- 1 Figure S1: Prognostic value of the lysine methytransferase family in patients with BCa.
- 2 A-M: The overall survival and disease-free survival outcomes of 13 lysine methytransferase in
- 3 TCGA-BLCA data (SETDB1, METTL21A, SETD1A, SETD8, NSD1, EHMT2, SMYD3, EZH2,
- 4 METTL22, SMYD2, SETD6, CAMKMT, SETD7).
- 5

### Figure S2: Correlation between lysine methytransferase family and immunotherapy response of patients with BCa.

- A-L: Correlations between 12 lysine methytransferase and immunotherapy response of patients
  with BCa in GSE173839 (SETDB1, METTL21A, SETD1A, NSD1, EHMT2, SMYD3, EZH2,
  METTL22, SMYD2, SETD6, CAMKMT, and SETD7).
- 11

#### 12 Figure S3: SETD7 was negatively correlated with the BCa immunescore of GSE69795.

A. Infiltration level of different immune cells in high- and low-SETD7 groups on the basis of
GSE69795 data. B. Correlation analysis of SETD7 and immunescore which was based on the
immune cell infiltration level of GSE69795 data. C. Expression of different immunomodulators in
high- and low-SETD7 groups on the basis of GSE69795 data. D. Expression of immune cells
effector genes in high and low SETD7 groups on the basis of GSE69795 data. E. Correlation
analysis between SETD7 and inhibitory immune checkpoints on the basis of GSE69795 data.

- 19
- 20 Figure S4: Associations between SETD7 and immune cells infiltration in TCGA BLCA.
- 21

22 Figure S5: The GO-GSEA and Hallmark-GSEA analyses of SETD7 in BCa.

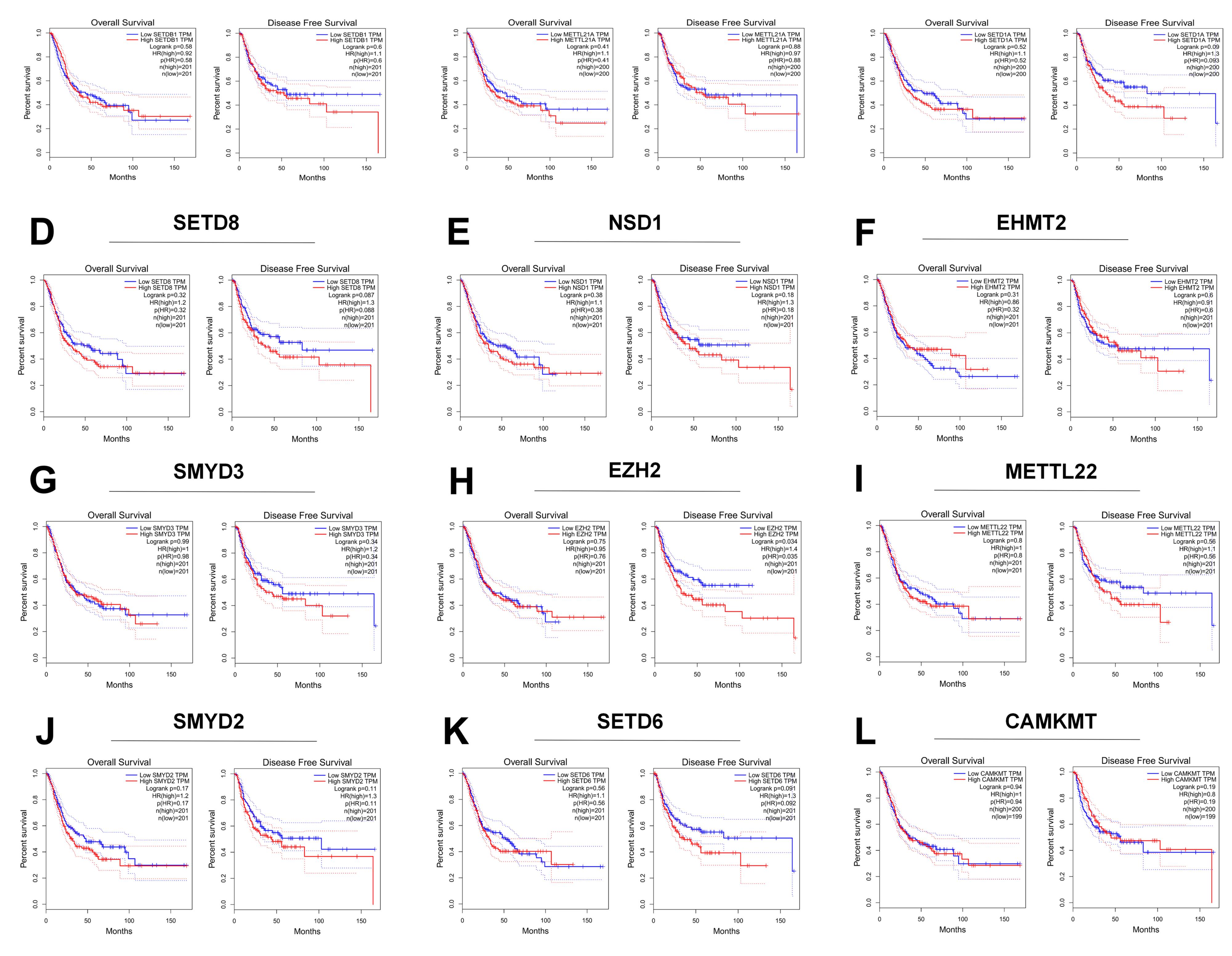
23

SETDB1

METTL21A

B

## SETD1A



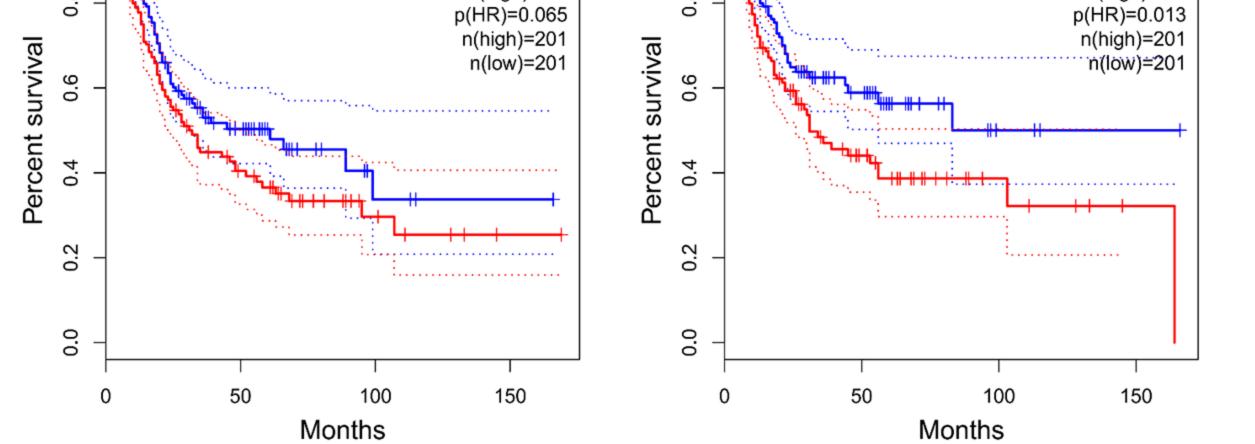
N SETD7 Overall Survival Disease Free Survival

