

Abundant copy-number loss of CYCLOPS and STOP genes in gastric adenocarcinoma

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Supplementary Tables

Table S1. Clinical and pathological information on tumors studied.

Category	Subcategory	All tumors	Tumors with ASCAT estimate	Tumors without ASCAT estimate	P-value, with vs. without ASCAT estimate	Test
Age (years)	Range	25-92	25-92	32-88	0.238	t
	Median	67	65	68		
Pathologist-estimated tumor content (%)	Range	0-90	0-90	5-60	0.034	One-sided Wilcoxon rank-sum
	Median	35	60	20		
Gender	Female	41	23	18	0.15	Fisher's exact
	Male	72	51	21		
Laurén classification	Diffuse	44	25	19	0.152	Fisher's exact (excluding "Mixed")
	Intestinal	62	44	18		
	Mixed	7	5	2		
TNM Stage	I	14	10	4	0.961	Chisq
	II	20	13	7		
	III	61	39	22		
	IV	18	12	6		
G-INT / G-DIF subtype	G-INT	57	42	15	0.062	Fisher's exact (excluding NC)
	G-DIF	45	25	20		
	NC	11	7	4		
Overall survival time (months)	Range	0.2-178.1	0.2-167.0	2.27-178.1	0.151	Kaplan-Meier log-rank ^a
	Median ^a	30.0	24.6	56.9		
Tumor grade	Poorly differentiated	69	44	25	0.935	Fisher's exact
	Moderately differentiated	40	27	13		
	Well differentiated	4	3	1		

t: t-test; G-INT: genomic intestinal [1]; G-DIF: genomic diffuse [1]; NC: not classifiable; Chisq: chi-squared test.

^a Median survival and Kaplan-Meier log-rank tests calculated by the survfit and survdiff functions in the R package "survival" (<http://cran.r-project.org/web/packages/survival/index.html>) [2].

Table S3. Values of parameters used in ASCAT analysis. See notes at end of table for explanations of the parameters.

Sample ID	ASCAT version	μ factor ^a	Germline BAF limits ^b	Min goodness of fit ^c	Segment length ^d
970005	2.0	1.5	0.35, 0.65	85	100
980011	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
980021	2.0	1.5	0.35, 0.65	85	100
980029	2.0	1.5	0.35, 0.65	85	100
980097	2.0	1.5	0.35, 0.65	85	100
980156	2.0	1.5	0.35, 0.65	85	100
980369	2.0	1.5	0.35, 0.65	65	100
980390	2.0	1.5	0.35, 0.65	65	800
980401	2.0	1.5	0.35, 0.65	85	100
980417	2.0	1.3	0.35, 0.65	85	100
980437	2.0	1.5	0.35, 0.65	85	100
980447	2.0	1.5	0.35, 0.65	65	100
990005	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
990010	2.0	1.9	0.35, 0.65	85	100
990041	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
990044	2.0	1.5	0.35, 0.65	85	100
990046	2.0	1.5	0.35, 0.65	65	100
990060	2.0	1.5	0.35, 0.65	85	100
990069	2.0	1.5	0.35, 0.65	85	100
990071	2.0	1.5	0.35, 0.65	85	100
990090	2.0	1.5	0.35, 0.65	85	100
990097	2.0	1.3	0.35, 0.65	85	100
990098	2.0	1.5	0.35, 0.65	65	800
990108	2.0	1.3	0.35, 0.65	65	100
990111	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
990170	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
990172	2.0	1.9	0.35, 0.65	75	100
990195	2.0	1.5	0.35, 0.65	85	100
990203	2.0	1.5	0.35, 0.65	85	100
990228	2.0	1.5	0.35, 0.65	85	100
990275	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
990300	2.0	1.3	0.35, 0.65	85	100
990339	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
990355	2.0	1.5	0.35, 0.65	85	100
990396	2.0	1.5	0.35, 0.65	85	100
990412	2.0	1.5	0.35, 0.65	65	100
990474	2.0	1.5	0.35, 0.65	85	100
990475	2.0	1.9	0.35, 0.65	85	100
990489	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
990515	2.0	1.5	0.35, 0.65	85	100
2000040	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
2000068	2.0	1.5	0.35, 0.65	85	100
2000085	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
2000088	2.0	1.5	0.35, 0.65	85	100
2000169	2.0	1.5	0.35, 0.65	65	100
2000175	2.0	1.5	0.35, 0.65	85	100
2000201	2.0	1.5	0.35, 0.65	85	100
2000242	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1

2000286	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
2000303	2.0	1.5	0.3, 0.7	85	100
2000362	2.0	1.5	0.35, 0.65	85	100
2000403	2.0	1.5	0.35, 0.65	65	100
2000433	2.0	1.5	0.35, 0.65	85	100
2000441	2.0	1.3	0.35, 0.65	85	100
2000877	2.0	1.5	0.35, 0.65	85	100
2000892	2.0	1.5	0.35, 0.65	85	100
20020011	2.0	1.9	0.35, 0.65	85	100
20020448	2.0	1.5	0.35, 0.65	65	800
20020720	2.0	1.5	0.35, 0.65	85	100
20263644	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
32226415	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
38877042	2.0	1.5	0.35, 0.65	85	100
46404174	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1
47492137	2.0	1.9	0.35, 0.65	85	100
57689477	2.0	1.5	0.35, 0.65	85	100
57701999	2.0	1.5	0.35, 0.65	85	100
58947266	2.0	1.5	0.35, 0.65	85	100
61669256	2.0	1.5	0.35, 0.65	85	100
66811693	2.0	1.5	0.35, 0.65	85	100
73291145	2.0	1.5	0.35, 0.65	85	100
76629543	2.0	1.5	0.35, 0.65	80	100
87622942	2.0	1.3	0.35, 0.65	85	100
91228050	2.0	1.9	0.35, 0.65	85	100
96141474	2.1	1.5	0.35, 0.65	85	as determined by ASCAT 2.1

^a μ factor is used by the segmentation algorithm to determine if the BAF is 0.5 or if there is allelic imbalance at that segment.

^b Germline BAF limits are used to remove from analysis those SNPs that are not heterozygous in the non-malignant samples; any probes with BAF values above or below these limits are considered homozygous.

^c Min goodness of fit is the minimum goodness of fit allowed for a sample; ASCAT evaluates the goodness of fit for a grid of possible values of average ploidy and tumor content, then picks the optimal solution which should have a goodness of fit value higher than this parameter.

^d Segment length is used by the segmentation algorithm in ASCAT 2.0, and refers to the number of informative probes in a segment.

Table S4. Tumors for which ASCAT was unable to estimate allele-specific copy numbers.

Sample ID	Problem
970003	Excessively variable LRR
970017	Flat BAF
980035	Flat BAF
980251	Flat BAF
980319	Flat BAF
980327	Flat BAF
980344	Excessively variable LRR
980386	Flat BAF
980418	Flat BAF
980436	Flat BAF
980442	Flat BAF
990015	Flat BAF
990024	Flat BAF
990068	Excessively variable LRR
990070	Apparently low tumor content
990089	Apparently low tumor content
990119	Flat BAF
990129	Excessively variable LRR
990136	Excessively variable LRR
990205	Excessively variable LRR
990247	Flat BAF
990413	Flat BAF
990424	Flat BAF
2000114	Flat BAF
2000159	Flat BAF
2000178	Flat BAF
2000238	Flat BAF
2000291	Flat BAF
2000346	Flat BAF
2000479	Flat BAF
2000617	Excessively variable LRR
2000920	Excessively variable LRR
2001159	Flat BAF
2001226	Excessively variable LRR
2001229	Flat BAF
2001241	Excessively variable LRR
37262942	Excessively variable LRR
43658255	Excessively variable LRR
65256293	Flat BAF

Table S5. LOH and copy number alterations in 74 gastric adenocarcinomas.

Sample ID	Average ploidy	Tumor content	Proportion of probes with		
			LOH	CN loss	CN gain
970005	2.57	0.58	0.58	0.11	0.00
980011	1.84	0.32	0.37	0.32	0.00
980021	2.81	0.77	0.33	0.00	0.03
980029	2.31	0.57	0.47	0.02	0.09
980097	2.09	0.54	0.02	0.00	0.00
980156	4.18	1	0.36	0.24	0.10
980369	4.08	0.25	0.11	0.01	0.00
980390	3.05	0.76	0.40	0.25	0.01
980401	2.08	0.32	0.15	0.00	0.02
980417	1.64	0.35	0.30	0.17	0.01
980437	4.19	0.6	0.00	0.01	0.00
980447	4.23	0.37	0.22	0.02	0.02
990005	1.97	0.39	0.08	0.03	0.00
990010	2.33	0.34	0.31	0.00	0.14
990041	2	0.27	0.22	0.07	0.00
990044	2.65	0.45	0.37	0.05	0.03
990046	3.91	0.36	0.15	0.16	0.01
990060	2.31	0.5	0.04	0.02	0.06
990069	2.98	1	0.47	0.35	0.02
990071	2.2	0.75	0.17	0.09	0.04
990090	3.41	0.48	0.23	0.31	0.07
990097	2.19	0.27	0.02	0.00	0.10
990098	3.09	0.88	0.33	0.37	0.02
990108	4.26	0.2	0.29	0.09	0.01
990111	2.47	1	0.23	0.00	0.06
990170	2	0.32	0.08	0.00	0.00
990172	2.94	0.45	0.35	0.50	0.06
990195	1.64	0.42	0.43	0.40	0.02
990203	1.81	0.48	0.37	0.27	0.03
990228	2.2	0.36	0.06	0.05	0.04
990275	3.56	0.53	0.34	0.11	0.10
990300	3.83	0.81	0.00	0.01	0.00
990339	2	0.29	0.15	0.06	0.00
990355	2	0.35	0.16	0.08	0.01
990396	2.14	0.41	0.51	0.15	0.09
990412	2.32	0.63	0.53	0.07	0.07
990474	2.3	0.18	0.00	0.00	0.08
990475	1.96	0.67	0.15	0.14	0.04
990489	2.01	0.25	0.07	0.02	0.00
990515	4.34	0.98	0.31	0.43	0.08
2000040	2	0.4	0.19	0.03	0.00
2000068	4.04	0.42	0.43	0.08	0.02
2000085	2	0.28	0.03	0.00	0.00
2000088	3.61	0.62	0.00	0.03	0.03
2000169	4.41	0.79	0.01	0.00	0.04
2000175	2.16	0.48	0.44	0.19	0.11

Table S5. LOH and copy number alterations in 74 gastric adenocarcinomas.

Sample ID	Average ploidy	Tumor content	Proportion of probes with		
			LOH	CN loss	CN gain
2000201	4.06	0.39	0.18	0.10	0.03
2000242	2	0.23	0.14	0.00	0.00
2000286	2	0.22	0.08	0.00	0.00
2000303	3.87	0.54	0.00	0.02	0.01
2000362	4.07	0.42	0.25	0.04	0.01
2000403	3.67	0.25	0.44	0.21	0.01
2000433	1.73	0.35	0.38	0.31	0.02
2000441	3.98	0.93	0.00	0.01	0.01
2000877	2.79	1	0.35	0.02	0.07
2000892	1.94	0.77	0.25	0.17	0.02
20020011	3.93	0.35	0.00	0.03	0.00
20020448	4.57	0.69	0.01	0.12	0.02
20020720	2.01	1	0.56	0.33	0.09
20263644	2	0.26	0.03	0.00	0.00
32226415	2	0.25	0.02	0.00	0.00
38877042	1.88	0.47	0.27	0.19	0.01
46404174	2	0.28	0.04	0.00	0.00
47492137	4	0.48	0.00	0.01	0.01
57689477	2.9	0.83	0.35	0.48	0.10
57701999	1.65	0.41	0.36	0.34	0.00
58947266	2.77	0.25	0.78	0.00	0.02
61669256	2.1	0.25	0.18	0.00	0.03
66811693	2.85	0.41	0.28	0.06	0.06
73291145	2.96	0.41	0.21	0.41	0.07
76629543	3.61	0.8	0.27	0.59	0.18
87622942	3.73	0.51	0.00	0.02	0.00
91228050	2.03	0.26	0.02	0.00	0.01
96141474	4.36	0.22	0.10	0.25	0.00
Average		0.50	0.22	0.12	0.03

NOTES:

LOH = loss of heterozygosity

CN loss = proportion of probes that show copy number < average ploidy of sample * 0.7

CN gain = proportion of probes that show copy number > average ploidy of the sample * 1.65

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy- number loss	STOP genes subject to copy-number loss
76629543	452	ABCD3,ACACB,ACSL1,ACTN1,ACVR2A,ACYP2,ADAMTS6,ADH7,ADORA3,ADRBK2,AGXT2L1,AHRR,AKAP12,AKAP7,ALB,ALDH3A2,ALG6,ALP K1,AMD1,ANGPTL3,ANKRD44,ANKRD55,ANXA10,AP3M2,AP3S1,APAF1,ARG2,ARHGAP11A,ARL6IP6,ASB15,ASB17,ASB5,ATG5,ATP5J,ATP6 V1E1,ATRNL1,AUH,AVPR1A,B3GALT1,BAHD1,BAI2,BAZ1A,BCL11A,BCL6,BDP1,BMI1,BPIL2,BPTF,BRAF,BRDT,BRWD1,BST1,BTBD8,BTC,BT G3,C10orf28,C10orf96,C12orf29,C14orf28,C14orf37,C14orf45,C15orf24,C15orf42,C17orf68,C19orf42,C19orf43,C2orf47,C4orf14,C5orf41,C6orf170, C8orf4,C9orf6,C9orf64,CALD1,CAPZA2,CARTPT,CASD1,CASP3,CASP6,CCDC28A,CCDC74A,CCDC74B,CCDC99,CCNB2,CCNG2,CD109,CD30 2,CD38,CDC123,CDC14A,CDH10,CDH9,CDKL2,CENPH,CGA,CH25H,CHCHD7,CHD1,CHI3L2,CHKA,CHUK,CLCC1,CLTC,CNOT4,COBLL1,COC H,COIL,COPS8,COQ10B,COX10,CPT2,CSF1,CTBS,CTLA4,CTNS,CTSL1,CXCL12,CXCL6,CYP26B1,CYP2C19,CYP4X1,DAAM1,DAP,DCN,DCTD ,DDX1,DFFA,DIABLO,DIS3L,DLG2,DNAH10,DNAH5,DNMT3L,DOCK2,DUXA,DYRK2,ECM2,EFCAB6,EGR1,EIF2AK2,EIF4A2,EIF4E2,ELMOD2,EN PP1,ENPP6,EPB41L2,EPHA5,ERAP2,ERI1,ERRFI1,ESR1,FAM175A,FAM81B,FAM84A,FAM8A1,FBXO22,FBXO25,FBXO3,FBXO34,FBXW7,FER, FGF19,FGF2,FGF7,FOS,FOXD2,FRK,FRZB,FSHR,G3BP1,GAB1,GAD1,GCA,GCNT2,GDF9,GEN1,GJA1,GMCL1,GNG5,GPD2,GPR125,GPR158, GPR21,GPR22,GRB14,GRIK1,GTDC1,GTFC3C6,HAT1,HCFC2,HDAC1,HERC3,HERC5,HES1,HMG1,HMHB1,HNRNP1,HNRNPUL1,HNRPLL,HT N1,HTR7,IBTK,IFNA1,IFNA13,IFNAR1,IFNW1,IFRD1,IFT81,IGF1,IL31RA,IL8,IMPAD1,INPP1,INVS,IQGAP1,IRAK3,IRAK4,ISL2,ITGA6,JAM2,JUB,K CNJ3,KCNN2,KCTD18,KIF20B,KLHDC1,KLHL6,KNG1,LAIR1,LIFR,LIP1,LIPJ,LMBRD2,LMO4,LPXN,LRAT,LRFN5,LRRC32,LRRIQ3,LUZP1,LYRM7, MAFG,MAP2K6,MAP3K1,MAPK10,MARCH6,MARS2,MCFD2,MEGF11,MEIS2,METT5D1,METTL3,METTL7A,MFF,MIA2,MIPOL1,MKX,MMADHC,M PP5,MS4A5,MSH6,MTF1,MTF2,MTFR1,MTHFD1,MTUS1,MUDENG,MYEOV,MYLIP,MYO1B,NAIP,NDRG2,NDUFA5,NF2,NHLRC2,NLRP9,NPY1R, NR0B2,NR2F2,NR3C2,NRIP1,NSUN6,NT5DC3,NTRK2,NUDT12,NUDT5,OAT,OGN,OLFML3,ORC4L,PAPOLG,PDE7A,PDHA2,PDZRN4,PENK,PG AP1,PHACTR4,PIGK,PJA2,PKP4,PLCE1,PLN,PLXNC1,PNRC1,PNRC2,POLR2D,PON2,PPP2CB,PPP3CB,PRDM1,PRDM8,PRKACB,PRKAR1A,P RKCA,PRKD1,PRTG,PTGER2,PTGR1,PTN,PTPLA,PTPRK,PTRH2,PTTG1,PTTG1IP,RAB2B,RAB33B,RABGGTB,RAD51C,RAD51L1,RAG2,RAI14 ,RARS2,RBP7,RCAN3,REV3L,RLN2,RNF111,RNF133,RNF170,RNF180,RNF44,RNFT1,RSBN1,RTN1,S1PR1,SAMD13,SCN1A,SDCBP,SEC31A,S EC63,SECISBP2,SEN2,SEN2,SEN2,SERAC1,SERINC1,SLC12A2,SLC19A3,SLC20A1,SLC20A2,SLC25A18,SLC38A2,SLC41A2,SLC46A2,SMU1,SNAI2,SNR NP48,SNX6,SNX9,SOC2, L1,STK17B,STK39,STON1- GTF2A1L,STRADB,STRN3,STXBP4,SUPT7L,SYNJ1,TANK,TARDBP,TAS1R1,TAS2R1,TEK,TEP1,TGFBR1,THAP3,THPO,TIGD2,TLR3,TLR4,TM9 SF3,TMEM144,TMEM56,TMEM59,TMPO,TNKS2,TP53,TPTE,TRAF3IP2,TRAPPC10,TRIM24,TSGA14,TTC9C,TTPA,TUSC3,UBE2U,UGT8,UHRF1 BP1L,USP32,USP33,USP34,USP45,USP53,VIP,VPS26A,VRK2,WHSC1L1,YIPF1,ZBTB1,ZBTB2,ZBTB25,ZBTB43,ZBTB6,ZNF253,ZNF254,ZNF32 6,ZNF330,ZNF417,ZNF43,ZNF549,ZNF571,ZNF587,ZNF626,ZNF644,ZNF664,ZNF675,ZNF800,ZNF804A,ZNF85,ZRANB2

