Figure S1. Whole transcriptome sequencing analysis pipeline and visualization. (A) Analysis pipeline for the identification of significant differentially expressed genes. (B) A volcano plot displaying the RNA-Sequencing results. FC, fold change.

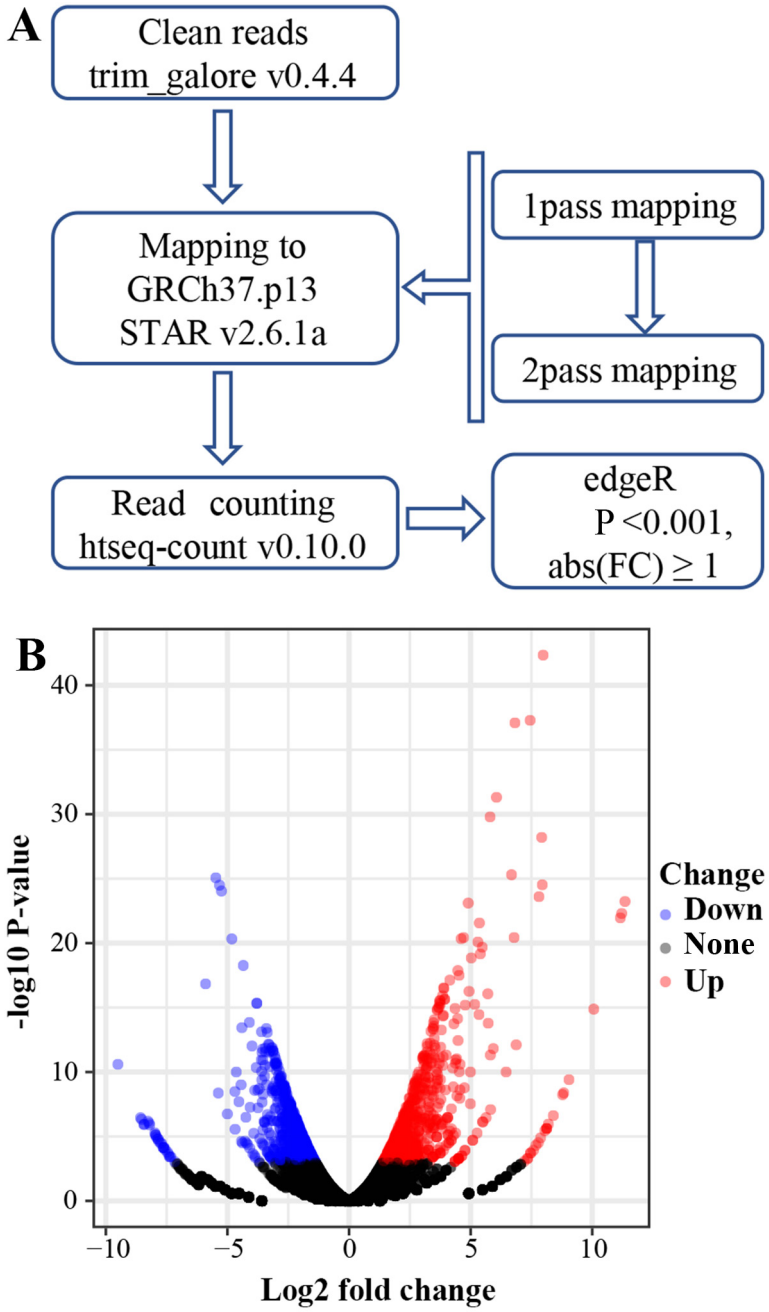


Figure S2. Analysis of dysregulated genes in TCGA-STAD and KM-plotter. (A) UpsetR software shows the intersecting sets of dysregulated genes in TCGA-STAD detected using the three different softwares. For each column, a single point without connecting lines represents the unique gene number detected by each method, while points with connecting lines represent overlap between the genes identified by the connected tools. The y-axis is gene counts, for which there is no unit. (B) Survival analysis using KM-plotter revealed that 10 of the 27 differentially expressed genes were significantly associated with survival. The x-axis means survival month in each plot. TCGA, The Cancer Genome Atlas; STAD, stomach adenocarcinoma; KM, Kaplan-Meier.

