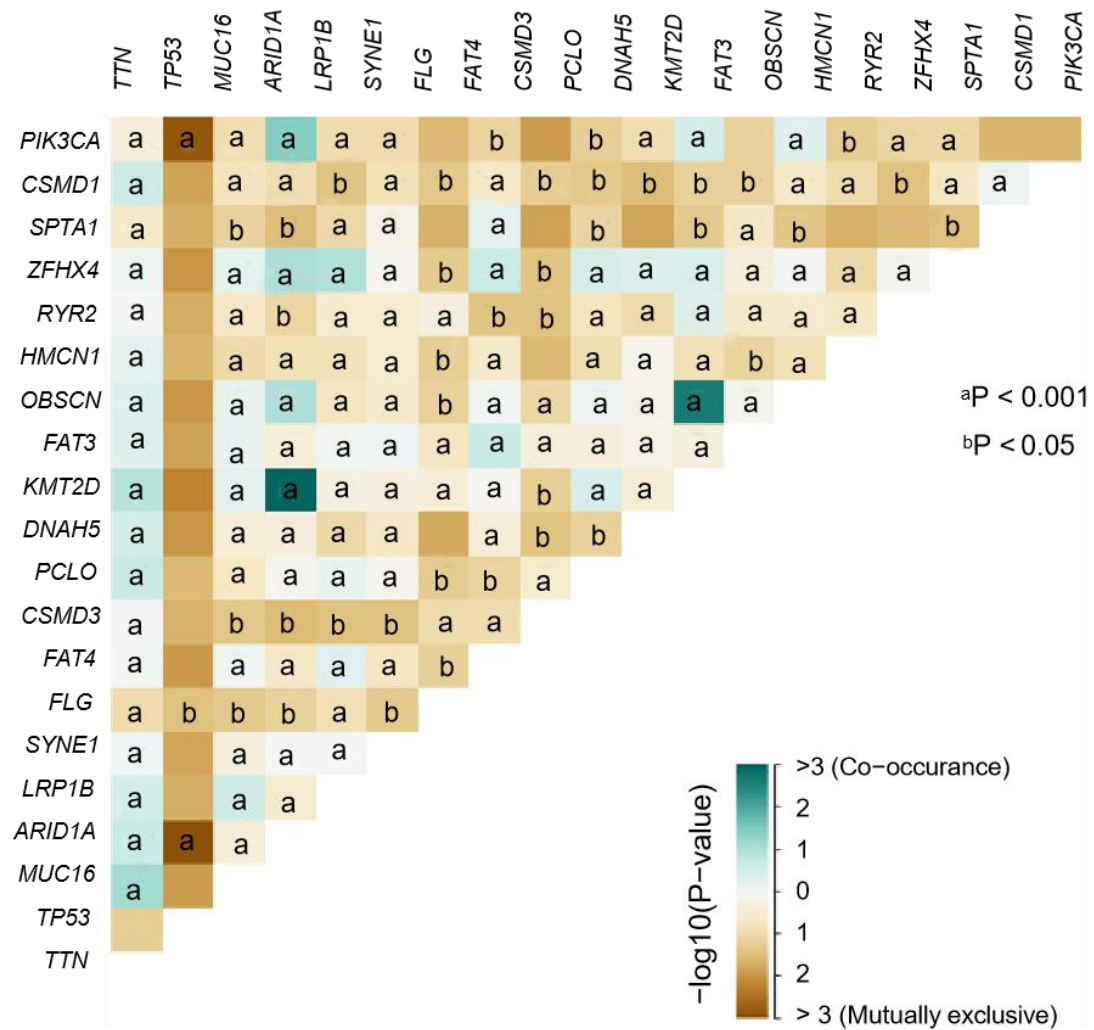
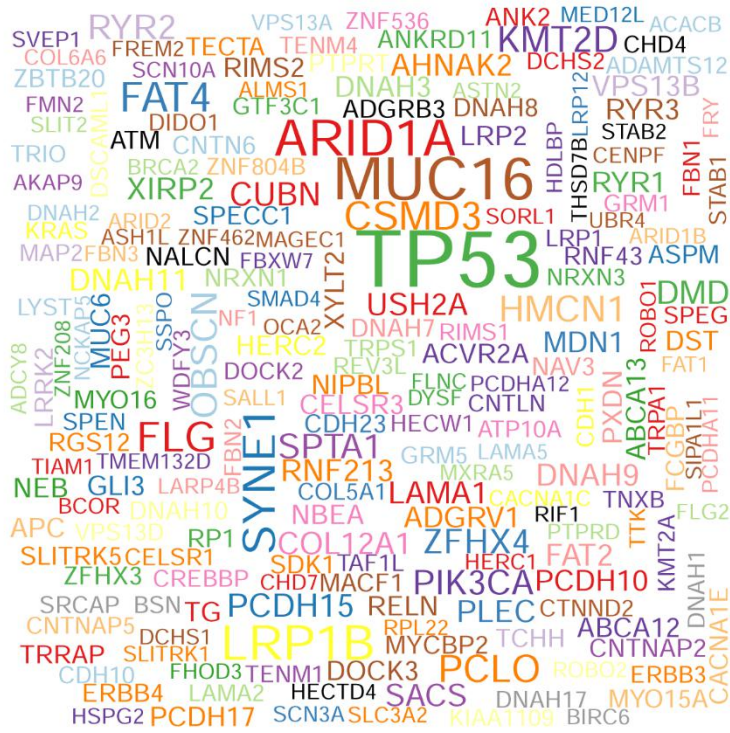


