
7 **HNSC.**

8 **Figure S3. Expression spectrum of m6A regulators in HPV-positive and negative**  
9 **CESC and survival analysis in HPV-related cancer.**

10 (A) Expression profiles of m6A regulators in HPV-positive and negative CESC. (B)  
11 Venn diagram of m6A regulators differentially expressed in tumor tissue and normal  
12 tissue in CESC and HNSC and HPV-positive and negative HNSC. (C) DFS survival  
13 map of m6A regulators. (D) Kaplan-Meier curve of m6A regulators in HNSC. (E)  
14 Kaplan-Meier curve of m6A regulators in CESC.

15 **Figure S4. Overall survival analysis of m6A regulators in HPV-related cancer.**

16 (A) Overall survival map of m6A regulators. (B) Kaplan-Meier curve of m6A  
17 regulators in HNSC. (C) Kaplan-Meier curve of m6A regulators in CESC.

18 **Figure S5. The landscape of genetic variations of m6A regulators in HNSC and**  
19 **CESC.**

20 (A) Overview of the types of mutation observed. (B) Breakdown of the observed  
21 substitution mutations. (C) Alteration frequency in HNSC and CESC. (D) Patients  
22 were divided into two groups with or without alterations on the m6A regulators. The

23 graph shows genes with the highest frequency in any group. (E) Mutation count,  
24 fraction genome altered, and MSIsensor scores in any group.

25 **Figure S6. METTL3 was involved in tumor immune response in HPV-related**  
26 **cancer.**

27 Patients were ranked according to METTL3 expression, and the top 50% of patients  
28 were in METTL3<sup>high</sup> status, otherwise, they were in METTL3<sup>low</sup> status. Enrichment  
29 analysis and visualization of the filtered DEGs were performed with clusterProfiler,  
30 org.Hs.eg.db, and the ggplot2 R package (R 3.6.3). (A-B) Enrichment analysis of  
31 differential genes in CESC. (C-D) GSEA analysis of differential genes in immune  
32 response-related pathways. (E-F) Enrichment analysis of differential genes in HNSC.

33 **Figure S7. Correlation of immune checkpoint molecules with METTL3**  
34 **expression in HPV-related cancer.**

35 (A) Relative mRNA expression level in C33A. (B) Correlation of immune checkpoint  
36 molecules and METTL3 expression in HNSC. P values are indicated as \*,  $P < 0.05$ ;  
37 \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ; and \*\*\*\*,  $P < 0.0001$ .

38 **Figure S8. Correlation of immune cell infiltration with METTL3 expression in**  
39 **HPV-associated cancers.**

40 (A) Correlation analysis of the number of immune cells and METTL3 expression in  
41 CESC using TIMER 2.0. (B) Correlation analysis of the number of immune cells and  
42 METTL3 expression in HNSC using TIMER 2.0.

43 **Figure S9. Immune cell infiltration levels in HPV-related cancer.**

44 Patients were ranked according to METTL3 expression, and the top 50% of patients

45 were in METTL3<sup>high</sup> status, otherwise, they were in METTL3<sup>low</sup> status. (A) The level  
46 of immune cell infiltration in CESC. (B) The level of immune cell infiltration in  
47 HNSC. P values are indicated as \*, P < 0.05; \*\*, P < 0.01; \*\*\*, P < 0.001; and \*\*\*\*, P  
48 < 0.0001.

49 **Figure S10. Clinical and immune relevance of METTL3 to OSCC.**

50 (A-B) The relationship between METTL3 and the prognosis of OSCC. (C) The  
51 diagnostic predictive value of METTL3 in OSCC. (D) Correlation between METTL3  
52 expression and immune cells infiltration. (E-F) Correlation between the expression of  
53 immune checkpoint molecules and the expression of METTL3.

