Figure S1. The profile of the MSI/LOH at 91 loci in tumor-related genes and 5 B5 loci in 90 patients with gastric cancer. The red color indicates the mutated MS and the green indicates the unmutated MS in each patient. MSI, microsatellite instability; LOH, loss of heterozygosity.

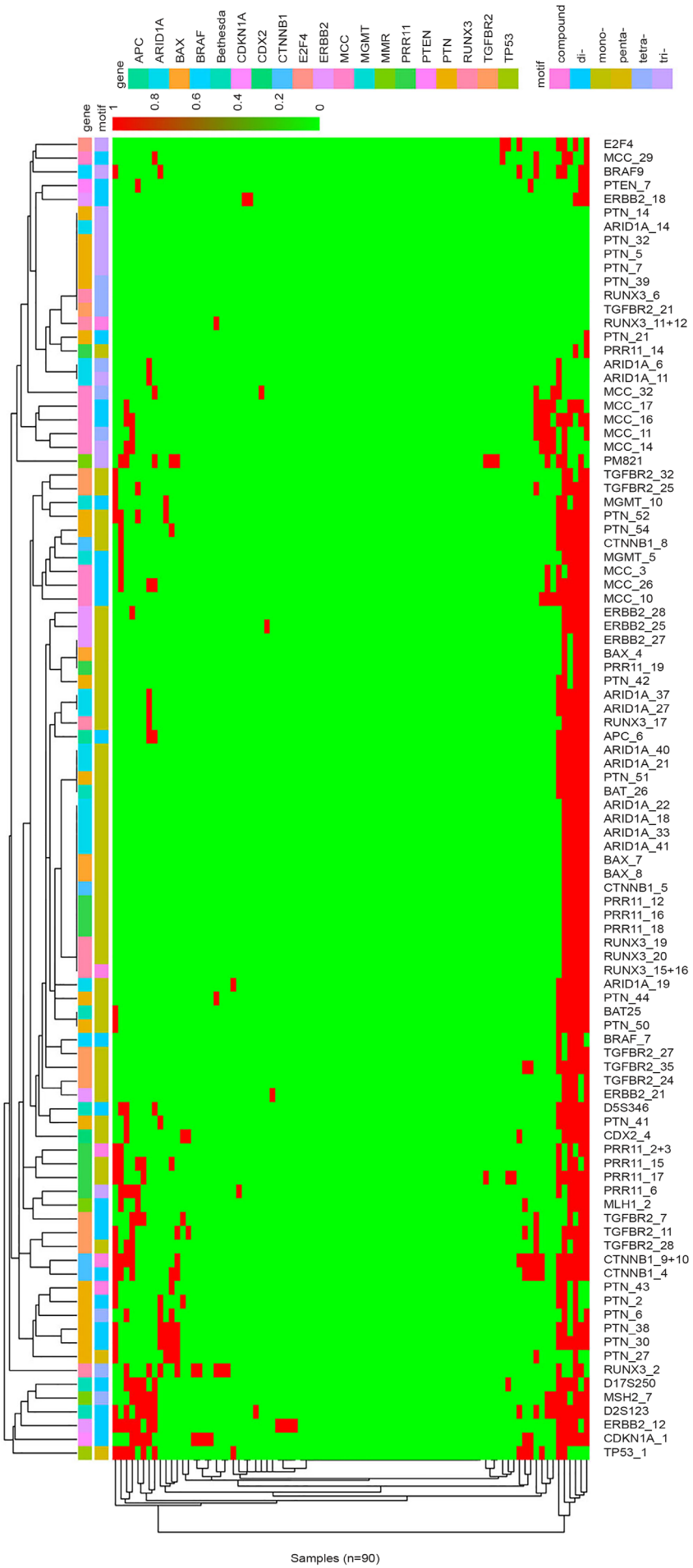

Figure S2. MSI/LOH profile of the 32 loci in the second set (n=136) of gastric cancer samples. MSI, microsatellite instability; LOH, loss of heterozygosity.

