

Supplementary Table S1. List of studied 409 oncogenes and tumor suppressor genes.

Gene names										
ABL1	BIRC2	COL1A1	ERCC4	GDNF	JUN	MDM4	NOTCH4	PMS1	SDHD	TLR4
ABL2	BIRC3	CRBN	ERCC5	GNA11	KAT6A	MEN1	NPM1	PMS2	9-Sep	TLX1
ACVR2A	BIRC5	CREB1	ERG	GNAQ	KAT6B	MET	NRAS	POT1	SETD2	TNFAIP3
ADAMTS20	BLM	CREBBP	ESR1	GNAS	KDM5C	MITF	NSD1	POU5F1	SF3B1	TNFRSF14
AFF1	BLNK	CRKL	ETS1	GPR124	KDM6A	MLH1	NTRK1	PPARG	SGK1	TNK2
AFF3	BMPR1A	CRTC1	ETV1	GRM8	KDR	MLLT10	NTRK3	PPP2R1A	SH2D1A	TOP1
AKAP9	BRAF	CSF1R	ETV4	GUCY1A2	KEAP1	MMP2	NUMA1	PRDM1	SMAD2	TP53
AKT1	BRD3	CSMD3	EXT1	HCAR1	KIT	MN1	NUP214	PRKAR1A	SMAD4	TPR
AKT2	BRIP1	CTNNA1	EXT2	HIF1A	KLF6	MPL	NUP98	PRKDC	SMARCA4	TRIM24
AKT3	BTK	CTNNB1	EZH2	HLF	KMT2A	MRE11A	PAK3	PSIP1	SMARCB1	TRIM33
ALK	BUB1B	CYLD	FANCA	HNF1A	KMT2C	MSH2	PALB2	PTCH1	SMO	TRIP11
AMER1	CARD11	CYP2C19	FANCC	HOOK3	KMT2D	MSH6	PARP1	PTEN	SMUG1	TRRAP
APC	CASC5	CYP2D6	FANCD2	HRAS	KRAS	MTOR	PAX3	PTGS2	SOCS1	TSC1
AR	CBL	DAXXF	FANCF	HSP90AA1	LAMP1	MTR	PAX5	PTPN11	SOX11	TSC2
ARID1A	CCND	DCC	FANCF	HSP90	LCK	MTRR	PAX7	PTPRD	SOX2	TSHR

	1		G	AB1							
ARID2	CCND2	DDB2	FAS	ICK	LIFR	MUC1	PAX8	PTPRT	SRC	UBR5	
ARNT	CCNE1	DDIT3	FBXW7	IDH1	LPHN3	MUTYH	PBRM1	RAD50	SSX1	UGT1A1	
ASXL1	CD79A	DDR2	FGFR1	IDH2	LPP	MYB	PBX1	RAF1	STK11	USP9X	
ATF1	CD79B	DEK	FGFR2	IGF1R	LRP1B	MYC	PDE4DIP	RALGDS	STK36	VHL	
ATM	CDC73	DICER1	FGFR3	IGF2	LTF	MYCL	PDGFB	RARA	SUFU	WAS	
ATR	CDH13A	DNMT3A	FGFR4	IGF2R	LTK	MYCN	PDGFR	RB1	SYK	WHSC1	
ATRX	CDH11	DPYD	FH	IKBKB	MAF	MYD88	PDGFRB	RECQL4	SYNE1	WRN	
AURKA	CDH2	DST	FLCN	IKBKE	MAFB	MYH11	PER1	REL	TAF1	WT1	
AURKB	CDH20	EGFR	FLI1	IKZF1	MAGEA1	MYH9	PGAP3	RET	TAF1L	XPA	
AURKC	CDH5	EML4	FLT1	IL2	MAGI1	NBN	PHOX2B	RHOH	TAL1	XPC	
AXL	CDK12	EP300	FLT3	IL21R	MALT1	NCOA1	PIK3C2B	RNAS	TBX22	XPO1	
BAI3	CDK4	EP400	FLT4	IL6ST	MAML2	NCOA2	PIK3CA	RNF2	TCF12	XRCC2	
BAP1	CDK6	EPHA3	FN1	IL7R	MAP2K1	NCOA4	PIK3CB	RNF213	TCF3	ZNF384	
BCL10	CDK8	EPHA7	FOXL2	ING4	MAP2K2	NF1	PIK3CD	ROS1	TCF7L1	ZNF521	
BCL11A	CDKN2A	EPHB1	FOXO1	IRF4	MAP2K4	NF2	PIK3CG	RPS6KA2	TCF7L2		
BCL11B	CDKN	EPHB4	FOXO	IRS2	MAP3	NFE2	PIK3R	RRM1	TCL1A		