 Of
 Low SETD7 TPM

 High SETD7 TPM

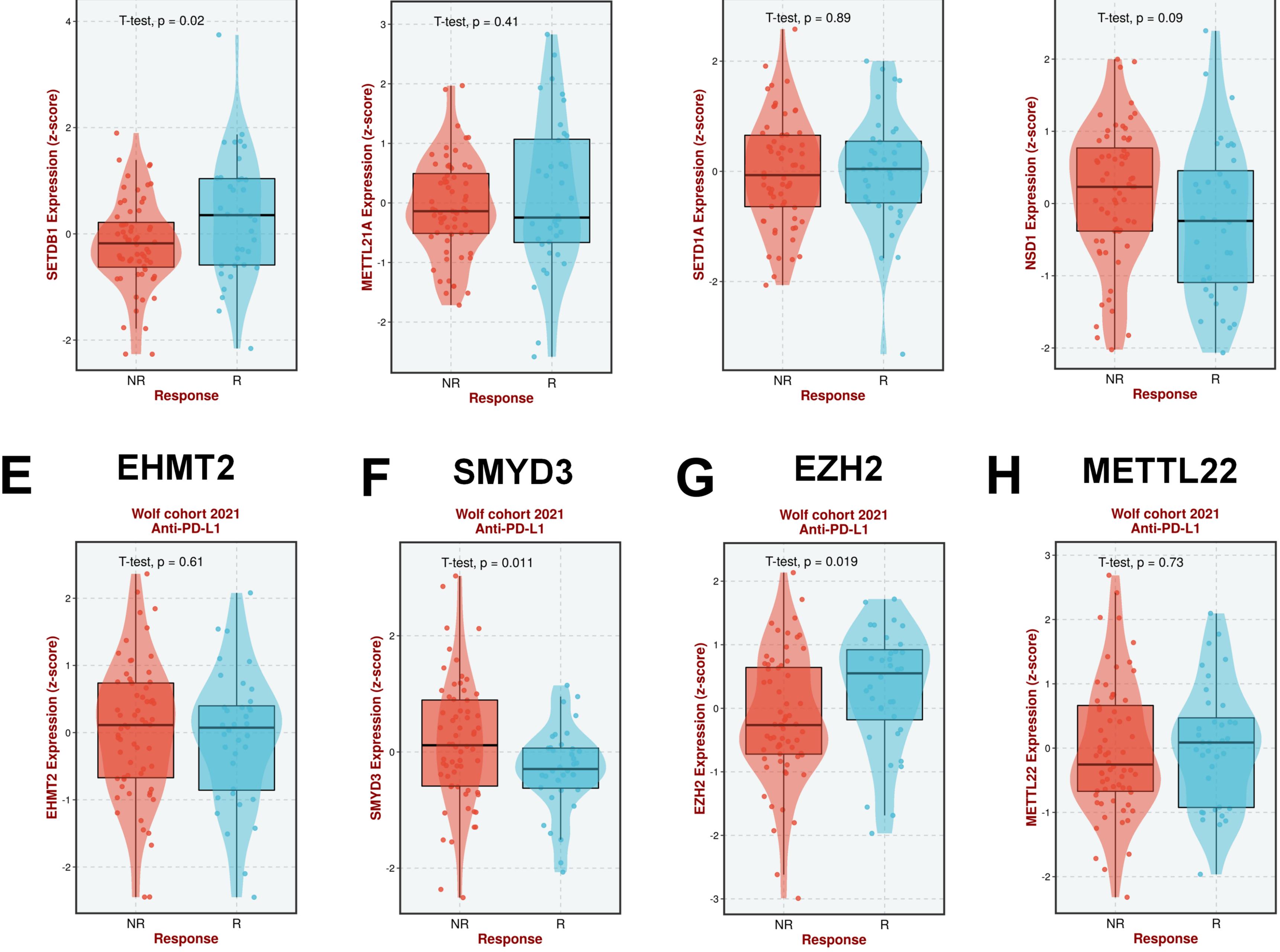
 Logrank p=0.064

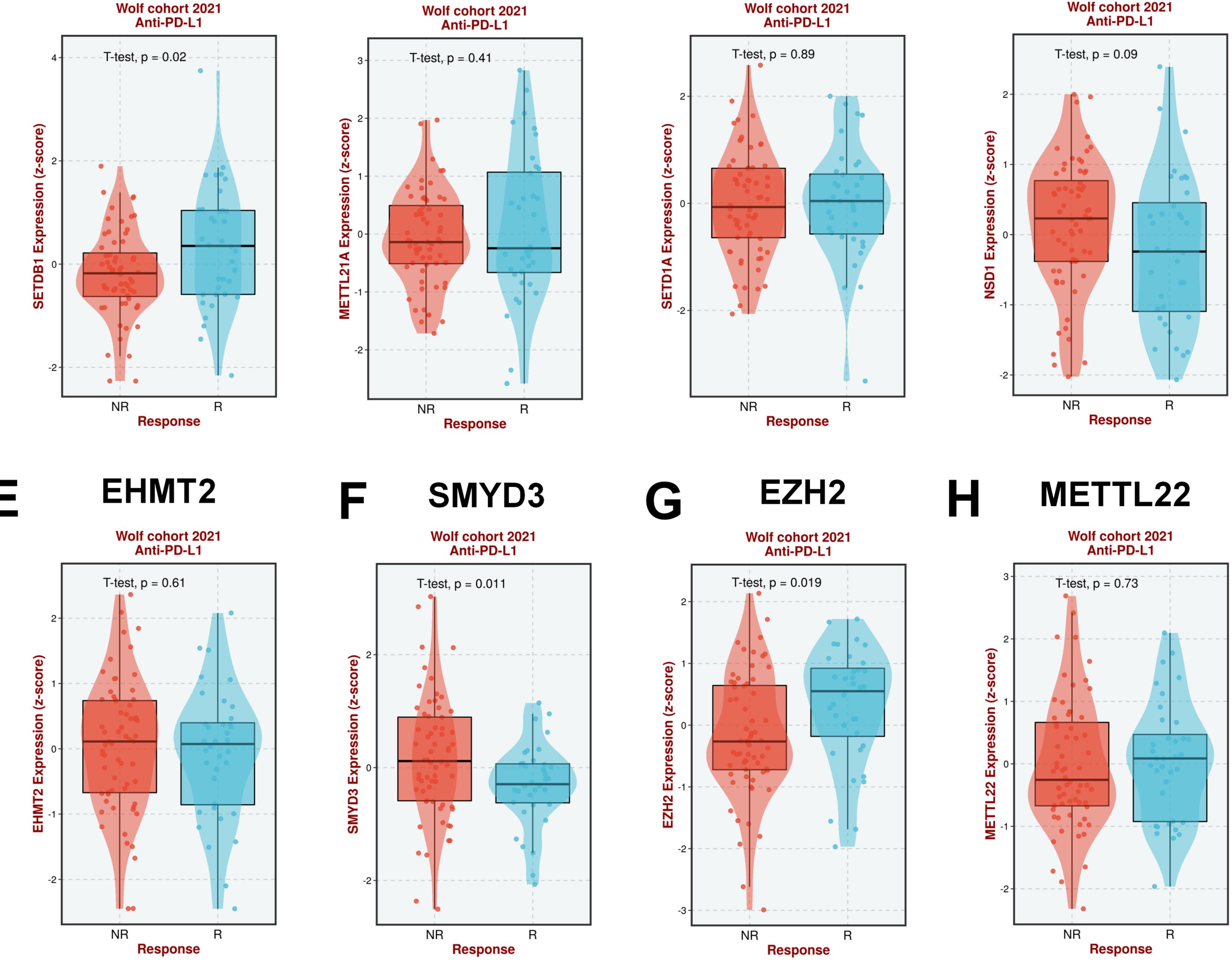
 HR(high)=1.3

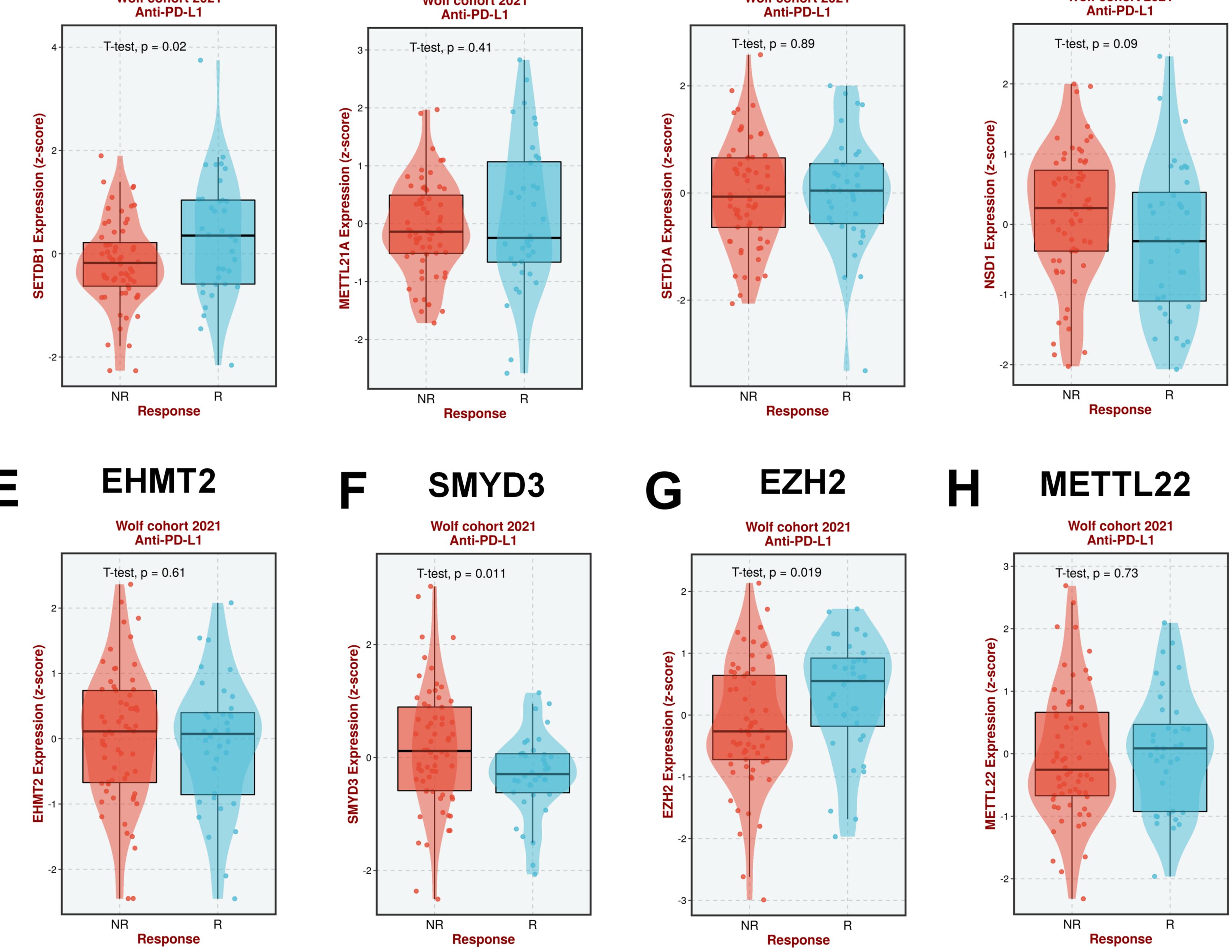


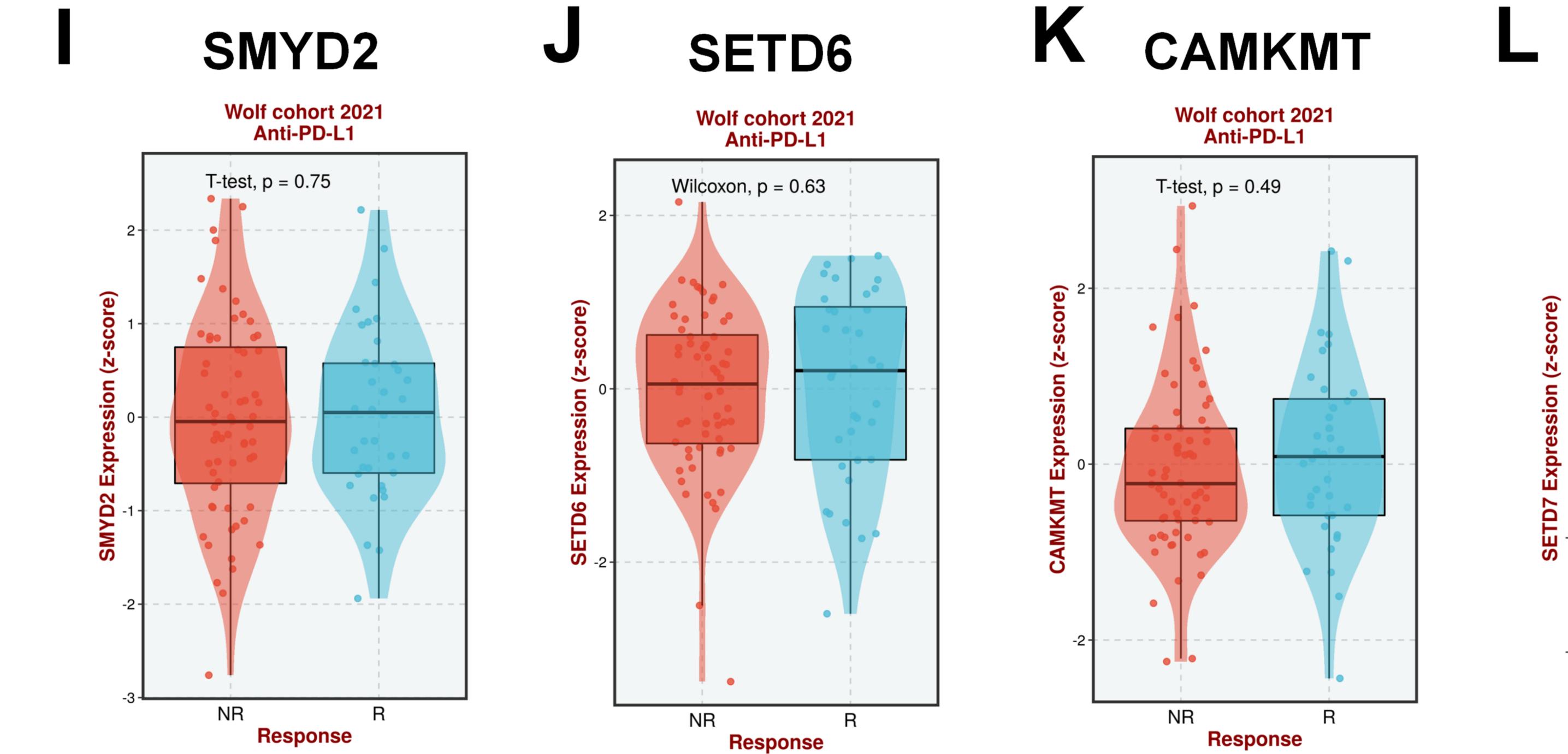
### С NSD1 SETD1A D METTL21A B SETDB1

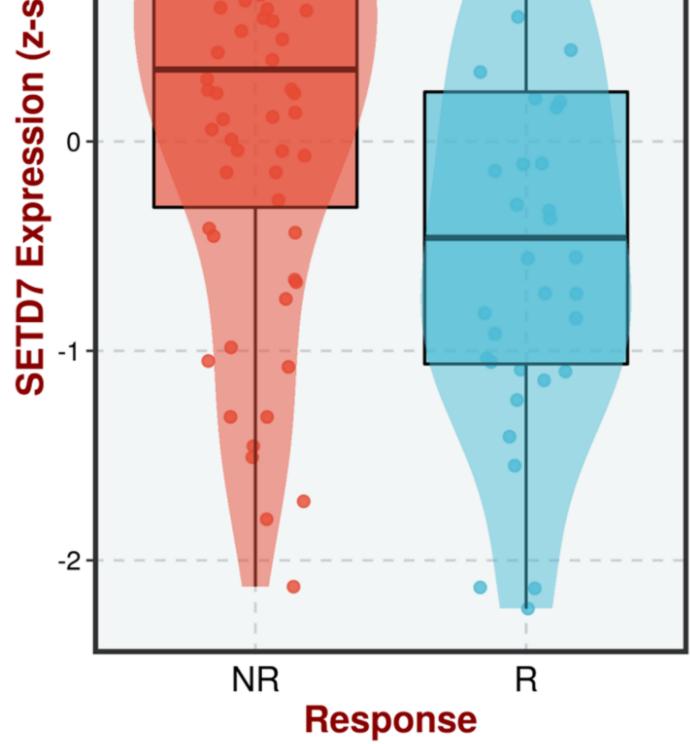
Wolf cohort 2021 Anti-PD-L1











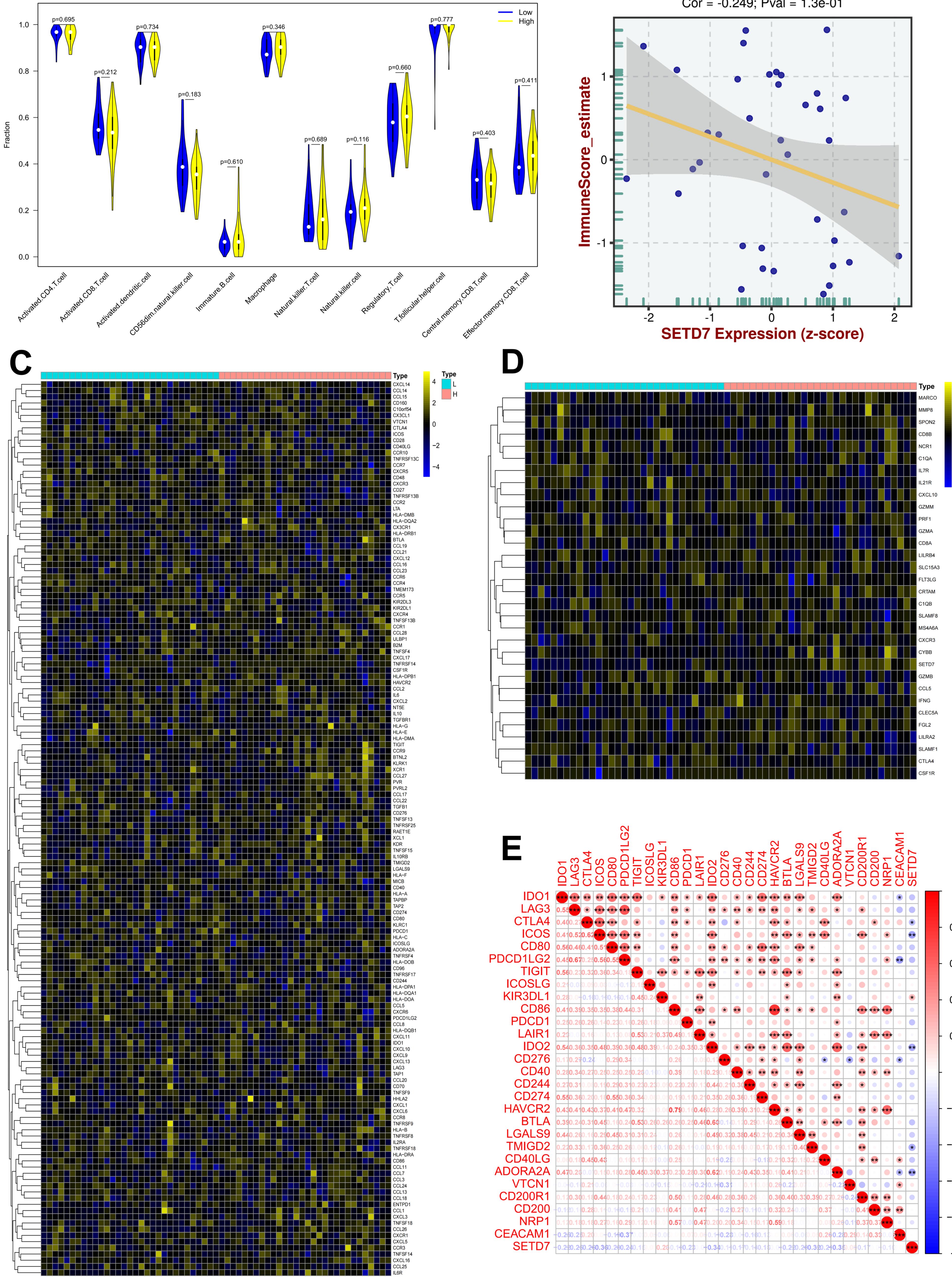
SETD7

Wolf cohort 2021

Anti-PD-L1

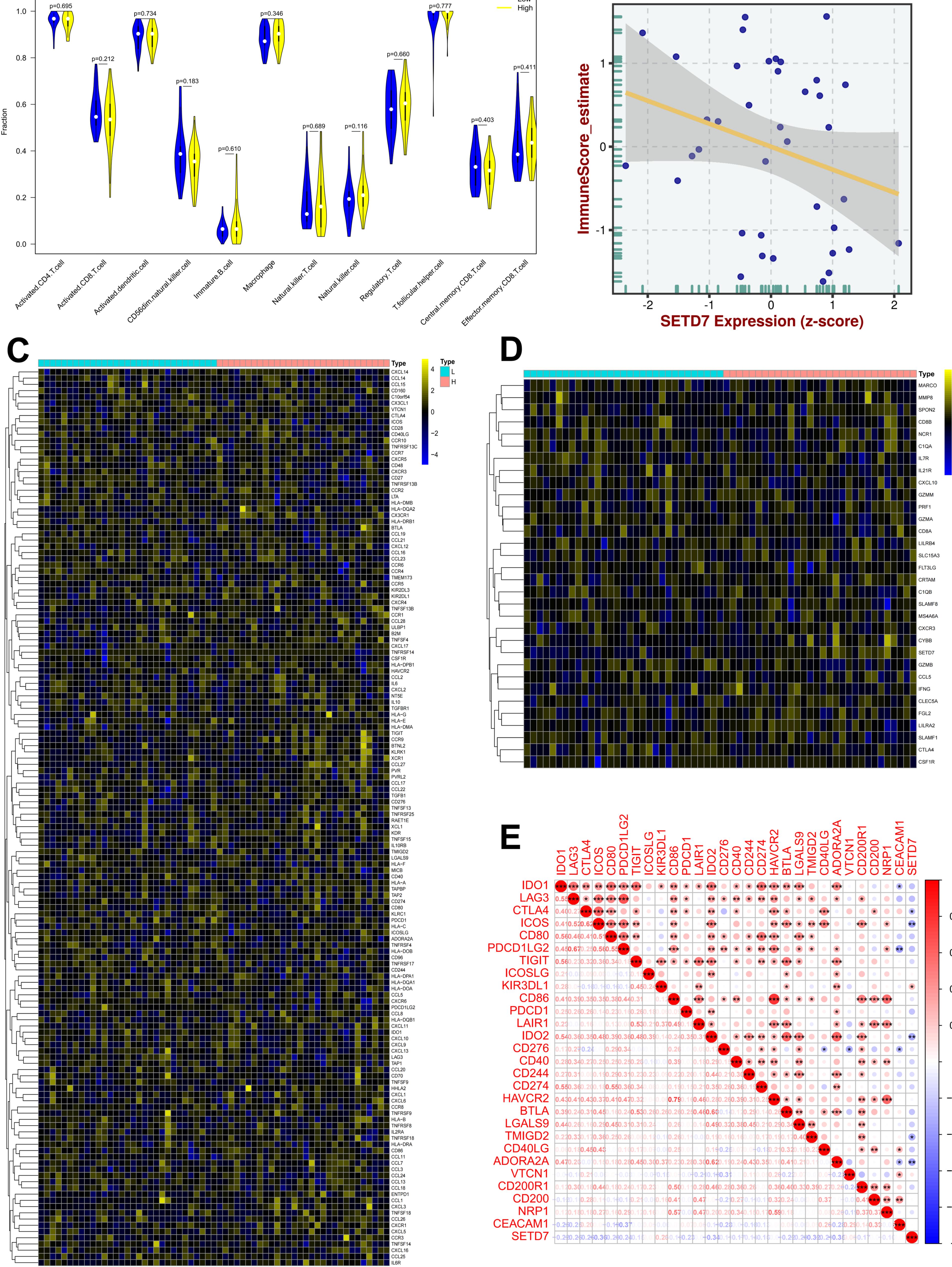
T-test, p = 0.0042

A



# **GSE69795**

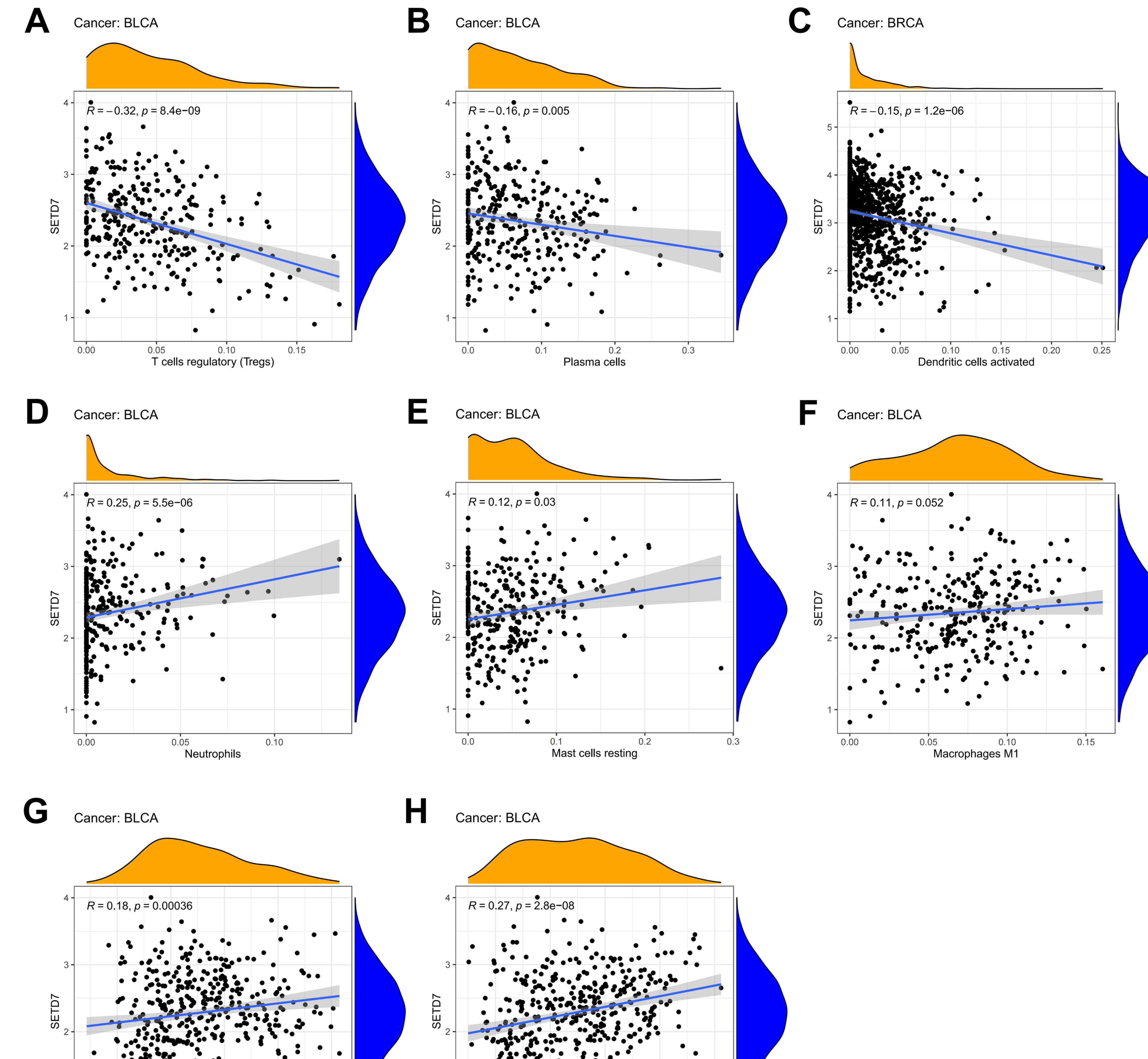
Cor = -0.249; Pval = 1.3e-01

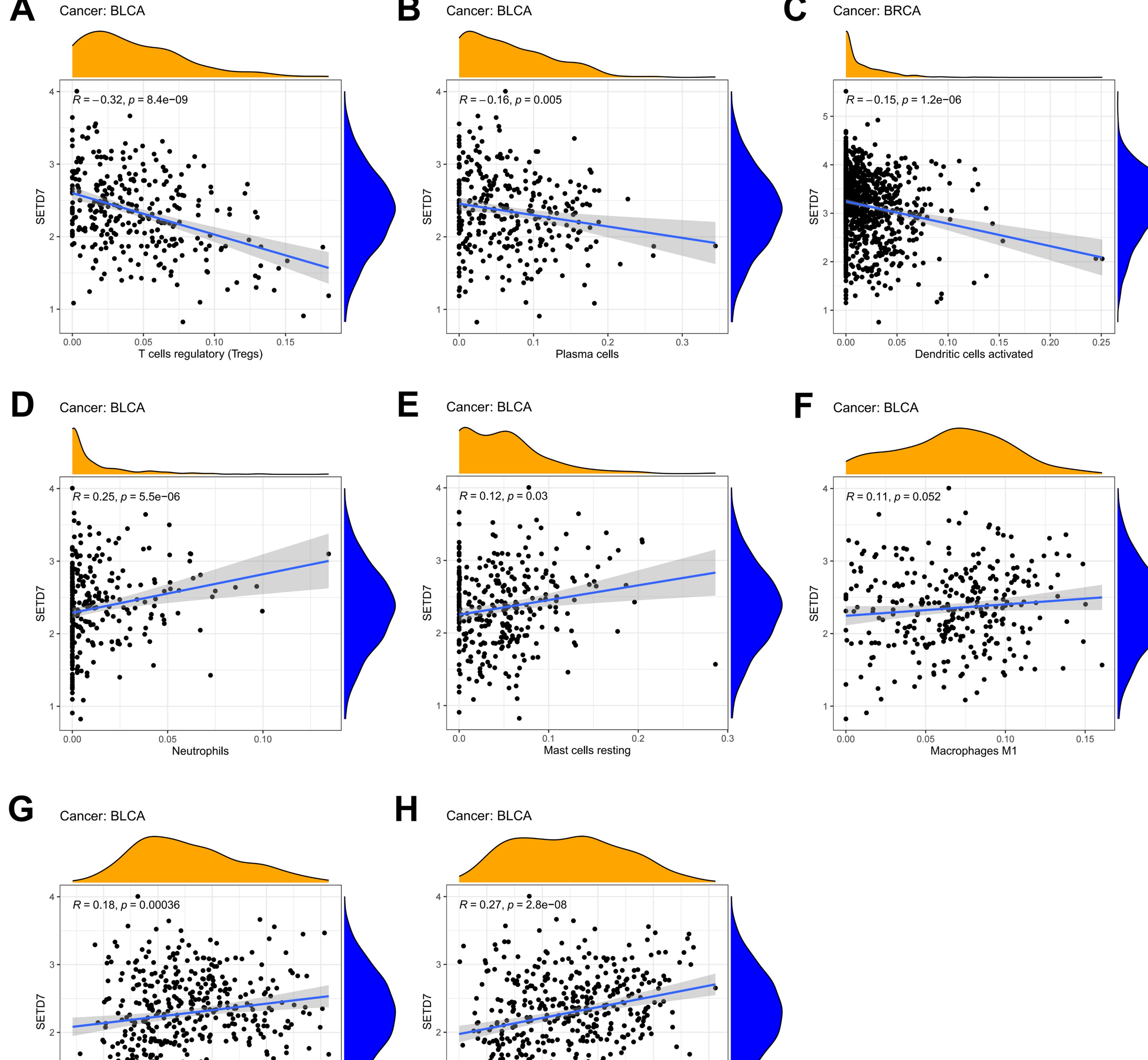


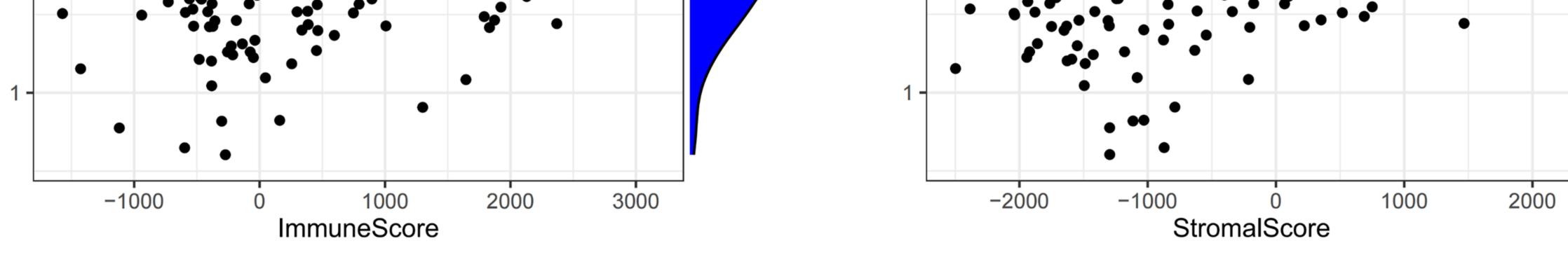
0.8

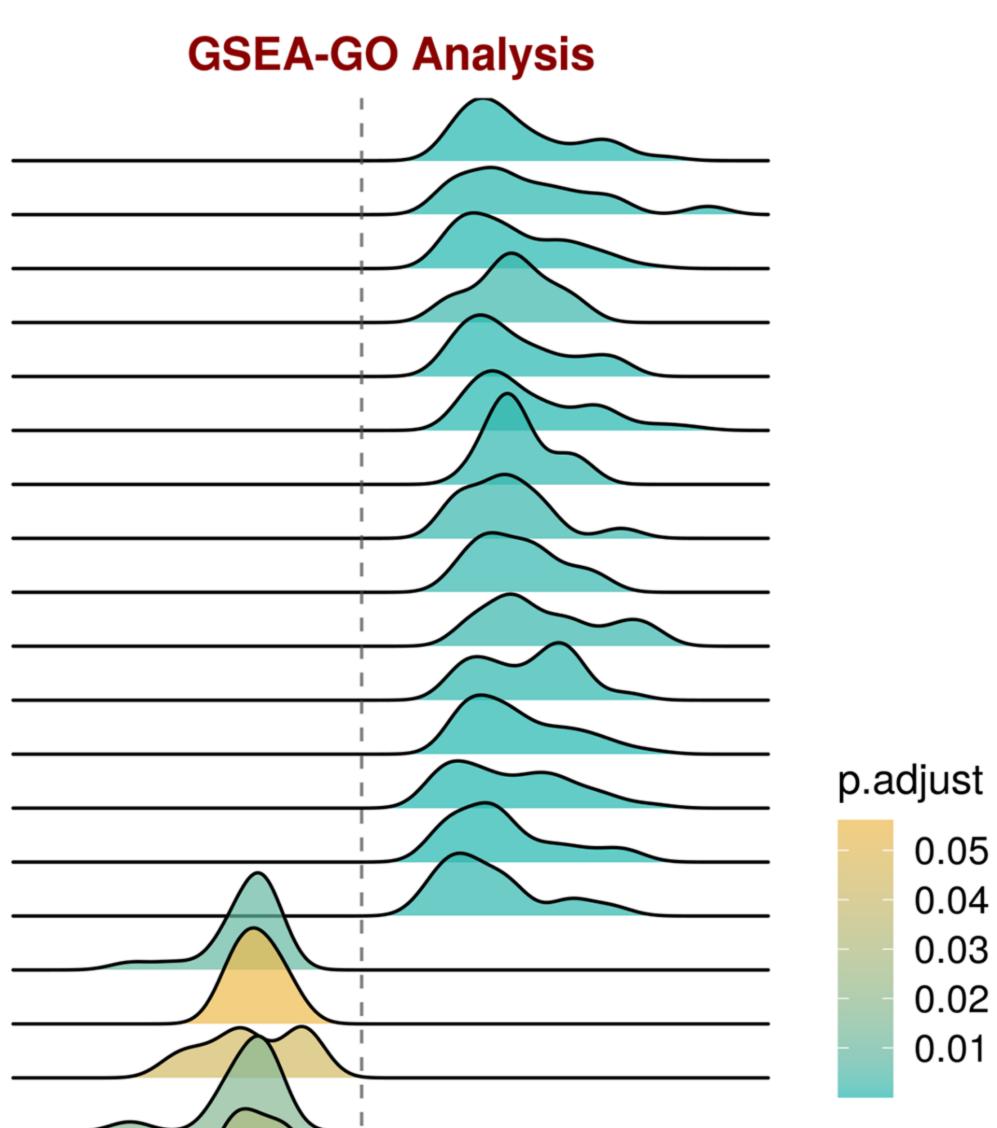