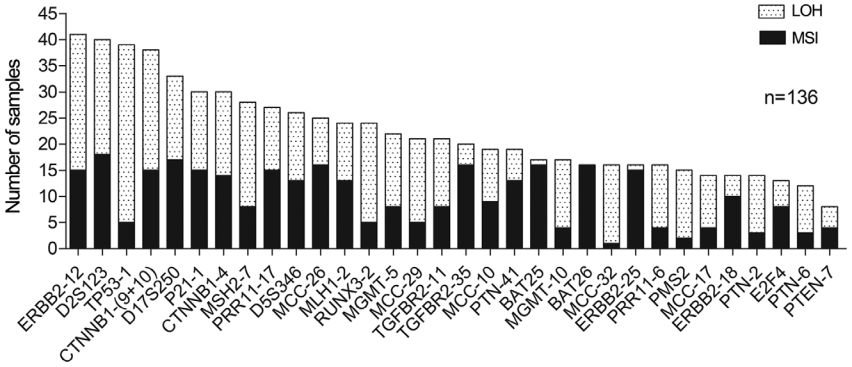

Table SI. Detailed information of the 91 MS loci.

Gene name	Locus name	Repeat unit	Primer sequence (5'-3')	Size, bp	Mg2+ concentration	AT, °C	Location
ARID1A	ARID1A-6	(TTTG)7	F: CAAGTGTCCATCCCAACT R: GGCAACCGAACGAGA	356	1.5	57.5	Intron 1
	ARID1A-11	(AAT)6	F: GGTTTCAACCAGTTAGCGGC R: AGAGAGCCAAAGCTACACGG	453	1.5	66.4	Intron 4
	ARID1A-14	(GCA)8	F: GACCACGACAGCACTATCCC R: ATCCATAGCAGCACCGAGAC	301	1.5	65.3	Exon 16
	ARID1A-18	(A)16	F: TTGATGGGTTAGGTAAGCCTG R: TGAGCAGCATTTGTTAGCTGC	424	1.5	66.4	Intron 1
	ARID1A-19	(T)26	F: GTAGTTTATCTGTTCTTGGGTCA R: TACTCGGGAGGCTGTGG	351	1.5	67	Intron 1
	ARID1A-21	(T)21	F: CCAGAAGGGTGATGTAGGA R: TGATTGTGCCTGTGGATAG	295	1.5	63.2	Intron 1
	ARID1A-22	(T)17	F: ACCACACCAGAGCTGGTAAA R: GCCAGGCTTTTCCAAGAAAGGA	410	1.5	64	Intron 1
	ARID1A-27	(T)19	F: TGGGTGAGGTGCTATTGTGT R: AAAGCCCAAACGTGGGAATG	318	2.5	67	Intron 4
	ARID1A-33	(T)20	F: TCTTGGCTGCTGTAACTCAGG R: ACTCCCATAGGCCGCTAAC	262	1.5	65	Intron 4
	ARID1A-37	(T)16	F: AAAATCCTGACCTCCAGTG R: AATCGCCCTATTCTACCTT	428	1.5	63.2	Intron 8
	ARID1A-40	(A)19	F: CTGGGCAACAGAGCGGGACT R: TTGGCTGAACAGTAGAGCAGATG GAAA	331	1.5	66.4	Intron 19
	ARID1A-41	(A)18	F: ATCCAGTTTACCCTGTGCTGT R: CAACTGCGAACTTCTTGGCTC	428	1.5	67	3'UTR
BAX	BAX-4	(A)22	F: CCATGGTCAGGGGTTGATCTT R: TTCAGCTCTCAGGGCAAATG	392	1.5	65	Intron 2
	BAX-7	(T)27	F: AGGGCAGAAGCGAGGAT R: CCTTGGTAACAGAGCGAGAC	401	1.5	67	Intron 2
	BAX-8	(A)17	F: GCAGGAGGATCACTTAAATCTG R: AGGATGAAGACCCGAAGG	386	1.5	64.4	Intron 2
CDX2	CDX2-4	(T)23	F: TCGCTACATCACCATCCG R: AGACCAACCTGGGTAAGACA	429	1.5	64.2	Intron 2
CTNNB1	CTNNB1-4	(TG)15	F: TGTTGGCAATTGGGGAAAAGAAT R: AAAGTAAGTGTTGCCAGCCC	264	1.5	65	Intron 7
	CTNNB1-5	(T)20	F: ACCCTGCTGTCCTTGAAGTATG R: GCTTCAGGCTTGAGGGAAACT	196	1.5	65	5'UTR
	CTNNB1-8	(T)21	F: CCTTAACTTTCTCCACCTAC R: CTCTTTGCACCTCACATT	295	1.5	60.8	Intron 12
	CTNNB1-(9+10)	(T)19+(T)25	F: CCTAGCCTTGCTTGTTA R: CCTCTTACTGATTTACCCT	405	1.5	57.5	3'UTR
E2F4	E2F4	(CAG)13	F: GGACAGTGGTGAGCTCAGTT R: TGGGTTCCATCCCCAATTCT	284	1.5	64.2	Exon 7
ERBB2	ERBB2-12	(AC)27	F: ACGACTCCTCCCGATTTCTG R: ACAGGGCTCTAGCTTCCGA	262	1.5	63	Intron 4
	ERBB2-18	(AC)15	F: CCATCAACTGCACCCA R: TGAGCCAAGATTGTACTACTG	427	1.5	67	Intron 18
	ERBB2-21	(A)16	F: TGAGCCTCCTTAGCTTGTCC R: TGCCGTTGAGCCTTTAGCAC	385	1.5	67	Intron 2
	ERBB2-25	(A)16	F: GTGCCTGCTTTAAGTGTGCTC R: TGCCCCTTGCCTTCTATTAGC	438	1.5	63	Intron 4
	ERBB2-27	(T)16	F: ACTTACTAGGCATGTGACCCT R: CTGGCGATAAAGCGAGAC	410	1.5	67	Intron 12
	ERBB2-28	(T)22	F: CGTGCCCAGCCAGATAC R: GCTGAGACAGGAGGATTGC	458	1.5	64.2	Intron 19
PRR11	PRR11-(2+3)	(AC)18+ (AG)10	F: TCCTCTGCATGTGCCAATTACT R: TTCCTGTTGGCTGTTCCAGT	251	1.5	61.1	Intron 1

