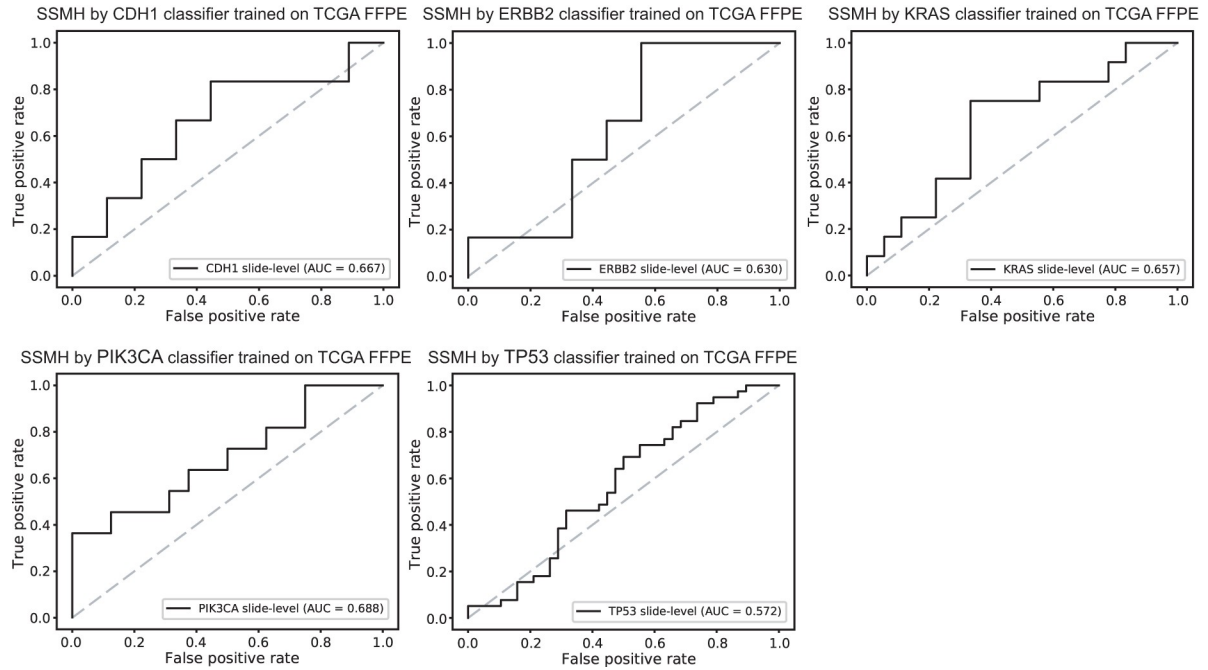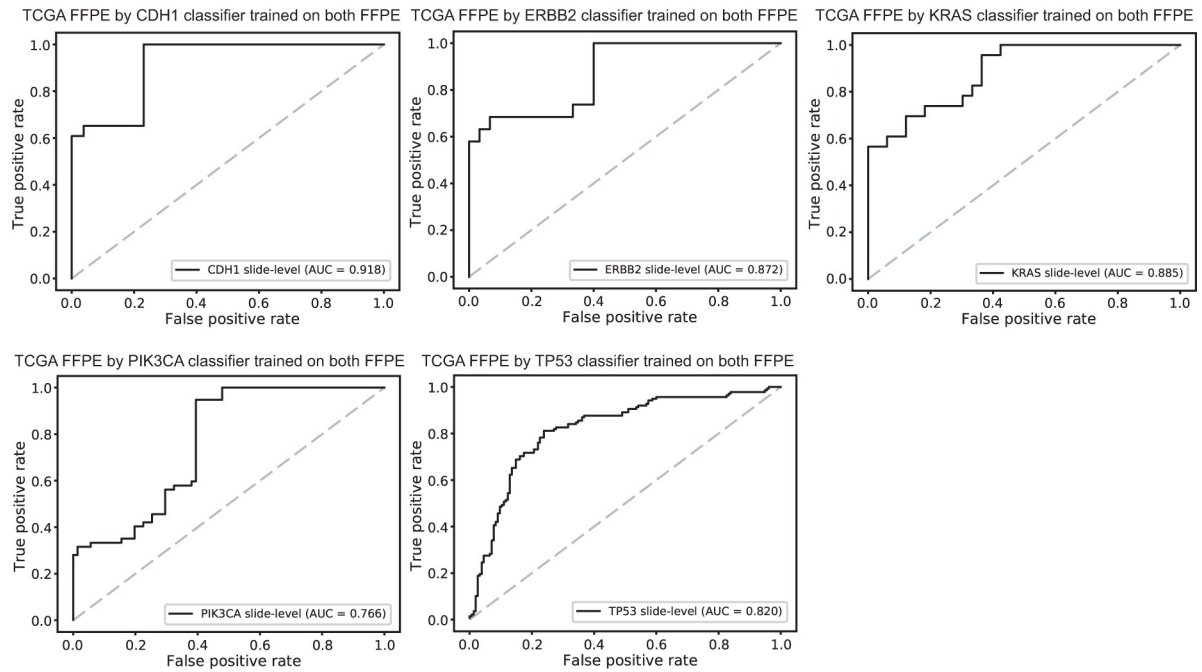**Supplementary Figure S1. Mutation prediction of CDH1, ERBB2, KRAS, PIK3CA, and TP53 genes for the SSMH gastric cancer tissue slides by the classifiers trained with TCGA FFPE data.**

