SUPPLEMENTARY FIGURE LEGENDS

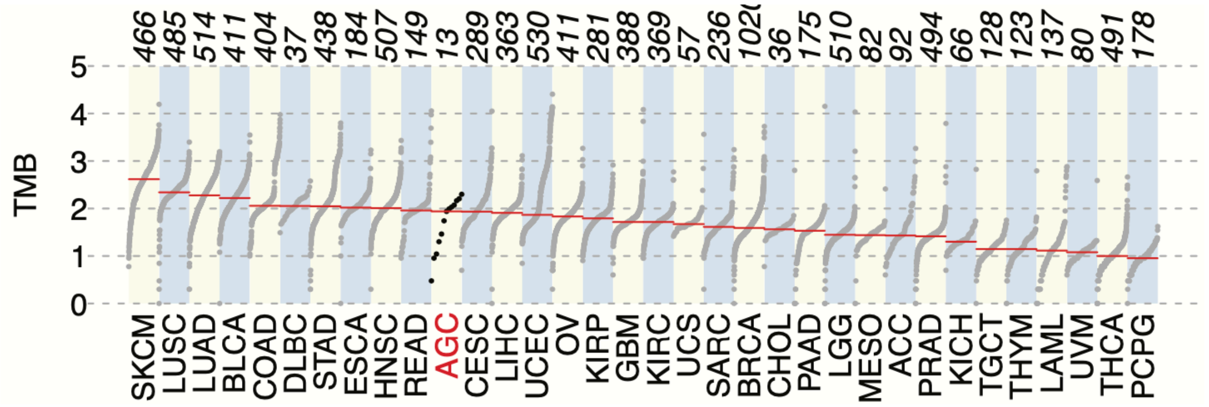

Figure S1. Mutational load of the advanced gastric cancer cohort.

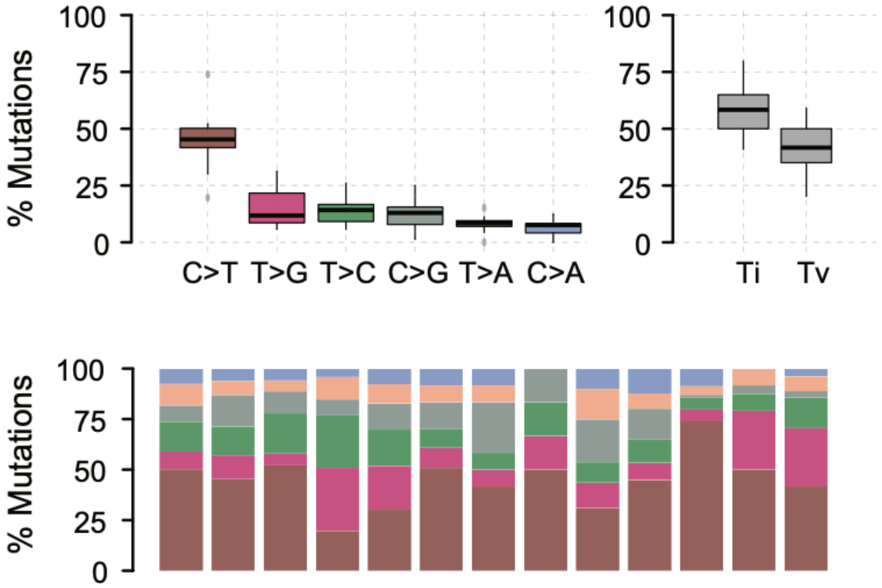

Figure S2. Classification of single-nucleotide variations.

SUPPLEMENTARY TABLES

Table S1. Focal copy number alterations identified by the Genomic Identification of Significant Targets in Cancer (GISTIC) algorithm in the study cohort.

Unique name	Number of genes	Number of samples	Variant classification	Cytoband	Wide peak limits	q-values
DP_5:16q11.2	11	8	Del	16q11.2	chr16:33294578-46723426	1.82E-06
DP_2:4q34.3	124	7	Del	4q34.3	chr4:160280551-191154276	0.0031908
AP_4:8q24.21	20	7	Amp	8q24.21	chr8:125730461-129029047	0.013246
DP_1:1p13.3	166	6	Del	1p13.3	chr1:102461462-121265007	0.084963
AP_2:7q31.2	11	5	Amp	7q31.2	chr7:115888553-116947663	0.09941
AP_1:7p11.2	11	6	Amp	7p11.2	chr7:53292358-56000794	0.14477
AP_3:8p23.1	2	6	Amp	8p23.1	chr8:12278702-12459239	0.14477
AP_5:12q14.3	39	5	Amp	12q14.3	chr12:65803552-71957037	0.14477
AP_7:17q12	7	4	Amp	17q12	chr17:37369541-37799779	0.14477
AP_8:19q12	18	5	Amp	19q12	chr19:23963713-31777953	0.14477
DP_3:8p21.2	18	3	Del	8p21.2	chr8:24209064-27325700	0.14822
DP_4:14q11.2	2	7	Del	14q11.2	chr14:19403660-19985576	0.14839
DP_6:21q22.3	11	8	Del	21q22.3	chr21:46924932-47715295	0.16068
AP_6:16q11.2	11	5	Amp	16q11.2	chr16:33783552-46733398	0.19368