Table SI. Continued.

Gene name	Locus name	Repeat unit	Primer sequence (5'-3')	Size, bp	Mg2+ concentration	AT, °C	Location
	PRR11-6	(AAT)11	F: ACACACCATCAGTCCCCCT R: GGAACATCCTATAAACACTGTT CTG	427	1.5	64.2	Intron 4
	PRR11-12	(T)21	F: TGGATGCTCAGTAGATGCTGC R: AGCGAAAATGGCTGTAGGTGG	393	1.5	64.2	Intron 1
	PRR11-14	(A)15	F: ATGCCACTGCACTCCATC R: CCAGCACTTCCCACCAG	421	1.5	67	Intron 2
	PRR11-15	(T)20	F: TGGCCTGAATTTCTCCATT R: GCCAAGATTGTGCTACCG	141	1.5	63.2	Intron 2
	PRR11-16	(T)26	F: TCTCTCTTCTGGCACACCAC R: GGGTTGGACTGACTTGAGCAC	476	1.5	67	Intron 2
	PRR11-17	(T)33	F: TGAGGGAGCCATCCA R: GAGCCAGTAGGTCAAGGT	481	1.5	63.2	Intron 4
	PRR11-18	(A)17	F: GCGGGCACCAGTAATC R: CTGTAAATGAGTTTGGGAAGT	292	1.5	65.3	Intron 4
	PRR11-19	(T)16	F: GGTTCCTGGTTATGATGGC R: GCGGTGGCTCACGTCTAT	472	1.5	65.3	Intron 4
RUNX3	RUNX3-2	(ATGG)11	F: TCACTACTCACCCCACAGGT R: CCATGTCCCACGTTGAAGGA	460	1.5	60.8	Intron 1
	RUNX3-6	(TCAT)6	F: CCCAGAGTGGAAACAAACA R: CTCCTCCTCATACATCAAAGC	340	1.5	60.8	Intron 1
	RUNX3-(11+12)	(TGAC)5+ (TGAA)6	F: ACCCAGACCCTATGAGCAGG R: GCTCCTTGCACAGCATTAGG	433	1.5	60.8	Intron4
	RUNX3-(15+16)	(T)15+ (T)16	F: GCTACTTTGTAGGGCTATGC R: GCGGATCACGAGGTCA	305	1.5	60.8	Intron 1
	RUNX3-17	(T)19	F: CCCATGCAGAAGGTACTTGA R: CAGGGAGTTGGAGGTTGC	295	1.5	65	Intron 1
	RUNX3-19	(T)25	F: GAAAGGGAGTGGTAGGGC R: CGAGCGTAGGCAACAAAC	423	1.5	63.2	Intron 3
	RUNX3-20	(T)21	F: TCTTGCCTCTTCTCCCTCTG R: CTGACCAATATGGTGAAACCC	312	1.5	65	Intron 4
	RUNX3-21	(A)16	F: AATCTTGCGACTCCTGGCAC R: CATCAGCGTTTCCCTCGTCC	379	2	66.4	3'UTR
TGFBR2	TGFBR2-7	(GA)13	F: ATCTCTGCACGAGGGTTGTT R: ACATCTCTGCAAAGGAATGTTGC	467	1.5	65	Intron 1
	TGFBR2-11	(TG)22	F: TAGGGACCAACCTGGTGTTTG F: TGGGCACCAGGATCAGAAGT	417	1.5	65	Intron 2
	TGFBR2-21	(ATTC)6	F: AGCCCAATCTCTCCTTTCAGC R: TTGGGTGCAAGTTGAGTCCC	294	1.5	65	Intron6
	TGFBR2-24	(T)16	F: AAGGCACTGGTAGCAAGTCA R: AGGCAATCTGTGAGTAAATGCC	494	1.5	64.2	Intron 1
	TGFBR2-25	(T)19	F: GCCAGATCATCACCCAT R: AGAAGTTCAAGAGCAGCAT	372	1.5	67	Intron 1
	TGFBR2-27	(T)22	F: CTAGGACTTGGAAAGGAGTAGCC R: GGTCTCTCTTGTGGTGAGTAGC	394	1.5	67	Intron 2
	TGFBR2-28	(T)22	F: TTCCTGCCCTTTGTTGTCCT R: GCCTGTTCTCCAACCAGTCA	252	1.5	65	Intron 2
	TGFBR2-32	(T)15	F: TTGAGGGCCATACTGTGCT R: AGCTTTGAAGCCACTCAGATG	430	1.5	67	Intron 4
	TGFBR2-35	(A)21	F: GCAAGCACACTGACTTCCAC R: CAAAGCAGTACCCCCGAGTT	345	1.5	63	Intron6
PTN	PTN-2	(AC)10	F: AGTGAAACCTCCTCTCTCCTCT R: CTCTTAGCACCCCTACCCCT	204	1.5	65.3	Non-coding
	PTN-5	(CTC)5	F: TGCCTTGATTGCTATTTGCTGT R: AGCAATTCAAGTAGCTTCTTAT GGA	496	1.5	60.8	Non-coding
	PTN-6	(TCAT)7	F: TTGCTTAAATACCGTCACGTCC R: TAGAGCCCAGCTCATTGTGTG	181	2	57.5	Non-coding

Table SI. Continued.