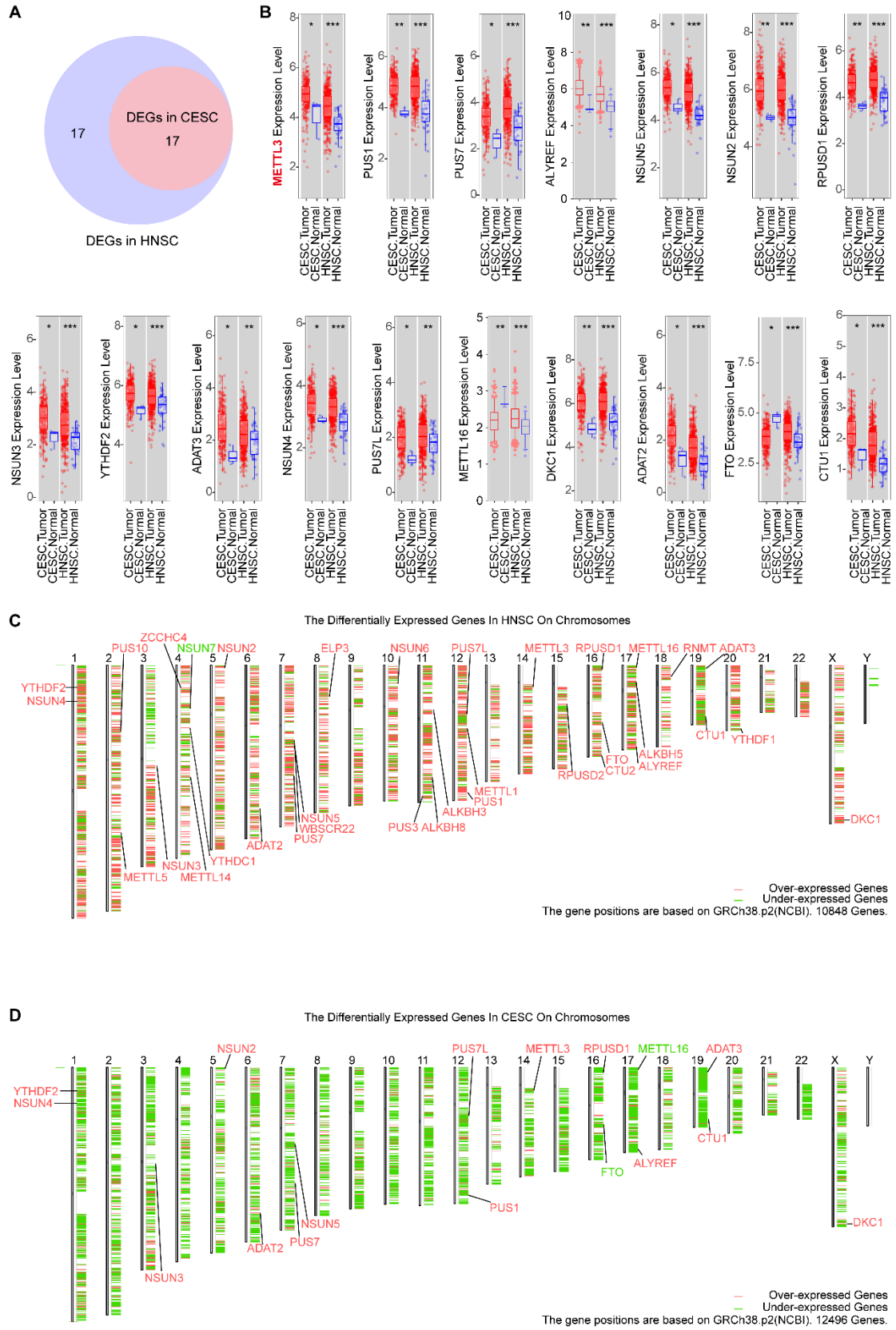
54

55 **Supplementary Table 1: Sequence of primers used in real-time PCR.**

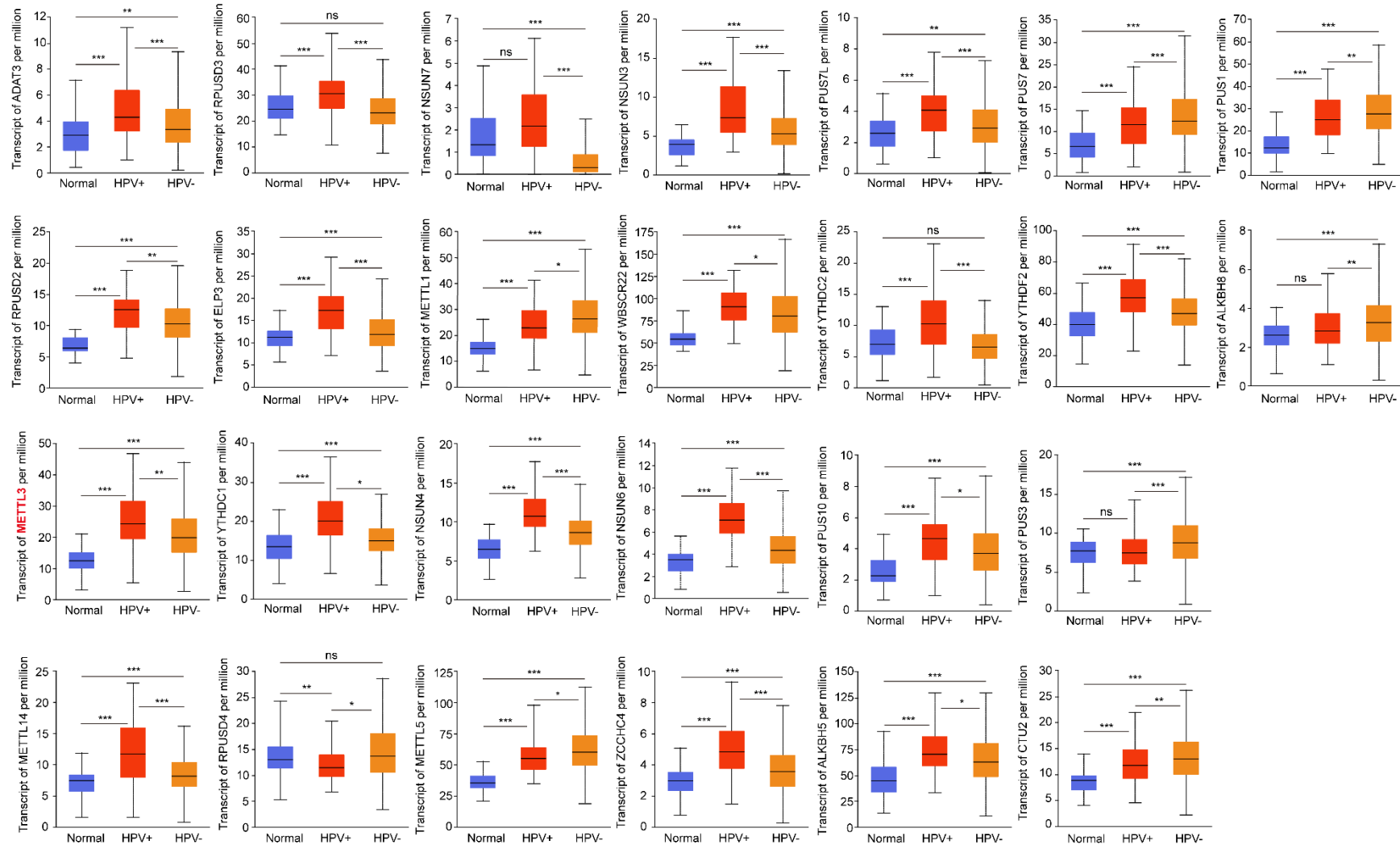
56

57

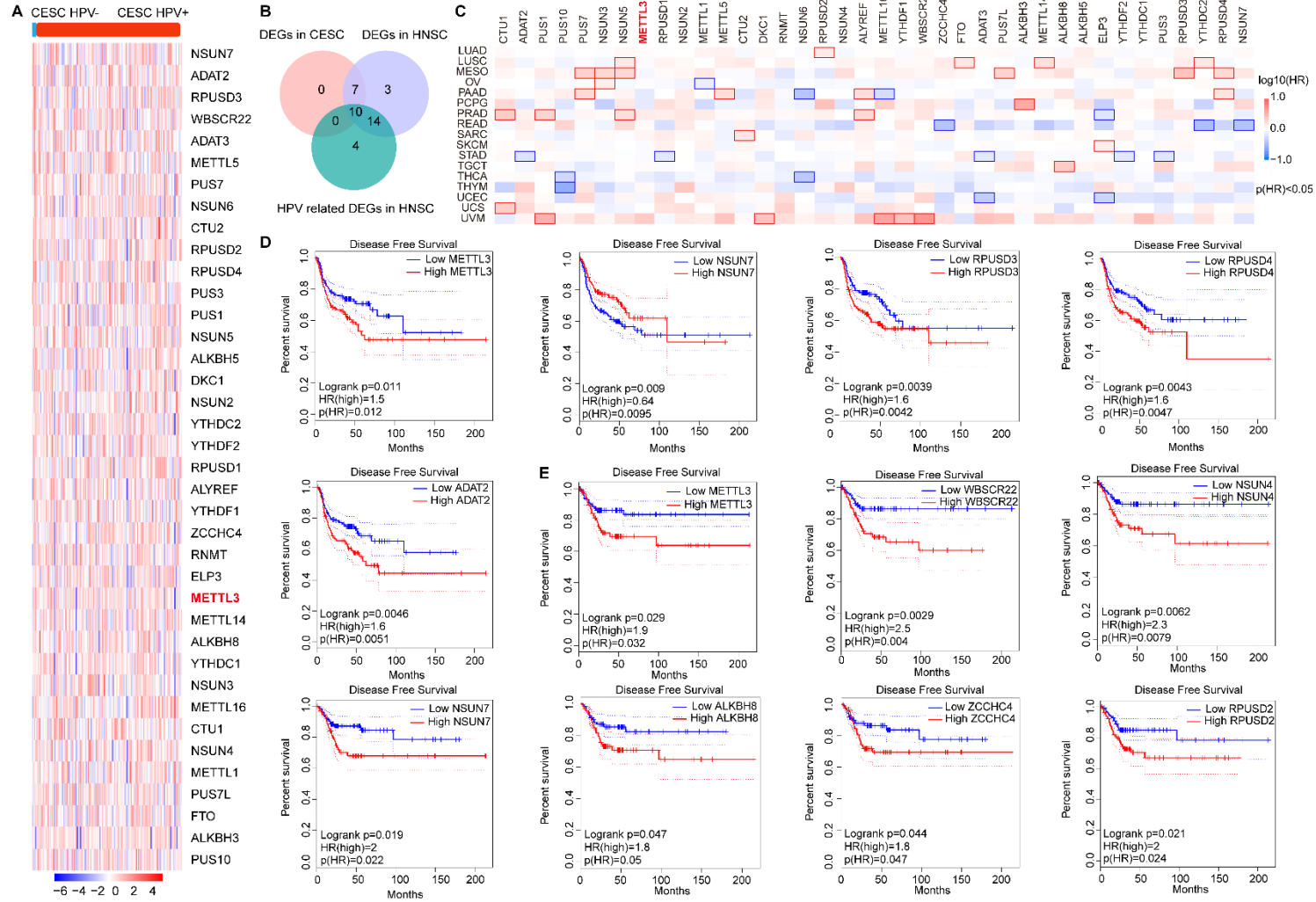