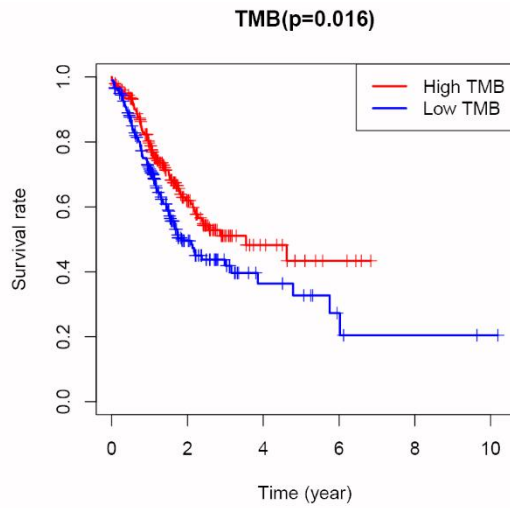
## Supplementary material



Supplementary Figure 1 The coincident and exclusive associations across mutated genes in gastric cancer.



**Supplementary Figure 2 Genecloud plot showed mutation information of genes in gastric cancer.**



**Supplementary Figure 3 Survival analysis to explore the overall survival of gastric cancer patients between the high- and low-TMB group.** The samples were classified into high- and low-TMB groups according to the median value as the cutoff value.

**Supplementary Table 1 Clinical characteristics of gastric cancer patients in each dataset**

<b>Clinical characteristic</b>	<b>Type</b>	<b>Whole</b>	<b>Train</b>	<b>Test</b>	<b>p-value</b>
Age	≤ 65	185	107	78	0.540
	> 65	235	144	91	
	Unknown	5	4	1	
Gender	Female	150	93	57	0.605
	Male	275	162	113	
Grade	G1-2	165	103	62	0.494
	G3	251	147	104	
	Unknown	9	5	4	
AJCC stage	Stage I-II	182	107	75	1
	Stage III-IV	217	128	89	
	Unknown	26	20	6	
T	T1-2	112	66	46	0.952
	T3-4	304	182	122	
	Unknown	9	7	2	
M	M0	374	225	149	0.996
	M1	29	18	11	
	Unknown	22	12	10	
N	N0	125	72	53	0.660
	N1-3	281	170	111	
	Unknown	19	13	6	

