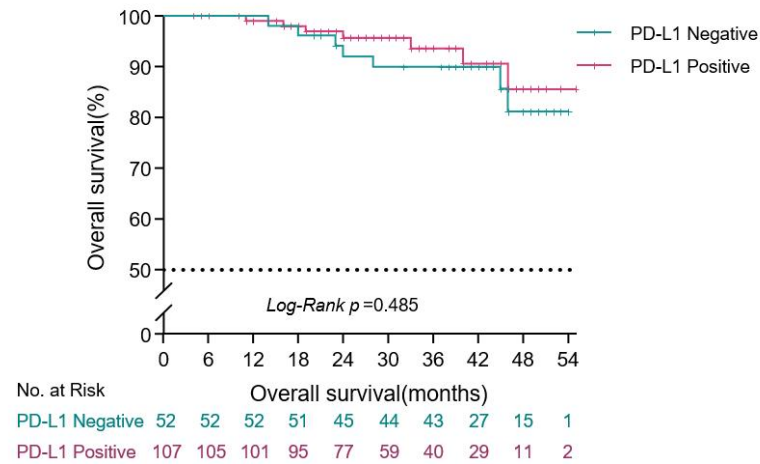
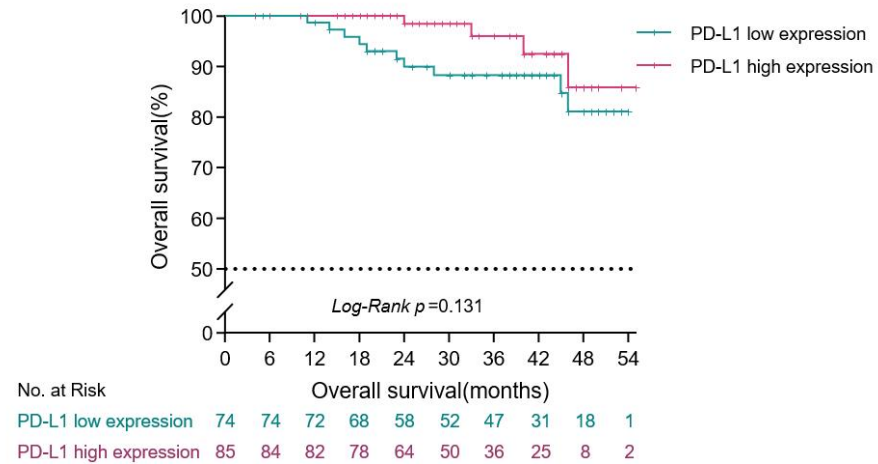


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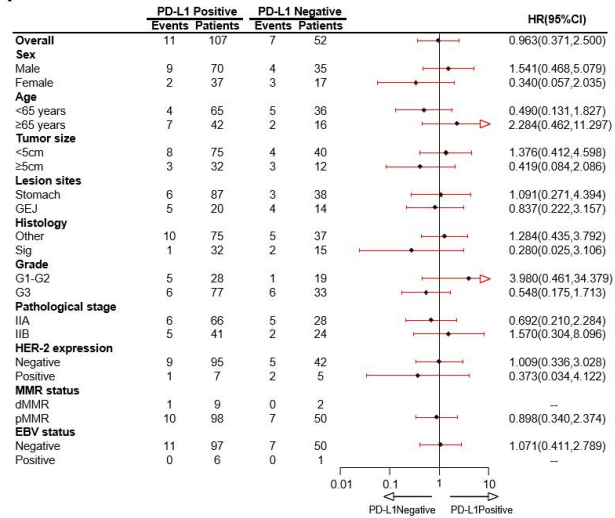


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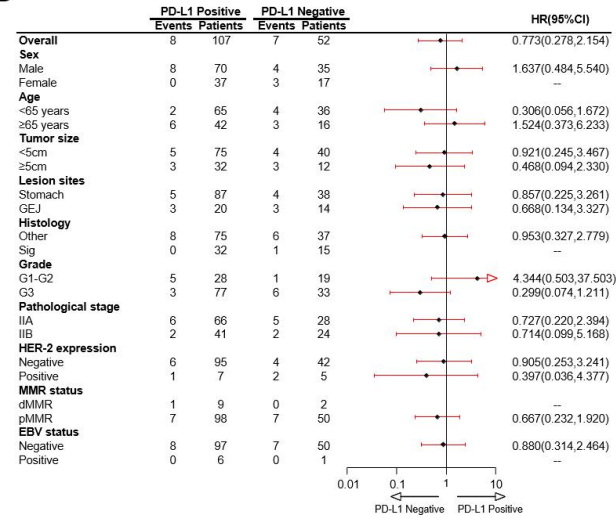


**Supplementary Figure 1 Sensitivity analyses of overall survival according to programmed death ligand-1 expression in patients with pathological stage II gastric or gastroesophageal junction cancer.** A: Kaplan-Meier curves showing overall survival (OS) between programmed death ligand-1 (PD-L1) positive and PD-L1-negative groups; B: Kaplan-Meier curves showing OS between high and low PD-L1 expression groups. No significant differences in OS were observed between the groups. PD-L1: Programmed death ligand-1.

