

Supplemental Material to:

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**Novel tumor suppressor candidates on chromosome 3
revealed by NotI-microarrays in cervical cancer**

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Table S1. Summary hybridization data of 48 cervical samples to NotI-microarrays.

* - gene names separated by “/” mean that NotI-site is common for these two genes.

№	NotI-site	Gene*	Gene Localization	Homozygous Del/Met		Hemizygous Del/Met	
				N	%	N	%
1	NL6-FJ5R (C)	LRRN1	3p26.2	1	2.1	20	41.7
2	NR5-IH18RS	BHLHE40	3p26.1	0	0.0	13	27.1
3	NR5-GP13R (C)	LMCD1	3p26-24	2	4.2	4	8.3
4	NL2B001R (D)	LOC440944/SETD5	3p25.3	0	0.0	1	2.1
5	NL1-BH17R (C)	LHFPL4/MTMR14	3p25.3	0	0.0	3	6.3
6	NR1-WA8R (C)	IL17RE	3p25.3	0	0.0	2	4.2
7	NL1106R (D)	IL17RC	3p25.3	0	0.0	1	2.1
8	NRLA404R (U)	VHL	3p25.3	1	2.1	16	33.3
9	NRLa098R (S)	IRAK2	3p25.3	0	0.0	1	2.1
10	NLMA188R (D)	TSEN2	3p25.2	0	0.0	0	0.0
11	NR1-NK17R (C)	CAND2	3p25.2	0	0.0	1	2.1
12	HSJ4-AB7R (C)	RPL32/IQSEC1	3p25.2	0	0.0	10	20.8
13	NLMP217R (D)	IQSEC1	3p25.2	0	0.0	2	4.2
14	NR1-XM13C	IQSEC1	3p25.2	0	0.0	15	31.3
15	NRL2062R (D)	NUP210	3p25.1	0	0.0	3	6.3
16	NR1-KJ5R (C)	FBLN2	3p25.1	0	0.0	7	14.6
17	NL1-VJ14R (C)	LOC285375	3p25.1	0	0.0	1	2.1
18	NR1-PL22R (C)	LOC285375	3p25.1	0	0.0	10	20.8
19	NL4-BK12R (C)	WNT7A	3p25	0	0.0	11	22.9
20	NLMP199R (D)	GRIP2/C3orf19	3p25.1	0	0.0	2	4.2
21	NL4-DP2RS	FGD5	3p25.1	0	0.0	10	20.8
22	NL1A177R (143D)	SH3BP5	3p24.3	0	0.0	0	0.0
23	APC1R	EAF1/METTL6	3p25.1	0	0.0	0	0.0
24	NL1G261R (D)	ANKRD28	3p25.1	0	0.0	0	0.0
25	NR1-AB20R (C)	ANKRD28	3p25.1	1	2.1	4	8.3
26	NL4-AP18R (C)	PLCL2	3p24.3	0	0.0	12	25.0
27	NL1-GC10C	HMGB1L5 (Pseudo)	3p24	0	0.0	4	8.3
28	NR1-WF18R (C)	UBE2E2	3p24.2	1	2.1	10	20.8
29	NL1-CJ4R (C)	NKIRAS1/RPL15	3p24.2	0	0.0	18	37.5
30	NL1-DG8R	THRB	3p24.2	0	0.0	2	4.2
31	NR1-KA8R (C)	THRB	3p24.2	4	8.3	0	0.0
32	NL4-BB6R (C)	THRB	3p24.2	4	8.3	7	14.6
33	NL3-CA11RS	LRRC3B	3p24	2	4.2	17	35.4
34	NRLa082R (D)	STT3B	3p23	0	0.0	3	6.3
35	NR5-FH23R (C)	STT3B	3p23	0	0.0	3	6.3
36	NL124R (D)	OSBPL10/ZNF860	3p22.3	0	0.0	0	0.0
37	NR5-FK11R (C)	CMTM8	3p22.3	0	0.0	3	6.3
38	NRL-063R (D)	CMTM6	3p22.3	1	2.1	5	10.4
39	NR1-EP7RS	CLASP2	3p22.3	0	0.0	3	6.3
40	NLMZ142R (D)	TRANK1	3p22.2	0	0.0	0	0.0
41	NL1A401R (D)	ITGA9	3p21.3	2	4.2	18	37.5
42	NLJ-003RD	CTDSPL	3p21.3	1	2.1	14	29.2
43	NL3a019r (d)	SLC22A13	3p21.3	0	0.0	0	0.0
44	AP20D (NLMP220D)	SCN5A	3p21	0	0.0	0	0.0
45	NL3003R (U)	GORASP1/TTC21A	3p22-p21.33	0	0.0	14	29.2

