Table S1 The 75 single nucleotide variants (SNVs) found in the GC tissue

Gene	Transcript	c.	p.	Mutation frequency
ARAF	NM_001654.4	c.1199G>A	p.R400H	13.90%
MED12	NM_005120.2	c.5711C>T	p.A1904V	13.80%
MLH1	NM_000249.3	c.791-1G>T	.	11.00%
BCORL1	NM_021946.4	c.5036C[7>6]	p.P1681Qfs*20	11.00%
ETV6	NM_001987.4	c.985G>A	p.A329T	10.00%
CHEK1	NM_001114121.2	c.1115G>A	p.R372Q	8.00%
SOX9	NM_000346.3	c.1004G>A	p.W335*	7.80%
RNASEL	NM_021133.3	c.172G[5>6]	p.W60Lfs*6	7.40%
FLT4	NM_182925.4	c.1790C>T	p.T597M	7.40%
CDH11	NM_001797.2	c.1196G>T	p.G399V	7.40%
ROS1	NM_002944.2	c.6773T>C	p.I2258T	7.30%
EP300	NM_001429.3	c.752A>G	p.N251S	7.20%
EPAS1	NM_001430.4	c.2254C>T	p.P752S	7.10%
SOX9	NM_000346.3	c.1033C[5>4]	p.P346Rfs*37	7.10%
JAK3	NM_000215.3	c.523C>T	p.R175*	7.10%
MTHFR	NM_005957.4	c.659C>T	p.A220V	6.90%
FAT1	NM_005245.3	c.9589C>A	p.L3197I	6.90%
B2M	NM_004048.2	c.19T[2>3]	p.L7Ffs*50	6.90%
PBRM1	NM_018313.4	c.4133G>A	p.G1378D	6.80%
FAM175A	NM_139076.2	c.299A>G	p.Y100C	6.80%
MAGI2	NM_012301.3	c.1609A>G	p.M537V	6.80%
NOTCH1	NM_017617.3	c.2644G>A	p.A882T	6.80%
POLE	NM_006231.2	c.5312C>T	p.T1771M	6.70%
AURKB	NM_004217.3	c.809A>G	p.N270S	6.70%
MPL	NM_005373.2	c.565G>A	p.A189T	6.60%
EPHB6	NM_004445.3	c.2130A>C	p.E710D	6.60%
BRCA2	NM_000059.3	c.6700T>G	p.F2234V	6.60%
RPTOR	NM_020761.2	c.928G>T	p.G310C	6.60%
SRC	NM_198291.1	c.1335G>T	p.K445N	6.60%
BARD1	NM_000465.2	c.943C>T	p.P315S	6.50%
ATR	NM_001184.3	c.1817G>A	p.G606D	6.50%
CDK12	NM_016507.2	c.2594T[4>3]	p.L866Cfs*2	6.50%
BRIP1	NM_032043.2	c.688T>C	p.S230P	6.50%
CD74	NM_001025159.2	c.797G>A	p.R266H	6.40%
ACTB	NM_001101.3	c.1022T>G	p.I341S	6.40%
DDR1	NM_001954.4	c.352T>A	p.Y118N	6.30%
B2M	NM_004048.2	c.35T>C	p.L12P	6.30%

Table S1 *(continued)*

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Table S1 *(continued)*

Gene	Transcript	c.	p.	Mutation frequency
NOTCH3	NM_000435.2	c.5062T>A	p.S1688T	6.30%
PIK3CA	NM_006218.2	c.1634A>G	p.E545G	6.20%
PDGFRB	NM_002609.3	c.1712_1713delCT	p.S571Cfs*4	6.20%
FAT2	NM_001447.2	c.2304G>T	p.E768D	6.20%
MAP2K1	NM_002755.3	c.199G>A	p.D67N	6.20%
SMAD4	NM_005359.5	c.290G>A	p.R97H	6.10%
EPCAM	NM_002354.2	c.497T>C	p.L166P	6.00%
XRCC1	NM_006297.2	c.637G>T	p.A213S	6.00%
IGF1R	NM_000875.3	c.3469A>G	p.T1157A	5.90%
CREBBP	NM_004380.2	c.4996G>A	p.A1666T	5.90%
RECQL4	NM_004260.3	c.3136GAG[2>1]	p.E1046[2>1]	5.80%
RECQL	NM_002907.3	c.1058A>C	p.K353T	5.80%
DICER1	NM_030621.3	c.1469G>A	p.R490H	5.80%
EPHA5	NM_004439.5	c.2810G>A	p.R937H	5.60%
ROS1	NM_002944.2	c.4596A[6>5]	p.N1534Ifs*69	5.60%
MLL2	NM_003482.3	c.7057C[5>4]	p.P2354Lfs*30	5.50%
RB1	NM_000321.2	c.2521-1G>T	.	5.50%
DOT1L	NM_032482.2	c.2011C>A	p.L671M	5.50%
POLD1	NM_002691.3	c.31_37delCCCGGGG	p.P11Cfs*28	5.50%
SMARCA4	NM_003072.3	c.265C>T	p.R89C	5.40%
FAM5C	NM_199051.1	c.1261G>A	p.E421K	5.30%
EPHB1	NM_004441.4	c.1789C>A	p.P597T	5.10%
NSD1	NM_022455.4	c.7703G>A	p.G2568E	5.10%
MLL	NM_001197104.1	c.11281T>G	p.L3761V	5.10%
BRCA2	NM_000059.3	c.9247A[7>6]	p.T3085Qfs*19	5.10%
ATR	NM_001184.3	c.3396T[7>8]	p.N1135*fs*1	5.00%
SMARCB1	NM_003073.3	c.1085AGA[3>2]	p.K363[2>1]	4.90%
BUB1	NM_004336.3	c.1753C>T	p.R585C	4.80%
EPHA5	NM_004439.5	c.1443A[6>5]	p.N483Tfs*18	4.60%
NSD1	NM_022455.4	c.7697C[4>5]	p.G2568Rfs*4	4.50%
EIF2AK3	NM_004836.5	c.2723AG[5>6]	p.S912Gfs*23	3.90%
MLL2	NM_003482.3	c.12560G>T	p.G4187V	2.40%
LRP1B	NM_018557.2	c.5656C>A	p.H1886N	1.80%
ARID1A	NM_006015.4	c.31_56delAGCAGCCTGGGCAA CCCGCCGCCGCC	p.S11Afs*91	1.30%
EP300	NM_001429.3	c.4432C>T	p.R1478C	1.30%
PTPRD	NM_002839.3	c.2569C>T	p.R857C	1.20%
ERRFI1	NM_018948.3	c.529T>A	p.S177T	1.10%
ERBB2	NM_004448.2	c.1805G>A	p.S602N	1.10%

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