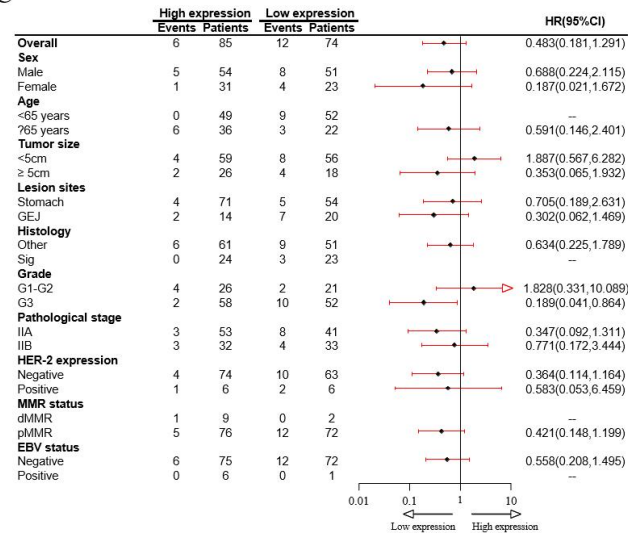
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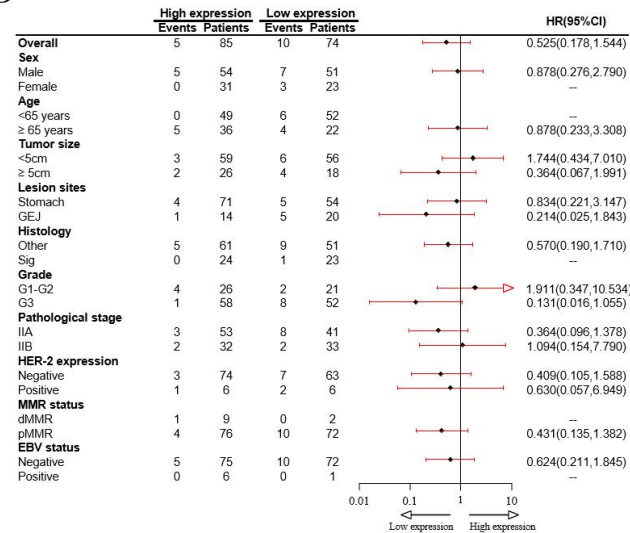
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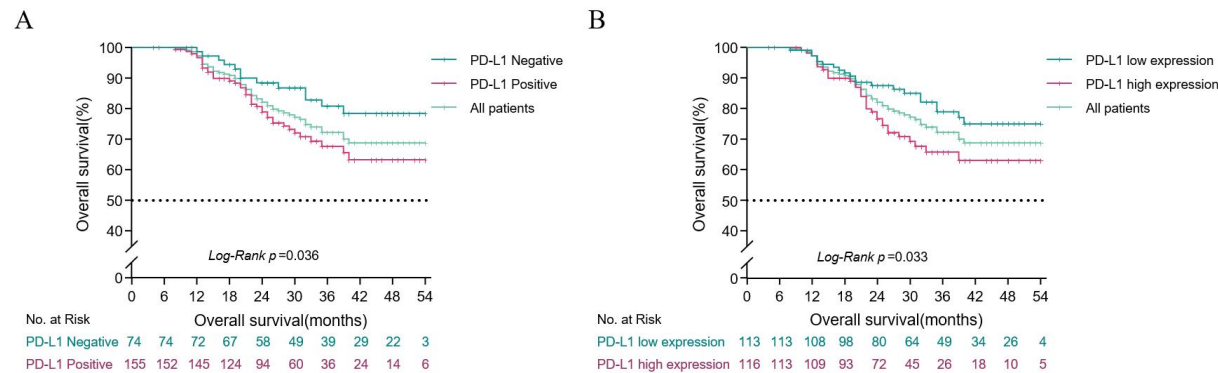
C