46	NL1308R (D)	MOBP	3p22.1	2	4.2	4	8.3
47	NR1-NK20R (C)	EIF1B	3p22.1	0	0.0	0	0.0
48	NR5-IB17R (C)	HIGD1A	3p22.1	0	0.0	3	6.3
49	NR1-PA6R (C)	FAM198A	3p22.1	0	0.0	4	8.3
50	NL3A009R (D)	SNRK	3p22.1	1	2.1	4	8.3
51	NL1232R (S)	ABHD5	3p21	0	0.0	1	2.1
52	NR1-AN24RS	ABHD5/C3orf77	3p21	0	0.0	12	25.0
53	NL2B007R (D)	ZDHHC3/EXOSC7	3p21.31	0	0.0	2	4.2
54	NL1320R (S)	SACM1L	3p21.3	0	0.0	2	4.2
55	NL3A010R (D)	SLC6A20	3p21.3	0	0.0	2	4.2
56	NLM-067R (D)	PRSS42/MYL3	3p21.31	0	0.0	7	14.6
57	NL3A006R (D)	NBEAL2	3p21.31	1	2.1	6	12.5
58	NR1-NJ3R (C)	CSPG5	3p21.3	0	0.0	0	0.0
59	J31A212R	DHX30	3p21.31	0	0.0	2	4.2
60	J31A219D	MAP4	3p21	0	0.0	0	0.0
61	NR1-KF21R (C)	MAP4	3p21	0	0.0	0	0.0
62	NR1-PM22R (C)	SHISA5	3p21.31	0	0.0	2	4.2
63	NL6-II3R	USP19	3p21.31	0	0.0	0	0.0
64	NL3A014R (D)	RHOA/TCTA	3p21.3	0	0.0	2	4.2
65	J32Z148D	RHOA/TCTA	3p21	0	0.0	0	0.0
66	NRL1	SEMA3F	3p21.3	0	0.0	0	0.0
67	NL3A001R (D)	GNAI2	3p21.31	1	2.1	6	12.5
68	NL1G210R (D)	MAPKAPK3	3p21.3	0	0.0	1	2.1
69	NL1Z216R (D)	MANF	3p21.1	0	0.0	0	0.0
70	NRLA097R	RBM15B	3p21.2	0	0.0	1	2.1
71	NR1-WH9R (C)	RRP9/PARP3	3p21.2	0	0.0	1	2.1
72	NRLA113R (D)	GPR62	3p21.1	0	0.0	1	2.1
73	NLM252R (D)	PCBP4	3p21	0	0.0	0	0.0
74	NL1243R (D)	ABHD14A	3p21.1	0	0.0	0	0.0
75	NL1245R (D)	ACY1	3p21.1	0	0.0	0	0.0
76	NR1-NC7RS	PPM1M	3p21.2	0	0.0	2	4.2
77	NL2G008R (D)	WDR82	3p21.2	0	0.0	0	0.0
78	AP32R (D)	PHF7/BAP1	3p21.1	0	0.0	1	2.1
79	NRL-143D	GLT8D1/SPCS1	3p21.1	0	0.0	0	0.0
80	NR1-DH18RS	CACNA2D3	3p21.1	0	0.0	2	4.2
81	NRL091R (S)	C3orf63	3p14.3	0	0.0	0	0.0
82	AP2R (D)	ARF4	3p21.2 - p21.1	0	0.0	0	0.0
83	NLMP223R (D)	ABHD6	3p14.3	0	0.0	1	2.1
84	NL1A358R (D)	ATXN7/THOC7	3p21.1-p12	0	0.0	0	0.0
85	NR1-NJ9R (C)	PRICKLE2	3p14.1	1	2.1	20	41.7
86	NR5-FL20R (C)	LRIG1	3p14	0	0.0	3	6.3
87	NL1-ZP13R (C)	KBTBD8	3p14	1	2.1	2	4.2
88	NL4-BN15R (C)	FAM19A4	3p14.1	0	0.0	8	16.7
89	NL2B063R (D)	FRMD4B/MITF	3p14.1	0	0.0	0	0.0
90	NL1-YL16RS	MITF	3p14.2-p14.1	0	0.0	5	10.4
91	NL1-BA6R	FOXP1	3p14.1	0	0.0	14	29.2
92	NL6-AF21R (C)	PDZRN3	3p13	1	2.1	15	31.3
93	924Z021R (D)	FRG2C	3p12.3	0	0.0	0	0.0
94	NR5-GE23R (C)	ROBO2	3p12.3	0	0.0	2	4.2
95	NL6-HG15R (C)	ROBO1	3p12.1	1	2.1	4	8.3
96	NR1-WE11RS	CGGBP1	3p12-p11.1	0	0.0	13	27.1
97	NR5-FK16RS	MINA	3q11.2	2	4.2	5	10.4