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy- number loss	STOP genes subject to copy-number loss
990172	361	AADACL2,ACACB,ACSL1,ACTN1,ADAMTS6,ADH7,AGTR1,AGXT2L1,ALDH3A2,ALG6,ALPK1,ANGPTL3,ANKRD55,AP3S1,APAF1,ARF4,ARG2,ARHGAP11A,ARIH2,ARL2BP,ARL6,ASB5,ASTE1,ATG3,ATP5J,ATRNL1,ATXN3,AUH,AVPR1A,AXIN1,BACE1,BAHD1,BAI2,BAZ1A,BCL6,BDP1,BPTF,BRWD1,BST1,BTG3,C10orf28,C10orf79,C10orf96,C11orf58,C12orf29,C14orf109,C14orf28,C14orf37,C14orf45,C15orf24,C15orf42,C16orf63,C16orf75,C17orf68,C19orf42,C19orf43,C3orf14,C3orf15,C3orf23,C4orf14,C4orf23,C5orf41,C9orf6,C9orf64,CADM2,CARTPT,CASP3,CASP6,CCDC99,CNB2,CCNG2,CCRL1,CD109,CD38,CDC42BPB,CDKL2,CDKN1A,CDKN3,CENPH,CEP70,CEP97,CGA,CH25H,CHD1,CHUK,COCH,COPS8,COX10,CP,CPT2,CRMP1,CSTA,CTDSPL,CTNS,CTSL1,CX3CR1,CXCL12,CYP2C19,CYP4X1,DAAM1,DCN,DCTD,DEPDC1,DFFA,DIABLO,DIS3L,DLG2, DNAH10,DNMT3L,DOCK2,DYRK2,ECM2,EGR1,EIF4A2,EIF4E2,ELMOD2,ENPP6,EPHA5,ERAP2,ERRFI1,FAM175A,FAM55A,FAM81B,FAM8A1,FBXO22,FBXO3,FBXO34,FBXW7,FER,FEZ1,FGF2,FGF7,FLNB,FOS,FOXD2,FXRD2,G3BP1,GAB1,GABRB1,GCNT2,GDF9,GNPDA2,GPR125,GPR15,GPR21,GRIK1,GRK4,GSK3B,GTF2H1,GTPBP8,HCFC2,HDAC1,HERC3,HERC5,HES1,HESX1,HMGN1,HMHB1,HNRNPH1,HTN1,HTR1F,HTR7, HYAL2,IBTK,IFNA1,IFNA13,IFNAR1,IFNW1,IFT81,IGF1,IL31RA,INA,INVS,IPP,IQCK,IQGAP1,IRAK3,IRAK4,ISL2,JAM2,JUB,KAT2B,KBTD3,KCN N2,KIF20B,KLHDC1,KLHL6,KNG1,KPNA4,LEKR1,LIPI,LIPJ,LNX1,LPXN,LRAT,LRFN5,LRRFIP2,LUZP1,L YRM7,MAFG,MAP2K6,MAP3K1,MAPK10,MEGF11,MEIS2,MELK,METT5D1,METTL3,METTL7A,MIA2,MICAL2,MIPOL1,MITF,MLH1,MME,MMP20,MPP5,MS4A5,MTF1,MTHFD1,MUDENG,MYLIP,NAIP,NDRG2,NDUFB4,NHLRC2,NMNAT3,NPY1R,NR0B2,NR1D2,NR3C2,NRIP1,NRIP3,NRSN1,NT5DC3,NTRK2,NUDT12,OAT,OGN,ORC6L,P2RY13,PARP15,PCGF3,PDHA2,PDZRN4,PFN2,PHACTR4,PHF7,PIK3R4,PJA2,PLCE1,PLCL2,PLSCR4,PLXNC1,PNRC1,PNRC2,PPARG,PPAT,PPP1R13B,PPP3CB,PRDM8,PRKAR1A,PRKCA,PRKD1,PRTG,PTGER2,PTGR1,PTP4A1,PTTG1,PTTG1IP,RAB2B,RAB33B,RAD18,RAD51L1,R AF1,RAG2,RARS2,RBP7,RCAN3,RLN2,RNF111,RNF13,RNF180,RNF44,RNF7,RPE65,RSRC1,RTN1,SEC31A,SECISBP2,SEN2,SEPSECS,SKIL,SLC25A31,SLC37A2,SLC38A2,SLC41A2,SLC46A2,SLC6A6,SLCO2A1,SMU1,SNRNP48,SNX6,SOC2,SORCS1,SOS2,SPATA18,SPATA4,SPG11,SPTLC1,SQRDL,SRD5A3,SRFBP1,SSR1,ST6GALNAC1,STAMBPL1,STRN3,SYNJ1,TARDBP,TAS1R1,TEK,TEP1,TESK2,TGFBR1,THAP3,THPO,THRB,TIGD2,TLR10,TLR3,TLR4,TM9SF3,TMEM144,TMEM165,TMEM59,TMPO,TNKS2,TP53,TPTE,TRAPPC10,TRIM39,TXK,UBE2E1,UBE2K,UBE2U,UGT8,UHRF1BP1L,USP45,USP53,VPS13A,VPS26A,YIPF1,ZBTB1,ZBTB25,ZBTB6,ZBTB9,ZKSCAN2,ZNF330,ZNF35,ZNF664,ZRANB2

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy- number loss	STOP genes subject to copy-number loss
57689477	360	ACACB,ACSL1,ACTN1,ACVR2A,ACYP2,ADAMTS6,ADH7,ADRBK2,AFF3,AGXT2L1,AHRR,ALB,ALDH3A2,ALG10,ALPK1,ANKRD44,ANKRD55,ANXA10,AP3S1,APAF1,ARG2,ARHGAP11A,ARL2BP,ARL6IP6,ASB15,ASB5,ATP5J,ATP6V1E1,ATXN3,AUH,AVPR1A,B3GALT1,BAHD1,BAZ1A,BCL11A,BDP1,BPIL2,BPTF,BRAF,BRWD1,BST1,BTC,BTG3,C12orf29,C12orf60,C13orf27,C13orf34,C14orf109,C14orf28,C14orf37,C14orf45,C15orf24,C17orf68,C2orf29,C2orf47,C4orf14,C4orf23,C5orf41,C9orf6,C9orf64,CALD1,CAPZA2,CARTPT,CASP3,CASP6,CCDC74A,CCDC74B,CCDC99,CCL22,CCNG2,CD302,CD38,CDC42BPB,CDH10,CDH9,CDKL2,CDKN1B,CDKN3,CENPH,CHD1,CLEC12A,CLEC2B,CLEC4A,CLTC,CNOT4,COBLL1,COCH,COIL,COPS8,COQ10B,COX10,CPB2,CREBL2,CRMP1,CTLA4,CTNS,CTSL1,CXCL6,CYP26B1,DAAM1,DAP,DCN,DCTD,DDX1,DIABLO,DNAH10,DNAH5,DNMT3L,DOCK2,DYRK2,ECM2,EFCAB6,EGR1,EIF2AK2,EIF4E2,ELMOD2,EMP1,ENPP6,ENTHD1,EP300,EPHA5,ERAP2,ERGIC2,FA2H,FAM175A,FAM81B,FAM84A,FBXL14,FBXL3,FBXO34,FBXW7,FER,FGF2,FGF7,FGFR1OP2,FKBP4,FOS,FOXF1,FRZB,FSHR,G3BP1,GAB1,GABRB1,GAD1,GCA,GCSH,GDF9,GEN1,GIMAP4,GMCL1,GNPDA2,GPC5,GPD2,GPR125,GPR180,GPR21,GPR22,GRB14,GRIK1,GRK4,GTDC1,HAT1,HCFC2,HERC3,HERC5,HMGNI1,HMHB1,HNRNP11,HNRPLL,HS6ST3,HTN1,IFNA1,IFNA13,IFNW1,IFRD1,IFT81,IGF1,IL1R1,IL31RA,IL8,INPP1,INVS,IRAK3,IRAK4,ITGA6,JAM2,JUB,KCNJ3,KCNN2,KCTD18,KLHDC1,KLHL36,KLRB1,KLRF1,KPNA3,KRAS,LIFR,LIG4,LIPT1,LMBRD2,LNX1,L RAT,LRFN5,L YRM7,MAB21L1,MAFG,MAP2K6,MAP3K1,MAPK10,MARCH6,MARS2,MCFD2,MCHR1,MEIS2,MELK,METTL3,METTL7A,MFAP5,MFF,MGP,MIA2,MIPOL1,MMADHC,MPP5,MSH6,MTHFD1,MUDENG,MYCBP2,MYO1B,NAE1,NAIP,NDRG2,NDUFA5,NF2,NPY1R,NR3C2,NT5DC3,NTRK2,NUDT12,OGN,OLFM4,ORC4L,ORC6L,PACSIN2,PAPOLG,PCDH9,PCGF3,PDHA2,PDZRN4,PGAP1,PJA2,PKP4,PLXNC1,POLR2D,PPAT,PPFIBP1,PPP1R13B,PRDM8,PRKAR1A,PRKCA,PRKD1,PRTG,PTGER2,PTGR1,PTN,PTRH2,PTTG1,PTTG1IP,RAB2B,RAB33B,RAD51C,RAD51L1,RAI14,RAP2A,RB1,RCBTB2,RLN2,RNF133,RNF180,RNF44,RNFT1,RTN1,SCN1A,SEC31A,SECISBP2,SEPSECS,SLC12A2,SLC19A3,SLC20A1,SLC25A17,SLC25A18,SLC25A31,SLC38A2,SLC41A2,SLC46A2,SMU1,SNX6,SOCS2,SOCS5,SOS2,SOX1,SPATA18,SPATA4,SPG11,SPTLC1,SQRDL,SRD5A3,SRFBP1,ST6GALNAC1,STK17B,STK39,STON1-GTF2A1L,STRADB,STRAP,STRN3,STXBP4,SUPT7L,SYNJ1,TANK,TAS2R1,TBC1D4,TEK,TEP1,TGFBR1,TIGD2,TLR10,TLR3,TLR4,TMEM144,TMEM165,TMPO,TP53,TRAPPC10,TRIM24,TSGA14,TXK,UBE2K,UCHL3,UGT8,UHRF1BP1L,USP32,USP34,USP53,VAPA,VPS13A,VRK2,ZBTB1,ZBTB25,ZBTB43,ZBTB6,ZFP1,ZIC2,ZNF254,ZNF330,ZNF43,ZNF664,ZNF675,ZNF800,ZNF804A,ZNF85