D

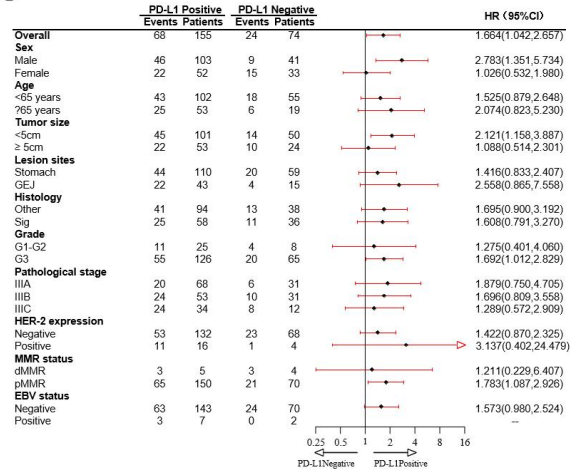


**Supplementary Figure 2 Forest plot of disease-free survival and overall survival of different programmed death ligand-1 expression in pathological stage II gastric or gastroesophageal junction cancer. A and B: Disease-free survival (DFS; A) and overall survival (OS; B) in the programmed death ligand-1 (PD-L1) positive and -negative groups; C and D: DFS (C) and OS (D) in the high and low PD-L1 expression groups. For subgroups with zero events in any patients, the HR was not calculated or shown. PD-L1: Programmed death ligand-1; GEJ: Gastroesophageal junction; MMR: Mismatch repair; EBV: Epstein-Barr virus.**

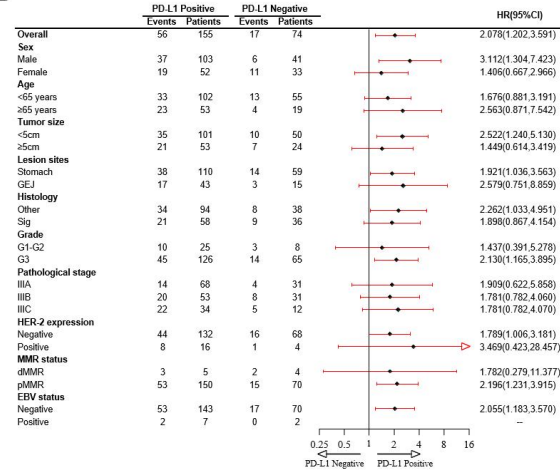


**Supplementary Figure 3 Sensitivity analyses of overall survival according to programmed death ligand-1 expression in patients with pathological stage III gastric or gastroesophageal junction cancer.** A: Kaplan-Meier curves showing overall survival (OS) between programmed death ligand-1 (PD-L1) positive and PD-L1 negative groups; B: Kaplan-Meier curves showing OS between high and low PD-L1 expression groups. Patients with PD-L1-positive or high expression had significantly shorter OS than those with PD-L1-negative or low expression. PD-L1: Programmed death ligand-1.

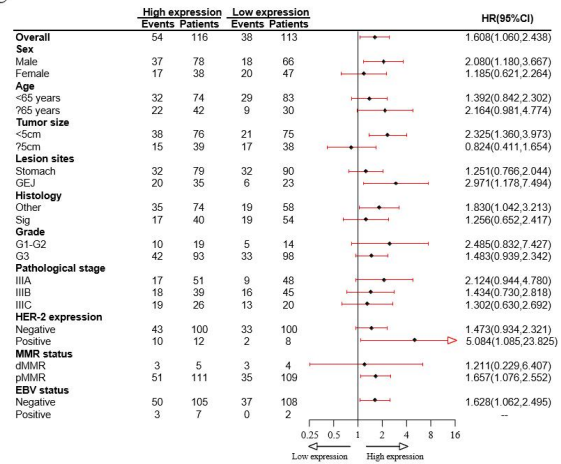
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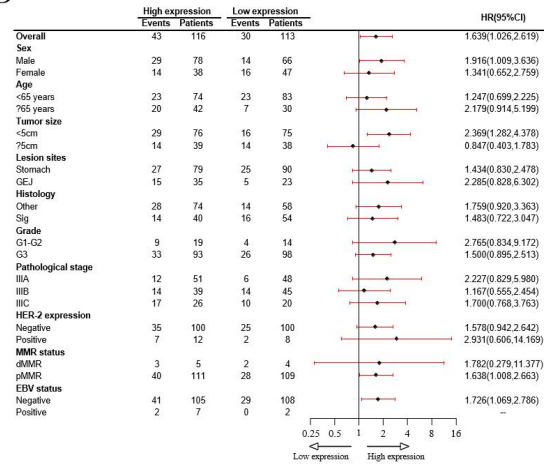
B



C



D



**Supplementary Figure 4 Forest plot of disease-free survival and overall survival of different programmed death ligand-1 expression in pathological stage III gastric or gastroesophageal junction cancer.** A and B disease-free survival (DFS; A) and overall survival (OS; B) in the programmed death ligand-1 (PD-L1) positive and -negative groups; C and D: DFS (C) and OS (D) in the high and low PD-L1 expression groups. For subgroups with zero events in any patients, the HR was not calculated or shown. PD-L1: Programmed death ligand-1; GEJ: Gastroesophageal junction; MMR: Mismatch repair; EBV: Epstein-Barr virus.