Gene name	Locus name	Repeat unit	Primer sequence (5'-3')	Size, bp	Mg2+ concentration	AT, °C	Location
	PTN-7	(CCT)5	F: TGGGTGGGTGTTTTGTGATG R: TACCACTGATTCTGCCCTCC	169	1.5	65.3	Non-coding
	PTN-14	(TTG)5	F: TAGATTCGTTTGCCGTCTGC R: AGGTGGAAACTAGAAGGGGTC	214	1.5	65.3	Non-coding
	PTN-21	(TG)11	F: ACCCTTGGTGCTTCCTTGTG R: GGTACTTCAGCTCACTTTTGCTT	197	1.5	66.4	Non-coding
	PTN-27	(TTTTG)5	F: CTGACTGGCTTGAGATGG R: AATGGGATGGCTGGA	297	2	60.8	Non-coding
	PTN-30	(AC)17	F: GCACAGACTAACCCAATCAGCA R: TCCACCTAATCATGTCCCCAC	261	1.5	65.3	Intron 4
	PTN-32	(TTG)5	F: GTTCCTTCCCTCTGACTGCT R: ACGTACTCCTTTCCCATCACTC	162	1.5	65.3	Intron 4
	PTN-38	(TG)10	F: GAACTCGTTAAAAGTGTTGTTTC R: CCCTGAAGGAAAAGGAGGGTT	280	1.5	57.5	Intron 4
	PTN-39	(CAGA)5	F: CCACTCTCACAGGCACTCTT R: TGCAGGGAAGAAATAGCCACAT	172	1.5	65.3	Intron 4
	PTN-41	(T)17	F: TGTTTTCAACACCAGTGCCC R: TAGGACCCCGAGACGATGTG	205	1.5	66.4	Non-coding
	PTN-42	(A)17	F: GTCAATGGTCACGACGCAAC R: CATGCCTGTTTCAGTTCAGCC	297	1.5	60.8	Non-coding
	PTN-43	(TA)9+(T)17	F: TAGATGAGGGCTTAGGAAGGT R: GGCTCTCAAACTTTAGTGTGTCTG	295	2.5	63.2	Non-coding
	PTN-44	(A)16	F: TGGGAGTCGGAGGTTG R: CAGGAGATTAGATGGGCTTA	209	1.5	67	Non-coding
	PTN-50	(A)27	F: AGCGCACATTTGTAATCC R: TGCTCCCGTTCACTTTT	272	1.5	63.2	Non-coding
	PTN-51	(A)22	F: AGTAACCTGCGGATGG R: CCTTGTAAGTTTGGGATT	168	1.5	57.5	Non-coding
	PTN-52	(A)19	F: GTCCCACGAGGAATACAG R: TTGTGCTAACAGGGTCATT	375	1.5	57.5	Non-coding
	PTN-54	(A)24	F: GGGGAGGGATAGCATT R: CCATCTCCAGGAAAGC	281	1.5	60.8	Intron 4
TP53	TP53-1	(AAAAT)8	F: GGCAATAAGAGCTGAGACTCC R: GACAAAACATCCCCTACCAAA	121	1.5	62	Intron 1
MSH2	MSH2-7	(AAAT)8	F: TTGCTCTCTTGCTATCTTG R: GCCCTCTACTGTCTCTCTG	127	1.5	60.7	Intron 7