Supplementary Figure S2. Mutation prediction of CDH1, ERBB2, KRAS, PIK3CA, and TP53 genes for the TCGA FFPE tissue slides by the classifiers trained with both TCGA and SSMH data.

Supplementary Table S1. List of TCGA IDs with specific mutation or all wild-type gene

\<CDH1 mutated\>	\<ERBB2 mutated\>	\<KRAS mutated\>	\<PIK3CA mutated\>	\<TP53A mutated\>	\<All wild-type\>
TCGA-VQ-A8PX	TCGA-BR-6802	TCGA-BR-8078	TCGA-D7-A4YV	TCGA-CD-8535	TCGA-HU-A4GC
TCGA-F1-6874	TCGA-IN-8663	TCGA-BR-8679	TCGA-VQ-A8PF	TCGA-BR-A4CR	TCGA-BR-A4J6
TCGA-BR-8592	TCGA-VQ-A8DT	TCGA-EQ-A4SO	TCGA-FP-7916	TCGA-HU-A4H4	TCGA-BR-A4J7
TCGA-D7-A4YU	TCGA-HU-A4H0	TCGA-D7-6815	TCGA-BR-8686	TCGA-VQ-A91Z	TCGA-BR-4279
TCGA-D7-8572	TCGA-VQ-A91D	TCGA-BR-4257	TCGA-BR-8381	TCGA-VQ-A91U	TCGA-CG-5718
TCGA-VQ-A924	TCGA-CG-4466	TCGA-BR-7703	TCGA-HU-A4H0	TCGA-VQ-AA6A	TCGA-CG-4472
TCGA-BR-A453	TCGA-VQ-A8PH	TCGA-B7-A5TJ	TCGA-BR-6706	TCGA-CG-5717	TCGA-HU-8610
TCGA-BR-6803	TCGA-BR-8487	TCGA-CD-A4MJ	TCGA-CG-4474	TCGA-BR-8678	TCGA-CG-5727
TCGA-VQ-A91K	TCGA-D7-A6EY	TCGA-CG-4442	TCGA-HU-A4H4	TCGA-CG-4449	TCGA-D7-A4YT
TCGA-IN-7808	TCGA-BR-7957	TCGA-VQ-A94T	TCGA-CD-8536	TCGA-CD-5800	TCGA-VQ-A8P3
TCGA-CD-A4MG	TCGA-BR-8588	TCGA-BR-6802	TCGA-VQ-A8PB	TCGA-BR-8484	TCGA-CG-5720
TCGA-VQ-A8PO	TCGA-BR-6566	TCGA-BR-4267	TCGA-BR-8366	TCGA-VQ-A8DT	TCGA-CD-5813
TCGA-D7-A6EY	TCGA-CG-4469	TCGA-BR-4201	TCGA-VQ-A91D	TCGA-CG-4438	TCGA-BR-8363
TCGA-BR-4292	TCGA-BR-4370	TCGA-BR-8687	TCGA-VQ-AA69	TCGA-CG-4477	TCGA-CG-4441
TCGA-D7-6518	TCGA-VQ-A8PB	TCGA-3M-AB46	TCGA-VQ-A8PP	TCGA-IN-7808	TCGA-BR-4362
TCGA-CG-4474	TCGA-HU-A4H8	TCGA-VQ-A91D	TCGA-VQ-A924	TCGA-D7-5578	TCGA-CG-5732
TCGA-BR-8364	TCGA-MX-A5UJ	TCGA-CD-5798	TCGA-CD-5800	TCGA-BR-6803	TCGA-IN-AB1V
TCGA-BR-6452	TCGA-VQ-A8PD	TCGA-BR-8368	TCGA-F1-6177	TCGA-D7-6527	TCGA-VQ-A8PY
TCGA-CD-5799	TCGA-BR-6852	TCGA-BR-8366	TCGA-BR-4361	TCGA-F1-A72C	TCGA-BR-8060