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy-number loss	STOP genes subject to copy-number loss
990515	328	AADACL2,ABCD3,ACSL1,ACTN1,ADAMTS6,ADH7,ADNP2,ADRBK2,AGTR1,AGXT2L1,AKAP12,ALB,ALG6,ALPK1,ANGPTL3,ANKRD55,ANXA10,AP3S1,ARF4,ARG2,ARIH2,ARL6,ASB15,ASB17,ASB5,ASTE1,ATG3,ATP5J,ATP6V1E1,ATRN1,ATXN3,AXIN1,B3GALT1,BAI2,BCL6,BDP1,BPIL2,BRAF,BRDT,BRWD1,BST1,BTBD8,BTC,BTG3,C10orf28,C10orf79,C10orf96,C14orf109,C14orf45,C16orf63,C16orf75,C19orf42,C19orf43,C3orf14,C3orf15,C3orf23,C4orf23,C5orf41,C9orf64,CADM2,CALD1,CARTPT,CASP3,CASP6,CCDC99,CCNG2,CCRL1,CD38,CDC42BPB,CDKL2,CDKN1B,CENPH,CEP70,CEP97,CH25H,CHD1,CHUK,CLEC12A,CLEC2B,CLEC4A,CNOT4,COPS8,CP,CPT2,CREBL2,CRMP1,CSTA,CTBS,CTDSPL,CTSL1,CX3CR1,CXCL12,CXCL6,CYP2C19,CYP4X1,DCTD,DEPDC1,DFFA,DNMT3L,DOCK2,EFCAB6,EGR1,EIF4A2,EIF4E2,ELMOD2,ENPP6,ENTHD1,EP300,EPAH5,ERAP2,ERI1,ERRFI1,ESR1,FAM175A,FAM81B,FBXL14,FBXO15,FBXO25,FBXW7,FER,FGF2,FKBP4,FLNB,FOS,FOXO2,G3BP1,GAB1,GDF9,GIMAP4,GNG5,GPR125,GPR15,GRIK1,GRK4,GSK3B,GTPBP8,HDAC1,HERC3,HERC5,HES1,HESX1,HMGN1,HMHB1,HNRNPH1,HTR1F,HTR7,HYAL2,IFNA1,IFNA13,IFNAR1,IFNW1,IL31RA,IL8,INA,IPP,IQCK,IRAK4,JAM2,KAT2B,KCNN2,KDSR,KIF20B,KLHL6,KLRB1,KLRF1,KNPNA4,LEKR1,LIP1,LIPJ,LMO4,LPXN,LRAT,LRRFIP2,LRRIQ3,LUZP1,LYRM7,MAP3K1,MAPK10,MCHR1,MELK,METTL7A,MFAP5,MFF,MITF,MLH1,MME,MPP5,MS4A5,MTF1,MTF2,MTHFD1,MTUS1,NAIP,NDUFA5,NDUFB4,NF2,NHLRC2,NMNAT3,NPY1R,NR0B2,NR1D2,NR3C2,NRIP1,NTRK2,NUDT12,OAT,P2RY13,PACSIN2,PARP15,PCGF3,PDHA2,PDZRN4,PFN2,PHACTR4,PHF7,PIGK,PIK3C3,PIK3R4,PJA2,PLCE1,PLCL2,PLSCR4,PMAIP1,PNRC2,PPARG,PPP1R13B,PPP2CB,PPP3CB,PRDM8,PRKACB,PTN,PTTG1,PTTG1IP,RAB33B,RABGGTB,RAD18,RAD51L1,RAF1,RBP7,RCAN3,RLN2,RNF13,RNF133,RNF180,RNF44,RNF7,ROCK1,RPE65,RSRC1,SAMD13,SCN1A,SEC31A,SENP2,SEPSECS,SERAC1,SERPINB7,SKIL,SLC12A2,SLC19A3,SLC25A17,SLC25A18,SLC25A31,SLC38A2,SLC6A6,SLCO2A1,SMAD2,SMAD4,SMU1,SNX9,SORCS1,SOX7,SPATA4,SFRBP1,SSX2IP,ST8SIA5,STAMBPL1,STK39,SYNJ1,TARDBP,TAS1R1,TEK,TESK2,THAP3,THPO,THRB,TIGD2,TLR10,TLR3,TM9SF3,TMEM144,TMEM56,TMEM59,TNKS2,TPTE,TRAPPC10,TRIM24,TSGA14,TTC9C,TUSC3,UBE2E1,UBE2K,UBE2U,UGT8,USP33,USP45,USP53,VIP,VPS13A,VPS26A,WHSC1L1,YIPF1,ZBTB1,ZBTB2,ZBTB25,ZKSCAN2,ZNF253,ZNF254,ZNF326,ZNF330,ZNF35,ZNF43,ZNF626,ZNF644,ZNF675,ZNF800,ZNF85,ZRANB2
73291145	305	ABCB1,ACSL1,ACTN1,ADAMTS6,ADH7,ADNP2,ADRBK2,AGXT2L1,AHRR,AIG1,ALB,ALPK1,ANKRD55,ANXA10,AP3M2,AP3S1,ARF4,ARG2,ARHGAP11A,ARIH2,ASB5,ATP12A,ATP5J,ATP6V1E1,BAHD1,BAZ1A,BDP1,BPIL2,BPTF,BRWD1,BST1,BTC,BTG3,C13orf27,C13orf34,C14orf28,C14orf37,C14orf45,C15orf24,C15orf42,C19orf42,C19orf43,C3orf14,C3orf23,C4orf14,C4orf23,C5orf41,C8orf4,CADM2,CARTPT,CASD1,CASP3,CASP6,CCDC99,CCNB2,CCNG2,CD38,CDH10,CDH2,CDH9,CDKL2,CDKN3,CENPH,CHCHD7,CHD1,CLTC,COCH,COIL,CPB2,CRMP1,CROT,CTDSPL,CX3CR1,CXCL6,DAAM1,DAP,DCTD,DIS3L,DNAH5,DNMT3L,DOCK2,EFCAB6,EGR1,ELMOD2,ENPP6,ENTHD1,EP300,EPAH5,ERAP2,ERI1,ESCO1,FA2H,FAM175A,FAM81B,FBXL3,FBXO15,FBXO22,FBXO25,FBXO34,FBXW7,FER,FGF2,FGF7,FGL2,FLNB,FOS,FOXF1,G3BP1,GAB1,GABRB1,GCSH,GDF9,GNPDA2,GPC5,GPR125,GPR180,GRIK1,GRK4,HERC3,HERC5,HESX1,HMGN1,HMHB1,HNRNPH1,HS6ST3,HTN1,HTR1F,HYAL2,IFNA1,IFNA13,IFNAR1,IFNW1,IL31RA,IL8,IMPAD1,IQGAP1,ISL2,JAM2,JUB,KAT2B,KCNN2,KDSR,KIAA1324L,KLHDC1,KLHL36,KPNA3,LIFR,LIG4,LIP1,LMBRD2,LNX1,LRAT,LRFN5,LRRFIP2,LYRM7,MAFG,MAP2K6,MAP3K1,MAPK10,MARCH6,MCHR1,MEGF11,MEIS2,MELK,METTL3,MIA2,MIPOL1,MITF,MLH1,MPP5,MTFR1,MTHFD1,MTUS1,MUDENG,MYCBP2,NAE1,NAIP,NDRG2,NF2,NPY1R,NR1D2,NR2F2,NR3C2,NRIP1,NUDT12,OLFAM4,PACSIN2,PCDH9,PCGF3,PDE7A,PDHA2,PENK,PHF7,PIK3C3,PJA2,PLCL2,PMAIP1,PON2,PPARG,PPAT,PPP2CB,PRDM8,PRKAR1A,PRKCA,PRKD1,PRTG,PTGER2,PTRH2,PTTG1,PTTG1IP,RAB2B,RAB33B,RAD18,RAD51C,RAD51L1,RAF1,RAI14,RAP2A,RB1,RCBTB2,RIOK3,RLN2,RNF111,RNF125,RNF138,RNF170,RNF180,RNF44,RNFT1,ROCK1,RSBN1L,RTN1,SACS,SDCBP,SEC31A,SEPSECS,SERPINB7,SLC12A2,SLC20A2,SLC25A17,SLC25A18,SLC25A31,SLC6A6,SMAD2,SMAD4,SMU1,SNAI2,SNX6,SOS2,SOX1,SOX7,SPATA18,SPATA4,SPG11,SQRDL,SRD5A3,SFRBP1,ST6GALNAC1,ST8SIA5,STOML3,STRN3,STXBP4,SUGT1,SYNJ1,TAS2R1,TBC1D4,TEK,TEP1,THRB,TIGD2,TLR10,TLR3,TMEM144,TMEM165,TMEM60,TPT1,TPTE,TPTE2,TRAM1,TRAPPC10,TPPA,TUSC3,TXK,UBE2E1,UBE2K,UCHL3,UGT8,USP12,USP32,USP53,UTRN,VAPA,WHSC1L1,ZBTB1,ZBTB25,ZFP1,ZIC2,ZNF253,ZNF254,ZNF330,ZNF35,ZNF43,ZNF626,ZNF675,ZNF85

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy-number loss	STOP genes subject to copy-number loss
990195	292	ACSL1,ACTN1,ACYP2,ADAMTS6,ADH7,ADNP2,ADRBK2,AGXT2L1,AHRR,ALB,ALPK1,ANKRD55,ANXA10,AP3S1,ARG2,ARL2BP,ASB5,ATP5J,ATP6V1E1,ATRN1,ATXN3,AUH,AXIN1,BAZ1A,BCL11A,BDP1,BMI1,BPIL2,BRWD1,BTC,BTG3,C10orf28,C10orf79,C10orf96,C11orf58,C14orf109,C14orf28,C14orf37,C14orf45,C16orf63,C16orf75,C19orf42,C19orf43,C4orf14,C4orf23,C5orf41,C9orf6,C9orf64,CARTPT,CASP3,CASP6,CCDC99,CC L22,CCNG2,CDC123,CDC42BPB,CDH10,CDH2,CDH9,CDKL2,CDKN1B,CDKN3,CENPH,CH25H,CHD1,CHUK,CLEC12A,CLEC2B,CLEC4A,COCH,CREBL2,CRMP1,CTSL1,CXCL12,CXCL6,CYP2C19,DAAM1,DAP,DCTD,DNAH5,DNMT3L,DOCK2,DUSP8,DUXA,ECM2,EFCAB6,EGR1,EIF2AK2,ELMOD2,EMP1,ENPP6,ENTHD1,EP300,EPA5,ERAP2,ERI1,FA2H,FAM175A,FAM81B,FBXL14,FBXO15,FBXO25,FBXO34,FBXW7,FER,FGF2,FKBP4,FOS,FOXF1,FSHR,G3BP1,GAB1,GABRB1,GCSH,GDF9,GNPDA2,GPR125,GPR158,GPR21,GRIK1,GRK4,GTTF2H1,HERC3,HERC5,HMGNI1,HMB1,HNRNP1,HNRNPUL1,HNRPLL,HTN1,HTR7,IFNA1,IFNA13,IFNAR1,IFNW1,IL31RA,IL8,INA,INVS,IQCK,JAM2,JUB,KCNN2,KDSR,KIF20B,KLHDC1,KLHL36,KLRB1,KLRF1,LAIR1,LIFR,LIPI,LIPJ,LMBRD2,LNX1,LRAT,LRFN5,L YRM7,MAFG,MAP3K1,MAPK10,MARCH6,MCFD2,MCHR1,MELK,METTL3,MFAP5,MIA2,MICAL2,MIPOL1,MKX,MPP5,MSH6,MTHFD1,MUDENG,NAE1,NAIP,NDRG2,NF2,NHLRC2,NLRP9,NPY1R,NR3C2,NRIP1,NRIP3,NSUN6,NTRK2,NUDT12,NUDT5,OAT,OGN,OLFML1,ORC6L,PACSIN2,PAPOLG,PDHA2,PIK3C3,PJA2,PLCE1,PMAIP1,PPAT,PPP1R13B,PPP3CB,PRDM8,PRKD1,PTGER2,PTGR1,PTPLA,PTTG1,PTTG1IP,RAB2B,RAB33B,RAD51L1,RAI14,RIOK3,RLN2,RNF125,RNF138,RNF180,RNF44,RTN1,SEC31A,SECISBP2,SEPSECS,SERPINB7,SLC12A2,SLC25A17,SLC25A18,SLC25A31,SLC46A2,SMAD2,SMAD4,SMU1,SNRNP48,SNX6,SOC5,SORCS1,SOS2,SOX7,SPATA18,SPATA4,SPTLC1,SRD5A3,SRFBP1,SSR1,ST6GALNAC1,ST8SIA5,STAMBPL1,STON1-GTF2A1L,STRN3,SUPT7L,SYNJ1,TAS2R1,TEK,TEP1,TGFBR1,TIGD2,TLR10,TLR3,TLR4,TM9SF3,TMEM144,TMEM165,TNKS2,TPTE,TRAPPC10,TKX,UBE2K,UBQLN,UGT8,USP34,USP53,VPS13A,VPS26A,VRK2,ZBTB1,ZBTB25,ZBTB43,ZBTB6,ZFP1,ZKSCAN2,ZNF214,ZNF253,ZNF254,ZNF330,ZNF417,ZNF43,ZNF549,ZNF587,ZNF626,ZNF675,ZNF85
990098	277	ACTN1,ADCY10,ADH7,AGXT2L1,AIG1,AKAP12,AKAP7,ALB,ALPK1,AMD1,ANXA10,ARF4,ARG2,ARHGAP11A,ARIH2,ARL2BP,ARL6,ASB5,ATG5,ATP5J,ATXN3,AUH,BAZ1A,BMI1,BRWD1,BST1,BTC,BTG3,C12orf60,C14orf109,C14orf28,C14orf37,C14orf45,C16orf63,C16orf75,C1orf49,C3orf14,C3orf23,C4orf14,C4orf23,C6orf170,C9orf6,C9orf64,CADM2,CASP6,CCDC28A,CCL22,CCNG2,CD109,CD1D,CD2AP,CD38,CD55,CDC123,CDC42BPB,CDH2,CDKL2,CDKN1A,CDKN1B,CDKN3,CEP97,CGA,CLEC12A,CLEC2B,CLEC4A,COCH,CREBL2,CTSK,CTSL1,CXCL6,DAAM1,DCTD,DISP1,ECM2,ELMOD2,EMP1,ENPP1,ENPP5,EPB41L2,EPA5,ERI1,ESCO1,ESR1,FA2H,FAM175A,FAM177B,FAM8A1,FBXL14,FBXO15,FBXO25,FBXO28,FBXO34,FBXW7,FCGR3A,FCGR3B,FCRL2,FGF2,FKBP4,FLNB,FMO5,FOS,FOXF1,FRK,GAB1,GABRB1,GCNT2,GCSH,GJA1,GNPDA2,GPR110,GPR125,GPR15,GRIK1,GSTA3,GTFC3C6,HERC3,HERC5,HESX1,HMGNI1,HORMAD1,HTN1,HTR1F,HYAL2,IBTK,IER5,IFNA1,IFNA13,IFNAR1,IFNW1,IL8,INVS,IQCK,JAM2,JUB,KCNK1,KDSR,KIF6,KIFAP3,KLHDC1,KLHL36,KLRB1,KLRF1,LEMD1,LIPI,LNX1,LRAT,LRFN5,LYST,MAPK10,METTL3,MFAP5,MGP,MIA2,MIPOL1,MITF,MPP5,MTHFD1,MTUS1,MUDENG,MYB,MYLIP,NAE1,NDRG2,NPY1R,NR1D2,NR3C2,NR5A2,NRIP1,NSUN1,NSUN6,NTRK2,NUDT5,OGN,OPN3,ORC6L,PDHA2,PHF7,PIK3C3,PLN,PMAIP1,PNRC1,PPAT,PPP1R13B,PRDM1,PRDM8,PRKD1,PSEN2,PTGER2,PTGR1,PTP4A1,PTPLA,PTPRK,RAB2B,RAB33B,RAD51L1,RARS2,REV3L,RGS2,RGS5,RHOU,RIOK3,RLN2,RNF125,RNF138,ROCK1,RTN1,RUSC1,SCYL3,SEC31A,SEC63,SECISBP2,SEPSECS,SERAC1,SERINC1,SERPINB7,SERPINC1,SLC19A2,SLC25A31,SLC46A2,SMAD2,SMAD4,SNRNP48,SNX10,SNX6,SNX9,SOS2,SOX7,SPATA18,SPATA4,SPTLC1,SRD5A3,SSR1,ST8SIA5,STRAP,STRN3,SYNJ1,SYT14,TAF1A,TEK,TEP1,TGFBR1,THRB,TIGD2,TLR10,TLR4,TMEM144,TMEM165,TNFSF4,TOR1AIP1,TPTE,TRAF3IP2,TRIM39,TRIM58,TUSC3,TKX,UBE2E1,UBE2K,UBR2,UGT8,URB2,USP45,USP53,UTRN,VAPA,VIP,VPS13A,YOD1,ZBTB1,ZBTB2,ZBTB25,ZBTB9,ZFP1,ZKSCAN2,ZNF281,ZNF330,ZNF35,ZNRF2

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy-number loss	STOP genes subject to copy-number loss
20020720	276	AADACL2, ABCB1, ABCD3, ACSL1, ACTN1, ADAMTS6, ADH7, ADORA3, AGTR1, AGXT2L1, ALB, ALG6, ALPK1, ANGPTL3, ANKRD55, ANXA10, AP3S1, ARF4, ARG2, ARIH2, ARL6, ASB15, ASB17, ASB5, ASTE1, ATG3, ATP5J, ATXN3, BAH1D1, BAI2, BAZ1A, BCL6, BDP1, BRAF, BRDT, BRWD1, BTBD8, BTC, BTG3, C14orf109, C14orf28, C14orf37, C14orf45, C3orf14, C3orf15, C3orf23, C4orf14, C5orf41, CADM2, CALD1, CAPZA2, CARTPT, CASD1, CASP3, CASP6, CDC99, CCNB2, CCNG2, CCRL1, CD2AP, CDC14A, CDC42BPB, CDKL2, CDKN3, CENPH, CEP70, CEP97, CHD1, CHI3L2, CLCC1, CNOT4, COCH, CP, CPT2, CROT, CSF1, CSTA, CTBS, CTDSPL, CX3CR1, CXCL6, CYP4X1, DAAM1, DCTD, DEPDC1, DFFA, DIABLO, DNMT3L, DOCK2, EGR1, EIF4A2, ELMOD2, ENPP5, ENPP6, EPHA5, ERAP2, ERFF1, FAM175A, FAM81B, FAM8A1, FBXO34, FBXW7, FER, FGF2, FGF7, FLNB, FOS, FOXD2, G3BP1, GAB1, GDF9, GIMAP4, GNG5, GPR110, GPR15, GPR22, GRIK1, GSK3B, GSTA3, GTPBP8, HDAC1, HERC3, HERC5, HES1, HESX1, HMGN1, HMHB1, HNRNP1, HTN1, HTR1F, HYAL2, IFNA1, IFNA13, IFNAR1, IFNW1, IFRD1, IL31RA, IL8, IPP, JAM2, KAT2B, KCNN2, KIAA1324L, KLHDC1, KLHL6, KNG1, KPNA4, LEKR1, LIPI, LMO4, LRAT, LRFN5, LRRFIP2, LRRIQ3, LUZP1, LYRM7, MAP3K1, MAPK10, MELK, MIA2, MIPOL1, MITF, MLH1, MME, MPP5, MTF1, MTF2, MTHFD1, MUDENG, MYLIP, NAIP, NDUFA5, NDUFB4, NMNAT3, NPY1R, NR0B2, NR1D2, NR3C2, NRIP1, NRSN1, NUDT12, OLFML3, P2RY13, PARP15, PDHA2, PFN2, PHACTR4, PHF7, PIGK, PIK3R4, PJA2, PLCL2, PLSCR4, PNRC2, PON2, PPARG, PPP1R13B, PRDM8, PRKACB, PRKD1, PRTG, PTGER2, PTN, PTTG1, PTTG1IP, RAB33B, RABGGTB, RAD18, RAD51L1, RAF1, RBP7, RCAN3, RLN2, RNF111, RNF13, RNF133, RNF180, RNF44, RNF7, RPE65, RSNB1, RSR1, RTN1, S1PR1, SAMD13, SEC31A, SENP2, SKIL, SLC12A2, SLC25A31, SLC6A6, SLCO2A1, SMU1, SNX6, SOS2, SPATA4, SPG11, SQRDL, SRFBP1, SSX2IP, ST7L, STRN3, SYNJ1, TARDBP, TAS1R1, TEK, TESK2, THAP3, THPO, THRB, TIGD2, TLR3, TMEM144, TMEM56, TMEM59, TPTE, TRAPPC10, TRIM24, TRIM39, TSGA14, UBE2E1, UBE2U, UBR2, UGT8, USP33, USP53, VAPA, YIPF1, ZBTB1, ZBTB25, ZNF326, ZNF330, ZNF35, ZNF644, ZNF800, ZRANB2
980011	271	ABCD3, ACSL1, ACVR2A, ADH7, ADNP2, ADORA3, AGXT2L1, AIG1, AKAP12, AKAP7, ALB, ALDH3A2, ALG6, ALPK1, AMD1, ANGPTL3, ANXA10, ARF4, ARIH2, ARL6IP6, ASB17, ASB5, ATG5, ATP5J, AUH, B3GALT1, BAI2, BAZ1A, BRDT, BRWD1, BST1, BTBD8, BTC, BTG3, C17orf68, C2orf47, C3orf14, C3orf23, C4orf14, C4orf23, C6orf170, C9orf6, C9orf64, CASP3, CASP6, CCDC28A, CCDC74A, CCDC74B, CCNG2, CD109, CD2AP, CD302, CD38, CDC14A, CDKL2, CDKN1A, CGA, CHI3L2, CLCC1, COBLL1, COCH, COPS8, COX10, CPT2, CRMP1, CSF1, CTBS, CTDSPL, CTLA4, CTNS, CTS1, CX3CR1, CXCL6, CYP4X1, DCTD, DDX1, DEPDC1, DFFA, ECM2, EIF4E2, ELMOD2, ENPP1, ENPP5, ENPP6, EPB41L2, EPHA5, ERFF1, ESR1, FAM175A, FAM84A, FAM8A1, FBXO15, FBXW7, FGF2, FLNB, FOXD2, FRK, GAB1, GABRB1, GAD1, GCA, GCNT2, GEN1, GJA1, GNG5, GNPD2, GPD2, GPR110, GPR125, GRB14, GRIK1, GRK4, GSTA3, GTDC1, GTF3C6, HAT1, HDAC1, HERC3, HERC5, HESX1, HMGN1, HTN1, HYAL2, IBTK, IFNA1, IFNA13, IFNAR1, IFNW1, IL8, INVS, IPP, ITGA6, JAM2, JUB, KAT2B, KCNJ3, KCTD18, KDSR, KIF6, LIPI, LMO4, LNX1, LRAT, LRFN5, LRRFIP2, LRRIQ3, LUZP1, MAPK10, METTL3, MIA2, MIPOL1, MLH1, MMADHC, MTF1, MTF2, MYB, MYLIP, NDRG2, NPY1R, NR0B2, NR1D2, NR3C2, NRIP1, NRSN1, NTRK2, OGN, OLFML3, ORC4L, PCGF3, PDHA2, PHACTR4, PHF7, PIGK, PIK3C3, PKP4, PLCL2, PLN, PMAIP1, PNRC1, PNRC2, POLR2D, PPARG, PPAT, PRDM1, PRDM8, PRKACB, PRKD1, PTP4A1, PTPRK, RAB2B, RAB33B, RABGGTB, RAD18, RAF1, RARS2, RBP7, RCAN3, REV3L, RLN2, RPE65, RSNB1, S1PR1, SAMD13, SCN1A, SEC31A, SEC63, SECISBP2, SEPSECS, SERAC1, SERINC1, SERPINB7, SLC25A31, SLC6A6, SMAD2, SMAD4, SNRNP48, SNX6, SNX9, SPATA18, SPATA4, SPTLC1, SRD5A3, SSR1, SSX2IP, ST7L, STSIA5, STK39, STRADB, STRN3, SUPT7L, SYNJ1, TANK, TARDBP, TAS1R1, TEK, TEPI1, TESK2, TGFB1, THAP3, THRB, TIGD2, TLR10, TLR3, TMEM144, TMEM165, TMEM56, TMEM59, TP53, TPTE, TRAF3IP2, TRIM39, TXK, UBE2E1, UBE2K, UBE2U, UBR2, UGT8, USP33, USP45, USP53, UTRN, VIP, VPS13A, YIPF1, ZBTB2, ZBTB9, ZNF326, ZNF330, ZNF35, ZNF644, ZRANB2