98	NL6-F020R (C)	DCBLD2	3q12.1;3	0	0.0	4	8.3
99	NLMA202R (D)	NIT2	3q12.2	0	0.0	1	2.1
100	NL1268R (P65D)	TMEM45A	3q12.2	0	0.0	0	0.0
101	924Z094R (D)	TFG	3q12.2	0	0.0	0	0.0
102	NLMZ(A)134R(S)	BBX	3q13.1	0	0.0	1	2.1
103	NL3-CI2R (C)	LOC285205	3q13.12	0	0.0	9	18.8
104	NLM187R (D)	BOC	3q13.2	0	0.0	1	2.1
105	NL2273R (D)	B4GALT4	3q13.3	0	0.0	0	0.0
106	NR1-WD23R (C)	LRRC58	3q13.33	0	0.0	1	2.1
107	NR5-FG18R (C)	FSTL1	3q13.33	1	2.1	3	6.3
108	NL2B006R (D)	SEMA5B	3q21.1	0	0.0	1	2.1
109	NL1-GK21R (C)	ROPN1/KALRN	3q13.3	0	0.0	9	18.8
110	NR5-CD6R (C)	ITGB5	3q21.2	0	0.0	1	2.1
111	NL4-BC8R (C)	ALDH1L1	3q21.3	0	0.0	11	22.9
112	NL1290R (D)	CHST13	3q21.3	0	0.0	8	16.7
113	NL1-YJ5R (C)	C3orf46/CHCHD6	3q21.3	0	0.0	9	18.8
114	NR1-NK11R (C)	CHCHD6	3q21.3	0	0.0	5	10.4
115	NL2A230R	ABTB1/PODXL2	3q21	0	0.0	2	4.2
116	NL1-DE18R	GATA2	3q21.3	0	0.0	3	6.3
117	NL4-BH3R (C)	GATA2	3q21.3	0	0.0	6	12.5
118	NR5-IG11RS	C3orf27	3q21	0	0.0	0	0.0
119	NL2B023R (NLMP23D)	C3orf27	3q21	0	0.0	0	0.0
120	AP4R (D)	RPN1	3q21.3	0	0.0	0	0.0
121	NRL084R (D)	RPN1/RAB7A	3q21.3	0	0.0	0	0.0
122	NLMP7R (D)	RAB7A	3q21.3	0	0.0	0	0.0
123	NR1-PH14R (C)	KIAA1257	3q21.3	0	0.0	1	2.1
124	NR1-EP10R (C)	PLXND1	3q22.1	0	0.0	0	0.0
125	NL1P9R (Z206D)	TMCC1	3q22.1	0	0.0	0	0.0
126	NL4-DJ11RS	TRH	3q13.3-q21	0	0.0	9	18.8
127	NR1-WD21R (C)	NEK11/NUDT16	3q22.1	5	10.4	3	6.3
128	AP45R (NLMZ073D)	TMEM108	3q21	0	0.0	2	4.2
129	NRL124R (D)	TOPBP1	3q22.1	0	0.0	0	0.0
130	NR5-IG2R (C)	KY	3q22.2	0	0.0	3	6.3
131	NL1A079R (D)	EPHB1	3q21-q23	0	0.0	13	27.1
132	NL1-FK10R (C)	PPP2R3A	3q22.1	2	4.2	8	16.7
133	NL2G249R (D)	NCK1	3q21	0	0.0	0	0.0
134	NR1-WJ2RS	SOX14	3q22-q23	0	0.0	10	20.8
135	NR1-WL7R (C)	DZIP1L	3q22.3	0	0.0	1	2.1
136	NL1-DJ10R (C)	ARMC8	3q22.3	0	0.0	0	0.0
137	NL1A278R (D)	MRAS	3q22.3	0	0.0	0	0.0
138	NR1-NO14R (C)	FOXL2/C3orf72	3q23	0	0.0	0	0.0
139	NL1-YD3R (C)	ACPL2	3q23	0	0.0	3	6.3
140	NR5-KB9R (C)	GK5	3q23	0	0.0	0	0.0
141	NL6-FB5R (C)	PAQR9	3q23	0	0.0	1	2.1
142	NR5-IO11R (C)	PAQR9	3q23	1	2.1	2	4.2
143	NR1-OG4R (C)	SLC9A9/C3orf58	3q24	0	0.0	0	0.0
144	NR1-PD1R	ZIC4	3q24	1	2.1	11	22.9
145	NL2Z262R (221S)	SIAH2	3q25	0	0.0	0	0.0
146	NL4-BI4RS	RAP2B	3q25.2	0	0.0	8	16.7
147	NL1-VC9R (C)	GPR149	3q25.2	1	2.1	2	4.2
148	NRL090R (S)	GMPS	3q24	0	0.0	4	8.3
149	NRLZ271R (D)	SSR3	3q25.31	0	0.0	0	0.0