Туре

													-	_																
PDCD1LG2	0.45 <b>0.6</b>	70.25	0.56	0.55	***				***		•	**	**	*	*	**	***		*	*		*	•			*	**			0.6
TIGIT	0.560.2	30.32	0.36	0.34	0.18	***		***	*	*	***	***	•	*		**	*	***	*	•		***					•			0.0
ICOSLG	0.2 <del>1</del> 0.0	80.09	0.08	0.0	80.13	0.15	***					**	•			•	•	*			•	*	•		•		•	•		
KIR3DL1	<b>0.28</b> 0.0	<del>(</del> 0.1	30.1-6	0.16	<b>50.1</b> 4	0.45	0.24	***		•	**		•	•		•	•	*	0	•	•	**		•		•	•	*		0.4
CD86	0.410.3	90.35	0.35	0.38	0.44	0.31	0.01	0.12	***		***	•	*	**			***	*	*	*			•	***	***	***				
PDCD1	0.250.2	60.26	0.14	0.23	0.16	0.26	0.18	0.06	0.09	***		**		•					•	•	•	*	•	•	•	•	•			
LAIR1	0.290.0	0.16	0.03	0.13	80.0	0.53	0.21	0.37	0.49	0.18	***	*	•				***	***		•		*		*	***	***	•	•	F 1	0.2