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy-number loss	STOP genes subject to copy-number loss
990069	271	ACSL1,ACTN1,ADAMTS6,ADH7,ADNP2,ADRBK2,AGXT2L1,ALB,ALDH3A2,ALPK1,ANKRD55,ANXA10,AP3S1,ARG2,ARHGAP11A,ARIH2,ARL2BP,ASB5,ATP6V1E1,ATRN1,ATXN3,AXIN1,BAHD1,BAZ1A,BDP1,BPIL2,BPTF,BST1,BTC,C10orf28,C10orf79,C10orf96,C14orf109,C14orf28,C14orf37,C14orf45,C15orf24,C15orf42,C16orf63,C16orf75,C17orf68,C19orf42,C19orf43,C3orf23,C4orf14,C4orf23,C5orf41,CARTPT,CASP3,CASP6,CCDC99,CCL22,CCL7,CCNB2,CCNG2,CD2AP,CD38,CDH2,CDKL2,CDKN1A,CDKN3,CENPH,CH25H,CHD1,CHUK,CLTC,COCH,COIL,COX10,CPB2,CPD,CRMP1,CTDSPL,CTNS,CX3CR1,CXCL6,CYP2C19,DAAM1,DCTD,DIS3L,DOCK2,EFCAB6,EGR1,ELMOD2,ENPP5,ENPP6,ENTHD1,EP300,EPHA5,ERAP2,ERI1,FA2H,FAM175A,FAM81B,FBXO15,FBXO22,FBXO25,FBXO34,FBXW7,FER,FGF2,FGF7,FOS,FOXF1,G3BP1,GAB1,GABRB1,GCSH,GDF9,GNPDA2,GPR110,GPR125,GRK4,HERC3,HERC5,HMHB1,HNRNP1,HTN1,HTR7,HYAL2,IL31RA,IL8,INA,IQCK,IQGAP1,ISL2,JUB,KAT2B,KCNN2,KDSR,KIF20B,KIF6,KLHDC1,KLHL36,KPNA3,LIPJ,LNX1,LRAT,LRFN5,LRRFIP2,LYRM7,MAFG,MAP2K6,MAP3K1,MAPK10,MCHR1,MEGF11,MEIS2,METTL3,MIA2,MIPOL1,MLH1,MPP5,MTHFD1,MTUS1,MUDENG,NAE1,NAIP,NDRG2,NF2,NHLRC2,NPY1R,NR1D2,NR2F2,NR3C2,NUDT12,OAT,OLFM4,OMG,ORC6L,PACIN2,PCDH9,PCGF3,PDHA2,PHF7,PIGW,PIK3C3,PJA2,PLCE1,PLCL2,PMAIP1,PPARG,PPAT,PPP2CB,PRDM8,PRKAR1A,PRKCA,PRKD1,PRTG,PTGER2,PTRH2,PTTG1,RAB2B,RAB33B,RAD18,RAD51C,RAD51L1,RAF1,RB1,RCBTB2,RIOK3,RNF111,RNF125,RNF135,RNF138,RNF180,RNF44,RNFT1,ROCK1,RTN1,SEC31A,SEPSECS,SERPINB7,SLC12A2,SLC25A17,SLC25A18,SLC25A31,SLC6A6,SLFN13,SMAD2,SMAD4,SNX6,SORCS1,SOS2,SOX7,SPATA18,SPATA4,SPG11,SQRDL,SRD5A3,SRFBP1,ST6GALNAC1,ST8SIA5,STAMBPL1,STRN3,STXBP4,SUGT1,TAOK1,TEP1,THRB,TIGD2,TLR10,TLR3,TM9SF3,TMEM144,TMEM165,TNKS2,TP53,TPT1,TUSC3,TKX,UBE2E1,UBE2K,UBR2,UGT8,USP32,USP53,VAPA,ZBTB1,ZBTB25,ZBTB9,ZFP1,ZKSCAN2,ZNF253,ZNF254,ZNF330,ZNF35,ZNF43,ZNF626,ZNF675,ZNF85
2000433	264	ABCD3,ACSL1,ACTN1,ADH7,ADORA3,AGXT2L1,ALB,ALG6,ALOX5AP,ALPK1,ANGPTL3,ANXA10,ARF4,ARG2,ARHGAP11A,ARIH2,ARL2BP,ASB15,ASB17,ASB5,ATP12A,ATXN3,BAHD1,BAI2,BAZ1A,BCL6,BRAF,BRCA2,BRDT,BST1,BTBD8,BTC,C11orf58,C14orf109,C14orf28,C14orf37,C14orf45,C15orf24,C19orf42,C19orf43,C3orf14,C3orf23,C4orf14,C4orf23,CALD1,CAPZA2,CASD1,CASP3,CASP6,CCL22,CCNB2,CCNG2,CD38,CDC14A,CDC42BPB,CDKL2,CDKN3,CHI3L2,CHKA,CLCC1,CNOT4,COCH,CPB2,CPT2,CRMP1,CSF1,CTBS,CTDSPL,CX3CR1,CXCL6,CYP4X1,DAA M1,DCTD,DEPDC1,DFFA,DIS3L,DUSP8,EIF4A2,ELMOD2,ENPP6,EPHA5,ERRF1,FA2H,FAM175A,FBXO22,FBXO3,FBXO34,FBXW7,FGF2,FGF7,FLNB,FOS,FOXD2,FOXF1,GAB1,GABRB1,GCSH,GIMAP4,GNG5,GNPDA2,GPR125,GPR22,GRK4,GTF2H1,HDAC1,HERC3,HERC5,HES1,HESX1,HTN1,HYAL2,IFNA1,IFNA13,IFNW1,IFRD1,IL8,IPP,ISL2,JUB,KAT2B,KLHDC1,KLHL36,KNG1,KPNA3,LMO4,LNX1,LPXN,LRAT,LRFN5,LRRFIP2,LRRIQ3,LUZP1,MAB21L1,MAPK10,MEGF11,MEIS2,METT5D1,METTL3,MIA2,MICAL2,MIPOL1,MLH1,MPP5,MS4A5,MTF1,MTF2,MTHFD1,MUDENG,N4BP2L2,NAE1,NDRG2,NDUFA5,NPY1R,NR0B2,NR1D2,NR3C2,NRIP3,OLFM4,OLFML1,OLFML3,ORC6L,PAK7,PCGF3,PDHA2,PDYN,PHACTR4,PHF7,PIGK,PLCL2,PNRC2,PON2,PPARG,PPAT,PPP1R13B,PRDM8,PRKACB,PRKD1,PRNP,PRTG,PTGER2,PTN,RAB2B,RAB33B,RABGGTB,RAD18,RAD51L1,RAF1,RAG2,RB1,RBP7,RCAN3,RCBTB2,RLN2,RNF111,RNF133,RNF24,RPE65,RSBN1,RTN1,S1PR1,SACS,SAMD13,SEC31A,SENP2,SEPSECS,SLC25A31,SLC6A6,SNX6,SOS2,SPATA18,SPATA4,SPG11,SQRDL,SRD5A3,SSX2IP,ST7L,STOML3,STRN3,SUGT1,TARDBP,TAS1R1,TEK,TEP1,TESK2,THAP3,THRB,TIGD2,TLR10,TLR3,TMEM144,TMEM165,TMEM56,TMEM59,TPT1,TPTE2,TRIM24,TSGA14,TTC9C,TKX,UBE2E1,UBE2K,UBE2U,UBQLNL,UGT8,USP12,USP33,USP53,YIPF1,ZBTB1,ZBTB25,ZFP1,ZNF214,ZNF253,ZNF254,ZNF326,ZNF330,ZNF35,ZNF43,ZNF626,ZNF644,ZNF675,ZNF800,ZNF85,ZRANB2

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy- number loss	STOP genes subject to copy-number loss
57701999	235	ACACB,ACYP2,ADAMTS6,ADNP2,ADRBK2,AIG1,AKAP12,AKAP7,ALB,ALDH3A2,ANKRD55,APAF1,ARF4,ARHGAP11A,ARIH2,AVPR1A,BAHD1,BAI2,BCL11A,BDP1,BMI1,BPIL2,BRWD1,BTC,C11orf58,C12orf29,C13orf27,C14orf45,C15orf24,C15orf42,C17orf68,C19orf42,C19orf43,C3orf14,C3orf23,C4orf14,C5orf41,C6orf170,C9orf64,CADM2,CARTPT,CCDC28A,CCDC99,CCNB2,CCNG2,CDC123,CDC42BPB,CDH2,CDKL2,CDKN1A,CENPH,COX10,CTDSPL,CTNS,CX3CR1,CXCL6,CYP26B1,DCN,DDX1,DIABLO,DIS3L,DNAH10,DNMT3L,DOCK2,DYRK2,EFCAB6,EIF2AK2,ENPP1,ENTHD1,EP300,EPB41L2,EPHA5,ESCO1,ESR1,FAM175A,FAM84A,FAM8A1,FBXO15,FBXO22,FGF7,FLNB,FOS,FRK,FSHR,GCNT2,GEN1,GJA1,GMCL1,GPC5,GPR158,GPR180,GRIK1,GTTF2H1,HCFC2,HERC3,HERC5,HESX1,HMG1,HMGB1,HNRNPUL1,HNRPLL,HS6ST3,HTN1,HTR1F,HYAL2,IFNA1,IFNA13,IFNAR1,IFNW1,IFT81,IGF1,IL31RA,IL8,IQGAP1,IRAK3,IRAK4,ISL2,KAT2B,KDSR,KIF6,LAIR1,LIG4,LNX1,LRRFIP2,LUZP1,MAFG,MAP2K6,MAP3K1,MAPK10,MCFD2,MCHR1,MEGF11,MEIS2,MELK,METTL7A,MITF,MKX,MLH1,MSH6,MTHFD1,MYB,MYLIP,NAIP,NF2,NLRP9,NR0B2,NR1D2,NR2F2,NRSN1,NSUN6,NT5DC3,NTRK2,NUDT5,PACSIN2,PAPOLG,PDZRN4,PHACTR4,PHF7,PIK3C3,PLCL2,PLN,PLXNC1,PMAP1,PNRC2,PPAT,PPP1R13B,PRDM8,PRKAR1A,PRTG,PTPLA,PTPRK,PTTG1,PTTG1IP,RAP2A,RCAN3,RIOK3,RLN2,RNF111,RNF125,RNF138,RNF180,ROCK1,SEC31A,SERAC1,SERINC1,SERPINB7,SLC25A17,SLC38A2,SLC41A2,SMAD2,SMAD4,SMU1,SNRNP48,SNX9,SOCS2,SOC5,SOX1,SPATA18,SPG11,SQRDL,SRD5A3,SSR1,ST6GALNAC1,ST8SIA5,STON1-GTF2A1L,SUPT7L,SYNJ1,TEK,THRB,TIGD2,TMEM165,TMPO,TP53,TRAPPC10,TRIM39,UBE2E1,UHRF1BP1L,USP34,UTRN,VIP,VRK2,ZBTB1,ZBTB2,ZBTB25,ZBTB9,ZIC2,ZNF253,ZNF254,ZNF35,ZNF43,ZNF571,ZNF626,ZNF664,ZNF675,ZNF85
990090	221	ACSL1,ACTN1,ADAMTS6,ADH7,ADNP2,ADRBK2,AGXT2L1,AIG1,AKAP12,AKAP7,ALB,ALPK1,ANXA10,ARG2,ARHGAP11A,ARL2BP,ASB5,ATP5J,ATP6V1E1,AUH,BAHD1,BDP1,BPIL2,BRWD1,BTC,BTG3,C10orf28,C10orf79,C14orf37,C14orf45,C15orf24,C15orf42,C4orf14,C4orf23,C6orf170,C8orf4,C9orf6,C9orf64,CARTPT,CASP3,CASP6,CCDC28A,CCL22,CCNB2,CCNG2,CD109,CDH2,CDKL2,CDKN3,CENPH,CH25H,CHUK,CLTC,COC,H,COIL,CRMP1,CTSL1,CXCL6,CYP2C19,DAAM1,DCTD,DNMT3L,ECM2,EFCAB6,ELMOD2,ENPP1,ENPP6,ENTHD1,EP300,EPB41L2,EPHA5,ERI1,ESR1,FA2H,FAM175A,FAM8A1,FBXO22,FBXO25,FBXO34,FBXW7,FGF2,FGF7,FOS,FOXF1,GAB1,GCNT2,GCSH,GIMAP4,GJA1,GPR125,GPR21,GRIK1,GRK4,HERC3,HERC5,HMG1,HTN1,HTR7,IFNA1,IFNA13,IFNAR1,IFNW1,IL8,INA,INVS,IQGAP1,ISL2,JAM2,KIF20B,KLHL36,LIP1,LIPJ,LRAT,MAFG,MAPK10,MCHR1,MEGF11,MEIS2,METTL3,MPP5,MTHFD1,MTUS1,MUDENG,MYB,MYLIP,NAE1,NAIP,NDRG2,NF2,NPY1R,NR2F2,NR3C2,NRIP1,NTRK2,NUDT12,OGN,PACSIN2,PCGF3,PDHA2,PIGW,PIK3C3,PLCE1,PLN,PPAT,PPP2CB,PRDM8,PRKD1,PRTG,PTGER2,PTGR1,PTP4A1,PTPRK,PTRH2,PTTG1IP,RAB2B,RAB33B,RAD51C,RAD51L1,RLN2,RNF111,RNF125,RNF138,RNF180,RNFT1,RTN1,SEC31A,SECISBP2,SEPSECS,SERAC1,SERINC1,SLC25A17,SLC25A18,SLC25A31,SLC46A2,SLFN13,SMAD2,SMAD4,SNRNP48,SNX9,SOX7,SPATA4,SPG11,SPPLC1,SQRDL,SRD5A3,SSR1,ST8SIA5,STAMBPL1,STRN3,STXBP4,SYNJ1,TEK,TEP1,TGFBR1,TIGD2,TLR10,TLR3,TLR4,TM9SF3,TMEM144,TMEM165,TNKS2,TPTE,TRAPPC10,TUSC3,UBE2K,UGT8,USP32,USP53,UTRN,VIP,VPS13A,VPS26A,WHSC1L1,ZBTB1,ZBTB2,ZBTB25,ZBTB43,ZBTB6,ZFP1,ZNF330