**Figure S1**



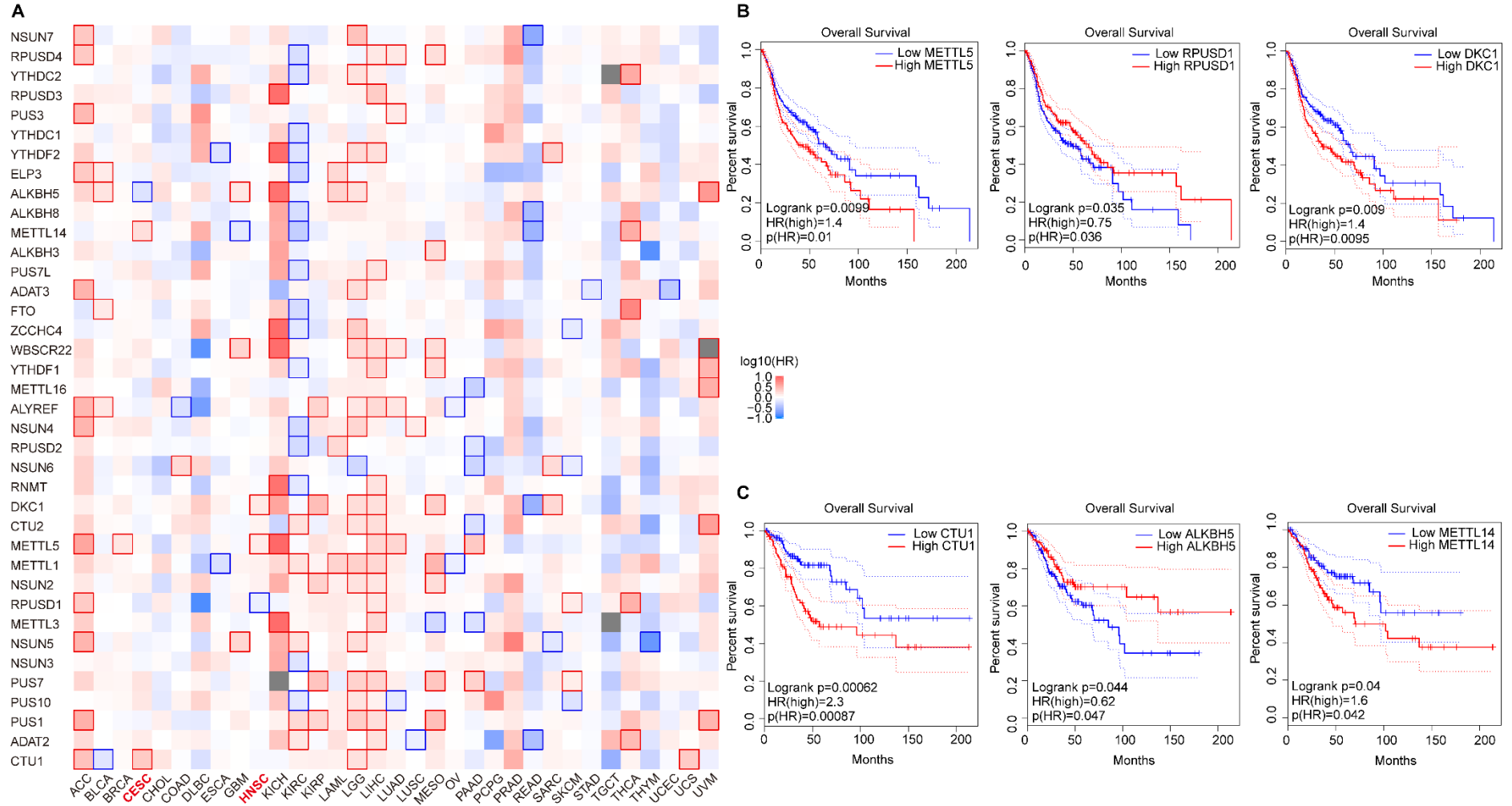
**Figure S2**



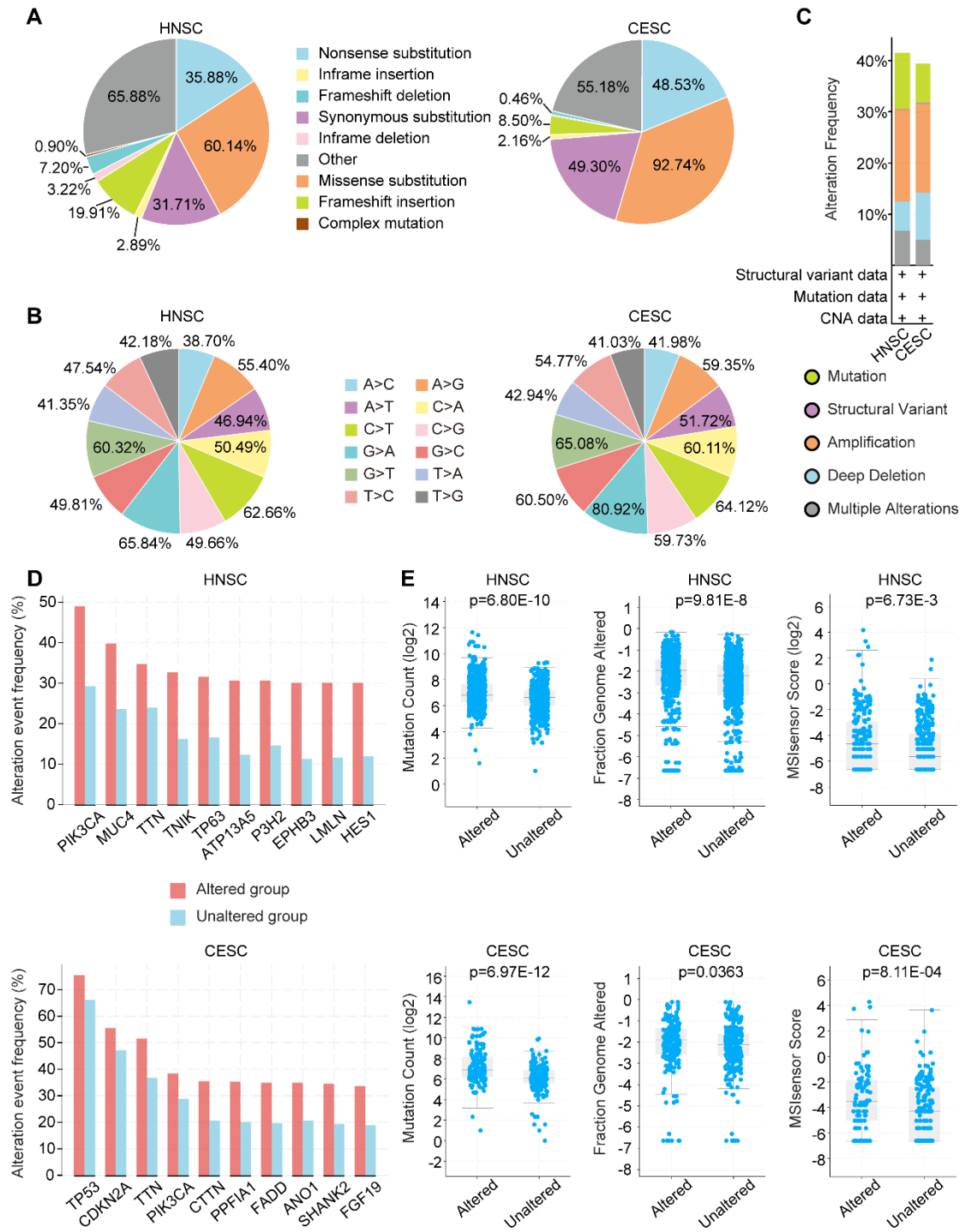
**Figure S3**



**Figure S4**

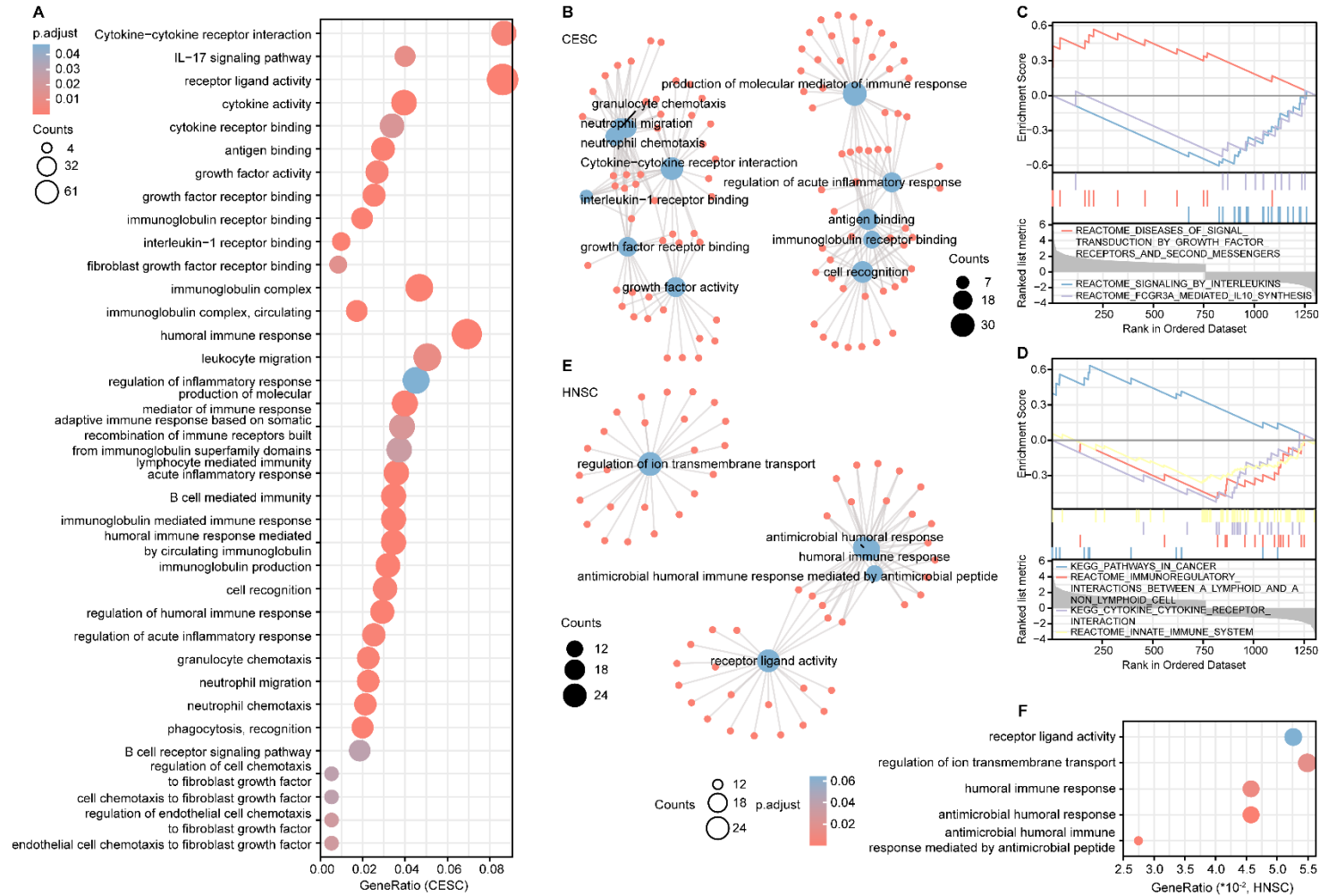