TCGA-MX-A5UG		TCGA-BR-4280	TCGA-CG-5722	TCGA-BR-4361	TCGA-BR-4188
TCGA-B7-A5TI		TCGA-VQ-A8PP	TCGA-VQ-A91W	TCGA-EQ-8122	TCGA-HJ-7597
TCGA-BR-8686		TCGA-VQ-A8PU	TCGA-BR-8591	TCGA-CG-4440	TCGA-BR-8372
TCGA-BR-A4IV		TCGA-BR-6705	TCGA-B7-5816	TCGA-D7-6528	TCGA-HU-A4G3
TCGA-FP-A8CX		TCGA-BR-8680	TCGA-D7-5577	TCGA-CD-8531	TCGA-HF-7136
TCGA-BR-A44T		TCGA-D7-A74A	TCGA-BR-6452	TCGA-CD-8526	TCGA-BR-A4IZ
		TCGA-BR-4368	TCGA-HF-A5NB	TCGA-B7-A5TN	TCGA-BR-7959
		TCGA-SW-A7EA	TCGA-CG-5721	TCGA-D7-6520	TCGA-CG-4300
		TCGA-VQ-AA69	TCGA-D7-A4YX	TCGA-FP-7735	TCGA-RD-A8MV
		TCGA-BR-7707	TCGA-HU-A4GX	TCGA-VQ-A94P	TCGA-IN-A6RP
		TCGA-BR-4361	TCGA-RD-A8NB	TCGA-VQ-A922	TCGA-HU-8244
		TCGA-B7-A5TK	TCGA-BR-6454	TCGA-BR-8081	TCGA-RD-A7C1
		TCGA-BR-8059	TCGA-D7-A6EZ	TCGA-BR-8077	TCGA-CD-8532
		TCGA-CD-8535	TCGA-D7-5578	TCGA-HU-A4HD	TCGA-HU-A4GJ
		TCGA-HF-A5NB	TCGA-CG-4442	TCGA-BR-A44U	TCGA-BR-A4QM
			TCGA-HU-8602	TCGA-IN-8462	TCGA-CD-5802
			TCGA-HU-A4GU	TCGA-VQ-A91N	TCGA-HU-A4HB
			TCGA-HU-8608	TCGA-CD-8530	TCGA-D7-6519
			TCGA-BR-8588	TCGA-HU-A4GD	TCGA-BR-A4J2
			TCGA-VQ-AA6K	TCGA-VQ-AA6I	TCGA-HU-A4H6
			TCGA-BR-7196	TCGA-BR-6565	TCGA-BR-A4J9
			TCGA-CD-5801	TCGA-BR-6457	TCGA-CG-5726
			TCGA-HU-A4GQ	TCGA-D7-A4YU	TCGA-VQ-A91Q
			TCGA-VQ-A91K	TCGA-IP-7968	TCGA-VQ-A91E
			TCGA-HF-7132	TCGA-BR-8683	TCGA-VQ-A927
			TCGA-CD-A4MI	TCGA-HU-A4GX	TCGA-CG-5728
			TCGA-BR-8081	TCGA-VQ-A8PH	TCGA-BR-8360
			TCGA-VQ-A8P2	TCGA-FP-A4BF	TCGA-FP-A4BE
			TCGA-FP-7998	TCGA-RD-A8N1	TCGA-HU-8245
			TCGA-D7-A747	TCGA-BR-4255	TCGA-CG-4443
			TCGA-BR-6707	TCGA-BR-7901	TCGA-VQ-A91A
			TCGA-HU-A4H3	TCGA-FP-8099	TCGA-BR-8362
			TCGA-B7-A5TK	TCGA-IN-7806	TCGA-VQ-AA6D
			TCGA-BR-7851	TCGA-CD-A48C	TCGA-D7-A6ET
			TCGA-HU-A4G2	TCGA-BR-8487	TCGA-D7-8574
			TCGA-BR-6455	TCGA-CD-A4MH	TCGA-KB-A6F7
			TCGA-B7-5818	TCGA-HU-A4GH	TCGA-CG-5725