AJCC: American Joint committee on Cancer

**Supplementary Table 2 Kyoto encyclopedia of genes and genomes enrichment analysis of the 23 miRNAs.**

<b>KEGG pathway</b>	<b>P value</b>	<b>Genes</b>	<b>miRNAs</b>
Hippo signaling pathway	5.11E-14	91	22
Signaling pathways regulating pluripotency of stem cells	8.95E-12	89	22
Fatty acid biosynthesis	3.91E-10	6	5
Proteoglycans in cancer	2.58E-08	108	23
TGF-beta signaling pathway	6.09E-08	48	20
Axon guidance	9.25E-08	71	20
Wnt signaling pathway	1.09E-06	80	22
Glioma	1.57E-06	39	22
Adherens junction	2.86E-06	47	19
ErbB signaling pathway	8.79E-06	53	21
Renal cell carcinoma	9.11E-06	42	19
Prostate cancer	1.38E-05	54	21
Pathways in cancer	2.96E-05	192	22
Prion diseases	7.15E-05	9	9
Glutamatergic synapse	9.99E-05	58	21
FoxO signaling pathway	0.000115887	72	20
Transcriptional misregulation in cancer	0.000138754	81	20
Ras signaling pathway	0.000170836	110	22
Prolactin signaling pathway	0.000212816	41	19
Mucin type O-Glycan biosynthesis	0.000216692	14	13
Chronic myeloid leukemia	0.000329074	44	19
Rap1 signaling pathway	0.000503535	102	22
Estrogen signaling pathway	0.000682824	51	20
Pancreatic cancer	0.000690922	38	20
PI3K-Akt signaling pathway	0.0008416	159	22

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Amphetamine addiction	0.000924743	36	21
Bacterial invasion of epithelial cells	0.000989305	44	19
Gap junction	0.001113391	44	17
Melanogenesis	0.001133416	54	22
Insulin signaling pathway	0.001388558	73	21
Neurotrophin signaling pathway	0.001605601	64	22
Biotin metabolism	0.002639475	2	2
Oocyte meiosis	0.003037703	56	20
Dopaminergic synapse	0.003044542	67	20
Thyroid hormone signaling pathway	0.003066049	61	22
Ubiquitin mediated proteolysis	0.003450723	67	19
Endometrial cancer	0.003817967	30	19
Glycosaminoglycan biosynthesis-heparan sulfate/heparin	0.003818634	13	14
Choline metabolism in cancer	0.003818634	54	19
T cell receptor signaling pathway	0.003914169	55	20
Long-term potentiation	0.003914169	38	21
cAMP signaling pathway	0.00477084	95	22
Cocaine addiction	0.005155046	25	20
Focal adhesion	0.005860759	98	21
AMPK signaling pathway	0.006330007	63	20
Endocytosis	0.00701708	93	20
Acute myeloid leukemia	0.00904192	31	18
CAMs	0.009202838	60	19

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KEGG: Kyoto encyclopedia of genes and genomes; CAMs: Cell adhesion molecules.

**Supplementary Table 3 Gene ontology enrichment analysis of the 23 miRNAs**

GO Category	<i>P</i> value	Gene s	miRNA s
Cellular nitrogen compound metabolic process	1.16E-12 6	1789	23
Biosynthetic process	1.45E-77	1465	23
Cellular protein modification process	1.52E-74	941	22
Neurotrophin TRK receptor signaling pathway	1.37E-41	136	22
Small molecule metabolic process	6.77E-40	828	22
Gene expression	8.66E-40	243	22
Fc-epsilon receptor signaling pathway	8.04E-34	91	22
Viral process	1.60E-32	199	21
Symbiosis, encompassing mutualism through parasitism	1.11E-31	218	21
Catabolic process	2.75E-28	676	23
Cellular component assembly	7.62E-27	482	22
Epidermal growth factor receptor signaling pathway	1.19E-24	112	22
Blood coagulation	2.61E-23	184	23
Mitotic cell cycle	5.30E-21	155	21
Membrane organization	6.10E-20	227	21
Nucleobase-containing compound catabolic process	1.07E-19	327	22
Biological_process	4.07E-19	5340	23
Cellular protein metabolic process	2.96E-18	166	22
Synaptic transmission	2.75E-17	174	21
Cell death	6.19E-17	334	22
Cell-cell signaling	8.07E-16	251	21
Fibroblast growth factor receptor signaling pathway	1.13E-15	94	22
Macromolecular complex assembly	2.79E-15	307	22