	2B		3		K7	L2	1		
BCL2	CDKN	EPHB6	FOXP	ITGA10	MAPK	NFKB	PIK3R	RUNX	TET1
	2C		1		1	1	2	1	
BCL2L1	CEBP	ERBB2	FOXP	ITGA9	MAPK	NFKB	PIM1	RUNX	TET2
	A		4		8	2		1T1	
BCL2L2	CHEK	ERBB3	FZR1	ITGB2	MARK	NIN	PKHD	SAMD	TFE3
	1				1		1	9	
BCL3	CHEK	ERBB4	G6PD	ITGB3	MARK	NKX2	PLAG1	SBDS	TGFBR
	2				4	-1			2
BCL6	CIC	ERCC1	GATA	JAK1	MBD1	NLRP	PLCG1	SDHA	TGM7
			1			1			
BCL9	CKS1	ERCC2	GATA	JAK2	MCL1	NOTC	PLEKH	SDHB	THBS1
	B		2			H1	G5		
BCR	CMPK	ERCC3	GATA	JAK3	MDM	NOTC	PML	SDHC	TIMP3
	1		3		2	H2			

Supplementary Table S2. The aqueous metabolites were defined in the CIN type from ESI+/- liquid chromatography-mass spectrometry.

CIN type		Metabolites	VIP score	Fold change (tumor/normal)	P value
LC-MS	1	3'-AMP	0.095	0.979	0.810
ESI-	2	Adenosine phosphosulfate	0.549	0.731	0.417
	3	Adenylsuccinic acid	0.110	1.070	0.824
	4	Alanine	1.000	2.371	0.196
	5	Ascorbic acid	1.793	0.514	0.171
	6	Aspartic acid	1.309	2.029	0.043*
	7	beta-citryl-L-glutamic acid	0.240	0.942	0.725
	8	Glutamic acid	1.005	1.427	0.061
	9	Glutathione	0.937	0.734	0.253
	10	Glycine	0.551	1.580	0.420
	11	Guanosine monophosphate	0.404	0.895	0.289
	12	Inosine	0.664	1.276	0.157
	13	Inosinic acid	1.572	0.506	0.008*
	14	Isoleucine	1.194	1.723	0.060
	15	Lactic acid	0.846	1.474	0.090
	16	NAD	0.254	0.952	0.602
	17	Oxidized glutathione	1.642	2.249	0.018*
	18	Phenylalanine	1.016	1.492	0.029*
	19	Taurine	0.079	1.094	0.878
	20	Tryptophan	0.760	1.367	0.105
	21	Tyrosine	1.408	1.758	0.074
	22	Uric acid	0.524	1.321	0.325
	23	Uridine 5'-monophosphate	1.035	1.522	0.030*
	24	Uridine diphosphate-N-acetylglucosamine	1.264	2.006	0.036*
	25	Xanthine	1.409	2.386	0.063

LC-MS	1	3'-AMP	0.163	1.074	0.653
ESI+	2	Acetylcarnitine	0.597	0.797	0.152
	3	Adenine	0.143	0.970	0.633
	4	Adenosine	1.133	1.795	0.020*
	5	ADP	0.572	0.813	0.084
	6	Alanine	0.061	1.093	0.892
	7	Butyrylcarnitine	1.218	0.590	0.014*
	8	Carnitine	0.553	1.330	0.159
	9	Choline	0.451	1.415	0.376
	10	Citicoline	1.751	2.886	0.033*
	11	Creatine	0.002	1.067	0.996
	12	Glutamic acid	1.219	2.101	0.011*
	13	Glutamine	1.039	1.923	0.041*
	14	Glutathione	1.214	0.582	0.042*
	15	Glycerophosphocholine	0.319	1.517	0.591
	16	Guanine	0.500	1.270	0.228
	17	Guanosine monophosphate	0.458	0.875	0.150
	18	Hexanoylcarnitine	0.951	0.642	0.068
	19	Histidine	0.057	0.997	0.895
	20	Hydroxyhexanoylcarnitine	1.883	0.397	0.013*
	21	Hypoxanthine	0.141	1.044	0.686
	22	Inosinic acid	2.046	0.359	0.018*
	23	Isoleucine	0.656	1.320	0.079
	24	Isovalerylcarnitine	1.657	0.346	0.004*
	25	Cysteinylglycine	1.071	0.649	0.091
	26	NAD	0.663	0.789	0.119
	27	Niacinamide	0.262	1.082	0.449
	28	Oxidized glutathione	1.157	1.748	0.005*
	29	Phenylalanine	0.834	1.373	0.011*
	30	Phosphocholine	0.963	1.800	0.052
	31	Proline	0.977	1.870	0.053

32	Propionyl-L-carnitine	1.011	0.590	0.055
33	Succinyladenosine	1.671	3.434	0.011*
34	Taurine	0.148	0.979	0.753
35	Threonine	1.714	0.394	0.006*
36	Tryptophan	0.380	1.187	0.375