TCGA-BR-4371	TCGA-IN-A7NR	TCGA-CD-8525
TCGA-D7-6815	TCGA-VQ-A91X	TCGA-3M-AB47
TCGA-BR-6802	TCGA-BR-A4IY	TCGA-CG-4465
TCGA-BR-4253	TCGA-BR-A4IU	TCGA-CD-A48A
TCGA-BR-8487	TCGA-HU-8604	TCGA-VQ-AA6J
TCGA-CG-4305	TCGA-CG-5721	TCGA-BR-8384
TCGA-BR-8589	TCGA-BR-A452	TCGA-VQ-AA6F
TCGA-BR-8680	TCGA-D7-6526	TCGA-CD-A486
	TCGA-BR-A4QI	TCGA-HU-8238
	TCGA-HU-A4GF	TCGA-BR-4369
	TCGA-CD-8528	TCGA-VQ-A925
	TCGA-D7-A6F0	TCGA-ZA-A8F6
	TCGA-CG-5734	TCGA-VQ-A8PZ
	TCGA-CD-5799	TCGA-BR-8677
	TCGA-BR-6456	TCGA-FP-8211
	TCGA-BR-A4PD	TCGA-BR-8296
	TCGA-HU-A4GN	TCGA-VQ-A8PJ
	TCGA-B7-A5TI	TCGA-CG-5719
	TCGA-VQ-A8E3	TCGA-BR-7722
	TCGA-CG-5723	TCGA-FP-8209
	TCGA-HU-A4GQ	TCGA-BR-7958
	TCGA-CD-A489	TCGA-CG-4475
	TCGA-D7-8576	TCGA-HU-A4G8
	TCGA-BR-4292	TCGA-IN-A6RO
	TCGA-D7-6525	TCGA-BR-6801
	TCGA-BR-A4J8	TCGA-KB-A6F5
	TCGA-VQ-A8PK	TCGA-D7-5579
	TCGA-BR-4366	TCGA-CG-4462
	TCGA-BR-8679	TCGA-BR-A4J4
	TCGA-D7-A6EV	TCGA-BR-8295
	TCGA-IN-A6RS	TCGA-BR-6709
	TCGA-RD-A8MW	TCGA-BR-8373
	TCGA-BR-8590	TCGA-BR-8676
	TCGA-FP-A9TM	TCGA-RD-A8N2
	TCGA-BR-7703	TCGA-IN-A6RN
	TCGA-RD-A8NB	TCGA-HF-7131
	TCGA-MX-A666	TCGA-CG-5733
	TCGA-HU-A4H3	TCGA-BR-4191
	TCGA-HU-A4GP	TCGA-HU-A4G6
	TCGA-VQ-A8DV	TCGA-CD-8529
	TCGA-BR-4357	TCGA-HF-7133
	TCGA-BR-A4PE	TCGA-MX-A663
	TCGA-IN-A7NU	TCGA-BR-A4J1
	TCGA-CG-4436	TCGA-KB-A93G
	TCGA-CD-8524	TCGA-VQ-A8PM
	TCGA-VQ-A94U	TCGA-F1-6875
	TCGA-VQ-A8E2	TCGA-EQ-5647
	TCGA-D7-6815	TCGA-CG-4476
	TCGA-BR-4256	TCGA-VQ-A928
	TCGA-BR-8297	TCGA-IN-A6RJ
	TCGA-D7-6817	TCGA-VQ-A8PQ
	TCGA-IN-A6RR	TCGA-BR-8284
	TCGA-D7-A6EX	TCGA-BR-7717
	TCGA-VQ-A8DU	TCGA-BR-8369
	TCGA-D7-6521	TCGA-HU-8249
	TCGA-VQ-A8PP	TCGA-CG-4301
	TCGA-3M-AB46	TCGA-BR-4183
	TCGA-VQ-A8PX	TCGA-HU-8243
	TCGA-VQ-A8DZ	TCGA-KB-A93H