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy-number loss	STOP genes subject to copy-number loss
2000403	196	ABCD3,ACSL1,ACVR2A,ADH7,ADORA3,AFF3,AGXT2L1,ALB,ALG6,ALPK1,ANGPTL3,ANKRD44,ANXA10,ARL6IP6,ASB17,ASB5,ATP5J,AXIN1,B3GALT1,BAI2,BMI1,BRDT,BRWD1,BST1,BTBD8,BTC,BTG3,C13orf27,C16orf63,C16orf75,C2orf29,C2orf47,C4orf14,C4orf23,CASP3,CASP6,CCDC74A,CCDC74B,CCNG2,CD302,CD38,CDC14A,CDKL2,CHI3L2,CLCC1,COBLL1,COPS8,COQ10B,CPT2,CRMP1,CSF1,CTBS,CTLA4,CXCL6,CYP4X1,DCTD,DEPDC1,DFFA,DNMT3L,EIF4E2,ELMOD2,ENPP6,EPHA5,ERRFI1,FAM175A,FBXL3,FBXW7,FGF2,FOXD2,FRZB,GAB1,GABRB1,GAD1,GCA,GNG5,GNPDA2,GPC5,GPD2,GPR125,GPR180,GRB14,GRIK1,GRK4,GTDC1,HAT1,HDAC1,HERC3,HERC5,HMG1,HS6ST3,HTN1,IFNA1,IFNA13,IFNAR1,IFNW1,IL1R1,IL8,INPP1,IPP,IQCK,ITGA6,JAM2,KCNJ3,KCTD18,LIG4,LIPI,LIPT1,LMO4,LNX1,LRAT,LRRIQ3,LUZP1,MAPK10,MARS2,MFF,MMADHC,MTF1,MTF2,MYCBP2,MYO1B,NPY1R,NR0B2,NR3C2,NRIP1,NSUN6,OLFML3,ORC4L,PCGF3,PDHA2,PGAP1,PHACTR4,PIGK,PKP4,PNRC2,POLR2D,PPAT,PRDM8,PRKACB,PTTG1IP,RAB33B,RABGGTB,RAP2A,RBP7,RCAN3,RPE65,RSBN1,S1PR1,SAMD13,SCN1A,SEC31A,SEPSECS,SLC19A3,SLC20A1,SLC25A31,SOX1,SPATA18,SPATA4,SRD5A3,SSX2IP,ST7L,STK17B,STK39,STRADB,SYNJ1,TANK,TARDBP,TAS1R1,TBC1D4,TEK,TESK2,THAP3,TIGD2,TLR10,TLR3,TMEM144,TMEM165,TMEM56,TMEM59,TPTE,TRAPPC10,TXK,UBE2K,UBE2U,UGHL3,UGT8,USP33,USP53,YIPF1,ZIC2,ZKSCAN2,ZNF107,ZNF326,ZNF330,ZNF644,ZNF804A,ZRANB2
990203	183	ABCD3,ACTN1,ADNP2,ADORA3,AHRR,ALDH3A2,ALG6,ANGPTL3,AP3M2,ARF4,ARG2,ARHGAP11A,ARIH2,ARL2BP,ASB17,BAHD1,BAI2,BRDT,BST1,BTBD8,C14orf45,C15orf24,C17orf68,C19orf43,C3orf14,C3orf23,C4orf23,C8orf4,CADM2,CCL22,CD109,CD2AP,CD38,CDC14A,CDH2,CDKN1A,CHI3L2,CLCC1,COX10,CPT2,CRMP1,CSF1,CTBS,CTDSPL,CTNS,CX3CR1,CYP4X1,DAP,DEPDC1,DFFA,DNAH5,EIF2AK2,ENPP5,ERI1,ERRFI1,FA2H,FAM8A1,FBXO15,FBXO25,FLNB,FOS,FOXD2,FOXF1,FSHR,GABRB1,GCNT2,GCSH,GNG5,GNPDA2,GPR110,GPR125,GRK4,GSTA3,HDAC1,HESX1,HNRPLL,HTR1F,HYAL2,IFNA1,IFNA13,IFNW1,IPP,KAT2B,KDSR,KIF6,KLHL36,LMO4,LPXN,LRRFIP2,LRRIQ3,LUZP1,MARCH6,MCFD2,MEIS2,MELK,MITF,MLH1,MS4A5,MSH6,MTF1,MTF2,MTUS1,MYLIP,NAE1,NR0B2,NR1D2,NRSN1,OLFML3,ORC6L,PCGF3,PHACTR4,PHF7,PIGK,PIK3C3,PLCL2,PMAIP1,PNRC2,PPARG,PPP2CB,PRKACB,PTP4A1,RABGGTB,RAD18,RAD51L1,RAF1,RBP7,RCAN3,RLN2,RNF125,RNF138,RNF170,ROCK1,RPE65,RSBN1,S1PR1,SAMD13,SEPSECS,SERPINB7,SLC20A2,SLC6A6,SMAD2,SMAD4,SMU1,SNRNP48,SOC5,SORCS1,SOX7,SPG11,SQRDL,SSR1,SSX2IP,ST7L,ST8SIA5,STON1-GTF2A1L,TARDBP,TAS1R1,TAS2R1,TEK,TESK2,THAP3,THRB,TLR10,TMEM56,TMEM59,TP53,TRIM39,TTC9C,TUSC3,TXK,UBE2E1,UBE2K,UBE2U,UBR2,USP33,VAPA,WHSC1L1,YIPF1,ZBTB9,ZFP1,ZNF326,ZNF35,ZNF644,ZRANB2
980390	181	ACSL1,ACTN1,ADAMTS6,ADH7,ADNP2,ADRBK2,AGXT2L1,ALB,ALPK1,ANKRD55,ANXA10,AP3S1,ARG2,ARL2BP,ASB5,ATP5J,ATP6V1E1,ATXN3,BAZ1A,BDP1,BPIL2,BST1,BTC,BTG3,C14orf109,C14orf28,C14orf37,C14orf45,C4orf14,C4orf23,C5orf41,CARTPT,CASP3,CASP6,CCDC99,CCL22,CCNG2,CD38,CDH2,CDKL2,CDKN3,CENPH,CHD1,COCH,CRMP1,CXCL6,DAAM1,DCTD,DOCK2,DUSP8,EGR1,ELMOD2,ENPP6,EPHA5,ERAP2,ESCO1,FA2H,FAM175A,FAM81B,FAM8A1,FBXO15,FBXO34,FBXW7,FER,FGF2,FOS,FOXF1,G3BP1,GAB1,GABRB1,GCNT2,GCSH,GDF9,GNPDA2,GPR125,GRIK1,GRK4,HERC3,HERC5,HMBB1,HNRNPH1,HTN1,IFNA1,IFNA13,IFNAR1,IFNW1,IL31RA,IL8,JAM2,JUB,KCNN2,KDSR,KLHDC1,KLHL36,LIPI,LNX1,LRAT,LRFN5,LYRM7,MAP3K1,MAPK10,METTL3,MIA2,MIPOL1,MPP5,MTHFD1,MUDENG,MYLIP,NAE1,NAIP,NDRG2,NFY2,NPY1R,NR3C2,NRIP1,NRIP3,NRSN1,NUDT12,OLFML1,ORC6L,PDHA2,PIK3C3,PJA2,PMAIP1,PPAT,PRDM8,PRKD1,PTGER2,PTTG1,RAB2B,RAB33B,RAD51L1,RGS2,RIOK3,RLN2,RNF125,RNF138,RNF180,RNF44,ROCK1,RTN1,SEC31A,SEPSECS,SERPINB7,SLC12A2,SLC25A18,SLC25A31,SMAD2,SMAD4,SMU1,SNRNP48,SNX6,SOS2,SPATA18,SPATA4,SRD5A3,SRFBP1,SSR1,ST8SIA5,STRN3,SYNJ1,TEK,TEP1,TIGD2,TLR10,TLR3,TMEM144,TMEM165,TPTE,TPTE2,TXK,UBE2K,UBQLN1,UGT8,USP53,VAPA,ZBTB1,ZBTB25,ZFP1,ZNF214,ZNF330

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy-number loss	STOP genes subject to copy-number loss
96141474	167	ACSL1,ADAMTS6,ADH7,ADNP2,AGXT2L1,AHRR,AIG1,AKAP12,AKAP7,ALB,ALPK1,AMD1,ANKRD55,ANXA10,AP3S1,ASB5,ATG5,ATP5J,AUH,BDP1,BRWD1,BTC,BTG3,C17orf68,C3orf14,C4orf14,C6orf170,C9orf6,C9orf64,CADM2,CARTPT,CASP3,CASP6,CCDC28A,CCNG2,CD109,CDH10,CDH9,CDKL2,CENPH,CGA,CHD1,COX10,CTNS,CTSL1,CXCL6,DAP,DCTD,DDX1,DNAH5,ECM2,EGR1,ELMOD2,ENPP1,ENPP6,EPB41L2,EPHA5,ERAP2,ESR1,FAM175A,FAM81B,FAM84A,FBXO15,FBXW7,FER,FGF2,FRK,GAB1,GDF9,GEN1,GJA1,GRIK1,GTFC36,HERC3,HERC5,HMG1,HMHB1,HTN1,HTR1F,IBTK,IFNA1,IFNA13,IFNAR1,IFNW1,IL31RA,IL8,INVS,JAM2,KCNN2,KDSR,LIFR,LMBRD2,LNX1,LRAT,LYRM7,MAP3K1,MAPK10,MARCH6,MITF,MYB,NAIP,NPY1R,NR3C2,NRIP1,NTRK2,NUDT12,OGN,PDHA2,PIK3C3,PJA2,PLN,PMAIP1,PNRC1,PPAT,PRDM1,PRDM8,PTGR1,PTP4A1,PTPRK,RAB33B,RAD18,RAI14,RARS2,REV3L,RLN2,RNF125,RNF138,RNF180,ROCK1,SEC31A,SEC63,SECISBP2,SERAC1,SELRINC1,SERPINB7,SLC12A2,SLC25A31,SLC46A2,SMAD2,SMAD4,SNX9,SPATA18,SPATA4,SPTLC1,SRD5A3,SRFBP1,ST8SIA5,SYNJ1,TAS2R1,TEK,TGFBR1,TIGD2,TLR3,TLR4,TMEM144,TMEM165,TP53,TRAF3IP2,UGT8,USP45,USP53,UTRN,VAPA,VIP,VPS13A,ZBTB2,ZNF330
38877042	157	ACSL1,ADAMTS6,ADH7,ADNP2,AGXT2L1,ALB,ALDH3A2,ALPK1,ANKRD55,ANXA10,AP3S1,ASB5,ATP5J,BDP1,BPTF,BRWD1,BST1,BTC,BTG3,C17orf68,C4orf14,C4orf23,C5orf41,C9orf6,CARTPT,CASP3,CASP6,CCDC99,CCL7,CCNG2,CD38,CDKL2,CENPH,CHD1,CLTC,COIL,COX10,CPD,CRMP1,CTNS,CXCL6,DCTD,DNMT3L,DOCK2,DUXA,EGR1,ELMOD2,ENPP6,EPHA5,ERAP2,FAM175A,FAM81B,FAM8A1,FBXW7,FER,FGF2,GAB1,GABRB1,GCNT2,GNPDA2,GPR125,GPR21,GRIK1,GRK4,HERC3,HERC5,HMG1,HMHB1,HNRNP1,HNRNPUL1,HTN1,IFNAR1,IL31RA,IL8,INVS,JAM2,KCNN2,KDSR,LAIR1,LIP1,LNX1,LRAT,MAFG,MAP2K6,MAP3K1,MAPK10,MYLIP,NAIP,NLRP9,NPY1R,NR3C2,NRIP1,NRSN1,NUDT12,OMG,PCGF3,PDHA2,PIGW,PIK3C3,PJA2,PMAIP1,PPAT,PRDM8,PRKAR1A,PRKCA,PTGR1,PTRH2,PTTG1,PTTG1IP,RAB33B,RAD51C,RNF135,RNF138,RNF180,RNF44,RNFT1,SEC31A,SEPSECS,SERPINB7,SLC25A31,SLC46A2,SLFN13,SMAD2,SMAD4,SNRNP48,SPATA18,SPATA4,SRD5A3,SRFBP1,SSR1,ST6GALNAC1,ST8SIA5,STXBPA4,SYNJ1,TAOK1,TGFBR1,TIGD2,TLR10,TLR3,TLR4,TMEM144,TMEM165,TP53,TPTE,TRAPPC10,TXK,UBE2K,UGT8,USP32,USP53,ZBTB43,ZBTB6,ZNF330,ZNF417,ZNF549,ZNF571,ZNF587
980156	155	ACSL1,ADAMTS6,ADH7,AGXT2L1,ALB,ALOX5AP,ALPK1,ANKRD55,ANXA10,AP3M2,AP3S1,ARL2BP,ASB5,ATP12A,ATP5J,ATRNL1,AXIN1,BDP1,BRCA2,BST1,BTC,C10orf28,C10orf79,C10orf96,C13orf27,C16orf75,C4orf23,C8orf4,C9orf6,CADM2,CARTPT,CASP3,CASP6,CCL22,CCNG2,CD38,CDKL2,CENPH,CH25H,CHD1,CHKA,CHUK,CRMP1,CXCL12,CXCL6,CYP26B1,CYP2C19,DCTD,EGR1,ELMOD2,ENPP6,EPHA5,ERAP2,FA2H,FAM175A,FAM81B,FBXO25,FBXW7,FER,FGF2,FOXF1,GAB1,GABRB1,GCSH,GDF9,GMCL1,GNPDA2,GPC5,GPR125,GPR180,GPR21,GRIK1,GRK4,HERC3,HERC5,HS6ST3,HTN1,HTR1F,HTR7,IFNA1,IFNA13,IFNW1,IL31RA,IL8,INA,JAM2,KCNN2,KIF20B,KLHL36,LIG4,LIPJ,LPXN,LRAT,LYRM7,MAB2L1,MAP3K1,MAPK10,MITF,MS4A5,N4BP2L2,NAE1,NAIP,NHLRC2,NPY1R,NR3C2,NUDT12,OAT,ORC6L,PCGF3,PDHA2,PHACTR4,PJA2,PLCE1,PPP2CB,PPP3CB,PRDM8,PTGR1,RAB33B,RAD51L1,RAP2A,RLN2,RNF170,RNF180,SACS,SEC31A,SEPSECS,SLC12A2,SLC20A2,SLC46A2,SMU1,SORCS1,SOX1,SPATA4,SRFBP1,STAMBPL1,STOML3,TIGD2,TLR10,TLR3,TLR4,TM9SF3,TMEM144,TNKS2,TPTE2,TTC9C,UBE2K,UGT8,USP12,USP53,VPS26A,WHSC1L1,ZBTB6,ZFP1,ZIC2,ZNF330
990046	145	AADACL2,ACSL1,ADH7,ADNP2,AGTR1,AGXT2L1,ALB,ALPK1,ANXA10,ARF4,ARIH2,ARL6,ASB5,ASTE1,ATG3,ATP5J,BCL6,BRWD1,BTC,BTG3,C12orf60,C3orf14,C3orf15,C3orf23,C4orf14,CADM2,CASP3,CASP6,CCNG2,CCRL1,CDKL2,CDKN1B,CEP70,CEP97,CLEC12A,CLEC2B,CLEC4A,CP,CREBL2,CSTA,CTDSPL,CX3CR1,CXCL6,DCTD,DNMT3L,EIF4A2,ELMOD2,EMP1,ENPP6,EPHA5,FAM175A,FBXL14,FBXO15,FBXW7,FGF2,FKBP4,FLNB,GAB1,GPR15,GRIK1,GSK3B,GTPBP8,HERC3,HERC5,HES1,HESX1,HMG1,HTN1,HTR1F,HYAL2,IFNAR1,IL8,JAM2,KAT2B,KDSR,KLHL6,KLRB1,KLRF1,KNG1,KPNA4,LEKR1,LIP1,LNX1,LRAT,LRRFIP2,MAPK10,MFAP5,MGP,MITF,MLH1,MME,NDUFB4,NMNAT3,NPY1R,NR1D2,NR3C2,NRIP1,P2RY13,PARP15,PDHA2,PFN2,PHF7,PIK3C3,PIK3R4,PLCL2,PLSCR4,PMAIP1,PPARG,PPAT,PRDM8,PTTG1IP,RAB33B,RAD18,RAF1,RNF13,RNF7,RSRC1,SEC31A,SENP2,SERPINB7,SKIL,SLC25A31,SLC6A6,SLCO2A1,SMAD2,SMAD4,SPATA18,SPATA4,SRD5A3,ST8SIA5,STRAP,SYNJ1,THPO,THRB,TIGD2,TLR3,TMEM144,TMEM165,TPTE,TRAPPC10,UBE2E1,UGT8,USP53,ZNF330,ZNF35