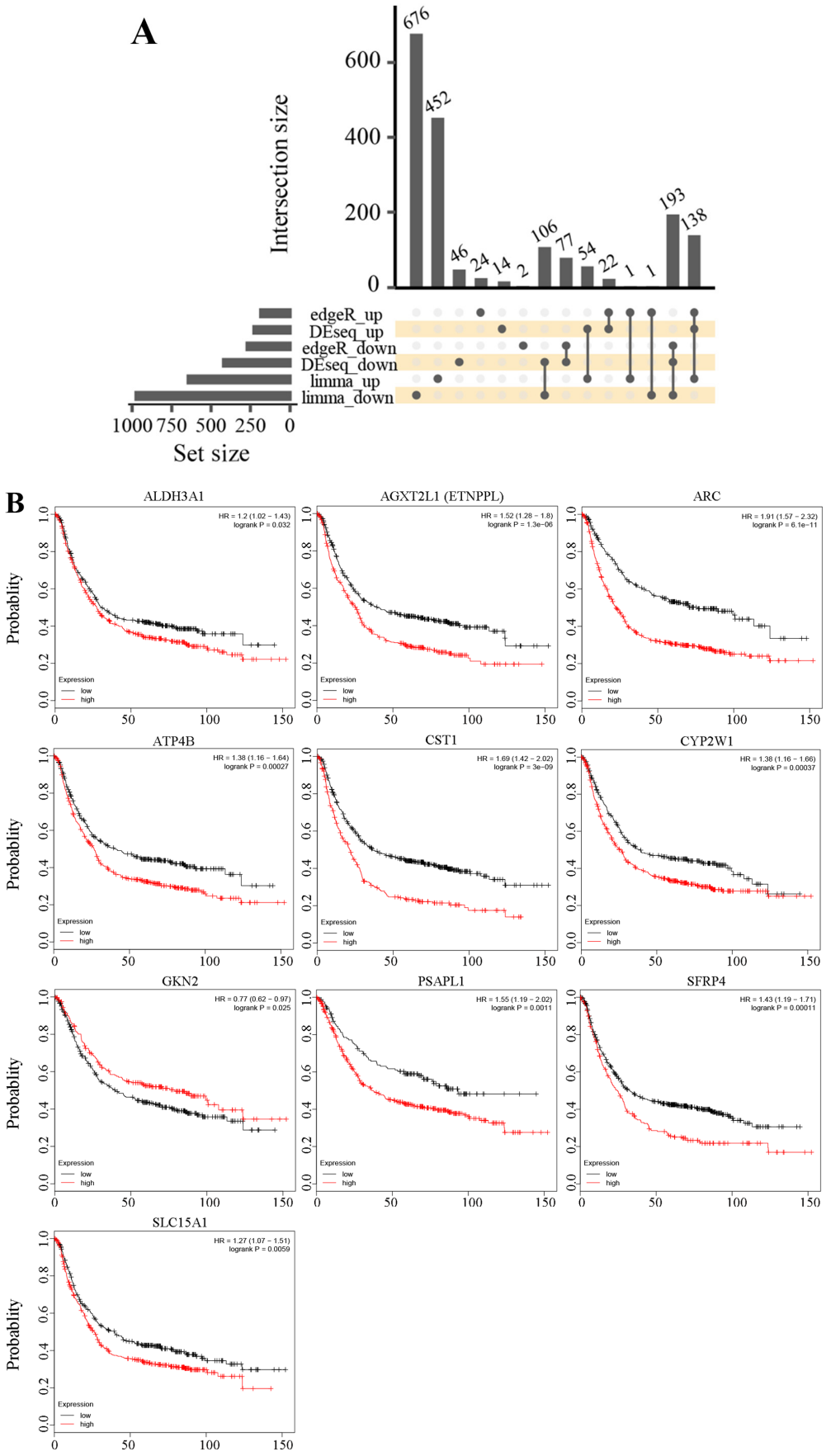


Table SI. Prediction of somatic mutations' functional effects.