Table S2. Genes contained in focal copy number alterations (CNA) in the study cohort: (A) amplification, (B) deletion.

(A)

cytoband	8q24.21	7q31.2	7p11.2	8p23.1	12q14.3	17q12	19q12	16q11.2
q value	0.013246	0.09941	0.14477	0.14477	0.14477	0.14477	0.14477	0.19368
residual q value	0.013246	0.09941	0.14477	0.14477	0.14477	0.14477	0.14477	0.19368
wide peak boundaries	chr8:125730461-129029047	chr7:115888553-116947663	chr7:53292358-56000794	chr8:12278702-12459239	chr12:65803552-71957037	chr17:37369541-37799779	chr19:23963713-31777953	chr16:33783552-46733398
genes in wide peak	hsa-mir-1206	CAPZA2	EGFR	FAM86B2	hsa-mir-1279	NEUROD2	CCNE1	hsa-mir-1826
	hsa-mir-1205	CAV1	HPVC1	LOC100506990	CPM	MED1	UQCRFS1	ORC6
	hsa-mir-1204	CAV2	SEC61G		IFNG	STARD3	URI1	VPS35
	MYC	MET	LANCL2		LYZ	CDK12	ZNF254	SHCBP1
	POU5F1B	WNT2	VOPP1		MDM2	PPP1R1B	ZNF536	ANKRD26P1
	PVT1	ST7	VSTM2A		CNOT2	FBXL20	POP4	LOC146481
	SQLE	TES	LOC285878		PTPRB	STAC2	TSHZ3	LOC283914
	MTSS1	ST7-AS1	14.Sep		PTPRR		PLEKHF1	FLJ26245
	KIAA0196	ST7-AS2	ZNF713		RAP1B		C19orf12	UBE2MP1
	TRIB1	ST7-OT3	FKBP9L		TSPAN8		DKFZp566F0947	LINC00273
	ZNF572	ST7-OT4	FLJ45974		YEATS4		LOC148145	LOC100130700
	LOC157381				HMGA2		LOC148189	
	FAM84B				DYRK2		LOC284395	
	NSMCE2				LGR5		VSTM2B	
	LOC727677				CCT2		RPSAP58	

	LOC100130231	FRS2	ZNF726
	MIR1205	CPSF6	LOC100101266
	MIR1206	IRAK3	LOC100505835
	MIR1204	GRIP1	
	PCAT1	KCNMB4	
		IL22	
		TMBIM4	
		SLC35E3	
		IL26	
		CAND1	
		MDM1	
		NUP107	
		LLPH	
		HELB	
		RAB3IP	
		BEST3	
		RPSAP52	
		MSRB3	
		LRRC10	
		MIR1279	
		SNORA70G	
		MIR3913-2	
		MIR3913-1	
		LOC100507250	

(B)

cytoband	16q11.2	4q34.3	1p13.3	8p21.2	14q11.2	21q22.3
q value	1.82E-06	0.0031908	0.084963	0.14822	0.14839	0.16068
residual q value	1.82E-06	0.0031908	0.084963	0.14822	0.14894	0.16068
wide peak boundaries	chr16:33294578-46723426	chr4:160280551-191154276	chr1:102461462-121265007	chr8:24209064-27325700	chr14:19403660-19985576	chr21:46924932-47715295
genes in wide peak	hsa-mir-1826	hsa-mir-1305	hsa-mir-942	hsa-mir-548h-4	POTEG	COL6A1
	VPS35	hsa-mir-4276	hsa-mir-320b-1	ADRA1A	LOC642426	COL6A2
	SHCBP1	hsa-mir-548t	hsa-mir-4256	BNIP3L		LSS
	ANKRD26P1	hsa-mir-1979	hsa-mir-197	DPYSL2		SLC19A1
	LOC146481	AGA	ADORA3	PTK2B		MCM3AP
	LOC283914	SLC25A4	ALX3	GNRH1		FTCD
	LOC390705	CASP3	AMPD1	NEFM		PCBP3
	FLJ26245	CLCN3	AMPD2	NEFL		YBEY
	UBE2MP1	CPE	AMY1A	PPP2R2A		C21orf56
	LINC00273	DCTD	AMY1B	ADAM7		MCM3AP-AS1
	LOC100130700	F11	AMY1C	PNMA2		LOC100129027
		ACSL1	AMY2A	TRIM35		
		FAT1	AMY2B	ADAMDEC1		
		FRG1	RHOC	KCTD9		
		GK3P	ATP1A1	EBF2		
		GPM6A	ATP5F1	DOCK5		
		HMGB2	CAPZA1	STMN4		
		HPGD	CASQ2	CDCA2		