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy-number loss	STOP genes subject to copy-number loss
2000175	142	ACSL1,ADAMTS6,ADH7,ADNP2,AGXT2L1,ALDH3A2,ALPK1,ANKRD55,ANXA10,ARF4,ARIH2,ASB5,ATP5J,BCL6,BDP1,BST1,BTG3,C12orf60,C17orf68,C19orf42,C19orf43,C3orf14,C3orf23,C4orf23,CADM2,CARTPT,CASP3,CASP6,CD38,CDH2,CDKN1B,CENPH,CLEC12A,CLEC2B,COX10,CREBL2,CRMP1,CTDSPL,CTNS,CX3CR1,DCTD,EIF4A2,ELMOD2,EMP1,ENPP6,FAM175A,FBXO15,FBXW7,FGF2,FLNB,G3BP1,GAB1,GABRB1,GNPDA2,GPR21,GRIK1,GRK4,HERC3,HERC5,HES1,HESX1,HTR1F,HYAL2,IFNA1,IFNA13,IFNW1,IL31RA,JAM2,KAT2B,KDSR,KLRF1,KNG1,LIPI,LRAT,LRRFIP2,MAP3K1,MAPK10,MELK,MGP,MITF,MLH1,NAIP,NPY1R,NR1D2,NR3C2,NRIP1,OAT,PCGF3,PDHA2,PHF7,PIK3C3,PLCL2,PMAIP1,PPARG,PRDM8,PTGR1,PTTG1,RAB33B,RAD18,RAF1,RIOK3,RLN2,RNF125,RNF138,RNF180,ROCK1,SEC31A,SENP2,SERPINB7,SLC25A31,SLC46A2,SLC6A6,SMAD2,SMAD4,SMU1,SPATA4,ST8SIA5,SYNJ1,TEK,THRB,TIGD2,TLR10,TLR3,TLR4,TMEM144,TP53,TPTE,TKX,UBE2E1,UBE2K,UGT8,USP53,ZBTB43,ZBTB6,ZNF253,ZNF254,ZNF330,ZNF35,ZNF43,ZNF626,ZNF675,ZNF85
980417	136	ACSL1,ADAMTS6,ADH7,AGXT2L1,AHRR,ALB,ALPK1,ANKRD55,ANXA10,AP3S1,ASB5,ATP5J,AUH,BDP1,BRWD1,BTC,BTG3,C11orf58,C19orf42,C19orf43,C4orf14,C5orf41,C9orf6,C9orf64,CARTPT,CASP3,CASP6,CCDC99,CCNG2,CDH10,CDH9,CDKL2,CENPH,CHD1,CTSL1,CXCL6,DAP,DCTD,DNAH5,DNMT3L,DOCK2,DUSP8,ECM2,EGR1,ELMOD2,ENPP6,EPAH5,ERAP2,FAM175A,FAM81B,FBXW7,FER,FGF2,G3BP1,GAB1,GDF9,GPR21,GRIK1,GTF2H1,HERC3,HERC5,HMG1,HMGB1,HNRNP1,HTN1,IFNAR1,IL31RA,IL8,INVS,JAM2,KCNN2,LIFR,LIPI,LMBRD2,LNX1,LRA T,LRRC6,LYRM7,MAP3K1,MAPK10,MARCH6,MICAL2,NAIP,NPY1R,NR3C2,NRIP1,NRIP3,NTRK2,NUDT12,OGN,OLFML1,PDHA2,PJA2,PPAT,PRDM8,PTGR1,PTTG1,PTTG1IP,RAB33B,RAI14,RNF180,RNF44,SEC31A,SECISBP2,SLC12A2,SLC25A31,SLC46A2,SPATA18,SPATA4,SPTLC1,SRD5A3,SREBP1,SYNJ1,TAS2R1,TGFB1,TIGD2,TLR3,TLR4,TMEM144,TMEM165,TPTE,TRAPPC10,UBQLN,UGT8,USP53,VPS13A,ZBTB43,ZBTB6,ZNF214,ZNF253,ZNF254,ZNF330,ZNF43,ZNF626,ZNF675,ZNF85
990396	124	ACSL1,ADH7,ADNP2,AGXT2L1,AIG1,AKAP12,AKAP7,ALOX5AP,ALPK1,AMD1,ARF4,ARHGAP11A,ARIH2,ASB5,ATG5,ATP12A,BRCA2,C13orf34,C15orf24,C1orf49,C3orf23,C4orf14,C6orf170,CASP3,CASP6,CCDC28A,CD109,CD55,CDH2,CGA,CPB2,CTDSPL,CX3CR1,DCTD,ENPP1,ENPP6,EPB41L2,EPAH5,ESR1,FBXL3,FBXO15,FLNB,FRK,GIMAP4,GJA1,GTF3C6,HESX1,HYAL2,IBTK,IER5,JUB,KAT2B,KDSR,KIFAP3,KPNA3,LNX1,LRRFIP2,LYST,MAB21L1,MEIS2,METTL3,MLH1,MYB,MYCBP2,N4BP2L2,NDRG2,NR1D2,OLFM4,OPN3,PCDH9,PHF7,PIK3C3,PLN,PMAIP1,PNRC1,PPAT,PRDM1,PTPRK,RAB2B,RARS2,RB1,RCBTB2,REV3L,RNF125,RNF138,SACS,SCYL3,SEC63,SERAC1,SERINC1,SERPINB7,SERPINC1,SLC19A2,SMAD2,SMAD4,SNX9,SPATA18,SPATA4,SRD5A3,ST8SIA5,STOML3,SUGT1,SYT14,TBC1D4,TEP1,THRB,TLR3,TMEM165,TNFSF4,TOR1AIP1,TPT1,TPTE2,TRAF3IP2,TRIM58,UBE2E1,UCHL3,UGT8,USP12,USP45,UTRN,VIP,YOD1,ZBTB2,ZNF35
990475	113	ACTN1,ADAMTS6,ADRBK2,ALDH3A2,ANKRD55,ARF4,ARG2,ARIH2,ATG3,ATP5J,ATP6V1E1,ATRN1,ATXN3,BPIL2,BRWD1,BTG3,C10orf28,C10orf79,C10orf96,C14orf109,C14orf37,C14orf45,C17orf68,C3orf15,C3orf23,CDC42BPB,CENPH,CH25H,CHUK,COX10,CSTA,CTDSPL,CTNS,CX3CR1,CYP2C19,DAAM1,DNMT3L,EFCAB6,ENTHD1,EP300,FAM8A1,FLNB,FOS,GCNT2,GRIK1,GSK3B,GSTA3,GTPBP8,HESX1,HMG1,HTR7,HYAL2,IFNA1,IFNA13,IFNAR1,IFNW1,IL31RA,INA,JAM2,KAT2B,KIF20B,LIPI,LIPJ,LRRFIP2,MAP3K1,MCHR1,MELK,MLH1,MPP5,MTHFD1,MUDENG,MYLIP,NAIP,NDUFB4,NF2,NHLRC2,NR1D2,NRIP1,NRSN1,PACIN2,PARP15,PHF7,PLCE1,PLCL2,PPARG,PPP1R13B,PTTG1IP,RAD18,RAD51L1,RAF1,RLN2,RNF180,RTN1,SLC25A17,SLC25A18,SLC6A6,SMU1,SNRNP48,SORCS1,SSR1,STAMBPL1,SYNJ1,TEK,THRB,TM9SF3,TNKS2,TP53,TPTE,TRAPPC10,UBE2E1,ZBTB1,ZBTB25,ZNF35

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy-number loss	STOP genes subject to copy-number loss
2000892	102	ACTN1,ADNP2,ALDH3A2,ARG2,ARHGAP20,ATXN3,AXIN1,BACE1,BAHD1,C14orf109,C14orf28,C14orf37,C14orf45,C17orf68,C5orf41,CCDC99,C CNB2,CDC42BPB,CDH2,CDKN3,COCH,COIL,COPS8,COX10,CTLA4,CTNS,DAAM1,DOCK2,EIF4E2,ERI1,FAM55A,FBXO15,FBXO25,FBXO34,FO S,FXVD2,G3BP1,GDF9,HMHB1,HNRNP1,IFNA1,IFNA13,IFNW1,INPP1,JUB,KBTBD3,KDSR,KLHDC1,LRFN5,MEIS2,METTL3,MFF,MMP20,MPP 5,MTHFD1,MTUS1,MUDENG,MYO1B,NDRG2,NR2F2,PGAP1,PIGW,PIK3C3,PMAIP1,POU2AF1,PPP1R13B,PPP2CB,PRKD1,PTG,PTGER2,PTT G1,RAB2B,RAD51L1,RDX,RIOK3,RLN2,RNF111,RNF125,RNF138,RNF44,RTN1,SERPINB7,SLC19A3,SLFN13,SMAD2,SMAD4,SOS2,SOX7,SPG 11,SQRDL,ST8SIA5,STK17B,STRADB,STRN3,STXBP4,TEK,TEP1,TP53,TPTE2,TUSC3,ZBTB1,ZBTB25
20020448	92	ADNP2,ADRBK2,AHRR,AKAP12,ALDH3A2,ARHGAP11A,ATP6V1E1,AXIN1,BAHD1,BAI2,BDP1,BPIL2,BPTF,C15orf24,C17orf68,C4orf23,CARTPT ,CCL7,CCNB2,CDC42BPB,CHKA,CLTC,COIL,COX10,CPD,CRMP1,CTNS,DIS3L,DNMT3L,DUSP8,EFCAB6,ENTHD1,EP300,ESR1,FBXO22,FBXO 25,FGF19,FGF7,FOXF1,GIMAP4,GRK4,HDAC1,HNRNP1,ISL2,MAFG,MAP2K6,MCHR1,MEGF11,MEIS2,MELK,MYEOV,NAE1,NAIP,NCOA6,NF2 ,NR0B2,OMG,PACIN2,PCGF3,PHACTR4,PIGW,PPP1R13B,PPP2CB,PRKAR1A,PRKCA,PRTG,PTRH2,PTTG1IP,RAD51C,RBL1,RNF111,RNF13 5,RNF44,RNFT1,SERAC1,SLC25A17,SLC25A18,SLFN13,SNX9,SOX1,SPG11,SQRDL,ST6GALNAC1,STXBP4,TAOK1,TP53,TRAPPC10,TRIM58, TTC9C,USP32,VIP,ZBTB2
990108	82	ACSL1,ADNP2,AHRR,ALDH3A2,ARIH2,ATP6V1E1,AXIN1,C17orf68,C19orf42,C19orf43,C4orf23,CASP3,CCL7,CDC42BPB,CHKA,CPD,CRMP1,CT NS,DIABLO,DNAH10,DNMT3L,DUSP8,DUXA,EFCAB6,EGR1,ENPP6,ENTHD1,EP300,FBXO25,FGF19,FOXF1,GRK4,HNRNP1,HNRNPUL1,HYA L2,KLHL36,LAIR1,LRR32,MAFG,MCHR1,MELK,METTL7A,MYEOV,NLRP9,OMG,PACIN2,PCGF3,PHF7,PIGW,PPARG,PPP1R13B,PTTG1IP,RA F1,RNF135,RNF44,SLC25A17,SLC25A18,SLC6A6,SLFN13,SMU1,SNRNP48,SOX1,SSR1,ST6GALNAC1,TAOK1,TLR3,TP53,TRAPPC10,TTC9C, VPS26A,ZBTB43,ZNF253,ZNF254,ZNF417,ZNF43,ZNF549,ZNF571,ZNF587,ZNF626,ZNF664,ZNF675,ZNF85
970005	78	ADAMTS6,ADH7,ADNP2,AGXT2L1,ALB,ALPK1,ANKRD55,AP3S1,BDP1,BST1,BTC,C4orf14,C4orf23,CARTPT,CASP6,CCNG2,CD38,CDKL2,CEN PH,CRMP1,CXCL6,EGR1,EPHA5,ERAP2,FAM175A,FAM81B,FBXO15,FER,FGF2,GABRB1,GDF9,GNPDA2,GPR125,GRK4,HERC3,HERC5,HTN1 ,IFNA1,IFNA13,IFNW1,IL31RA,IL8,KCNN2,KDSR,LNX1,LRYM7,MAP3K1,MAPK10,NAIP,PCGF3,PDHA2,PIK3C3,PJA2,PMAIP1,PPAT,PRDM8,RLN 2,RNF125,RNF138,RNF180,SEC31A,SEPSECS,SERPINB7,SLC12A2,SMAD2,SMAD4,SPATA18,SRD5A3,SFRBP1,ST8SIA5,TEK,TIGD2,TLR10,T MEM165,TKX,UBE2K,UGT8,USP53
990041	74	ACTN1,ALDH3A2,AMD1,ARG2,ATXN3,BAI2,BAZ1A,BPTF,C14orf109,C14orf28,C14orf37,C14orf45,C17orf68,CCL7,CDC42BPB,CDKN3,CLTC,CO CH,COIL,COX10,CPD,CTNS,DAAM1,FBXO34,FOS,GTFC6,HDAC1,JUB,KLHDC1,LRFN5,LUZP1,MAFG,MAP2K6,METTL3,MIA2,MIPOL1,MPP5, MTF1,MTHFD1,MUDENG,NDRG2,NR0B2,OMG,PHACTR4,PIGW,PNRC2,PPP1R13B,PRKAR1A,PRKCA,PRKD1,PTGER2,PTRH2,RAB2B,RAD51 C,RAD51L1,RCAN3,REV3L,RNF135,RNFT1,RTN1,SEC63,SLFN13,SNX6,SOS2,ST6GALNAC1,STRN3,STXBP4,TAOK1,TEP1,TP53,TRAF3IP2,U SP32,ZBTB1,ZBTB25
990275	68	AFF3,ALDH3A2,ATXN3,AUH,BRAF,BRWD1,C14orf109,C17orf68,C19orf42,C19orf43,C2orf29,C5orf41,C9orf6,C9orf64,CCDC99,CDC42BPB,COX1 0,CTNS,CTSL1,DNAH10,DNMT3L,DOCK2,ECM2,ERI1,FBXO25,FOS,GIMAP4,HMG1,IL1R1,INVS,LIPT1,LNX1,MELK,METTL3,MTUS1,NDRG2,N TRK2,OAT,OGN,PPP1R13B,PPP2CB,PTGR1,PTTG1IP,RAB2B,RAG2,RGS2,SECISBP2,SLC46A2,SMU1,SOX7,SPATA18,SPTLC1,TEP1,TGFB1 ,TLR4,TP53,TRAPPC10,TUSC3,VPS13A,VPS26A,ZNF253,ZNF254,ZNF43,ZNF571,ZNF626,ZNF664,ZNF675,ZNF85
2000201	62	AIG1,AKAP12,AKAP7,ALDH3A2,AMD1,ARHGAP11A,ATG5,BAHD1,C15orf24,C15orf42,C17orf68,C6orf170,CCDC28A,CCNB2,CD109,CGA,COX10 ,CTNS,DIS3L,ENPP1,EPB41L2,ESR1,FBXO22,FGF7,FRK,GJA1,GTFC6,IBTK,IFNA1,IFNA13,IFNW1,IQAP1,ISL2,MEGF11,MEIS2,MELK,MYB,N R2F2,PLN,PNRC1,PRDM1,PTG,PTP4A1,PTPRK,RARS2,REV3L,RLN2,RNF111,SEC63,SERAC1,SERINC1,SMU1,SNX9,SPG11,SQRDL,TEK,TP 53,TRAF3IP2,USP45,UTRN,VIP,ZBTB2

