Supplementary Table 2. Association between the *FGFR2* amplification status and clinicopathological features

Factors		*FGFR2* amplification status				
		Tissue$^+$ctDNA$^+$ (n=6)		Tissue$^-$ctDNA$^+$ (n=6)		*P* value
Age (average ± SD)		61.5 ± 17.7		62.5 ± 11.9		0.748
Sex	Male	3	(50.0)	4	(66.7)	1.000
	Female	3	(50.0)	2	(33.3)	
ECOG PS	0	4	(66.7)	4	(66.7)	1.000
	1 or 2	2	(33.3)	2	(33.3)	
Location	EGJ	1	(16.7)	1	(16.7)	1.000
	Gastric	5	(83.3)	5	(83.3)	
Histology	Intestinal	1	(16.7)	3	(50.0)	0.546
	Diffuse	5	(83.3)	3	(50.0)	
HER2 status (IHC/FISH)	Negative	5	(83.3)	5	(83.3)	1.000
	Positive	1	(16.7)	1	(16.7)	
Number of organs with metastasis	≤ 2	4	(66.7)	4	(66.7)	1.000
	≥ 3	2	(33.3)	2	(33.3)	
Site of metastasis	Lymph node	6	(100.0)	5	(83.3)	1.000
	Peritoneum	3	(50.0)	3	(50.0)	1.000
	Liver	1	(16.7)	2	(33.3)	1.000

[*] The left subcolumn (without parentheses) represents the number of patients and the right subcolumn (with parentheses) represents the percentage of patients.

Abbreviations: ctDNA, circulating tumor DNA; SD, standard deviation; ECOG PS, Eastern Cooperative Oncology Group performance status; EGJ, esophagogastric junction; IHC, immunohistochemistry; FISH, fluorescence in situ hybridization.