IDO2	<b>0.5</b> 40.3	60.35	0.48	0.39	0.36	0.48	0.39	0.14	0.24	0.3	0.3 <sup>,</sup>	***		*	***	**	*	***	***			***		***	•			**		
CD276	0.17 <mark>0.2</mark>	70.24	0.00	0.29	0.34	0.0	10.0	0.02	0.26	0.0	0.0	9 <mark>0.1</mark> 7	***			*	*		*		*		*	*			*			
CD40	0.28 <mark>0.3</mark>	40.27	0.25	0.25	0.25	0.20	0.1	90.0	0.39	0.0	0.18	0.29	0.1	***	*	**	**	•	**		•		•	**	*	**	•		F	0
CD244	0.270.3	10.08	0.19	0.29	0.31	0.23	0.23	0.09	0.22	0.20	0.1	3 <b>0.4</b> 4	0.21	0.30	***		*	*	***	•	•	***	•	*						
CD274	<b>0.55</b> 0.3	60.20	0.18	0.55	0.36	0.34	0.08	0.05	0.19	0.1	<b>0.2</b> ′	10.3	0.20	0.36	0.19	***						**	•	•						
HAVCR2	0.430.4	10.43	0.37	0.41	0.47	0.32	0.04	0.06	0.79	0.10	0.4	60.28	0.26	0.39	0.31	0.2	***	*	*					**	*	***		•	F -	-0.2
BTLA	<b>0.39</b> 0.2	40.31	0.45	0.16	0.24	0.53	0.26	0.26	0.26	0.2	0.4	0.60	0.1	0.12	0.29	0.14	0.26	***	**		*	***		**			•			
LGALS9	<b>0.44</b> 0.2	<b>6</b> 0.16	0.29	0.45	0.31	0.31	0.24	0.0	0.26	0.0	0.14	0.49	0.32	0.38	0.45	0.21	0.29	0.34	***	**			•	**	•		•			
TMIGD2	0.22 <mark>0.3</mark>	<b>3</b> 0.17	0.36	0.25	0.26	0.06	0.12	0.1	0.26	0.14	0.0	0.19	0.16	0.16	0.07	0.17	0.19	0.17	0.40	***			•	**	•	•	•	*	F -	-0.4
CD40LG	0.06 <mark>0.1</mark>	80.45	0.43	0.0	0.10	0.17	0.07	0.0	0.25	0.0	0.0	0.1	0.2	D.07	0.0	0.1	0.21	0.32	0.15	0.23	***	•	•	*	**	•	*			