HSP90AA4P
ING2
IRF2
KLKB1
MTNR1A
NEK1
NPY1R
NPY5R
MSMO1
TLL1
TLR3
VEGFC
GLRA3
SORBS2
SAP30
HAND2
MFAP3L
ADAM29
ANXA10
KLHL2
SCRG1
DUX4
PALLD
ANP32C
FAM149A
CD2
CD53
CD58
CHI3L2
COL11A1
CSF1
CELSR2
FCGR1B
GNAI3
GNAT2
GSTM1
GSTM2
GSTM3
GSTM4
GSTM5
HMGCS2
HSD3B1
HSD3B2
IGSF3
KCNA2
KCNA3
KCNA10
KCNC4
KCND3
MOV10

FBXO8	NGF
DUX2	NHLH2
PDLIM3	NOTCH2
SPOCK3	NRAS
AADAT	OVGP1
GALNT7	PSMA5
CLDN22	PTGFRN
C4orf27	RAP1A
1.Mar	SORT1
NEIL3	SARS
C4orf43	SLC16A1
UFSP2	STXBP3
DDX60	SYCP1
CDKN2AIP	TAF13
ODZ3	TBX15
LRP2BP	TSHB
FSTL5	WNT2B
STOX2	CSDE1
KIAA1430	TTF2
SH3RF1	SLC16A4
SPCS3	CD101
TRAPPC11	LRIG2
MLF1IP	TSPAN2
NBLA00301	BCAS2
WWC2	WARS2

CEP44
SNX25
TKTL2
CBR4
MGC45800
DDX60L
NAF1
WDR17
ZFP42
SPATA4
ENPP6
ASB5
C4orf38
C4orf39
TRIM60
TMEM192
RWDD4
CCDC111
TRIML2
CCDC110
CYP4V2
LOC285441
LOC285501
LOC339975
TRIML1
CEPT1
VAV3
HBXIP
AP4B1
PHTF1
AHCYL1
WDR3
MAN1A2
ADAM30
DDX20
NTNG1
WDR47
CLCC1
PTPN22
PHGDH
CHIA
GPSM2
SLC25A24
HAO2
TRIM33
RSBN1
GDAP2
FAM46C
ST7L
PRPF38B

ANKRD37
LOC389247
TRIM61
HELT
LOC401164
FAM92A3
HSP90AA6P
C4orf47
DUX4L4
GALNTL6
FRG2
SLED1
FLJ38576
DUX4L6
DUX4L5
DUX4L3
MIR578
LINC00290
LOC728175
DUX4L2
LOC731424
CLDN24
LOC100288255
MIR1305
MIR4276
PRMT6
SLC22A15
RNPC3
LRIF1
CTTNBP2NL
FAM212B
TMEM167B
OLFML3
AMIGO1
KIAA1324
RBM15
DCLRE1B
WDR77
EPS8L3
VTCN1
DENND2D
SIKE1
TRIM45
VANGL1
GPR61
REG4
PROK1
PSRC1
ATP1A1OS
FAM40A

MIR3945	ZNF697
LOC100505989	HENMT1
LOC100506013	MAB21L3
LOC100506085	ATXN7L2
LOC100506122	C1orf194
LOC100506229	HSD3BP4
	DRAM2
	C1orf88
	C1orf162
	SYT6
	NBPF4
	RP11-165H20.1
	DENND2C
	FNDC7
	UBL4B
	SPAG17
	HIPK1
	AKR7A2P1
	AKNAD1
	MAGI3
	FAM19A3
	FAM102B
	SYPL2
	CYB561D1
	PPM1J

	HIST2H2BA
	MYBPHL
	NBPF7
	SLC6A17
	MIR197
	LOC440600
	BCL2L15
	PGCP1
	SRG7
	CYMP
	LOC643441
	LOC644242
	LOC648740
	NBPF6
	FAM72B
	SCARNA2
	MIR942
	LOC100129138
	LOC100129269
	LOC100287722
	MIR320B1
	MIR4256
	LOC100506343