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy-number loss	STOP genes subject to copy-number loss
2000068	53	ADRBK2, ARHGAP20, ATP5J, ATP6V1E1, BACE1, BPIL2, BRWD1, BTG3, DIABLO, DNMT3L, EFCAB6, ENTHD1, EP300, ERFFI1, FAM55A, FEZ1, FXYD2, GRIK1, HMGN1, IFNA1, IFNA13, IFNAR1, IFNW1, JAM2, JRKL, KBTBD3, LIPI, MCHR1, MELK, METTL7A, MMP20, MRE11A, NF2, NRIP1, PACSIN2, POU2A F1, PTTG1IP, RDX, RLN2, ROCK1, SLC25A17, SLC25A18, SLC37A2, SLC38A2, SMU1, SYNJ1, TAF1D, TAS1R1, TEK, THAP3, TPTE, TRAPPC10, VAPA
66811693	52	ABCD3, ADORA3, ALG6, ANGPTL3, AP3S1, ASB17, BRDT, BTBD8, CDC14A, CHD1, CHI3L2, CLCC1, COPS8, CSF1, CTBS, DEPDC1, EGR1, EIF4E2, ERA P2, FAM81B, FER, GDF9, GNG5, HMHB1, KCNN2, KDSR, LMO4, LRR1Q3, LYRM7, MTF2, NUDT12, OLFML3, PIGK, PJA2, PMAIP1, PRKACB, RABGGTB, R PE65, RSBN1, S1PR1, SAMD13, SERPINB7, SLC12A2, SRFBP1, SSX2IP, ST7L, TMEM56, UBE2U, USP33, ZNF326, ZNF644, ZRANB2
990355	49	AP3S1, ARF4, ARIH2, BDP1, C3orf14, C3orf23, C5orf41, CADM2, CARTPT, CCDC99, CHD1, CTDSP1, CX3CR1, DOCK2, EGR1, ERAP2, FAM81B, FER, FL NB, G3BP1, GDF9, HESX1, HMHB1, HNRNP1, HTR1F, HYAL2, KAT2B, KCNN2, LRRFIP2, LYRM7, MITF, MLH1, NAIP, NR1D2, NUDT12, PHF7, PJA2, PLC L2, PPARG, PTTG1, RAD18, RAF1, RNF44, SLC12A2, SLC6A6, SRFBP1, THRB, UBE2E1, ZNF35
990071	48	ACSL1, ADNP2, ALDH3A2, ASB5, AXIN1, BST1, C17orf68, C4orf23, CASP3, CD38, CDH2, CHD1, COX10, CRMP1, CTNS, DCTD, ENPP6, ERAP2, ER11, FA M81B, FBXO15, FBXO25, FER, FEZ1, GPR125, GRK4, KDSR, LUZP1, NUDT12, PCGF3, PIK3C3, PJA2, PMAIP1, RIOK3, RNF125, RNF138, SEPSECS, SER PINB7, SLC25A31, SLC37A2, SMAD2, SMAD4, SOX7, SPATA4, ST8SIA5, TLR3, TP53, TUSC3
990412	40	AP3M2, ARHGAP20, BACE1, C19orf42, C19orf43, C8orf4, C9orf64, ER11, FAM55A, FBXO25, FEZ1, FXYD2, IFNA1, IFNA13, IFNW1, KBTBD3, LPXN, MELK, MS4A5, MTUS1, NTRK2, POU2AF1, PPP2CB, RDX, RLN2, RNF170, SLC20A2, SLC37A2, SMU1, SOX7, TEK, TUSC3, VPS13A, WHSC1L1, ZNF253, ZNF25 4, ZNF43, ZNF626, ZNF675, ZNF85
990044	40	ADNP2, ALG10, ARHGAP11A, BAH1, C12orf60, C15orf24, CDH2, CDKN1B, CLEC12A, CLEC2B, CLEC4A, CREBL2, EMP1, ERGIC2, FBXL14, FBXO15, F GF7, FGFR1OP2, FKBP4, KDSR, KLRB1, KLRF1, KRAS, LRFN5, MEIS2, MFAP5, MGP, PIK3C3, PMAIP1, PPFIBP1, RIOK3, RNF125, RNF138, SERPINB7, SMAD2, SMAD4, SPG11, SQRDL, ST8SIA5, STRAP
2000040	30	C14orf28, C4orf23, CRMP1, DFFA, ERFFI1, FAM8A1, GCNT2, GRK4, KLHDC1, LRFN5, LUZP1, METTL3, MIA2, MYLIP, NDRG2, NR0B2, NRSN1, PCGF3, P NRC2, RAB2B, RBP7, RCAN3, SLC20A1, SNRNP48, SOS2, SSR1, TARDBP, TAS1R1, TEP1, THAP3
990339	30	ADNP2, ARL2BP, BST1, C4orf23, CCL22, CD38, CDH2, CRMP1, FA2H, FBXO15, FOXF1, GCNT2, GCSH, GPR125, GRK4, KDSR, KLHL36, NAE1, ORC6L, P CGF3, PMAIP1, RIOK3, RNF125, RNF138, SEPSECS, SERPINB7, SMAD4, SNRNP48, SSR1, ZFP1
990228	25	AUH, C9orf6, C9orf64, CTSL1, ECM2, GPR21, IFNA1, IFNA13, IFNW1, INVS, MELK, NTRK2, OGN, PTGR1, RLN2, SECISBP2, SLC46A2, SMU1, SPTLC1, TE K, TGFB1, TLR4, VPS13A, ZBTB43, ZBTB6
20020011	22	AGXT2L1, ALPK1, ARF4, CADM2, CASP6, FBXO15, FGF2, FLNB, GABRB1, GNPDA2, HESX1, HTR1F, KDSR, PHF7, PMAIP1, SERPINB7, SLC25A31, SMA D4, TXK, UBE2K, UGT8, USP53
980029	22	BAZ1A, C12orf60, CDC123, CDKN1B, CLEC12A, CLEC2B, CLEC4A, CREBL2, EMP1, ERGIC2, FBXL14, FGFR1OP2, FKBP4, KLRB1, KLRF1, MFAP5, MGP , MIPOL1, NUDT5, PPFIBP1, SNX6, STRAP
2000088	20	ADCY1, AP3M2, C8orf4, CHCHD7, ER11, FBXO25, IMPAD1, MTFR1, MTUS1, PDE7A, PENK, PPP2CB, RNF170, SDCBP, SLC20A2, SNAI2, SOX7, TTPA, TU SC3, WHSC1L1
990489	16	ATXN3, C14orf109, C19orf42, C19orf43, CDC42BPB, CXCL12, DUSP8, MAFG, PPP1R13B, ST6GALNAC1, ZNF253, ZNF254, ZNF43, ZNF626, ZNF675, ZN F85
990060	16	ADH7, ALDH3A2, C17orf68, COPS8, COX10, CTNS, EIF4E2, FAM175A, HERC3, HERC5, MAPK10, PDHA2, PRDM8, SEC31A, TIGD2, TP53
980447	14	ATP5J, ATXN3, BRWD1, BTG3, C14orf109, DNMT3L, GRIK1, HMGN1, JAM2, LIPI, NRIP1, PTTG1IP, TPTE, TRAPPC10

Table S6. STOP genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of STOP genes subject to copy- number loss	STOP genes subject to copy-number loss
990300	14	<i>C12orf60,CDKN1B,CLEC12A,CLEC2B,CLEC4A,CREBL2,EMP1,FBXL14,FKBP4,KLRB1,KLRF1,MFAP5,MGP,STRAP</i>
87622942	13	<i>ARL2BP,BTG3,CCL22,FA2H,FOXF1,GCSH,KLHL36,LIPI,NAE1,NRIP1,ORC6L,TPTE,ZFP1</i>
990005	13	<i>ADNP2,FBXL14,FBXO15,FKBP4,KDSR,PIK3C3,PMAIP1,RNF125,RNF138,SERPINB7,SMAD2,SMAD4,ST8SIA5</i>
2000362	12	<i>BACE1,FAM55A,FEZ1,FXVD2,IFNA1,IFNA13,IFNW1,MELK,RLN2,SLC37A2,SMU1,TEK</i>
2000303	12	<i>AP3M2,C8orf4,ERI1,FBXO25,FOXF1,MTUS1,PPP2CB,RNF170,SLC20A2,SOX7,TUSC3,WHSC1L1</i>
2000877	8	<i>ATG3,BMI1,FAM81B,GPR15,GTPBP8,LPXN,LRFN5,RLN2</i>
990097	6	<i>DFFA,ERF1,RBP7,TARDBP,TAS1R1,THAP3</i>
980437	6	<i>ATP5J,BTG3,JAM2,LIPI,NRIP1,TPTE</i>
980369	5	<i>ALDH3A2,C17orf68,COX10,CTNS,TP53</i>
91228050	2	<i>ADNP2,FBXO15</i>
2000441	1	<i>GIMAP4</i>
2000169	1	<i>DCTD</i>
46404174	1	<i>SKIL</i>
990170	1	<i>PDHA2</i>
980021	0	
61669256	0	
990111	0	
2000242	0	
990474	0	
32226415	0	
990010	0	
58947266	0	
980401	0	
47492137	0	
980097	0	
2000286	0	
2000085	0	
20263644	0	

Avg 91.11

Table S7. CYCLOPS genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of CYCLOPS genes subject to copy-number loss	CYCLOPS genes subject to copy-number loss
76629543	39	<i>ALDH2,BMP8A,CEBPG,CPT1B,CSF3R,EEF1A1,EEF2,EIF2B2,ENC1,EPHB2,ETFDH,FBXO6,GRIK5,HPGD,LSM4,OBP2A,PABPN1,PAFAH1B1,PARK7,PGF,PMPCB,POLG,PSMA4,PSMC2,PSMC4,RBM17,RPS11,RPS15,RPS9,SF3A2,SMC2,SMU1,SNRNP70,SRP68,TIE1,TIMM50,UBA52,UBE2L6,ZNF583</i>
990195	29	<i>ADSL,ASCL3,EEF2,EIF2B2,ENC1,ETFDH,GRIK5,HPGD,LSM4,NUTF2,OBP2A,PABPN1,PDGFB,PGF,PHF5A,POLR2F,PSMC4,RBM17,RPS11,RPS15,RPS9,SBK1,SF3A2,SMC2,SMU1,SNRNP70,TIMM50,UBA52,ZNF583</i>
990172	28	<i>ALDH2,ASCL3,BMP8A,CSF3R,EEF1A1,EEF2,EIF2B2,ENC1,EPHB2,ETFDH,FBXO6,HPGD,LSM4,PABPN1,PAFAH1B1,PARK7,PGF,POLG,PSMA4,RPS15,SBK1,SF3A2,SMC2,SMU1,SRP68,TIE1,UBA52,UBE2L6</i>
57701999	27	<i>ADSL,ALDH2,CEBPG,CPT1B,EEF2,EIF2B2,EPHB2,GRIK5,LSM4,PAFAH1B1,PDGFB,PGF,PHF5A,POLG,POLR2F,PSMA4,PSMC4,RBM17,RPS11,RPS15,RPS9,SF3A2,SMU1,SNRNP70,SRP68,TIMM50,UBA52</i>
2000433	26	<i>ASCL3,BMP8A,CSF3R,EEF2,EIF2B2,EPHB2,ETFDH,FBXO6,HPGD,LSM4,NUPL1,NUTF2,PABPN1,PARK7,PCNA,PGF,PMPCB,PSMA4,PSMC2,RPS15,SF3A2,SNRNP70,TIE1,UBA52,UBE2L6,USPL1</i>
990515	24	<i>ADSL,BMP8A,CPT1B,CSF3R,EEF2,EIF2B2,ENC1,EPHB2,ETFDH,FBXO6,HPGD,LSM4,PARK7,PDGFB,PGF,PHF5A,POLR2F,RPS15,SBK1,SF3A2,SMU1,TIE1,UBA52,UBE2L6</i>
57689477	23	<i>ADSL,ALDH2,CPT1B,EEF2,EIF2B2,ENC1,ETFDH,HPGD,NUTF2,OBP2A,PABPN1,PAFAH1B1,PDGFB,PGF,PHF5A,PMPCB,POLR2F,PSMC2,RPS15,SF3A2,SMC2,SMU1,SRP68</i>
990069	23	<i>ADSL,CPT1B,EEF2,EIF2B2,ENC1,ETFDH,HPGD,LSM4,NUTF2,PABPN1,PAFAH1B1,PDGFB,PGF,PHF5A,POLG,POLR2F,PSMA4,RPS15,SBK1,SF3A2,SRP68,TIAF1,UBA52</i>
73291145	22	<i>ADSL,CPT1B,EEF2,EIF2B2,ENC1,ETFDH,HPGD,LSM4,NUPL1,NUTF2,PABPN1,PDGFB,PGF,PHF5A,POLG,POLR2F,PSMA4,RPS15,SF3A2,SMU1,SRP68,UBA52</i>
990108	21	<i>ADSL,CEBPG,CPT1B,GRIK5,LSM4,OBP2A,PAFAH1B1,PDGFB,PHF5A,POLR2F,PSMC4,RPS11,RPS9,SBK1,SMU1,SNRNP70,SRP68,TIAF1,TIMM50,UBA52,ZNF583</i>
38877042	16	<i>CEBPG,ENC1,ETFDH,GRIK5,HPGD,OBP2A,PAFAH1B1,PSMC4,RPS11,RPS9,SMC2,SNRNP70,SRP68,TIAF1,TIMM50,ZNF583</i>
990203	16	<i>BMP8A,CSF3R,EEF1A1,EEF2,EIF2B2,EPHB2,FBXO6,NUTF2,PAFAH1B1,PARK7,PGF,RPS15,SF3A2,SMU1,TIE1,UBE2L6</i>
990090	16	<i>ADSL,CPT1B,EEF1A1,EIF2B2,ENC1,ETFDH,HPGD,NUTF2,OBP2A,PDGFB,PGF,PHF5A,POLG,POLR2F,PSMA4,SMC2</i>

Table S7. CYCLOPS genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of CYCLOPS genes subject to copy- number loss	CYCLOPS genes subject to copy-number loss
20020720	14	<i>BMP8A,CSF3R,EIF2B2,ENC1,EPHB2,ETFDH,FBXO6,HPGD,PARK7,PGF,PMPCB,PSMC2,SMU1,TIE1</i>
980011	12	<i>BMP8A,CSF3R,EEF1A1,EPHB2,ETFDH,FBXO6,HPGD,PABPN1,PAFAH1B1,PARK7,SMC2,TIE1</i>
990275	12	<i>CPT1B,EEF2,EIF2B2,LSM4,OBP2A,PAFAH1B1,PGF,RPS15,SF3A2,SMC2,SMU1,UBA52</i>
20020448	11	<i>ADSL,CPT1B,ENC1,NUTF2,OBP2A,PAFAH1B1,PDGFB,PHF5A,POLR2F,SRP68,TIAF1</i>
980417	11	<i>ASCL3,EEF2,ENC1,ETFDH,HPGD,LSM4,OBP2A,RPS15,SF3A2,SMC2,UBA52</i>
2000403	10	<i>BMP8A,CSF3R,EPHB2,ETFDH,FBXO6,HPGD,PARK7,RBM17,SBK1,TIE1</i>
2000175	10	<i>EEF2,ENC1,ETFDH,HPGD,LSM4,PAFAH1B1,RPS15,SF3A2,SMU1,UBA52</i>
990098	9	<i>EEF1A1,EIF2B2,ETFDH,HPGD,NUTF2,PABPN1,PGF,RBM17,SMC2</i>
990475	9	<i>ADSL,CPT1B,EIF2B2,PAFAH1B1,PDGFB,PGF,PHF5A,POLR2F,SMU1</i>
980390	9	<i>ASCL3,EIF2B2,ENC1,ETFDH,HPGD,NUTF2,PABPN1,PGF,SMU1</i>
980156	8	<i>ENC1,ETFDH,HPGD,NUPL1,NUTF2,SMC2,SMU1,USPL1</i>
2000068	8	<i>ADSL,CPT1B,FBXO6,PARK7,PDGFB,PHF5A,POLR2F,SMU1</i>
990041	8	<i>CSF3R,EIF2B2,EPHB2,PABPN1,PAFAH1B1,PGF,SRP68,TIAF1</i>
990412	7	<i>EEF2,LSM4,RPS15,SF3A2,SMU1,UBA52,UBE2L6</i>
990489	6	<i>EEF2,LSM4,RPS15,SF3A2,SRP68,UBA52</i>
2000892	6	<i>CPT1B,EIF2B2,PABPN1,PAFAH1B1,PGF,PSMA4</i>
96141474	6	<i>EEF1A1,ENC1,ETFDH,HPGD,PAFAH1B1,SMC2</i>
2000362	5	<i>EEF2,OBP2A,RPS15,SF3A2,SMU1</i>
2000201	5	<i>EEF1A1,PAFAH1B1,POLG,PSMA4,SMU1</i>
990396	5	<i>EEF1A1,HPGD,NUPL1,PABPN1,USPL1</i>
2000040	3	<i>EPHB2,FBXO6,PARK7</i>
990228	3	<i>OBP2A,SMC2,SMU1</i>
990071	3	<i>EPHB2,HPGD,PAFAH1B1</i>
2000242	2	<i>RPS15,SF3A2</i>
990097	2	<i>FBXO6,PARK7</i>
990046	2	<i>ETFDH,HPGD</i>
87622942	1	<i>NUTF2</i>
980369	1	<i>PAFAH1B1</i>
970005	1	<i>ENC1</i>
980029	1	<i>RBM17</i>
2000877	1	<i>UBE2L6</i>
990060	1	<i>PAFAH1B1</i>
990339	1	<i>NUTF2</i>
990355	1	<i>ENC1</i>

Table S7. CYCLOPS genes that are subject to copy-number loss (copy number < 0.7 times the average ploidy) in each tumor.

