

Supplementary documentation

Supplementary Tables

Table S1. Correlations between *FCGBP* alterations and top altered genes in HNSC patients ($n = 522$)

A Gene Symbol	B Gene Symbol	Neither	A Not B	B Not A	Both	Log2 (OR)	<i>q</i> -Value	Tendency
<i>TP53</i>	<i>CDKN2A</i>	112	139	44	214	1.970	< 0.001	Co-occurrence
<i>CDKN2A</i>	<i>FAT1</i>	201	165	50	93	1.180	< 0.001	Co-occurrence
<i>TP53</i>	<i>FAT1</i>	126	240	30	113	0.984	0.009	Co-occurrence
<i>TTN</i>	<i>SI</i>	253	167	39	50	0.958	0.012	Co-occurrence
<i>FCGBP</i>	<i>FAT1</i>	354	12	129	14	1.679	0.012	Co-occurrence
<i>FCGBP</i>	<i>SI</i>	404	16	79	10	1.676	0.019	Co-occurrence
<i>TP53</i>	<i>TTN</i>	102	190	54	163	0.696	0.020	Co-occurrence
<i>FCGBP</i>	<i>TP53</i>	153	3	330	23	1.830	0.037	Co-occurrence

HNSC: head-neck squamous cell carcinoma; ***TP53*:** tumor protein p53; ***CDKN2A*:** cyclin-dependent kinase inhibitor; ***TTN*:** titin; ***SI*:** sucrose-isomaltase; ***FCGBP*:** Fc gamma binding protein; **OR:** Odds Ratio

Table S2. Intersection analysis of interacted proteins with *FCGBP* and *FCGBP*-associated co-expressed genes

Gene Symbol	Combined Score	¹ <i>p</i> -Value (co-Expressed Genes)	² mRNA Correlation	<i>p</i> -Value (mRNA Correlation)
<i>TFF3</i>	0.983	8.27E-17	0.357	3.02E-16
<i>CLCA1</i>	0.789	*	-0.003	*
<i>CDHR5</i>	0.731	*	0.069	*
<i>CHURC1</i>	0.689	*	0.087	*
<i>NPTX2</i>	0.654	*	0.057	*
<i>PCDH17</i>	0.629	*	0.112	1.32E-02
<i>NAALADL1</i>	0.593	6.29E-08	0.304	6.01E-12
<i>ZG16</i>	0.583	4.72E-03	-0.144	1.40E-03
<i>C1QC</i>	0.574	5.93E-03	0.178	7.40E-05
<i>NPAS4</i>	0.555	*	0.13	3.74E-03

¹***p* value in co-expressed genes:** *p* value of mRNA correlation between *FCGBP* and *FCGBP*-associated co-expressed genes by LinkedOmics; ²**mRNA correlation:** R value of Spearman's correlation by TIMER2.0.

**p* > 0.05

Supplementary Figures

Figure S1.