Gene	Chromosome	Position	Reference allele	Alternation	Type	AA. Change	Cosmic82	Final prediction
ALMS1	2	73677678	G	A	Non-SNV	p.V1341I	Y	U
ALMS1	2	73677679	T	G	Non-SNV	p.V1341G	N	U
BPNT1	1	220236175	C	A	Non-SNV	p.S144I	N	D
CELF3	1	151678708	TGC	-	Non-FS DEL	p.322_323del	Y	U
CNN2	19	1037646	C	-	FS DEL	p.T187fs	Y	U
DBT	1	100672005	CC	-	FS DEL	p.G402fs	N	U
FADS6	17	72889676	-	GGCTCCGTAGGTT CCATGGGCTCCG TAGGTTCCATGGGC TCCGTAGGTTCCA TGGGCTCCGT AGGTTCCATC	Non-FS INS	p.P6delins PMEPTEP MEPTEPMEP TEPMEPTEP	N	U
FRG1	4	190878577	A	G	Non-SNV	p.N153D	Y	D
HLA-DRB1	6	32549613	G	A	Stop/gain	p.Q125X	N	U
IFNA4	9	21187341	C	A	Stop/gain	p.E64X	N	U
KRTAP5-3	11	1629062	C	G	Non-SNV	p.C185S	N	P
LOC100129697	16	89016668	T	A	Non-SNV	p.C48S	N	U
MUC2	11	1092884	C	T	Non-SNV	p.T1568M	Y	U
MUC4	3	195512837	A	G	Non-SNV	p.S1872P	Y	U
MUC6	11	1016779	G	A	Non-SNV	p.H2008Y	Y	U
MUC6	11	1017485	G	T	Non-SNV	p.N1772K	N	U
NEFL	8	24810424	CTT	-	Non-FS DEL	p.510_511del	Y	U
OR2T4	1	248524966	-	GCTCT	FS INS	p.P28fs	N	U
POU3F1	1	38512309	GCC	-	Non-FS DEL	p.35_36del	Y	U
RPGR	X	38145268	CCTTCCTCCT CTTCCCCCTC CCCTTCT	-	Non-FS DEL	p.986_995del	N	U
RPTN	1	152127898	GTAGTGGGA ACTCTGGCCT TGTCTGTCTG TCTGACCATA GTGGGAACT CTGGCCTTGT CTCTGTCCAT CTGACT	-	Non-FS DEL	p.536_559del	N	U
SLC25A5	X	118604476	-	CTGACCTCAT	FS INS	p.T247fs	N	U
SLC8A2	19	47935681	TCC	-	Non-FS DEL	p.710_711del	Y	U
SLC9B1	4	103822332	G	A	Non-SNV	p.T497I	N	U
TAS2R31	12	11183760	G	A	Non-SNV	p.L59F	Y	D

Table SI. Continued.

Gene	Chromosome	Position	Reference allele	Alternation	Type	AA. Change	Cosmic82	Final prediction
TCHH	1	152082500	C	T	Non-SNV	p.G1065R	Y	U
TUBGCP6	22	50659268	A	G	Non-SNV	p.S1174P	N	U
ZNF730	19	23329093	GAATTCA TACTG	-	Non-FS DEL	p.416_420del	N	U
ZNF880	19	52888049	C	A	Non-SNV	p.Q406K	Y	U

Non-SNV, non-synonymous single nucleotide variation; non-FS DEL, non-frameshift deletion; non-FS INS, non-frameshift insertion; CGC, Cancer Gene Census; CPG, Cancer Predisposition Genes; P, possibly damaging; D, deleterious; U, uncertain significance; Y, yes; N, no; AA, amino acid.