Post-translational protein modification	1.80E-14	71	18
Cellular lipid metabolic process	7.70E-14	66	19
Platelet activation	1.90E-13	87	23
Response to stress	2.08E-13	719	22
Fc-gamma receptor signaling pathway involved in phagocytosis	3.42E-13	38	17
Phosphatidylinositol-mediated signaling	9.13E-12	67	21
Cell junction organization	1.83E-11	72	19
Inositol phosphate metabolic process	1.54E-10	27	21
Protein complex assembly	6.70E-10	257	22
Axon guidance	1.12E-09	180	20
Cell junction assembly	1.48E-09	33	15
Insulin receptor signaling pathway	2.20E-09	77	22
Cell motility	5.00E-09	204	21
Water-soluble vitamin metabolic process	6.86E-09	33	16
Toll-like receptor TLR1:TLR2 signaling pathway	1.08E-08	30	17
Toll-like receptor TLR6:TLR2 signaling pathway	1.08E-08	30	17
Transcription initiation from RNA polymerase II promoter	1.31E-08	90	22
Vitamin metabolic process	1.54E-08	35	16
Toll-like receptor 10 signaling pathway	3.62E-08	28	17
TRIF-dependent toll-like receptor signaling pathway	1.49E-07	30	17
Toll-like receptor 9 signaling pathway	2.58E-07	31	17
Anatomical structure morphogenesis	3.21E-07	49	18
Transcription, DNA-templated	3.34E-07	812	23
Cellular component disassembly involved in execution phase of apoptosis	6.17E-07	22	15
G2/M transition of mitotic cell cycle	1.23E-06	60	18
Toll-like receptor 5 signaling pathway	1.33E-06	28	17



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mRNA metabolic process	1.33E-06	69	18
Platelet degranulation	1.97E-06	31	21
Immune system process	2.09E-06	486	22
MyD88-independent toll-like receptor signaling pathway	3.07E-06	30	17
Phospholipid metabolic process	3.41E-06	65	20
DNA metabolic process	3.41E-06	244	22
Glycosaminoglycan metabolic process	3.68E-06	40	16
Activation of signaling protein activity involved in unfolded protein response	8.93E-06	27	13
Toll-like receptor 2 signaling pathway	9.04E-06	31	17
Energy reserve metabolic process	1.05E-05	39	17
Regulation of defense response to virus by virus	1.83E-05	15	10
mRNA 3'-end processing	2.19E-05	20	17
Toll-like receptor 3 signaling pathway	2.31E-05	31	17
Post-Golgi vesicle-mediated transport	2.51E-05	24	19
Cytoskeleton organization	3.08E-05	222	21
Phosphatidylinositol biosynthetic process	3.49E-05	29	19
Termination of RNA polymerase II transcription	3.78E-05	21	17
Toll-like receptor 4 signaling pathway	4.46E-05	36	17
Innate immune response	7.85E-05	225	22
Protein N-linked glycosylation via asparagine	8.74E-05	37	16
Cell-cell junction organization	9.94E-05	35	14
Chromatin organization	0.000122	48	19
	504		
Sulfur compound metabolic process	0.000130	93	20
	867		
Intrinsic apoptotic signaling pathway	0.000153	30	17
	368		

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Positive regulation of protein insertion into Mitochondrial membrane involved in apoptotic signaling pathway	0.000171062	15	14
RNA metabolic process	0.000208589	73	19
Toll-like receptor signaling pathway	0.000264048	39	17
Nucleocytoplasmic transport	0.000333541	123	22
Glycerophospholipid biosynthetic process	0.000447608	31	18
Cytoskeleton-dependent intracellular transport	0.000527807	42	17
Nervous system development	0.000579354	154	21
Regulation of transcription from RNA polymerase II promoter in response to hypoxia	0.000616919	15	13
Cellular component movement	0.000770948	41	19
In utero embryonic development	0.000778339	129	21
Positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	0.000906307	25	18
Activation of phospholipase C activity	0.00104359	26	17
Stress-activated MAPK cascade	0.00122618	21	16
Homeostatic process	0.001286395	247	22

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Transforming growth factor beta receptor signaling pathway	0.001508 017	70	20
Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	0.001578 375	25	18
Leukocyte migration	0.001579 931	40	19
Extracellular matrix organization	0.001843 385	118	21
Positive regulation of signal transduction	0.002355 362	33	17
Extracellular matrix disassembly	0.002464 755	35	18
Long-chain fatty-acyl-CoA biosynthetic process	0.002561 874	9	7
Positive regulation of muscle cell differentiation	0.003287 519	15	16
MyD88-dependent toll-like receptor signaling pathway	0.003413 695	32	19
Nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	0.005660 975	15	14
3'-phosphoadenosine 5'-phosphosulfate metabolic process	0.006734 151	9	10
Adherens junction organization	0.006734 151	19	14
Cell cycle arrest	0.006734 151	68	20
Muscle cell differentiation	0.008676 313	21	19
G1/S transition of mitotic cell cycle	0.008699	61	20

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Chondroitin sulfate metabolic process	0.008728	17	11
	059		
Vesicle-mediated transport	0.008728	310	22
	059		

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GO: Gene ontology.