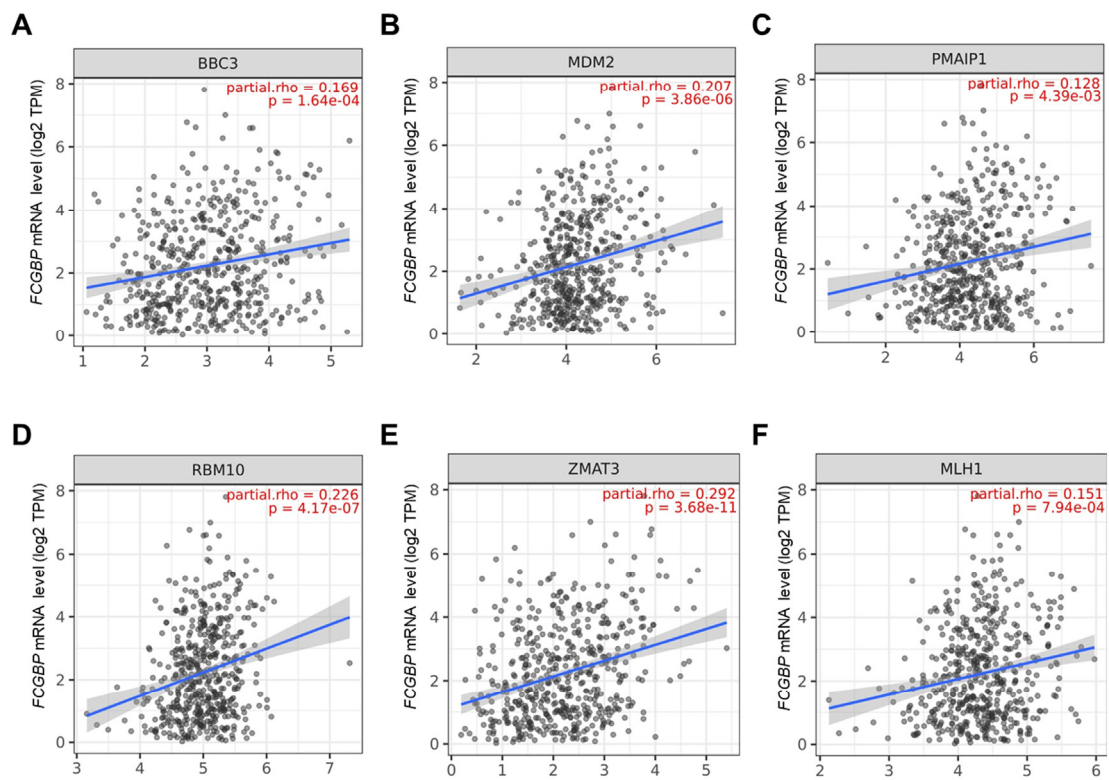


Figure S1. The correlations between *FCGBP* and the target genes of *TP53*.

(A–F) *FCGBP* is positively associated with *BBC3*, *MDM2*, *PMAIP1*, *RBM10*, *ZMAT3*, and *MLH1*.

Figure S2.