150	NR1-NM7R (C)	B3GALNT1	3q25	0	0.0	3	6.3
151	NLMP208R (D)	FNDC3B	3q26.31	0	0.0	0	0.0
152	NRLa114R (D)	TBL1XR1	3q26.32	0	0.0	1	2.1
153	NLMP137R (D)	PIK3CA	3q26.3	0	0.0	1	2.1
154	NL1-ZD4R	SOX2	3q26.3-27	0	0.0	6	12.5
155	924A053R (D)	ATP11B	3q27	0	0.0	0	0.0
156	NLMP224R (D)	ATP11B	3q27	0	0.0	0	0.0
157	NLMP91R (D)	LAMP3	3q26.3-q27	0	0.0	0	0.0
158	NL1-BM8R (C)	B3GNT5/MCF2L2	3q28	0	0.0	2	4.2
159	NR5-CM3R (C)	PARL	3q27.1	0	0.0	2	4.2
160	NL2B011R (D)	ABCC5	3q27	0	0.0	0	0.0
161	NRL117R (D)	VWA5B2	3q27.1	0	0.0	0	0.0
162	NL2B017R (D)	EIF4G1	3q27-qter	0	0.0	0	0.0
163	NL1088R (D)	CLCN2	3q27-q28	0	0.0	2	4.2
164	NR1-WB21R (C)	EPHB3	3q21-qter	0	0.0	2	4.2
165	NL1Z302R (D)	MAGEF1	3q13	0	0.0	1	2.1
166	AP19R (S)	ETV5	3q28	0	0.0	0	0.0
167	NL1-GJ12R (C)	ST6GAL1	3q27-28	0	0.0	3	6.3
168	NR1-AK24R	BCL6	3q27	0	0.0	7	14.6
169	NL1A313R (S)	LOC339929	3q27.3	0	0.0	0	0.0
170	NL1-YH24R (S)	LEPREL1	3q28	0	0.0	0	0.0
171	NR1-NH1R (C)	FGF12	3q28	1	2.1	12	25.0
172	NL2B060R (D)	HES1 (LOC100505920)	3q28-q29	0	0.0	1	2.1
173	AP34R (D)	LOC100507391	3q29	0	0.0	0	0.0
174	NR1-AM11R (C)	C3orf21	3q29	0	0.0	4	8.3
175	NLG26R (D)	TNK2/APOD	3q26.2-qter/3q29	0	0.0	0	0.0
176	NL2Z252R (D)	TFRC	3q29	0	0.0	0	0.0
177	HSJ-DP22RS	C3orf43	3q29	0	0.0	1	2.1
178	NLMA216R (S)	C3orf34/PIGX	3q29	0	0.0	0	0.0
179	NRL094R (D)	BDH1	3q29	0	0.0	0	0.0
180	NR1-PF24RS	LRCH3	3q29	0	0.0	0	0.0