PTEN	PTEN-7	(TA)10	F: CTTTTAGAATAATGACACC R: ATAATAGAGAAACAGGAAC	149	1.5	55.4	Intron 6
APC	APC-6	(AC)17	F: AACTTATTTCATTCCTGT R: TTGTATCATCTCCTCTTC	176	1.5	51.3	Intron 10
MGMT	MGMT-5	(GT)22	F: AAACGGGAACTTTCAGAC R: AAATCACTAGGCACCAAC	226	1.5	60.7	Intron 2
	MGMT-10	(AC)12	F: AAGACTTCAAGGGAGAC R: AAAGAAAGGAAAAACAA	177	1.5	51.3	Intron 2
CDKN1A	CDKN1A-1	(GT)19	F: TTCGTTGCTCCCGTCTAT R: GCTCTTGTGCCGTCTCTG	180	1.5	60.8	Intron 1
MCC	MCC-3	(TG)16	F: CTTGATTCCTTGCCC R: ACCTCTGTCGCTGCT	285	1.5	60.7	Intron 1
	MCC-10	(AT)10	F: GCCATACCCACTTCC R: GCTCATCACCCTGCT	241	1.5	62	Intron 1
	MCC-11	(TGAA)6	F: ACTTATCTATCTTTCC R: AGTTATTTAGTGTCTG	226	1.5	48.3	Intron 2
	MCC-14	(TTG)7	F: CTGCTTGGTGTTCTA R: ATCATGCCATTGTAC	190	1.5	55.4	Intron 2
	MCC-16	(CA)15	F: CCTAAGAAAATACGACAAC R: CAAAGACAGGAGAGAGAGT	271	1.5	60.7	Intron 3
	MCC-17	(TG)9	F: AATGAACTTGCAGAC R: AAAGATGGTGAATAA	191	1.5	46.2	Intron 3

Table SI. Continued.

Gene name	Locus name	Repeat unit	Primer sequence (5'-3')	Size, bp	Mg2+ concentration	AT, °C	Location
	MCC-26	(TG)23	F: GCTCTCCCTCTCCATC R: CCTTCAGCATCCCTAC	238	1.5	62	Intron 4
	MCC-29	(GA)11	F: AAATCCCCCCAACATCTC R: CCTGTCAATAGCCACTGC	182	1.5	62	Intron 8
	MCC-32	(TTGT)5	F: ATCCATTATCCAGCA R: AACACAGTGAGACCC	191	1.5	51.3	Intron 15
MLH1	MLH1-2	(TA)12	F: TCATACTAGCTTCTTTC R: ACCTTATCACTACTTCC	223	1.5	51.9	Intron 11
BRAF	BRAF-9	(TTG)14	F: TAGAGACAGAGTTTCG R: CAGTTAGGATTTGAAG	276	1.5	51.3	Intron 13
	BRAF-7	(GT)13	F: GCCTTAAAGTAGGAGACA R: TATGAAGAGTGGGGAAAT	278	1.5	51.3	Intron 3
PMS2	PMS2-1	(AAT)9	F: ATGCCATTGCCCTCTA R: TGCCCCACTTCCTACT	197	1.5	60.7	Intron 1

MS, microsatellite; AT, annealing temperature.