**Supplementary Table 1 Tumor microenvironment analysis of programmed death ligand-1 high expression in patients with locally advanced gastric or gastroesophageal junction cancer**

Cell type or other indicators	Marker	Area	Cell number, cells/mm <sup>2</sup> (positive rate, %)							
			Pathological stage II				Pathological stage III			
			Patient	Patient	Patient	Patient	Patient	Patient	Patient	Patient
			1	2	3	4	5	6	7	8
Total T cells	CD3+	Tumor	2414	836	349.35	426.86	-	-	156	2425
			(19.42)	(9.52)	(6.92)	(4.93)			(1.93)	(21.48)
		Stroma	2704	133	1310.70	193.33	-	-	1079	472
			(21.86)	(1.86)	(14.11)	(2.31)			(11.77)	(3.47)
Cytotoxic T cells	CD8+	Tumor	10	223	316.51	192.42	388	95	13	890
			(0.08)	(2.77)	(5.19)	(1.89)	(6.13)	(1.28)	(0.13)	(7.97)
		Stroma	44	16	780.68	137.63	68	1159	4	32
			(0.27)	(0.21)	(7.72)	(1.27)	(0.97)	(4.16)	(0.04)	(0.25)
PD-1 positive effector	PD-1+CD8+ T	Tumor	0	0	32.04	28.86	-	-	0	31
			(0.00)	(0.00)	(0.52)	(0.28)			(0.00)	(0.27)
		Stroma	4	0	148.48	4.37	-	-	0	1

cells			(0.02)	(0.00)	(1.47)	(0.04)			(0.00)	(0.01)
Helper T Cells	CD3+CD4+	Tumor	471	10	48.19	124.50			32	1271
			(3.79)	(0.12)	(0.95)	(1.44)	-	-	(0.39)	(11.26)
		Stroma	384	3	303.58	57.69			398	258
			(3.10)	(0.04)	(3.27)	(0.69)	-	-	(4.34)	(1.90)
Regulatory T cells	CD3+CD4+FoxP3+	Tumor	88	0	11.41	26.68			14	347
			(0.71)	(0.00)	(0.23)	(0.31)	-	-	(0.17)	(3.08)
		Stroma	13	0	49.79	18.71			39	40
			(0.11)	(0.00)	(0.54)	(0.22)	-	-	(0.42)	(0.29)
PD-L1 positive macrophages	PD-L1+CD68+	Tumor	4	2	107.64	3.21	16	9	0	246
			(0.03)	(0.02)	(1.76)	(0.03)	(0.26)	(0.12)	(0.00)	(2.20)
		Stroma	25	0	68.69	0.00	8	28	14	365
			(0.16)	(0.00)	(0.68)	(0.00)	(0.11)	(0.10)	(0.12)	(2.93)
M1 macrophages	CD68+CD163-	Tumor	232	54	130.07	93.00	265	57	136	181
			(1.78)	(0.67)	(2.13)	(0.91)	(4.19)	(0.76)	(1.33)	(1.62)
		Stroma	208	234	167.44	69.91	230	187	465	412
			(1.28)	(3.07)	(1.65)	(0.65)	(3.28)	(0.67)	(3.89)	(3.31)



