

Table S6. Candidate oncogenes and tumor suppressor genes identified by correlating expression arrays with aCGH data.

Genes that are up-regulated and are frequently gained in human GCs							
Gene Symbol	Chr	Percentage Gained*	Fold Up Regulation [#]	Gene Symbol	Chr	Percentage Gained*	Fold Up Regulation [#]
RNF115	1	17.74	1.41	ESRP1	8	17.74	1.41
BCL9	1	17.74	1.33	PTDSS1	8	19.35	1.52
SF3B4	1	20.97	1.6	MTDH	8	19.35	2.06
ANP32E	1	20.97	2.22	LAPTM4B	8	19.35	1.55
TARS2	1	20.97	1.52	STK3	8	19.35	1.82
PRUNE	1	20.97	1.36	COX6C	8	19.35	1.38
S100A7	1	20.97	1.51	AZIN1	8	24.19	1.65
ILF2	1	20.97	1.69	SLC25A32	8	24.19	1.56
SLC39A1	1	20.97	1.62	NUDCD1	8	24.19	2.08
TPM3	1	20.97	1.52	RAD21	8	25.81	1.8
UBE2Q1	1	20.97	1.28	DSCC1	8	25.81	1.56
FLAD1	1	20.97	1.6	MRPL13	8	25.81	1.83
EFNA1	1	20.97	1.37	DERL1	8	30.65	1.27
GBA	1	20.97	1.29	ATAD2	8	30.65	2.58
FAM189B	1	20.97	1.39	FAM91A1	8	30.65	2.6
ASH1L	1	20.97	1.51	PVT1	8	40.32	2.11
MSTO1	1	20.97	1.33	FAM49B	8	37.1	1.92
DAP3	1	20.97	1.6	ASAP1	8	37.1	1.85
SMG5	1	20.97	1.41	PHF20L1	8	37.1	1.43
GPATCH4	1	20.97	1.37	EIF2C2	8	35.48	1.37
MRPL24	1	20.97	1.31	PTK2	8	37.1	1.52
NUF2	1	20.97	2.17	RHPN1	8	35.48	1.54
UCK2	1	20.97	1.53	PUF60	8	35.48	1.6
CREG1	1	22.58	1.88	GRINA	8	35.48	2.22
CACYBP	1	19.35	2.1	EXOSC4	8	35.48	1.29
STX6	1	17.74	1.44	C8orf30A	8	35.48	1.44
SMG7	1	19.35	1.31	FBXL6	8	35.48	1.58
ARPC5	1	19.35	1.6	RECQL4	8	35.48	2.07
TPR	1	19.35	1.47	ARHGAP39	8	35.48	1.78
ZNF281	1	16.13	1.75	C8orf33	8	35.48	1.65
KIF21B	1	16.13	1.39	SETX	9	16.13	1.44
IPO9	1	16.13	1.62	NOTCH1	9	20.97	2.41
ARL8A	1	16.13	1.3	GTPBP4	10	11.29	1.97
UBE2T	1	14.52	2.06	PFKP	10	12.9	1.4
KDM5B	1	14.52	1.3	TAF3	10	11.29	1.31
SNRPE	1	14.52	1.82	UPF2	10	12.9	1.51
NUCKS1	1	14.52	1.46	NUDT5	10	12.9	1.46
CD46	1	16.13	1.85	CDC123	10	12.9	1.52
TRAF5	1	16.13	1.51	SEPHS1	10	11.29	1.49
NEK2	1	14.52	1.71	CD9	10	11.29	1.59
SMYD2	1	14.52	1.59	MLLT10	10	9.68	1.35