Homo + Hemi Del/Met		Amplification/ Demet		Retention		No info	
N	%	N	%	N	%	N	%
21	43.8	0	0.0	26	54.2	1	2.1
13	27.1	0	0.0	23	47.9	12	25.0
6	12.5	0	0.0	25	52.1	17	35.4
1	2.1	0	0.0	46	95.8	1	2.1
3	6.3	0	0.0	44	91.7	1	2.1
2	4.2	0	0.0	44	91.7	2	4.2
1	2.1	0	0.0	27	56.3	20	41.7
17	35.4	0	0.0	28	58.3	3	6.3
1	2.1	0	0.0	33	68.8	14	29.2
0	0.0	0	0.0	45	93.8	3	6.3
1	2.1	0	0.0	46	95.8	1	2.1
10	20.8	0	0.0	27	56.3	11	22.9
2	4.2	0	0.0	46	95.8	0	0.0
15	31.3	0	0.0	10	20.8	23	47.9
3	6.3	0	0.0	44	91.7	1	2.1
7	14.6	0	0.0	21	43.8	20	41.7
1	2.1	0	0.0	40	83.3	7	14.6
10	20.8	0	0.0	36	75.0	2	4.2
11	22.9	0	0.0	29	60.4	8	16.7
2	4.2	0	0.0	45	93.8	1	2.1
10	20.8	0	0.0	20	41.7	18	37.5
0	0.0	0	0.0	47	97.9	1	2.1
0	0.0	0	0.0	47	97.9	1	2.1
0	0.0	0	0.0	47	97.9	1	2.1
5	10.4	0	0.0	41	85.4	2	4.2
12	25.0	0	0.0	36	75.0	0	0.0
4	8.3	0	0.0	44	91.7	0	0.0
11	22.9	0	0.0	25	52.1	12	25.0
18	37.5	1	2.1	26	54.2	3	6.3
2	4.2	0	0.0	26	54.2	20	41.7
4	8.3	0	0.0	1	2.1	43	89.6
11	22.9	0	0.0	19	39.6	18	37.5
19	39.6	0	0.0	8	16.7	21	43.8
3	6.3	0	0.0	42	87.5	3	6.3
3	6.3	0	0.0	34	70.8	11	22.9
0	0.0	0	0.0	48	100.0	0	0.0
3	6.3	0	0.0	43	89.6	2	4.2
6	12.5	1	2.1	29	60.4	12	25.0
3	6.3	0	0.0	44	91.7	1	2.1
0	0.0	0	0.0	48	100.0	0	0.0
20	41.7	0	0.0	25	52.1	3	6.3
15	31.2	0	0.0	16	33.3	17	35.4
0	0.0	0	0.0	30	62.5	18	37.5
0	0.0	0	0.0	48	100.0	0	0.0
14	29.2	0	0.0	18	37.5	16	33.3