TCGA-FP-8631	TCGA-VQ-A8P5
TCGA-VQ-A91V	TCGA-VQ-A8PS
TCGA-CD-5804	TCGA-CG-4460
TCGA-F1-6874	TCGA-CG-4306
TCGA-D7-A6F2	TCGA-BR-4367
TCGA-CG-4469	TCGA-BR-4294
TCGA-IN-A6RL	TCGA-D7-8575
TCGA-IN-A7NT	TCGA-BR-8367
TCGA-RD-A8N9	TCGA-CD-5803
TCGA-VQ-A923	TCGA-CG-5724
TCGA-VQ-A8E7	TCGA-HU-A4GY
TCGA-BR-8289	TCGA-RD-A8N4
TCGA-D7-6818	TCGA-BR-8690
TCGA-D7-6820	TCGA-BR-6710
TCGA-BR-8682	TCGA-HU-A4H5
TCGA-CG-4466	TCGA-CG-4455
TCGA-HU-A4H2	TCGA-RD-A8N6
TCGA-VQ-AA68	TCGA-VQ-AA64
TCGA-VQ-A8P2	TCGA-BR-8365
TCGA-FP-7829	TCGA-VQ-A8DL
TCGA-BR-7715	TCGA-VQ-A8PT
TCGA-BR-6458	TCGA-BR-6563
TCGA-BR-8080	TCGA-BR-4187
TCGA-VQ-A8E0	TCGA-CG-5730
TCGA-VQ-AA6G	TCGA-BR-A4QL
TCGA-BR-7716	TCGA-VQ-A92D
TCGA-BR-8361	TCGA-D7-6522
TCGA-KB-A93J	TCGA-RD-A7BS
TCGA-BR-7197	TCGA-BR-7723
TCGA-VQ-A91Y	TCGA-BR-4184
TCGA-IN-A6RI	TCGA-BR-7704
TCGA-CD-A487	TCGA-CD-8534
TCGA-BR-A4CS	TCGA-D7-8579
TCGA-BR-4363	TCGA-D7-A74B
TCGA-D7-6518	TCGA-D7-8573
TCGA-D7-8578	TCGA-D7-A4Z0
TCGA-CG-4444	TCGA-VQ-A8P8
TCGA-VQ-A94O	TCGA-BR-8380
TCGA-BR-A4PF	TCGA-BR-8291
TCGA-SW-A7EB	TCGA-D7-A748
TCGA-D7-6822	TCGA-BR-8370
TCGA-VQ-A8PE	TCGA-D7-6524
TCGA-VQ-A91S	TCGA-CD-8533
TCGA-BR-8286	TCGA-BR-A4J5
TCGA-VQ-AA6B	TCGA-VQ-A94R
	TCGA-BR-8485
	TCGA-CG-4304
	TCGA-CG-4437
	TCGA-F1-A448
	TCGA-IN-AB1X
	TCGA-D7-8570
	TCGA-BR-8371
	TCGA-BR-8382
	TCGA-RD-A8N5
	TCGA-HU-A4GT
	TCGA-BR-6564
	TCGA-CD-8527
	TCGA-D7-A4YY
	TCGA-HF-7134

