

B

	TTN [233]	TP53 [200]	MUC16 [138]	LRP1B [118]	SYNE1 [111]	ARID1A [110]	CSMD3 [105]	FAT4 [ 93]	FLG [ 93]	PCL0 [ 85]	HMCN1 [ 83]	CSMD1 [ 79]	OBSCN [ 79]	ZFHX4 [ 79]	DNAH5 [ 78]	RYR2 [ 77]	SPTA1 [ 76]	KMT2D [ 73]	FAT3 [ 72]	PIK3CA [ 69]			
PIK3CA [ 69]	*	*	•	•	*	*		•		·	·		*	*	*	*	·	*	·				
FAT3 [ 72]	*		*	*	*	*	*	*	*	*	•	•	*	*	*	*	*	*					
KMT2D [ 73]	*	·	*	*	*	*	*	*	*	*	*	*	*	*	*	*	·						
SPTA1 [ 76]	·		•	·	*			·		*		*	·										
RYR2 [ 77]	*		*	*	*	*		÷	*	*	*	·	*	*	*								
DNAH5 [ 78]	*		*	*	*	*	•	*		·	*	•	*	*									
ZFHX4 [ 79]	*		*	*	*	*	*	*	÷	*	·	*	*		★ P < 0.001								
OBSCN [ 79]	*		*	*	*	*	·	*	*	*	*	*			• P < 0.05								
CSMD1 [ 79]	*		*	·	*	*	·	*		·	*												
HMCN1 [ 83]	*		*	*	*	*	•	*	*	*													
PCLO [ 85]	*		·	*	*	*	*	*	·														
FLG [ 93]	·	·	·	·	*	·	·	÷															
FAT4 [ 93]	*		*	*	*	*	*																
CSMD3 [105]	*		·	*	÷	·							>3 (Co-occurence) 2										
ARID1A [110]	*	*	*	•	*																		
SYNE1 [111]	*		*	*							(a	Ì											
LRP1B [118]	*	·	*								lev	2		- 1									
MUC16 [138]	*										ď	-		- 0	)								
TP53 [200]											-log10/P-value)	<u>ר</u> ה		- 1									
TTN [233]											Ī	2		2	3 (1	Mutu	ally	exc	lusiv	ve)			

**Supplementary Figure 1 Gastric cancer mutation information.** A: The plot showing the variant classification, variant type, SNV class, variants per sample, top 10 mutated genes in the TCGA cohort; B: The correlation matrix demonstrated the correlations of the top 20 mutated genes.