Table SII. Mutation profile of 91 MS in 90 gastric cancer samples.

Rank	MS locus	MSI	LOH	MSI+LOH
1	ERBB2-12	6	11	17
2	CDKN1A-1	7	9	16
3	CTNNB1-(9+10)	5	11	16
4	CTNNB1-4	8	7	15
5	PRR11-17	6	7	13
6	TP53-1	2	11	13
7	MSH2-7	5	7	12
8	PMS2-1	2	10	12
9	RUNX3-2	2	10	12
10	PTN-30	6	5	11
11	TGFBR2-11	5	6	11
12	MCC-16	3	7	10
13	MCC-26	6	4	10
14	PRR11-6	3	7	10
15	PTN-38	5	5	10
16	PTN-52	5	5	10
17	CDX2-4	5	4	9
18	MCC-10	6	3	9
19	PRR11-15	3	6	9
20	APC-6	4	4	8
21	BRAF-9	3	5	8
22	MCC-17	2	6	8
23	PTN-41	6	2	8
24	PTN-54	5	3	8
25	TGFBR2-25	5	3	8
26	TGFBR2-28	3	5	8
27	TGFBR2-35	5	3	8
28	TGFBR2-7	3	5	8
29	ARID1A-19	5	2	7
30	ARID1A-27	5	2	7
31	ARID1A-37	5	2	7
32	CTNNB1-8	5	2	7
33	E2F4	4	3	7
34	MCC-11	2	5	7
35	MCC-3	3	4	7
36	MGMT-10	3	4	7
37	MLH1-2	4	3	7
38	PTN-44	5	2	7
39	PTN-50	5	2	7
40	ARID1A-21	5	1	6
41	ARID1A-40	5	1	6
42	ERBB2-18	3	3	6
43	ERBB2-25	5	1	6
44	ERBB2-28	5	1	6
45	MCC-14	1	5	6
46	MCC-29	1	5	6
47	MGMT-5	3	3	6
48	PRR11-(2+3)	1	5	6
49	PTN-2	2	4	6
50	PTN-27	0	6	6
51	PTN-51	5	1	6
52	PTN-6	3	3	6
53	RUNX3-17	4	2	6
54	ARID1A-18	5	0	5
55	ARID1A-22	5	0	5
56	ARID1A-33	5	0	5
57	ARID1A-41	4	1	5
58	BAX-7	5	0	5
59	BAX-8	5	0	5

Table SII. Continued.

Rank	MS locus	MSI	LOH	MSI+LOH
60	CTNNB1-5	5	0	5
61	ERBB2-21	4	1	5
62	MCC-32	0	5	5
63	PRR11-12	5	0	5
64	PRR11-16	5	0	5
65	PRR11-18	5	0	5
66	PRR11-19	3	2	5
67	PTN-42	5	0	5
68	PTN-43	1	4	5
69	RUNX3-(15+16)	5	0	5
70	RUNX3-19	5	0	5
71	RUNX3-20	5	0	5
72	TGFBR2-27	5	0	5
73	TGFBR2-32	4	1	5
74	BAX-4	3	1	4
75	BRAF-7	1	3	4
76	ERBB2-27	4	0	4
77	PTEN-7	1	3	4
78	TGFBR2-24	4	0	4
79	ARID1A-11	0	2	2
80	ARID1A-6	0	2	2
81	PRR11-14	1	1	2
82	PTN-21	0	1	1
83	RUNX3-(11+12)	0	1	1
84	ARID1A-14	0	0	0
85	PTN-14	0	0	0
86	PTN-32	0	0	0
87	PTN-39	0	0	0
88	PTN-5	0	0	0
89	PTN-7	0	0	0
90	RUNX3-6	0	0	0
91	TGFBR2-21	0	0	0

MS, microsatellite; MSI, microsatellite instability; LOH, loss of heterozygosity.