Table SII. Detection of structural variation and fusion genes using Delly.

Chr1	Pos1	Chr2	Pos2	Gene1	Gene2	Fusion	Database
11	47660326	11	47663929	MTCH2	MTCH2	Deletion within transcript: Mid-exon	NR
12	104359834	12	104373638	TDG	TDG	Deletion within transcript: Mid-exon	NR
4	1800697	4	1801985	FGFR3	FGFR3	Deletion of 2 exons: in frame	CGC
1	225247226	1	225293671	DNAH14	DNAH14	Duplication of 6 exons: In frame	NR
10	53984355	10	54034100	PRKG1	PRKG1	Duplication of 3 exons: In frame	NR
2	135260558	2	135262058	TMEM163	TMEM163	Duplication within transcript: Mid-exon	CGC
3	195505767	3	195510182	MUC4	MUC4	Duplication within transcript: Mid-exon	CGC
3	195510897	3	195513776	MUC4	MUC4	Duplication within transcript: Mid-exon	NR
1	25622261	1	25724021	RHD	RHCE	Protein Fusion: In frame (RHCE:RHD)	NR
1	25626301	1	25720137	RHD	RHCE	Protein Fusion: In frame (RHD:RHCE)	NR
1	39959046	1	40252786	BMP8A	BMP8B	Protein Fusion: In frame (BMP8A:BMP8B)	NR
11	71590436	4	9447197	LOC100129216	DEFB131	Protein Fusion: In frame (DEFB131: LOC100129216)	NR
17	15508282	17	18661985	CDRT1	FBXW10	Protein Fusion: In frame (CDRT1:FBXW10)	NR
17	15641589	17	18541754	TBC1D26	TBC1D28	Protein Fusion: In frame (TBC1D26:TBC1D28)	NR
18	47106188	2	163609544	LIPG	KCNH7	Protein Fusion: In frame (LIPG:KCNH7)	NR
19	12404731	19	12550988	ZNF44	ZNF443	Protein Fusion: In frame (ZNF44:ZNF443)	NR
19	15838939	19	15918676	OR10H2	OR10H1	Protein Fusion: Mid-exon (OR10H1:OR10H2)	NR
2	130941022	2	132248867	MZT2B	MZT2A	Protein Fusion: In frame (MZT2B:MZT2A)	NR
21	11082665	7	152078406	BAGE2	KMT2C	Protein Fusion: In frame (KMT2C:BAGE2)	CGC
7	5939546	7	6865133	CCZ1	CCZ1B	Protein Fusion: In frame (CCZ1:CCZ1B)	NR

Chr, chromosome; pos, position; CGC, Cancer Gene Census; CPG, Cancer Predisposition Genes; NR, not reported.

Table SIII. Detection of copy number variation using FACETS.