Sample	Number of CYCLOPS genes subject to copy- number loss	CYCLOPS genes subject to copy-number loss
980021	0	
61669256	0	
2000441	0	
2000169	0	
20020011	0	
990111	0	
980447	0	
2000088	0	
990474	0	
66811693	0	
990300	0	
32226415	0	
46404174	0	
990010	0	
58947266	0	
91228050	0	
980401	0	
990170	0	
47492137	0	
980097	0	
2000286	0	
980437	0	
2000303	0	
990005	0	
2000085	0	
20263644	0	
990044	0	
Avg	6.81	

Table S8. CYCLOPS genes subject to copy-number loss in 74 gastric adenocarcinomas. Copy-number loss is defined as a region where genomic copy number is < 0.7 times the average ploidy.

Gene	Gene name	Number of tumors where gene is subject to loss	Median mRNA level (RMA)		Difference	Percent reduction in tumors with copy-number loss	P-value ^b	FDR ^b
			Copy-number loss	No copy-number loss or gain ^a				
<i>SMU1</i>	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	20	6.26	6.47	-0.21	14	0.001	0.027
<i>RBM17</i>	RNA binding motif protein 17	6	7.34	7.63	-0.29	18	0.002	0.040
<i>EEF2*</i>	eukaryotic translation elongation factor 2	16	12.56	12.88	-0.32	20	0.005	0.070
<i>SRP68</i>	signal recognition particle 68kDa	11	9.37	9.59	-0.22	14	0.006	0.070
<i>ETFDH*</i>	electron-transferring-flavoprotein dehydrogenase	20	6.51	7.37	-0.86	45	0.007	0.070
<i>PABPN1</i>	poly(A) binding protein, nuclear 1	13	8.06	8.37	-0.31	19	0.009	0.073
<i>PMPCB</i>	peptidase (mitochondrial processing) beta	4	6.96	7.10	-0.15	10	0.015	0.108
<i>POLG</i>	polymerase (DNA directed), gamma	7	5.98	6.15	-0.18	12	0.022	0.138
<i>ENC1*</i>	ectodermal-neural cortex 1 (with BTB domain)	18	9.27	9.90	-0.62	35	0.028	0.154
<i>TIMM50</i>	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	5	6.96	7.32	-0.36	22	0.065	0.271
<i>SF3A2</i>	splicing factor 3a, subunit 2, 66kDa	17	7.24	7.78	-0.54	31	0.065	0.271
<i>ALDH2</i>	aldehyde dehydrogenase 2 family (mitochondrial)	4	10.87	11.22	-0.35	21	0.066	0.271
<i>EEF1A1</i>	eukaryotic translation elongation factor 1 alpha 1	9	11.78	11.90	-0.11	8	0.074	0.279
<i>PSMA4</i>	proteasome (prosome, macropain) subunit, alpha type, 4	9	10.77	10.83	-0.06	4	0.085	0.296
<i>PAFAH1B1</i>	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	20	7.86	8.13	-0.27	17	0.091	0.298
<i>SNRNP70</i>	small nuclear ribonucleoprotein 70kDa (U1)	5	7.38	7.44	-0.06	4	0.097	0.298
<i>NUPL1</i>	nucleoporin like 1	4	6.05	6.34	-0.29	18	0.113	0.325
<i>POLR2F</i>	polymerase (RNA) II (DNA directed) polypeptide F	11	7.00	7.03	-0.02	2	0.121	0.330
<i>RPS15</i>	ribosomal protein S15	17	8.84	8.90	-0.07	5	0.144	0.371
<i>CPT1B</i>	carnitine palmitoyltransferase 1B (muscle)	13	6.09	6.27	-0.18	12	0.174	0.417
<i>HPGD</i>	hydroxyprostaglandin dehydrogenase 15-(NAD)	22	7.76	7.97	-0.21	14	0.179	0.417
<i>UBA52</i>	ubiquitin A-52 residue ribosomal protein fusion product 1	14	12.54	12.71	-0.16	11	0.187	0.417
<i>USPL1</i>	ubiquitin specific peptidase like 1	3	5.40	5.65	-0.25	16	0.205	0.437
<i>TIE1</i>	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	8	4.87	5.11	-0.24	16	0.241	0.477
<i>PGF</i>	placental growth factor	18	7.69	7.76	-0.07	4	0.243	0.477
<i>PARK7</i>	parkinson protein 7	11	12.17	12.24	-0.07	5	0.302	0.557
<i>PSMC2</i>	proteasome (prosome, macropain) 26S subunit, ATPase, 2	4	8.45	9.07	-0.62	35	0.316	0.557
<i>NUTF2</i>	nuclear transport factor 2	13	8.55	8.59	-0.04	3	0.347	0.557
<i>GRIK5</i>	glutamate receptor, ionotropic, kainate 5	5	5.77	5.86	-0.09	6	0.361	0.557
<i>ADSL</i>	adenylosuccinate lyase	11	9.44	9.48	-0.03	2	0.374	0.557
<i>PHF5A</i>	PHD finger protein 5A	11	8.65	8.63	0.03	-2	0.374	0.557

Table S8. CYCLOPS genes subject to copy-number loss in 74 gastric adenocarcinomas. Copy-number loss is defined as a region where genomic copy number is < 0.7 times the average ploidy.

Gene	Gene name	Number of tumors where gene is subject to loss	Median mRNA level (RMA)		Difference	Percent reduction in tumors with copy-number loss	P-value ^b	FDR ^b
			Copy-number loss	No copy-number loss or gain ^a				
<i>CEBPG</i>	CCAAT/enhancer binding protein (C/EBP), gamma	4	8.04	8.36	-0.32	20	0.385	0.557
<i>BMP8A</i>	bone morphogenetic protein 8a	8	5.41	5.52	-0.11	7	0.387	0.557
<i>UBE2L6</i>	ubiquitin-conjugating enzyme E2L 6	7	9.03	9.50	-0.46	27	0.387	0.557
<i>EPHB2</i>	EPH receptor B2	12	6.86	7.16	-0.30	19	0.405	0.563
<i>TIAF1</i>	TGFB1-induced anti-apoptotic factor 1	5	6.48	6.38	0.10	-7	0.413	0.563
<i>PDGFB</i>	platelet-derived growth factor beta polypeptide	11	5.55	5.64	-0.09	6	0.449	0.592
<i>OBP2A</i>	odorant binding protein 2A	11	5.34	5.43	-0.09	6	0.459	0.592
<i>ZNF583</i>	zinc finger protein 583	4	4.10	4.03	0.07	-5	0.476	0.599
<i>PSMC4</i>	proteasome (prosome, macropain) 26S subunit, ATPase, 4	5	9.43	9.40	0.03	-2	0.520	0.637
<i>SMC2</i>	structural maintenance of chromosomes 2	13	6.86	6.53	0.33	-26	0.577	0.689
<i>RPS11</i>	ribosomal protein S11	5	10.64	10.63	0.01	-1	0.601	0.701
<i>EIF2B2</i>	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa	18	8.43	8.30	0.14	-10	0.726	0.810
<i>CSF3R</i>	colony stimulating factor 3 receptor (granulocyte)	9	7.12	6.95	0.18	-13	0.728	0.810
<i>RPS9</i>	ribosomal protein S9	5	9.60	9.58	0.03	-2	0.809	0.881
<i>FBXO6</i>	F-box protein 6	11	8.52	7.89	0.63	-55	0.859	0.915
<i>ASCL3</i>	achaete-scute complex homolog 3 (Drosophila)	5	5.26	5.21	0.05	-3	0.903	0.941
<i>SBK1</i>	SH3-binding domain kinase 1	6	6.34	5.56	0.78	-71	0.979	0.980
<i>LSM4</i>	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	14	7.93	7.60	0.34	-26	0.980	0.980
<i>SNPRB</i>	small nuclear ribonucleoprotein polypeptides B and B1	1	10.63	10.55	0.08	-6	**	**
<i>PCNA</i>	proliferating cell nuclear antigen	1	10.12	10.48	-0.36	22	**	**
<i>ETV2</i>	ets variant 2	0						
<i>LSM7</i>	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0						
<i>MTHFD2L</i>	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	0						
<i>PUF60</i>	poly-U binding splicing factor 60KDa	0						

* Subject to copy-number loss in $\geq 10\%$ of tumors and median expression reduction $\geq 20\%$ and FDR ≤ 0.25

** We computed the p value only when we had at least 2 samples where the gene is subject to copy-number loss

Highlighted green cell indicate median expression reduction $\geq 10\%$ and FDR ≤ 0.25

^a copy-number equal to average ploidy

^b p values by one-sided Wilcoxon rank-sum test; FDR (false discovery rate) by the R p.adjust function with the 'fdr' method (Benjamini and Hochberg, 1995)

RMA = Robust Multiarray Average

Table S9. Multivariate Cox proportional hazards analysis of overall survival.

Variable	Hazard ratio	95% confidence interval	p
Copy-number loss in 3p as in Table 1	3.57	1.24 - 10.31	0.018
Copy-number loss in 5q as in Table 1	4.57	1.05 - 19.86	0.042
Copy-number loss in 17p as in Table 1	0.09	0.03 - 0.29	0.00009
Copy-number loss in 18q as in Table 1	2.05	0.84 - 5.02	0.117
Copy-number loss in 21q as in Table 1	0.28	0.08 - 1.08	0.064
Age	1.06	1.01 - 1.10	0.01
Stage 2	0.63	0.13 - 3.16	0.573
Stage 3	15.78	3.65 - 68.18	0.0002
Stage 4	20.90	3.85 - 113.28	0.0004

Calculated using the coxph function in the R package survival.

This table shows the final model after applying the R function step to a starting model that included the following additional variables: copy-number loss in 4, 9p, 14q, 19p, gender, tumor grade, Lauren classification, G-INT/G-DIF subtype.

Table S10. Univariate tests of association between copy-number loss of specific chromosomal arms as in Table 1 and clinical characteristics; none are significant after taking multiple hypothesis testing into account.

Clinical characteristic	Statistical test	Copy-number loss								
		3p	4	5q	9p	14q	17p	18q	19p	21q
Gender	Fisher's exact test	1.0000	0.2509	0.7009	1.0000	0.3172	0.7616	0.7328	0.2057	0.7101
Lauren classification	Fisher's exact test	1.0000	0.5800	0.3705	0.0192	0.7566	0.6688	0.3525	0.2768	0.6208
TNM stage	Cochran-Armitage test ^a	0.2792	0.1257	0.1257	0.5170	0.8224	0.2882	0.6738	0.9299	0.5788
Tumor grade^b	Fisher's exact test	1.0000	1.0000	0.0576	0.0023	0.6426	1.0000	0.0421	0.3595	0.1478
G-INT/G-DIF subtype	Fisher's exact test	0.7132	1.0000	0.6985	0.5123	0.3449	0.1365	1.0000	0.1998	1.0000
Adjuvant treatment	Fisher's exact test	0.1124	0.6348	1.0000	0.6697	0.5725	0.2585	0.1863	1.0000	0.1124

^a As implemented in the function `independence_test` in the R "coin" package (<http://cran.r-project.org/web/packages/coin/index.html>); we used the quadratic test statistic.

^b We combined undifferentiated and poorly differentiated because of the small number of undifferentiated tumors; we combined moderately differentiated and well differentiated because of the small number of well-differentiated tumors.

Table S11. Comparisons of current results to Yustein et al. [3]

Chromosome arm	Yustein		Current results		P value*	FDR*
	LOH	No LOH	LOH	No LOH		
1p	7	11	21	53	0.40	0.76
1q	4	14	6	68	0.10	0.49
2p	6	12	20	54	0.57	0.82
2q	7	11	19	55	0.38	0.76
3p	13	5	27	47	0.01	0.26
3q	4	14	13	61	0.74	0.87
4p	10	8	26	48	0.18	0.63
4q	6	12	24	50	1.00	1.00
5p	6	12	17	57	0.37	0.76
5q	11	7	26	48	0.06	0.44
6p	7	11	18	56	0.24	0.63
6q	4	14	16	58	1.00	1.00
7p	4	14	8	66	0.24	0.63
7q	6	12	17	57	0.37	0.76
8p	8	10	22	52	0.27	0.65
8q	7	11	9	65	0.01	0.26
9p	9	9	36	38	1.00	1.00
9q	7	11	24	50	0.59	0.82
10p	6	12	14	60	0.21	0.63
10q	8	10	17	57	0.08	0.45
11p	7	11	18	56	0.24	0.63
11q	5	13	24	50	0.78	0.87
12p	5	13	15	59	0.53	0.82
12q	7	11	14	60	0.11	0.49
13q	10	8	18	56	0.02	0.26
14q	4	14	22	52	0.77	0.87
15q	5	13	16	58	0.55	0.82
16p	3	15	10	64	0.71	0.87
16q	7	11	17	57	0.23	0.63
17p	12	6	40	34	0.43	0.76
17q	5	13	23	51	1.00	1.00
18p	6	12	20	54	0.57	0.82
18q	11	7	26	48	0.06	0.44
19p	6	12	20	54	0.57	0.82
19q	5	13	17	57	0.76	0.87
20p	6	12	9	65	0.07	0.44
20q	3	15	9	65	0.70	0.87
21q	4	14	25	49	0.41	0.76
22q	6	12	22	52	0.78	0.87

* P values by two-sided Fisher's exact tests; FDR (false discovery rate) by the R p.adjust function with the 'fdr' method [4].

We were unable to locate marker D21S413 (Table 2 in [3]) in the literature; therefore 21q is represented by only one locus in our data.

Table S12. Top ranked CYCLOPS genes and their frequency of loss in reference [5] (3131 samples) and in our 74 samples.

Gene	Frequency of loss in reference	Number of our samples where it is subject to copy-number loss	Frequency of loss in our samples	P value*	FDR*
<i>PSMC2</i>	0.1	4	0.05	0.2382	0.372
<i>EIF2B2</i>	0.17	18	0.24	0.1169	0.254
<i>EEF2</i>	0.27	16	0.22	0.3538	0.520
<i>PHF5A</i>	0.23	11	0.15	0.1221	0.254
<i>HPGD</i>	0.26	22	0.30	0.5030	0.635
<i>RPS15</i>	0.28	17	0.23	0.4311	0.599
<i>SNRPB</i>	0.13	1	0.01	0.0011	0.009
<i>POLR2F</i>	0.22	11	0.15	0.1562	0.300
<i>USPL1</i>	0.27	3	0.04	6.82E-07	1.70E-05
<i>SMC2</i>	0.21	13	0.18	0.5637	0.671
<i>SMU1</i>	0.25	20	0.27	0.6848	0.778
<i>PUF60</i>	0.08	0	0.00	0.0037	0.018
<i>RPS11</i>	0.19	5	0.07	0.0060	0.021
<i>POLG</i>	0.17	7	0.09	0.1137	0.254
<i>ZNF583</i>	0.2	4	0.05	0.0009	0.009
<i>CPT1B</i>	0.25	13	0.18	0.1730	0.309
<i>BMP8A</i>	0.12	8	0.11	0.8579	0.933
<i>TIE1</i>	0.11	8	0.11	1.0000	1.000
<i>SF3A2</i>	0.27	17	0.23	0.5082	0.635
<i>SNRNP70</i>	0.19	5	0.07	0.0060	0.021
<i>RBM17</i>	0.2	6	0.08	0.0110	0.034
<i>PCNA</i>	0.12	1	0.01	0.0016	0.010
<i>PSMA4</i>	0.18	9	0.12	0.2215	0.369
<i>LSM4</i>	0.2	14	0.19	1.0000	1.000
<i>EEF1A1</i>	0.2	9	0.12	0.1049	0.254

* P values for frequency of loss in gastric cancer versus the cancers in reference [5] by two-sided Fisher's exact tests; FDR (false discovery rate) by the R p.adjust function with the 'fdr' method [4].

Supplementary References

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