CENPF	1	14.52	2.83	BMI1	10	11.29	1.8
LYPLAL1	1	12.9	1.47	WAC	10	11.29	1.4
IARS2	1	12.9	2.14	MAP3K8	10	11.29	1.59
TAF1A	1	12.9	1.62	KIF5B	10	11.29	1.56
CNIH4	1	16.13	1.34	PARD3	10	12.9	1.35
LBR	1	14.52	2.19	METTL10	10	12.9	1.46
LIN9	1	14.52	2.08	BCCIP	10	12.9	1.58
PARP1	1	14.52	1.8	GLRX3	10	11.29	1.61
ABCB10	1	14.52	1.46	DYRK2	12	8.06	1.31
C1orf198	1	14.52	2.07	RAP1B	12	8.06	1.33
TSNAX	1	14.52	1.66	NUP107	12	8.06	2
C1orf31	1	12.9	1.42	MDM2	12	8.06	1.69
TARBP1	1	12.9	1.48	CPSF6	12	9.68	1.72
IRF2BP2	1	12.9	1.68	FRS2	12	9.68	1.27
CHML	1	12.9	1.54	RAB3IP	12	9.68	1.49
ADSS	1	11.29	1.66	POMP	13	14.52	1.59
FAM36A	1	11.29	1.74	SLC7A1	13	14.52	1.45
AHCTF1	1	11.29	1.93	RFC3	13	11.29	2.03
LAPTM4A	2	12.9	1.38	C13orf23	13	11.29	1.52
DHX57	2	14.52	1.46	DGKH	13	11.29	1.95
VPS54	2	8.06	1.33	NUFIP1	13	11.29	1.54
RUVBL1	3	9.68	2.07	ZC3H13	13	11.29	1.49
RAB7A	3	11.29	1.43	RNASEH2B	13	17.74	1.55
CDV3	3	9.68	1.39	PIBF1	13	12.9	1.75
ATP1B3	3	12.9	2.36	TGDS	13	14.52	1.49
HPS3	3	16.13	1.71	RAP2A	13	14.52	1.65
CP	3	16.13	1.47	IPO5	13	14.52	1.64
GFM1	3	16.13	1.6	DOCK9	13	14.52	1.93
ECT2	3	17.74	3.66	ING1	13	17.74	1.49
ACTL6A	3	17.74	2.03	ANKRD10	13	17.74	1.99
FXR1	3	17.74	1.84	ATP11A	13	19.35	1.92
DVL3	3	19.35	1.49	CUL4A	13	19.35	1.51
ECE2	3	19.35	1.78	TFDP1	13	14.52	1.79
EIF4G1	3	19.35	1.48	MED1	17	17.74	1.57
CLCN2	3	19.35	1.49	CDK12	17	17.74	1.56
MAGEF1	3	19.35	1.32	GRB7	17	17.74	1.44
RFC4	3	19.35	2.03	PSMD3	17	12.9	1.59
PPP1R2	3	17.74	1.27	CDC6	17	12.9	1.99
FBXO45	3	17.74	1.83	TOP2A	17	12.9	2.27
SENP5	3	17.74	1.77	KRT23	17	11.29	1.88
CCDC127	5	29.03	1.26	ACLY	17	14.52	1.64
PDCD6	5	29.03	1.36	EFTUD2	17	11.29	1.33
TRIP13	5	29.03	1.83	PHB	17	11.29	1.33
NKD2	5	29.03	1.53	MED13	17	12.9	1.51
SLC12A7	5	29.03	1.33	TANC2	17	12.9	1.36
LPCAT1	5	29.03	2.17	PRKCA	17	11.29	1.33

MED10	5	22.58	1.27	NOL11	17	11.29	1.71
NSUN2	5	22.58	1.82	FDXR	17	11.29	1.51
PAPD7	5	22.58	1.34	SUMO2	17	11.29	1.38
FAM173B	5	22.58	1.34	RBCK1	20	27.42	1.45
CCT5	5	22.58	1.89	TBC1D20	20	27.42	1.28
TRIO	5	25.81	1.62	SIRPA	20	27.42	1.84
ANKH	5	22.58	1.87	STK35	20	27.42	1.33
RNASEN	5	22.58	1.59	SNRPB	20	27.42	1.39
ZFR	5	27.42	1.82	MRPS26	20	27.42	1.49
SUB1	5	27.42	1.48	CDC25B	20	29.03	1.62
RAD1	5	25.81	1.6	PCNA	20	25.81	1.75
BRIX1	5	25.81	2.33	GPCPD1	20	24.19	1.53
C5orf33	5	25.81	1.4	PLCB1	20	27.42	1.34
NIPBL	5	24.19	1.45	MKKS	20	27.42	1.34
C5orf28	5	24.19	1.31	ESF1	20	30.65	2.2
MRPS30	5	24.19	1.48	SNX5	20	29.03	1.49
FLOT1	6	14.52	1.3	NAA20	20	30.65	1.53
TCF19	6	14.52	1.67	NANP	20	35.48	1.58
CSNK2B	6	14.52	1.3	HM13	20	41.94	1.39
MSH5	6	14.52	1.29	TPX2	20	41.94	3.2
VAR5	6	14.52	1.3	TM9SF4	20	38.71	1.27
EHMT2	6	14.52	1.3	PLAGL2	20	32.26	1.59
SNRPC	6	16.13	1.48	POFUT1	20	32.26	1.88
TOMM6	6	19.35	1.48	E2F1	20	41.94	1.48
BYSL	6	19.35	1.73	AHCY	20	41.94	1.39
RPL7L1	6	19.35	1.29	ITCH	20	41.94	1.45
MEA1	6	19.35	1.27	PIGU	20	41.94	1.35
CUL7	6	19.35	1.26	PROCR	20	41.94	1.34
XPO5	6	20.97	1.92	CPNE1	20	41.94	1.88
CDC5L	6	17.74	1.43	NFS1	20	41.94	1.54
INTS1	7	12.9	1.37	RBM39	20	41.94	1.41
EIF3B	7	11.29	1.73	DLGAP4	20	41.94	1.3
C1GALT1	7	11.29	1.53	C20orf24	20	41.94	1.46
C1GALT1	7	11.29	1.34	C20orf117	20	41.94	1.39
MACC1	7	11.29	1.54	RPN2	20	41.94	1.72
KLHL7	7	11.29	1.69	BLCAP	20	40.32	1.67
HNRNPA2B1	7	12.9	1.93	RPRD1B	20	40.32	1.64
CBX3	7	12.9	1.62	IFT52	20	41.94	1.61
SKAP2	7	12.9	1.65	MYBL2	20	41.94	2.17
LOC100289444	7	12.9	1.89	C20orf111	20	41.94	1.4
HOXA13	7	12.9	1.65	SERINC3	20	41.94	1.68
AVL9	7	12.9	1.82	YWHAB	20	41.94	1.36
KBTBD2	7	11.29	1.75	TOMM34	20	41.94	1.36
FKBP9	7	11.29	1.44	STK4	20	41.94	1.71
STARD3NL	7	11.29	1.6	UBE2C	20	41.94	2.97
PSMA2	7	8.06	1.43	TP53RK	20	41.94	1.25