Chr	Start	End	CN	Type	Gene	Database	CDS length
2	20187672	20190900	4	DUP	WDR35	NR	144
2	20191101	20247650	0	DEL	LAPTM4A	NR	597
2	20191101	20247650	0	DEL	MATN3	NR	1,469
2	20355792	20530450	0	DEL	PUM2	NR	3,221
2	20355792	20530450	0	DEL	SDC1	NR	938
2	20777101	20906150	0	DEL	GDF7	NR	1,355
2	20777101	20906150	0	DEL	HS1BP3	NR	1,186
2	20777101	20906150	0	DEL	LDAH	NR	277
2	20914451	21012750	0	DEL	LDAH	NR	707
4	1782501	1812666	25	DUP	FGFR3	CGC	2,444
4	8194101	8213528	26	DUP	SH3TC1	NR	249
4	130016051	131946400	3	DUP	C4orf33	NR	605
4	152178751	153716718	3	DUP	FAM160A1	NR	3,134
4	152178751	153716718	3	DUP	FBXW7	CGC	2,135
4	152178751	153716718	3	DUP	GATB	NR	1,687
4	152178751	153716718	3	DUP	PRSS48	NR	1,046
4	152178751	153716718	3	DUP	TIGD4	NR	1,540
4	152178751	153716718	3	DUP	TMEM154	NR	559
6	37955401	42203650	0	DEL	APOBEC2	NR	677
6	37955401	42203650	0	DEL	BTBD9	NR	1,849
6	37955401	42203650	0	DEL	BYSL	NR	1,321
6	37955401	42203650	0	DEL	C6orf132	NR	3,572
6	37955401	42203650	0	DEL	CCND3	CGC	884
6	37955401	42203650	0	DEL	DAAM2	NR	3,231
6	37955401	42203650	0	DEL	DNAH8	NR	1,4216
6	37955401	42203650	0	DEL	FOXP4	NR	2,059
6	37955401	42203650	0	DEL	FRS3	NR	1,484
6	37955401	42203650	0	DEL	GLO1	NR	561
6	37955401	42203650	0	DEL	GLP1R	NR	1,405
6	37955401	42203650	0	DEL	GUCA1A	NR	610
6	37955401	42203650	0	DEL	GUCA1B	NR	607
6	37955401	42203650	0	DEL	KCNK16	NR	974
6	37955401	42203650	0	DEL	KCNK17	NR	1,004
6	37955401	42203650	0	DEL	KCNK5	NR	1,505
6	37955401	42203650	0	DEL	KIF6	NR	2,468
6	37955401	42203650	0	DEL	LRFN2	NR	2,372
6	37955401	42203650	0	DEL	MDFI	NR	745
6	37955401	42203650	0	DEL	MED20	NR	643
6	37955401	42203650	0	DEL	MOCS1	NR	1,168
6	37955401	42203650	0	DEL	MRPS10	NR	613
6	37955401	42203650	0	DEL	NCR2	NR	836
6	37955401	42203650	0	DEL	NFYA	NR	1,053
6	37955401	42203650	0	DEL	OARD1	NR	464
6	37955401	42203650	0	DEL	PGC	NR	1,176
6	37955401	42203650	0	DEL	PRICKLE4	NR	1,161
6	37955401	42203650	0	DEL	SAYSD1	NR	554
6	37955401	42203650	0	DEL	TAF8	NR	942
6	37955401	42203650	0	DEL	TFEB	CGC	1,482
6	37955401	42203650	0	DEL	TOMM6	NR	227
6	37955401	42203650	0	DEL	TREM1	NR	709
6	37955401	42203650	0	DEL	TREM2	NR	698
6	37955401	42203650	0	DEL	TREML1	NR	942
6	37955401	42203650	0	DEL	TREML2	NR	971
6	37955401	42203650	0	DEL	TREML4	NR	608
6	37955401	42203650	0	DEL	TRERF1	NR	539
6	37955401	42203650	0	DEL	TSPO2	NR	516
6	37955401	42203650	0	DEL	UNC5CL	NR	1,565
6	37955401	42203650	0	DEL	USP49	NR	2,072
6	37955401	42203650	0	DEL	ZFAND3	NR	576

Table SIII. Continued.