M2 macrophages	CD68+CD163+	Tumor	18	26	192.22	19.24	142	3	7	198
			(0.14)	(0.32)	(3.15)	(0.19)	(2.24)	(0.04)	(0.06)	(1.77)
		Stroma	18	163	409.30	15.29	61	14	13	173
			(0.11)	(2.15)	(4.05)	(0.14)	(0.86)	(0.05)	(0.11)	(1.39)
Natural killer (NK) cells	CD56bright	Tumor	1	0	0.00	0.00	0	6	0	13
			(0.01)	(0.00)	(0.00)	(0.00)	(0.00)	(0.08)	(0.00)	(0.12)
		Stroma	4	0	0.00	0.00	0	28	0	33
			(0.03)	(0.00)	(0.00)	(0.00)	(0.00)	(0.10)	(0.00)	(0.25)
	CD56dim	Tumor	54	0	62.77	0.00	24	72	0	7
			(0.43)	(0.00)	(1.24)	(0.00)	(0.38)	(0.96)	(0.00)	(0.06)
B cells	CD20+	Stroma	194	0	201.18	0.00	8	354	23	22
			(1.57)	(0.00)	(2.17)	(0.00)	(0.11)	(1.27)	(0.25)	(0.17)
		Tumor	101	3	0.63	31.12	-	-	3	395
			(0.81)	(0.03)	(0.01)	(0.36)	-	-	(0.04)	(3.50)
		Stroma	647	9	3.61	9.35	-	-	62	817
			(5.23)	(0.12)	(0.04)	(0.11)	-	-	(0.67)	(6.01)
PD-1	PD-1+	Tumor	75	18	171.71	378.43	-	-	38	132

positive cell		Stroma	(0.57)	(0.22)	(2.81)	(3.71)		(0.37)	(1.18)
			185	93	804.29	327.69	-	160	260
			(1.14)	(1.22)	(7.95)	(3.03)	-	(1.33)	(2.09)
TPS	PD-L1+ (E1 L3N antibody)		<1%	<1%	0.16	<1%	<1%	<1%	0.03
CPS	PD-L1+ (E1 L3N antibody)		<1	<1	16	<1	<1	<1	18
Tertiary lymphoid structure <sup>1</sup>	CD3+、CD20+ /		0.15	0	0	0	-	0.47	0.36
			4829.10	0	0	0	-	29136.70	42672.07

<sup>1</sup>The count and density of tertiary lymphatic structures are filled in the table. The unit is number/mm<sup>2</sup> (μm<sup>2</sup>/mm<sup>2</sup>).

TME: Tumor microenvironment; G/GEJC: Gastric or gastroesophageal junction cancer.

**Supplementary Table 2 Clinicopathological features associated with Programmed death ligand-1 positive group in pathological stage III gastric or gastroesophageal junction cancer**

Variables	PD-L1 positive ( <i>n</i> = 155)	PD-L1 negative ( <i>n</i> = 74)	Statistic	<i>P</i> value
Sex [n(%)]			2.618	0.106

Male	103 (66.5%)	41 (55.4%)		
Female	52 (33.5%)	33 (44.6%)		
Age (mean $\pm$ SD)	58.57 $\pm$ 12.47	55.22 $\pm$ 13.34	-1.859	0.064
Tumor size [n(%)]			0.088	0.767
< 5cm	101 (65.6%)	50 (67.6%)		
$\geq$ 5cm	53 (34.4%)	24 (32.4%)		
Lesion sites [n(%)]			1.609	0.205
Stomach	110 (71.9%)	59 (79.7%)		
GEJ	43 (28.1%)	15 (20.3%)		
Histology [n(%)]			2.255	0.133
Sig	58 (38.2%)	36 (48.6%)		
Other	94 (61.8%)	38 (51.4%)		
Grade [n(%)]			1.227	0.268
G1-G2	25 (16.6%)	8 (11.0%)		
G3	126 (83.4%)	65 (89.0%)		
Pathological stage [n(%)]			1.670	0.434
pIIIA	68 (43.9%)	31 (41.9%)		

pIIIB	53 (34.2%)	31 (41.9%)		
pIIIC	34 (21.9%)	12 (16.2%)		
HER-2 expression [n(%)]			1.619	0.203
Negative	132 (89.2%)	68 (94.4%)		
Positive	16 (10.8%)	4 (5.6%)		
MMR status [n(%)]			0.185	0.667
dMMR	5 (3.2%)	4 (5.4%)		
pMMR	150 (96.8%)	70 (94.6%)		
EBV status [n(%)]			0.093	0.761
Negative	143 (95.3%)	70 (97.2%)		
Positive	7 (4.7%)	2 (2.8%)		
Ki-67 index (mean $\pm$ SD)	62.85 $\pm$ 21.90	52.85 $\pm$ 23.97	-3.125	0.002
Postoperative adjuvant chemotherapy [n(%)]			0.064	0.801
Yes	100 (64.5%)	49 (66.2%)		
No	55 (35.5%)	25 (33.8%)		

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GEJ: Gastroesophageal junction; Sig: Signet ring cell carcinoma; pIII: Pathological stage III; MMR: Mismatch repair; dMMR: Deficient mismatch repair; pMMR: Proficient mismatch repair; EBV: Epstein-Barr virus; PD-L1: Programmed death ligand-1.