**Figure S5**



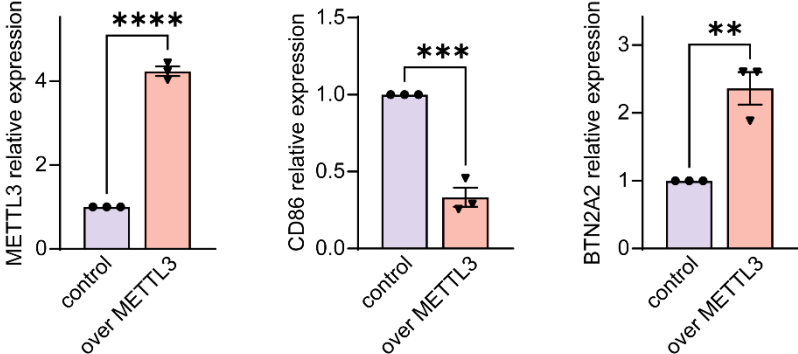


**Figure S6**

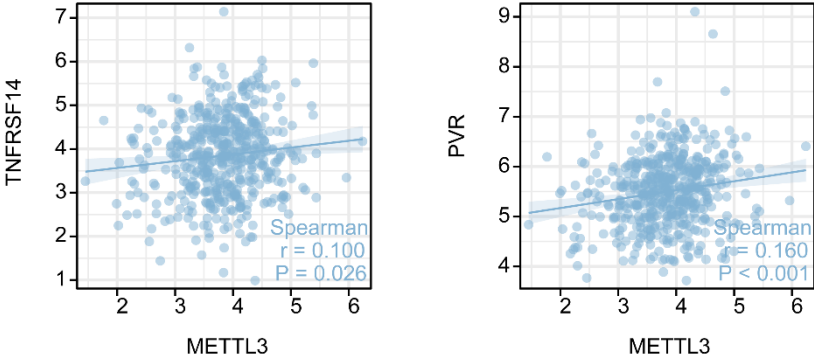


**Figure S7**

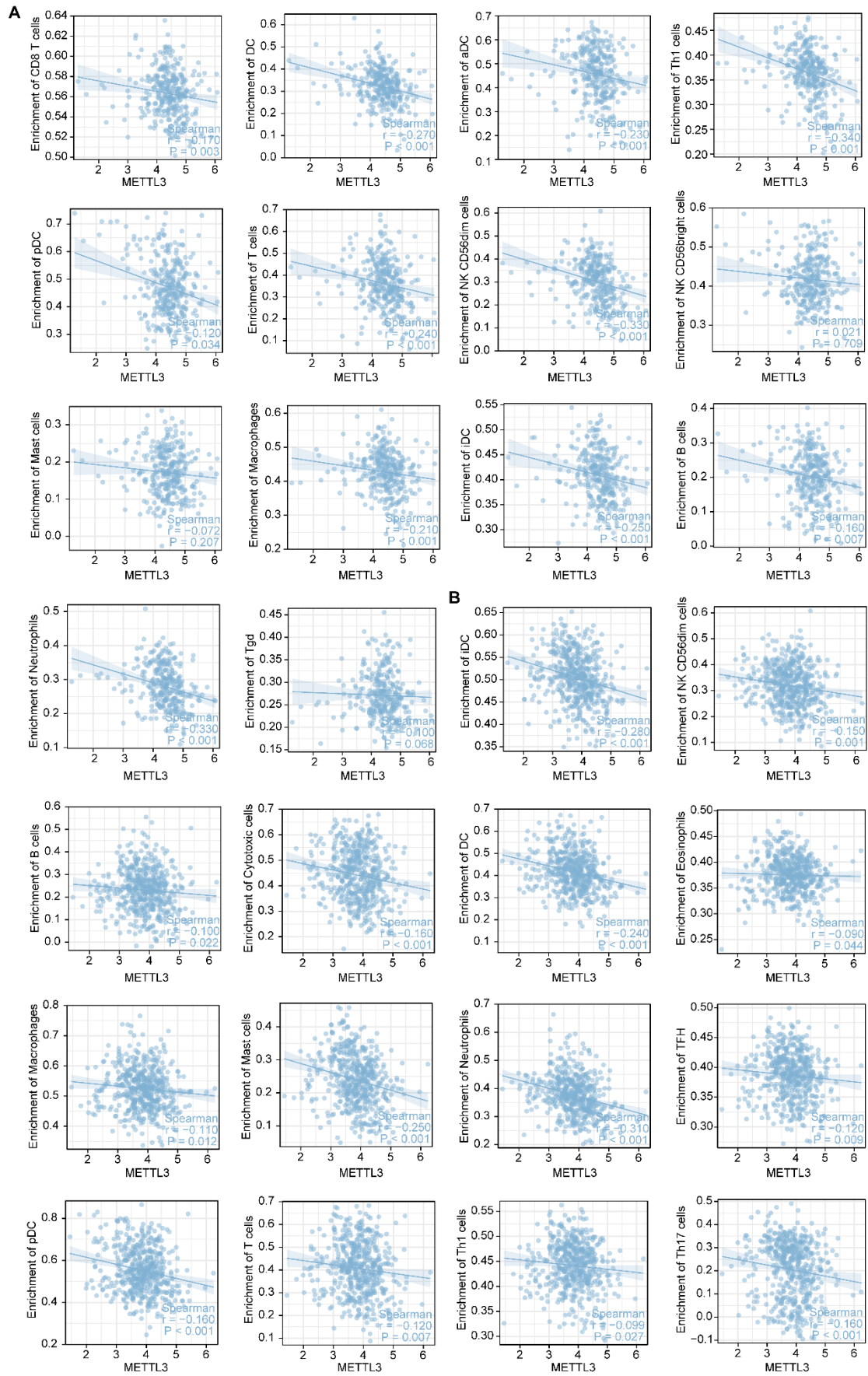
**A**



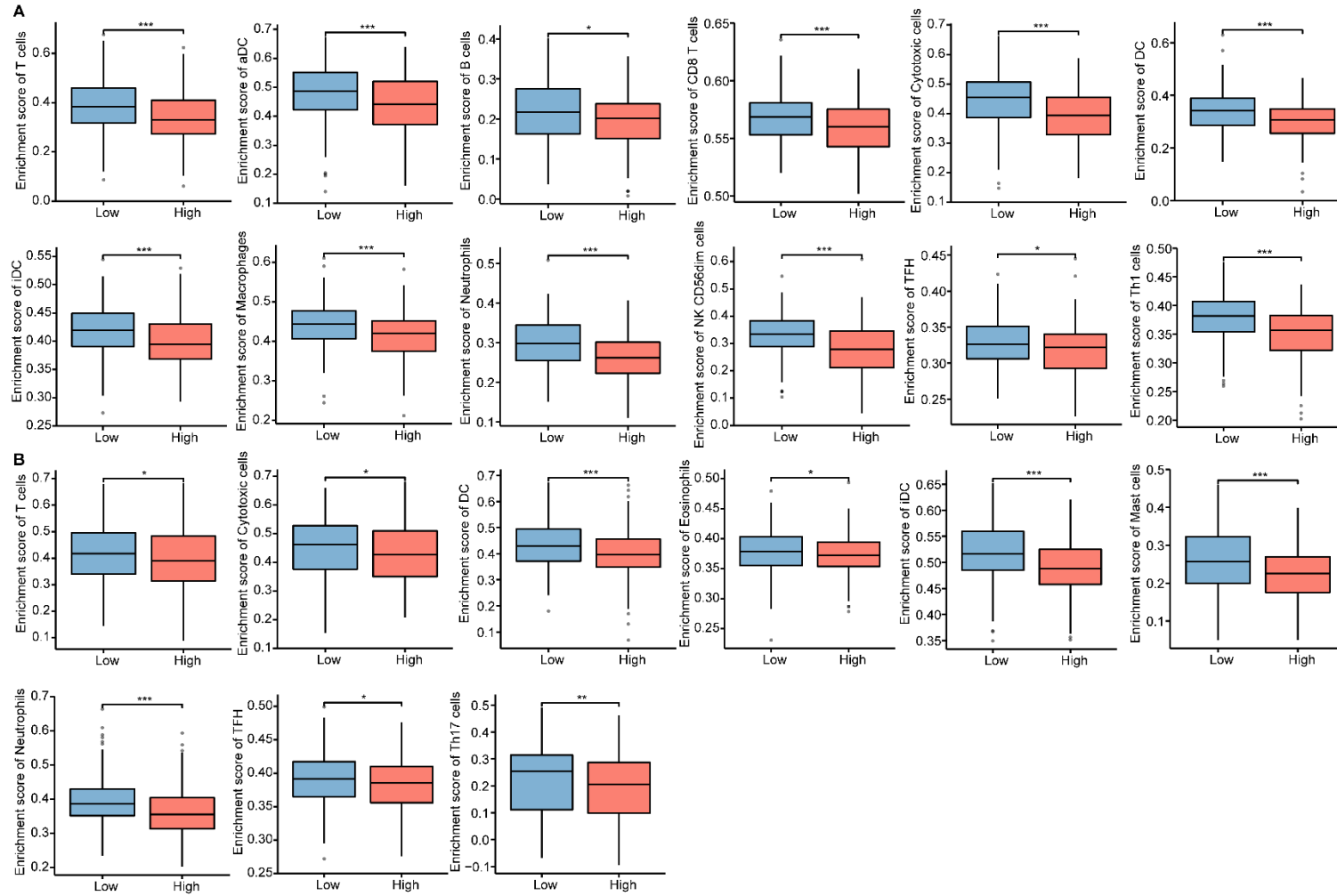