C7orf44	7	8.06	1.35	NCOA3	20	41.94	1.68
H2AFV	7	8.06	1.35	ZNFX1	20	41.94	1.62
PURB	7	8.06	1.47	NCRNA00275	20	41.94	1.75
IGFBP3	7	8.06	2.62	RNF114	20	43.55	1.66
TNS3	7	8.06	1.39	DPM1	20	41.94	1.61
MRPS17	7	11.29	1.6	ATP9A	20	41.94	1.31
SLC25A40	7	8.06	1.79	ZNF217	20	40.32	1.51
SRI	7	8.06	1.27	AURKA	20	37.1	2.36
FZD1	7	8.06	1.27	C20orf43	20	37.1	1.61
ANKIB1	7	8.06	1.48	RAE1	20	37.1	1.72
PEX1	7	8.06	1.27	RBM38	20	37.1	1.47
CDK6	7	8.06	1.55	PMEPA1	20	37.1	3.05
SAMD9L	7	8.06	1.49	RAB22A	20	37.1	1.65
CCDC132	7	8.06	1.51	VAPB	20	37.1	1.37
MCM4	8	16.13	2.14	VAPB	20	37.1	1.32
UBE2V2	8	16.13	1.56	STX16	20	37.1	1.79
CHCHD7	8	16.13	1.27	GNAS	20	37.1	1.32
IMPAD1	8	16.13	1.78	ATP5E	20	37.1	1.22
SNHG6	8	17.74	1.59	CDH26	20	35.48	1.8
CSPP1	8	17.74	1.57	PSMA7	20	30.65	1.66
NCOA2	8	22.58	1.31	LAMA5	20	30.65	1.78
TRAM1	8	22.58	1.47	COL9A3	20	30.65	2.01
LACTB2	8	22.58	2.06	C20orf11	20	30.65	1.4
MRPS28	8	17.74	1.4	ARFGAP1	20	30.65	1.27
IMPA1	8	17.74	1.78	SLC2A4RG	20	33.87	1.36
OSGIN2	8	17.74	2.22	TPD52L2	20	35.48	1.75
NBN	8	17.74	1.96	PRPF6	20	35.48	1.31
PDP1	8	17.74	1.83				

Genes that are down-regulated and are frequently lost in human GCs

Gene Symbol	Chr	Percentage Lost*	Fold Down Regulation [#]	Gene Symbol	Chr	Percentage Lost*	Fold Down Regulation [#]
SYTL1	1	8.06	1.75	UQCRQ	5	9.68	1.52
FAM107A	3	12.9	2.27	MYO5B	18	24.19	1.58
S100P	4	12.9	3.48	NEDD4L	18	24.19	1.58
OCIAD2	4	9.68	1.37	SEC11C	18	24.19	1.6
PLAC8	4	9.68	3.27	CYB5A	18	25.81	2.1
IQGAP2	5	17.74	1.48	CBR1	21	11.29	2.25

*Percentage of GC samples with gain or loss at the specific gene loci. [#]Average fold of up-regulation or down-regulation of the gene comparing GC with non-tumor gastric samples.