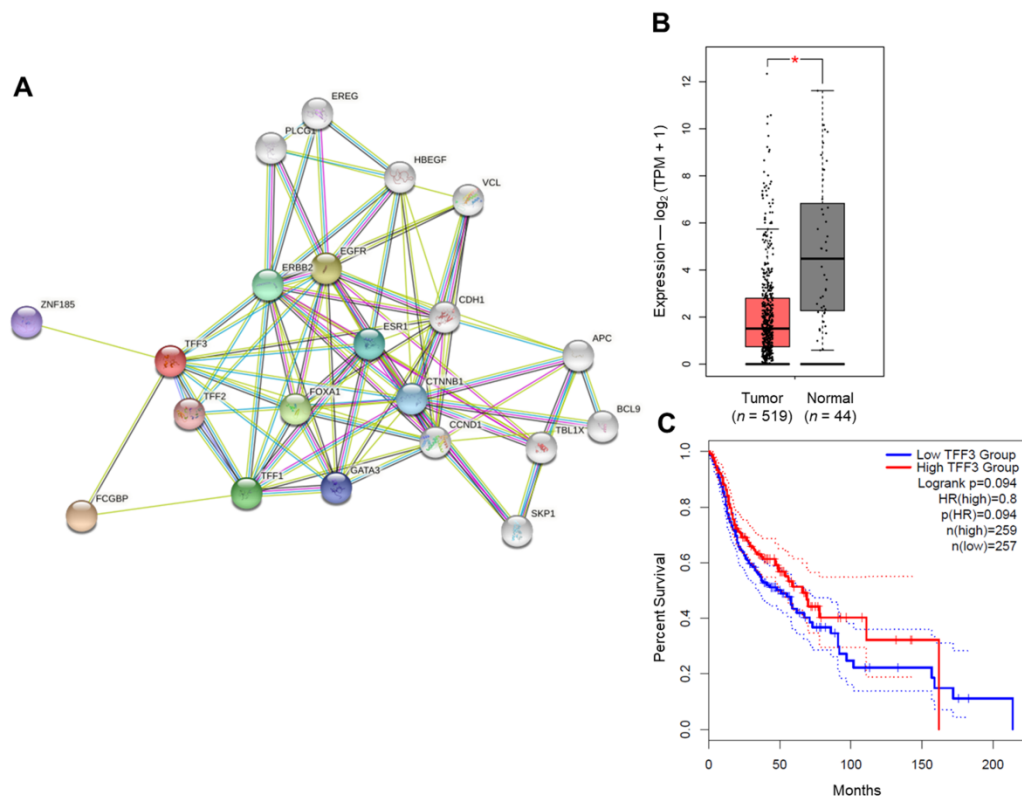


Figure S2. The interacting network, expression levels, and survival analysis of TFF3. (A) Close interaction between TFF3 and EGFR. (B) The expression level of *TFF3* in patients with HNSC (GEPIA2). (C) Kaplan-Meier curve showed overall survival of HNSC patients with high *TFF3* and low *TFF3* levels.

Figure S3.

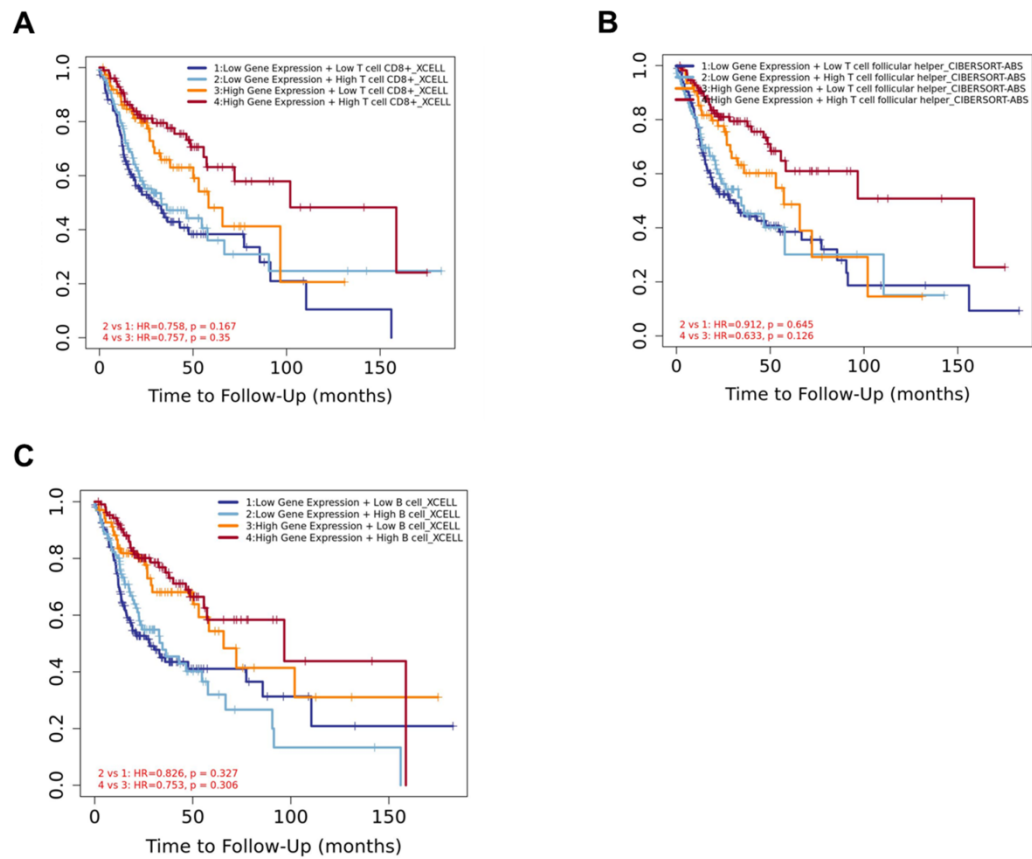


Figure S3. Survival analyses by high- and low- levels of *FCGBP* and infiltration rates of immune cells.

(A–C) The prognostic values of infiltration levels of CD8+, follicular helper T cells, and B cells by different *FCGBP* expressions.