Chr	Start	End	CN	Type	Gene	Database	CDS length
10	122150551	122422650	0	DEL	PLPP4	NR	823
10	122457898	122786200	0	DEL	WDR11	NR	3,704
10	122823876	123395200	0	DEL	FGFR2	CGC	2486
10	123468060	123665100	0	DEL	ATE1	NR	981
10	123665339	123682725	0	DEL	ATE1	NR	416
10	123682851	123704600	0	DEL	ATE1	NR	172
11	1535751	2137939	30	DUP	CTSD	NR	1,248
11	1535751	2137939	30	DUP	DUSP8	NR	1,884
11	1535751	2137939	30	DUP	HOTS	NR	457
11	1535751	2137939	30	DUP	IFITM10	NR	690
11	1535751	2137939	30	DUP	KRTAP5-1	NR	838
11	1535751	2137939	30	DUP	KRTAP5-2	NR	535
11	1535751	2137939	30	DUP	KRTAP5-3	NR	718
11	1535751	2137939	30	DUP	KRTAP5-4	NR	689
11	1535751	2137939	30	DUP	KRTAP5-5	NR	715
11	1535751	2137939	30	DUP	KRTAP5-6	NR	391
11	1535751	2137939	30	DUP	LSP1	NR	1,414
11	1535751	2137939	30	DUP	MRPL23	NR	467
11	1535751	2137939	30	DUP	SYT8	NR	1,218
11	1535751	2137939	30	DUP	TNNI2	NR	555
11	1535751	2137939	30	DUP	TNNT3	NR	792
12	9172443	11351400	3	DUP	A2M	NR	4,461
12	9172443	11351400	3	DUP	CD69	NR	605
12	9172443	11351400	3	DUP	CLEC12A	NR	835
12	9172443	11351400	3	DUP	CLEC12B	NR	837
12	9172443	11351400	3	DUP	CLEC1A	NR	849
12	9172443	11351400	3	DUP	CLEC1B	NR	696
12	9172443	11351400	3	DUP	CLEC2A	NR	530
12	9172443	11351400	3	DUP	CLEC2B	NR	454
12	9172443	11351400	3	DUP	CLEC2D	NR	591
12	9172443	11351400	3	DUP	CLEC7A	NR	750
12	9172443	11351400	3	DUP	CLEC9A	NR	732
12	9172443	11351400	3	DUP	CLECL1	NR	579
12	9172443	11351400	3	DUP	EIF2S3L	NR	1,420
12	9172443	11351400	3	DUP	GABARAPL1	NR	358
12	9172443	11351400	3	DUP	KLRB1	NR	684
12	9172443	11351400	3	DUP	KLRC1	NR	708
12	9172443	11351400	3	DUP	KLRC2	NR	702
12	9172443	11351400	3	DUP	KLRC3	NR	780
12	9172443	11351400	3	DUP	KLRC4	NR	481
12	9172443	11351400	3	DUP	KLRC4-KLRK1	NR	658
12	9172443	11351400	3	DUP	KLRD1	NR	565
12	9172443	11351400	3	DUP	KLRF1	NR	705
12	9172443	11351400	3	DUP	KLRF2	NR	630
12	9172443	11351400	3	DUP	KLRK1	NR	658
12	9172443	11351400	3	DUP	MAGOHB	NR	452
12	9172443	11351400	3	DUP	OLR1	NR	828
12	9172443	11351400	3	DUP	PRH1	NR	607
12	9172443	11351400	3	DUP	PRH1-TAS2R14	NR	535
12	9172443	11351400	3	DUP	PRH2	NR	504
12	9172443	11351400	3	DUP	PRR4	NR	408
12	9172443	11351400	3	DUP	PZP	NR	4,485
12	9172443	11351400	3	DUP	SMIM10L1	NR	208
12	9172443	11351400	3	DUP	STYK1	NR	1,278
12	9172443	11351400	3	DUP	TAS2R10	NR	925
12	9172443	11351400	3	DUP	TAS2R13	NR	913
12	9172443	11351400	3	DUP	TAS2R14	NR	955
12	9172443	11351400	3	DUP	TAS2R19	NR	901
12	9172443	11351400	3	DUP	TAS2R20	NR	931

Table SIII. Continued.