6	12.5	0	0.0	33	68.8	9	18.8
0	0.0	1	2.1	46	95.8	1	2.1
3	6.3	1	2.1	41	85.4	3	6.3
4	8.3	1	2.1	41	85.4	2	4.2
5	10.4	0	0.0	25	52.1	18	37.5
1	2.1	0	0.0	47	97.9	0	0.0
12	25.0	0	0.0	12	25.0	24	50.0
2	4.2	0	0.0	43	89.6	3	6.3
2	4.2	0	0.0	41	85.4	5	10.4
2	4.2	0	0.0	45	93.8	1	2.1
7	14.6	0	0.0	37	77.1	4	8.3
7	14.6	0	0.0	12	25.0	29	60.4
0	0.0	0	0.0	46	95.8	2	4.2
2	4.2	0	0.0	39	81.3	7	14.6
0	0.0	1	2.1	33	68.8	14	29.2
0	0.0	0	0.0	39	81.3	9	18.8
2	4.2	0	0.0	39	81.3	7	14.6
0	0.0	0	0.0	45	93.8	3	6.3
2	4.2	0	0.0	41	85.4	5	10.4
0	0.0	0	0.0	33	68.8	15	31.3
0	0.0	0	0.0	47	97.9	1	2.1
7	14.6	0	0.0	21	43.8	20	41.7
1	2.1	0	0.0	46	95.8	1	2.1
0	0.0	0	0.0	48	100.0	0	0.0
1	2.1	0	0.0	46	95.8	1	2.1
1	2.1	0	0.0	46	95.8	1	2.1
1	2.1	0	0.0	47	97.9	0	0.0
0	0.0	0	0.0	40	83.3	8	16.7
0	0.0	0	0.0	44	91.7	4	8.3
0	0.0	0	0.0	45	93.8	3	6.3
2	4.2	0	0.0	22	45.8	24	50.0
0	0.0	0	0.0	37	77.1	11	22.9
1	2.1	1	2.1	44	91.7	2	4.2
0	0.0	0	0.0	35	72.9	13	27.1
2	4.2	0	0.0	38	79.2	8	16.7
0	0.0	0	0.0	39	81.3	9	18.8
0	0.0	0	0.0	39	81.3	9	18.8
1	2.1	0	0.0	43	89.6	4	8.3
0	0.0	0	0.0	48	100.0	0	0.0
21	43.8	0	0.0	24	50.0	3	6.3
3	6.3	0	0.0	43	89.6	2	4.2
3	6.3	0	0.0	42	87.5	3	6.3
8	16.7	0	0.0	38	79.2	2	4.2
0	0.0	0	0.0	46	95.8	2	4.2
5	10.4	0	0.0	27	56.3	16	33.3
14	29.2	0	0.0	29	60.4	5	10.4
16	33.3	0	0.0	31	64.6	1	2.1
0	0.0	0	0.0	40	83.3	8	16.7
2	4.2	1	2.1	41	85.4	4	8.3
5	10.4	0	0.0	25	52.1	18	37.5
13	27.1	0	0.0	21	43.8	14	29.2
7	14.6	0	0.0	16	33.3	25	52.1