TCGA-BR-8285
TCGA-RD-A7BW
TCGA-BR-6453
TCGA-VQ-A8PC
TCGA-CG-5716
TCGA-BR-A4CQ
TCGA-RD-A8N0
TCGA-ZQ-A9CR
TCGA-RD-A7BT

Supplementary Table S2. Numbers of tissue patches used for the training of the mutation prediction models.

CDH1		ERBB2		KRAS		PIK3CA		TP53	
TCGA Frozen Tissue Slides									
Wild-type	Mutated	Wild-type	Mutated	Wild-type	Mutated	Wild-type	Mutated	Wild-type	Mutated
118,203	86,772	104,071	74,015	206,305	149,357	352,142	238,625	575,891	416,928
TCGA FFPE Tissue Slides									
Wild-type	Mutated	Wild-type	Mutated	Wild-type	Mutated	Wild-type	Mutated	Wild-type	Mutated
111,407	72,973	98,436	69,599	129,189	82,801	287,570	189,927	648,819	483,691
TCGA+SSMH FFPE Tissue Slides									
Wild-type	Mutated	Wild-type	Mutated	Wild-type	Mutated	Wild-type	Mutated	Wild-type	Mutated
123,052	85,530	114,770	79,237	161,360	102,740	345,306	225,218	701,325	547,789

Supplementary Table S3. Average numbers of training epochs for the mutation prediction models.

TCGA Frozen Tissue Slides				
CDH1	ERBB2	KRAS	PIK3CA	TP53
10.9	14.7	13.1	7.0	8.4
TCGA FFPE Tissue Slides				
CDH1	ERBB2	KRAS	PIK3CA	TP53
12.3	19.2	10.3	5.7	5.9
TCGA+SSMH FFPE Tissue Slides				
CDH1	ERBB2	KRAS	PIK3CA	TP53
13.1	11.0	6.7	10.6	8.1

Supplementary Table S4. Accuracy, sensitivity, specificity, and F1 score of the classification results of mutation prediction models.

SSMH FFPE Tissue Slides classified by a classifier trained with TCGA datasets				
	Accuracy	Sensitivity	Specificity	F1 score
CDH1	0.666	0.500	0.777	0.545
ERBB2	0.600	0.833	0.444	0.625
KRAS	0.600	0.833	0.444	0.625
PIK3CA	0.703	0.272	1.000	0.428
TP53	0.597	0.923	0.263	0.699
SSMH FFPE Tissue Slides classified by a classifier trained with both TCGA and SSMH datasets				
	Accuracy	Sensitivity	Specificity	F1 score
CDH1	0.800	0.666	0.888	0.727
ERBB2	0.800	0.666	0.888	0.727
KRAS	0.833	1.000	0.722	0.827
PIK3CA	0.666	1.000	0.437	0.709
TP53	0.784	0.939	0.625	0.815
TCGA FFPE Tissue Slides classified by a classifier trained with both TCGA and SSMH datasets				
	Accuracy	Sensitivity	Specificity	F1 score
CDH1	0.877	1.000	0.769	0.884
ERBB2	0.755	1.000	0.600	0.760
KRAS	0.767	0.956	0.636	0.771
PIK3CA	0.757	0.947	0.605	0.776
TP53	0.774	0.811	0.741	0.772