Chr	Start	End	CN	Type	Gene	Database	CDS length
12	9172443	11351400	3	DUP	TAS2R30	NR	961
12	9172443	11351400	3	DUP	TAS2R31	NR	931
12	9172443	11351400	3	DUP	TAS2R42	NR	946
12	9172443	11351400	3	DUP	TAS2R43	NR	931
12	9172443	11351400	3	DUP	TAS2R46	NR	931
12	9172443	11351400	3	DUP	TAS2R50	NR	901
12	9172443	11351400	3	DUP	TAS2R7	NR	958
12	9172443	11351400	3	DUP	TAS2R8	NR	931
12	9172443	11351400	3	DUP	TAS2R9	NR	940
12	9172443	11351400	3	DUP	TMEM52B	NR	557
12	9172443	11351400	3	DUP	YBX3	NR	1,128
12	11351664	12303750	0	DEL	BCL2L14	NR	989
12	11351664	12303750	0	DEL	ETV6	CGC	1,367
12	11351664	12303750	0	DEL	LRP6	NR	1,858
12	11351664	12303750	0	DEL	PRB1	NR	999
12	11351664	12303750	0	DEL	PRB2	NR	1,254
12	11351664	12303750	0	DEL	PRB3	NR	934
12	11351664	12303750	0	DEL	PRB4	NR	747
12	12303900	17560791	3	DUP	APOLD1	NR	842
12	12303900	17560791	3	DUP	ARHGDIB	NR	611
12	12303900	17560791	3	DUP	ART4	NR	948
12	12303900	17560791	3	DUP	ATF7IP	NR	3,852
12	12303900	17560791	3	DUP	BORCS5	NR	595
12	12303900	17560791	3	DUP	C12orf60	NR	739
12	12303900	17560791	3	DUP	CDKN1B	CGC/CPG	599
12	12303900	17560791	3	DUP	CREBL2	NR	367
12	12303900	17560791	3	DUP	DDX47	NR	1,380
12	12303900	17560791	3	DUP	DERA	NR	966
12	12303900	17560791	3	DUP	DUSP16	NR	2,004
12	12303900	17560791	3	DUP	EMP1	NR	478
12	12303900	17560791	3	DUP	EPS8	NR	2,489
12	12303900	17560791	3	DUP	ERP27	NR	829
12	12303900	17560791	3	DUP	FAM234B	NR	1,882
12	12303900	17560791	3	DUP	GPR19	NR	1,249
12	12303900	17560791	3	DUP	GPRC5A	NR	1,077
12	12303900	17560791	3	DUP	GPRC5D	NR	1,041
12	12303900	17560791	3	DUP	GRIN2B	NR	4,467
12	12303900	17560791	3	DUP	GSG1	NR	1,096
12	12303900	17560791	3	DUP	GUCY2C	NR	3,249
12	12303900	17560791	3	DUP	H2AFJ	NR	391
12	12303900	17560791	3	DUP	HEBP1	NR	574
12	12303900	17560791	3	DUP	HIST4H4	NR	313
12	12303900	17560791	3	DUP	LMO3	NR	508
12	12303900	17560791	3	DUP	LRP6	NR	2,876
12	12303900	17560791	3	DUP	MANSC1	NR	1,299
12	12303900	17560791	3	DUP	MGP	NR	392
12	12303900	17560791	3	DUP	MGST1	NR	471
12	12303900	17560791	3	DUP	PDE6H	NR	255
12	12303900	17560791	3	DUP	PLBD1	NR	1,673
12	12303900	17560791	3	DUP	PTPRO	NR	3,677
12	12303900	17560791	3	DUP	RERG	NR	604
12	12303900	17560791	3	DUP	SLC15A5	NR	1,749
12	12303900	17560791	3	DUP	SMCO3	NR	679
12	12303900	17560791	3	DUP	STRAP	NR	1,063
12	12303900	17560791	3	DUP	WBP11	NR	1,937
12	133806401	133841202	3	DUP	ANHX	NR	379

CGC, Cancer Gene Census; CN, copy number of the genes; CPG, Cancer Predisposition Genes; NR, not reported; DEL, deletion; DUP, duplication; Chr, chromosome.

Table SIV. GO and KEGG enrichments for somatic mutations using clusterProfiler.