Supplementary Table S3. The aqueous metabolites were defined in the non-CIN type from ESI+/- liquid chromatography-mass spectrometry.

non-CIN type		Metabolites	VIP score	Fold change (tumor/normal)	P value
LC-MS	1	3'-AMP	0.716	0.786	0.346
ESI-	2	Adenosine phosphosulfate	1.584	0.554	0.057
	3	Adenylsuccinic acid	0.027	1.020	0.970
	4	Alanine	1.707	1.583	0.170
	5	Ascorbic acid	0.429	1.276	0.762
	6	Aspartic acid	1.501	1.597	0.051
	7	beta-citryl-L-glutamic acid	0.812	1.222	0.274
	8	Glutamic acid	0.908	1.198	0.190
	9	Glutathione	0.740	0.771	0.344
	10	Glycine	0.051	0.988	0.937
	11	Guanosine monophosphate	0.188	0.928	0.774
	12	Inosine	0.430	1.210	0.536
	13	Inosinic acid	0.489	0.703	0.632
	14	Isoleucine	1.163	1.643	0.158
	15	Lactic acid	0.813	1.219	0.156
	16	NAD	1.584	0.599	0.047*
	17	Oxidized glutathione	1.013	0.768	0.323
	18	Phenylalanine	0.907	1.336	0.157
	19	Taurine	0.960	1.287	0.140
	20	Tryptophan	0.391	1.174	0.536
	21	Tyrosine	0.707	1.162	0.553
	22	Uric acid	0.434	1.043	0.565
	23	Uridine 5'-monophosphate	0.561	1.065	0.607
	24	Uridine diphosphate-N-acetylglucosamine	0.332	1.238	0.742
	25	Xanthine	2.360	2.085	0.007*

LC-MS	1	3'-AMP	0.344	0.868	0.565
ESI+	2	Acetylcarnitine	0.704	0.827	0.181
	3	Adenine	0.575	0.740	0.396
	4	Adenosine	1.060	1.509	0.265
	5	ADP	0.929	0.754	0.202
	6	Alanine	0.088	1.013	0.896
	7	Butyrylcarnitine	1.000	0.758	0.074
	8	Carnitine	0.024	0.925	0.973
	9	Choline	0.444	0.688	0.614
	10	Citicoline	2.026	2.321	0.094
	11	Creatine	0.079	1.017	0.908
	12	Cysteinylglycine	0.747	0.799	0.202
	13	Glutamic acid	1.424	1.688	0.031*
	14	Glutamine	1.369	1.954	0.069
	15	Glutathione	0.569	0.839	0.336
	16	Glycerophosphocholine	0.433	0.553	0.682
	17	Guanine	1.225	1.499	0.059
	18	Guanosine monophosphate	0.110	0.949	0.855
	19	Hexanoylcarnitine	0.887	0.830	0.060
	20	Histidine	0.860	0.965	0.446
	21	Hydroxyhexanoycarnitine	1.964	0.460	0.095
	22	Hypoxanthine	0.522	1.228	0.404
	23	Inosinic acid	0.328	0.498	0.817
	24	Isoleucine	0.570	1.193	0.283
	25	Isovalerylcarnitine	0.885	0.582	0.333
	26	NAD	1.561	0.579	0.030*
	27	Niacinamide	0.960	1.244	0.064
	28	Oxidized glutathione	1.678	1.676	0.019*
	29	Phenylalanine	0.314	1.119	0.558
	30	Phosphocholine	0.088	0.830	0.915

31	Proline	1.542	1.569	0.003*
32	Propionyl-L-carnitine	1.147	0.500	0.168
33	Succinyladenosine	1.929	3.207	0.031*
34	Taurine	0.675	1.224	0.262
35	Threonine	0.476	0.678	0.626
36	Tryptophan	0.139	1.000	0.808

Supplementary Table S4. Alteration genes of GC patients in TCGA system and Lauren system.

Patient	TCGA system	Lauren system	Number of alteration gene	Percentage of alteration gene
1	CIN type	intestinal	218	53.30%
2		intestinal	148	35.90%
3		intestinal	120	29.30%
4		mixed	97	23.70%
5		intestinal	64	15.60%
6		intestinal	58	14.20%
7		mixed	49	12.00%
8		intestinal	41	10.00%
9		mixed	32	7.80%
1	non-CIN type	mixed	17	4.20%
2		diffuse	13	3.20%
3		diffuse	12	2.90%
4		mixed	12	2.90%
5		intestinal	11	2.70%
6		diffuse	8	2.00%
7		diffuse	5	1.20%
8		diffuse	3	0.70%
9		diffuse	2	0.50%
10		mixed	2	0.50%