ADORA2A	<b>0.47</b> 0.2	<mark>6</mark> 0.0'	0.15	0.18	0.28	0.45	0.30	0.37	0.23	0.28	0.3	0.62	0.19	0.24	0.43	0.3	0.16	<b>0.4</b> 1	0.21	0.11	0.0						*	**		• •
VTCN1	0.0-0.1	0.21	0.0	9.04	0.0	30.0-	0.0	<b>0.1</b>	ສ. <b>ດ</b> ຄ	0.0	0.2	10.1	80.3	0.0	0.11	0.08	0.20	0.2	0.07	0.0	0.07	0.2			•		*	•	F -	-0.6
CD200R1	0.12 <mark>0.3</mark>	<b>0</b> 0.18	0.44	0.18	0.24	0.17	0.23	0.03	0.50	0.1	0.2	80.46	0.28	0.36	0.26	0.03	0.36	0.40	0.33	0.39	0.27	0.26	0.2		**	**				
CD200	- <b>0.1<del>/</del>20</b> .1	0.28	0.14	0.1	0.14	0.21	0.0	0.16	0.41	0.0	0.4	0.0-	0.2	0.27	<sup>•</sup> 0.1-	10.1	0.32	0.24	0.0	D.03	0.37	0.0	0.0	<b>0.4</b> 1	***	**	**	-		0.0
NRP1	0.12 <mark>0.1</mark>	80.18	0.27	0.16	0.29	0.12	0.16	0.03	0.57	0.0	0.4	70.20	0.20	0.34	0.15	0.17	0.59	0.18	0.00	0.01	90.0	0.26	0.1	0.37	0.37	***	•		F -	-0.8
CEACAM1	0.250.2	<b>D.20</b>	0.02	0.1 <del>(</del>	0.3	0.0	0.05	0.0	0.00	0.0	0.0	0.1-	0.2	<b>8</b> 0.0	0.1	30.1	0.00	0.08	0.0	0.08	0.20	0.2	0.29	0.14	0.39	0.0	***			
SETD7	0.220.2	50.2	60.36	<b>0.2</b> 6	0.2	0.1	0.03	0.20	0.1	0.2	<b>3</b> 0.0	0.3	0.1	10.1	70.1 <del>.</del>	0.1	<b>50.0</b> -	0.2	20.24	<b>0.3</b> :	20.24	0.3	0.08	0.1	70.0	0.1	0.01	***		_1
																													 	1









Cotranslational protein targeting to membrane Positive regulation of protein modification by small protein conjugation or removal Nuclear pore organization Establishment of protein localization to endoplasmic reticulum Endoplasmic reticulum to golgi vesicle mediated transport