A, GO enrichment analysis

ID	Description	P-value	Q-value	Gene	Count
GO:0030277	Maintenance of gastrointestinal epithelium	$2.5x10^{-6}$	0.001	MUC6, MUC2, MUC4	3
GO:0010669	Epithelial structure maintenance	$6.2x10^{-6}$	0.001	MUC6, MUC2, MUC4	3
GO:0016266	O-glycan processing	$7.5x10^{-5}$	0.006	MUC6, MUC2, MUC4	3
GO:0002223	Stimulatory C-type lectin receptor signaling pathway	$9.0x10^{-5}$	0.006	MUC6, MUC2, MUC4	3
GO:0002220	Innate immune response activating cell surface receptor signaling pathway	$1.0x10^{-4}$	0.006	MUC6, MUC2, MUC4	3
GO:0022600	Digestive system process	$3.0x10^{-4}$	0.014	MUC6, MUC2, MUC4	3
GO:0006493	Protein O-linked glycosylation	$3.4x10^{-4}$	0.014	MUC6, MUC2, MUC4	3
GO:0045109	Intermediate filament organization	$4.0x10^{-4}$	0.015	TCHH, NEFL	2
GO:0030216	Keratinocyte differentiation	$6.5x10^{-4}$	0.021	KRTAP5-3, TCHH, RPTN, POU3F1	4
GO:0007586	Digestion	$7.8x10^{-4}$	0.023	MUC6, MUC2, MUC4	3
GO:0009913	Epidermal cell differentiation	$1.2x10^{-3}$	0.032	KRTAP5-3, TCHH, RPTN, POU3F1	4
GO:0045104	Intermediate filament cytoskeleton organization	$2.0x10^{-3}$	0.042	TCHH, NEFL	2
GO:0045103	Intermediate filament-based process	$2.1x10^{-3}$	0.042	TCHH, NEFL	2
GO:0043588	Skin development	$2.1x10^{-3}$	0.042	KRTAP5-3, TCHH, RPTN, POU3F1	4
GO:0002429	Immune response-activating cell surface receptor signaling pathway	$2.2x10^{-3}$	0.042	MUC6, MUC2, MUC4, HLA-DRB1	4
GO:0002768	Immune response-regulating cell surface receptor signaling pathway	$2.8x10^{-3}$	0.051	MUC6, MUC2, MUC4, HLA-DRB1	4
GO:0008544	Epidermis development	$3.1x10^{-3}$	0.051	KRTAP5-3, TCHH, RPTN, POU3F1	4
GO:0001894	Tissue homeostasis	$3.2x10^{-3}$	0.051	MUC6, MUC2, MUC4	3
GO:0031424	Keratinization	$3.3x10^{-3}$	0.051	KRTAP5-3, TCHH, RPTN	3
GO:0048871	Multicellular organismal homeostasis	$3.4x10^{-3}$	0.051	MUC6, MUC2, ALMS1, MUC4	4

B, KEGG enrichment analysis

ID	Description	P-value	Q-value	Gene	Count
hsa05164	Influenza A	0.001	0.064	HLA-DRB1, IFNA4, SLC25A5	3
hsa05320	Autoimmune thyroid disease	0.002	0.064	HLA-DRB1, IFNA4	2
hsa04217	Necroptosis	0.021	0.208	IFNA4, SLC25A5	2
hsa04022	cGMP-PKG signaling pathway	0.022	0.208	SLC8A2, SLC25A5	2
hsa05152	Tuberculosis	0.025	0.208	HLA-DRB1, IFNA4	2
hsa04020	Calcium signaling pathway	0.027	0.208	SLC8A2, SLC25A5	2
hsa05168	Herpes simplex virus 1 infection	0.028	0.208	ZNF730, HLA-DRB1, IFNA4	3
hsa05169	Epstein-Barr virus infection	0.031	0.208	HLA-DRB1, IFNA4	2
hsa05166	Human T-cell leukemia virus 1 infection	0.036	0.216	HLA-DRB1, SLC25A5	2

GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.