**B**



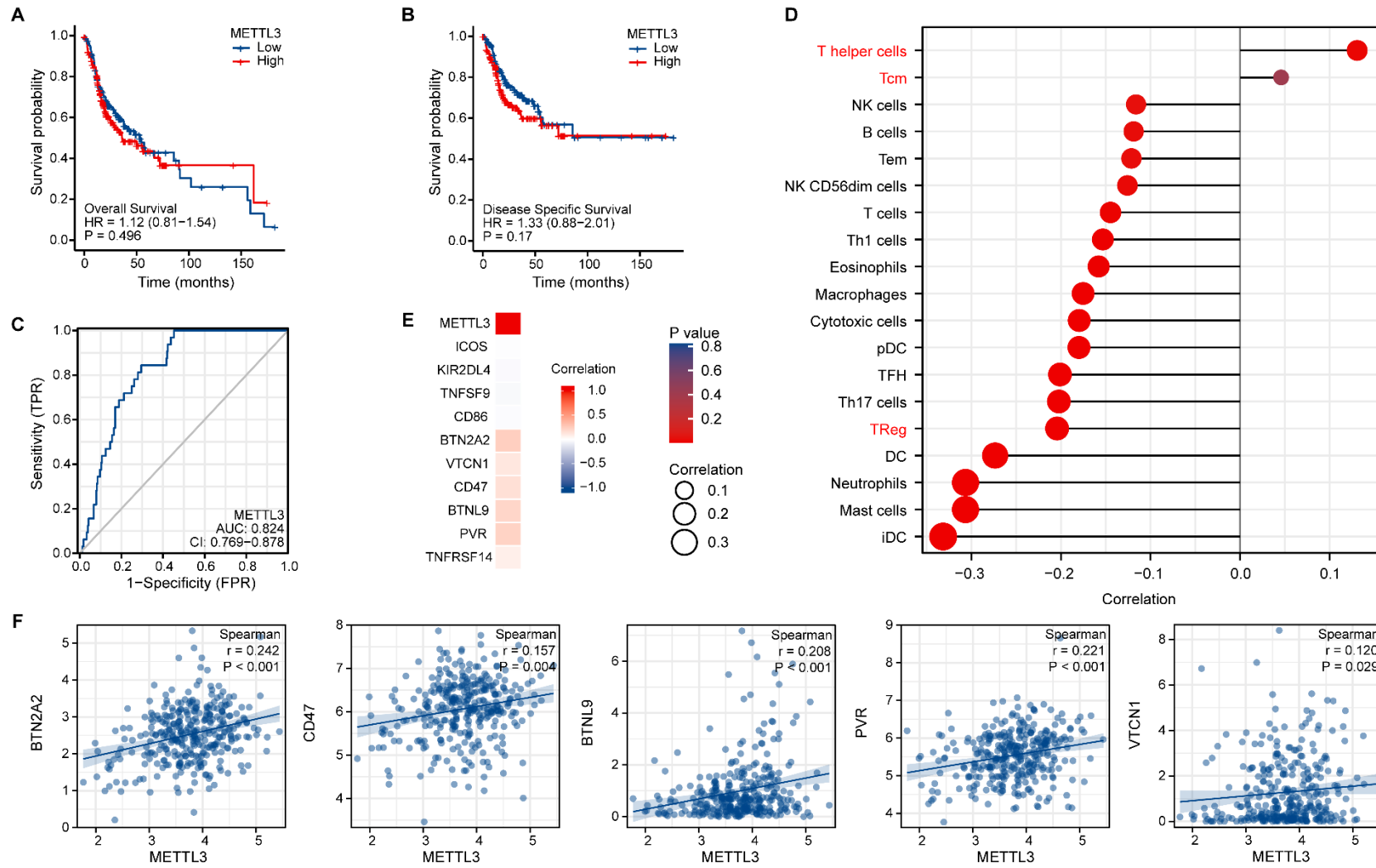
**Figure S8**



**Figure S9**



**Figure S10**



**Supplementary Table 1: Sequence of primers used in real-time PCR.**

Primer	Sequence (5'to3')