Nuclear pore complex assembly

Protein localization to condensed chromosome

Protein localization to endoplasmic reticulum

Positive regulation of telomerase rna localization to cajal body

Endoplasmic reticulum tubular network organization

Attachment of spindle microtubules to kinetochore

Regulation of protein modification by small protein conjugation or removal

Regulation of macroautophagy

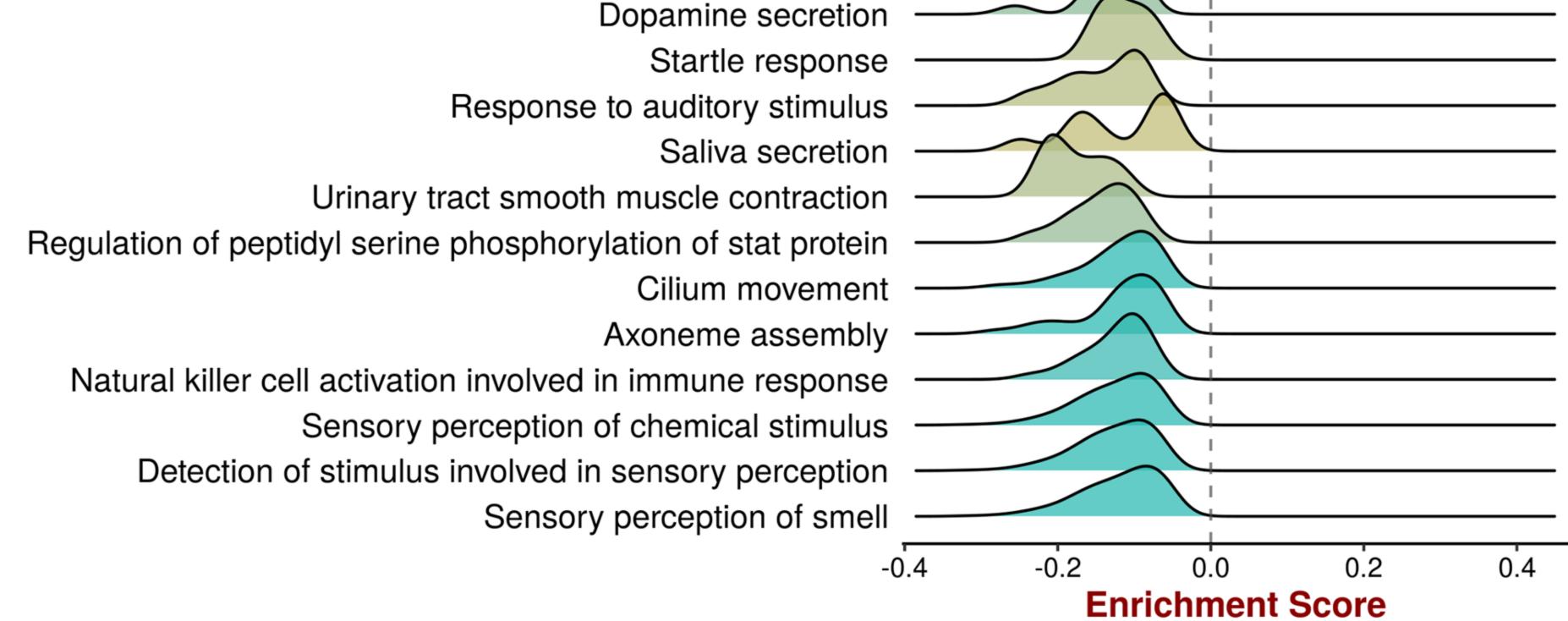
Iron ion homeostasis

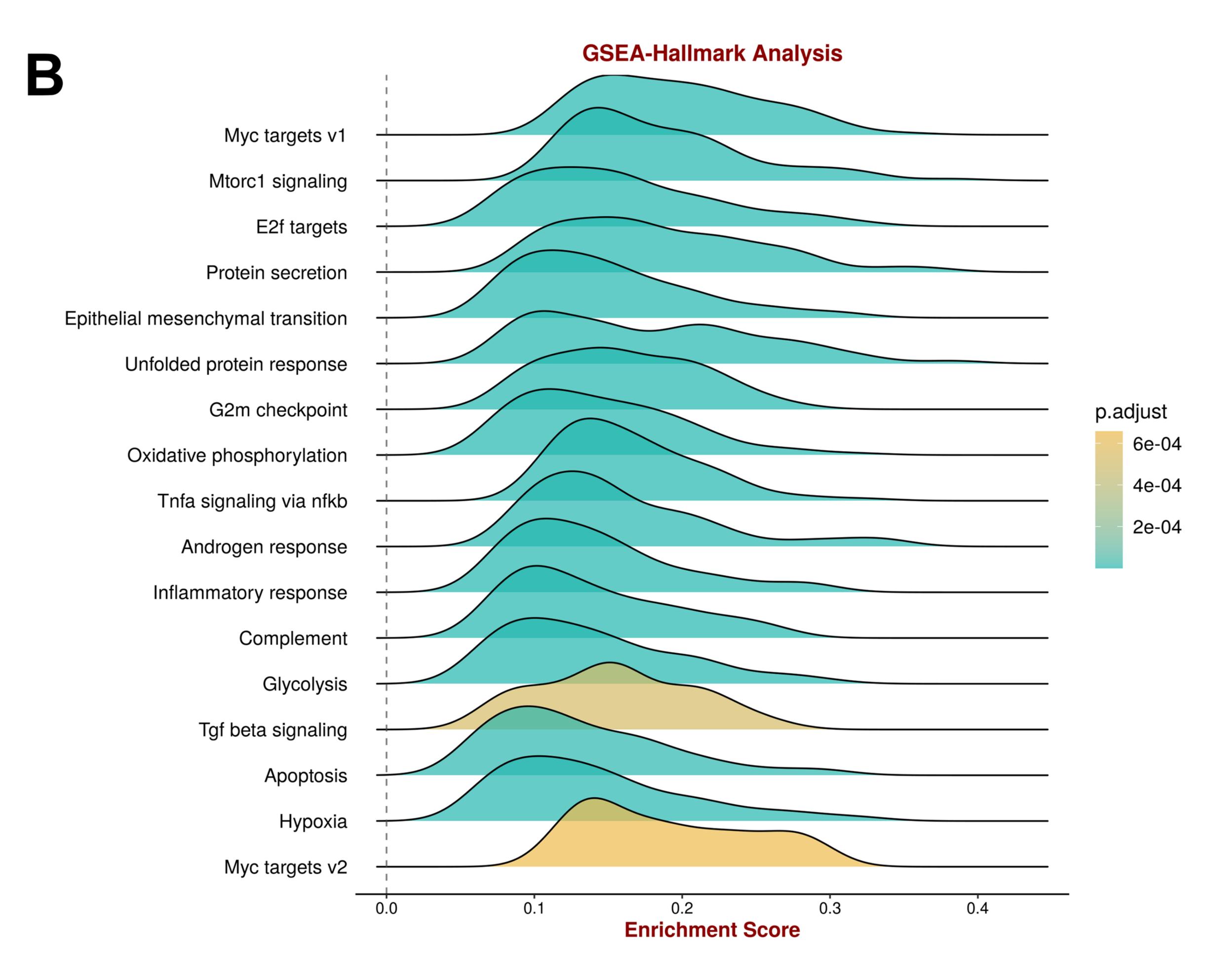
De novo protein folding

Catecholamine secretion

Prepulse inhibition

Peristalsis





Primers		Sequence (5'-3')
SETD7	Forward	5'-ATGGATAGCGACGACGAGATG-3'
	Reverse	5'-GCAGAACCCGTGCGGTAAT-3'
PD-L1	Forward	5'-TGGCATTTGCTGAACGCATTT-3'
	Reverse	5'-TGCAGCCAGGTCTAATTGTTTT-3'
β-Actin	Forward	5'-CTCCATCCTGGCCTCGCTGT-3'
	Reverse	5'-GCTGTCACCTTCACCGTTCC-3'

Table S4: All PCR primers used in this research

ID	logFC	AveExpression	P.Value			
CD27	-1.05843677	10.68337821	0.000476409			
KDR	0.921726243	10.94967268	0.001037254			
CCL27	1.076677996	6.888451478	0.003797654			
CCR9	0.371974514	5.96194796	0.005139314			
CXCL17	0.922135828	13.56727185	0.005310415			
TNFRSF17	-1.113525306	7.600444778	0.005756879			
TNFRSF13B	-0.837040918	11.36619321	0.009039589			
CX3CR1	0.861538602	8.406087679	0.010659964			
KLRK1	0.461059444	7.095738245	0.015614535			
CCR6	-0.357586301	12.50209037	0.026900344			
HHLA2	0.283602898	5.447229856	0.033298687			
CXCR6	-0.66946613	10.52301643	0.047939565			
CCR2	0.498545176	7.366932452	0.049446249			

Table S5: Differentially expressed chemokines, chemokine receptors, MHCmolecules, and immunostimulators in high and low SETD7 groups of GSE69795.

Table S6: Differentially expressed immune cell (CD8<sup>+</sup>T cell, NK cell, Macrophage, Th1 cell, and DC cell) related effector genes in high and low SETD7 groups of GSE69795.

ID	logFC	AveExpression	P. Value
SETD7	1.090535255	11.05232836	9.542E-06
GZMB	-0. 468495417	12.54022642	0.019992446
GZMA	-0. 481960831	12.19780344	0.024910009
SLAMF1	-0.701155072	8.632630496	0.03135724