TNFSF9-F	GGCTGGAGTCTACTATGTCTTCT
TNFSF9-R	ACCTCGGTGAAGGGAGTCC
BTN2A2-F	GGGCCAGCTAATCCCATCC
BTN2A2-R	GGTGATTCTTCCCCGGTACTC
CD274-F	GCTGCACTAATTGTCTATTGGGA
CD274-R	AATTCGCTTGTAGTCGGCACC
CD47-F	TCCGGTGGTATGGATGAGAAA
CD47-R	ACCAAGGCCAGTAGCATTCTT
PVR-F	GGACGGCAAGAATGTGACCT
PVR-R	GGTCGTGCTCCAATTATAGCCT
METTL3-F	AGATGGGGTAGAAAGCCTCCT
METTL3-R	TGGTCAGCATAGGTTACAAGAGT
GAPDH-F	ACAAC TTTGGTATCGTGGAAGG
GAPDH-R	GCCATCACGCCACAGTTTC
KIR2DL4-F	TCCCTGTCCCTGAGCTCTAC
KIR2DL4-R	AAGGTCACGTTCTCTCCTGC
CD86-F	AGGCAACAATGAGCAGACCA
CD86-R	ACTATGGCTTGTTGGGTGGG
VTCN1-F	CTGCCTCTCAGCCCTTACCT
VTCN1-R	GCCTTCTGCTTTTGGCTTCTT