4	8.3	0	0.0	29	60.4	15	31.3
1	2.1	1	2.1	43	89.6	3	6.3
0	0.0	0	0.0	48	100.0	0	0.0
0	0.0	0	0.0	48	100.0	0	0.0
1	2.1	0	0.0	36	75.0	11	22.9
9	18.8	0	0.0	27	56.3	12	25.0
1	2.1	0	0.0	45	93.8	2	4.2
0	0.0	1	2.1	47	97.9	0	0.0
1	2.1	0	0.0	46	95.8	1	2.1
4	8.3	1	2.1	33	68.8	10	20.8
1	2.1	0	0.0	43	89.6	4	8.3
9	18.8	0	0.0	20	41.7	19	39.6
1	2.1	0	0.0	44	91.7	3	6.3
11	22.9	0	0.0	33	68.8	4	8.3
8	16.7	0	0.0	21	43.8	19	39.6
9	18.8	0	0.0	23	47.9	16	33.3
5	10.4	0	0.0	39	81.3	4	8.3
2	4.2	0	0.0	41	85.4	5	10.4
3	6.3	0	0.0	24	50.0	21	43.8
6	12.5	0	0.0	19	39.6	23	47.9
0	0.0	0	0.0	47	97.9	1	2.1
0	0.0	0	0.0	46	95.8	2	4.2
0	0.0	0	0.0	42	87.5	6	12.5
0	0.0	0	0.0	43	89.6	5	10.4
0	0.0	0	0.0	44	91.7	4	8.3
1	2.1	0	0.0	45	93.8	2	4.2
0	0.0	2	4.2	43	89.6	3	6.3
0	0.0	0	0.0	45	93.8	3	6.3
9	18.8	1	2.1	29	60.4	9	18.8
8	16.7	0	0.0	0	0.0	40	83.3
2	4.2	0	0.0	44	91.7	2	4.2
0	0.0	0	0.0	43	89.6	5	10.4
3	6.3	1	2.1	22	45.8	22	45.8
13	27.1	0	0.0	20	41.7	15	31.3
10	20.8	0	0.0	17	35.4	21	43.8
0	0.0	0	0.0	25	52.1	23	47.9
10	20.8	0	0.0	35	72.9	3	6.3
1	2.1	0	0.0	45	93.8	2	4.2
0	0.0	0	0.0	45	93.8	3	6.3
0	0.0	0	0.0	41	85.4	7	14.6
0	0.0	0	0.0	46	95.8	2	4.2
3	6.3	0	0.0	44	91.7	1	2.1
0	0.0	0	0.0	48	100.0	0	0.0
1	2.1	0	0.0	44	91.7	3	6.3
3	6.3	0	0.0	15	31.3	30	62.5
0	0.0	0	0.0	40	83.3	8	16.7
12	25.0	1	2.1	15	31.3	20	41.7
0	0.0	0	0.0	40	83.3	8	16.7
8	16.7	0	0.0	24	50.0	16	33.3
3	6.3	3	6.3	3	6.3	39	81.3
4	8.3	0	0.0	37	77.1	7	14.6
0	0.0	0	0.0	43	89.6	5	10.4

3	6.3	0	0.0	40	83.3	5	10.4
0	0.0	0	0.0	40	83.3	8	16.7
1	2.1	0	0.0	40	83.3	7	14.6
1	2.1	0	0.0	42	87.5	5	10.4
6	12.5	1	2.1	27	56.3	14	29.2
0	0.0	0	0.0	40	83.3	8	16.7
0	0.0	0	0.0	47	97.9	1	2.1
0	0.0	0	0.0	35	72.9	13	27.1
2	4.2	0	0.0	45	93.8	1	2.1
2	4.2	0	0.0	44	91.7	2	4.2
0	0.0	0	0.0	41	85.4	7	14.6
0	0.0	0	0.0	43	89.6	5	10.4
0	0.0	0	0.0	44	91.7	4	8.3
2	4.2	0	0.0	40	83.3	6	12.5
2	4.2	0	0.0	41	85.4	5	10.4
1	2.1	0	0.0	34	70.8	13	27.1
0	0.0	0	0.0	45	93.8	3	6.3
3	6.3	0	0.0	44	91.7	1	2.1
7	14.6	0	0.0	30	62.5	11	22.9
0	0.0	0	0.0	47	97.9	1	2.1
0	0.0	0	0.0	42	87.5	6	12.5
13	27.1	0	0.0	23	47.9	12	25.0
1	2.1	0	0.0	45	93.8	2	4.2
0	0.0	0	0.0	43	89.6	5	10.4
4	8.3	0	0.0	42	87.5	2	4.2
0	0.0	0	0.0	47	97.9	1	2.1
0	0.0	0	0.0	28	58.3	20	41.7
1	2.1	0	0.0	42	87.5	5	10.4
0	0.0	1	2.1	45	93.8	2	4.2
0	0.0	0	0.0	37	77.1	11	22.9
0	0.0	0	0.0	47	97.9	1	2.1

Table S2. Main characteristics of thirty TSGs and newly identified TSGs candidates with high deletions/methylation frequency in cervical cancer.

Gene symbol and location	Protein Function*	Involvement in cancer
<i>LRRN1</i> 3p26.2	Leucine rich repeat neuronal 1 is required for formation of neuromeric boundaries during neural development. ^{1, 2} A single-pass transmembrane protein with 12 extracellular leucine-rich repeats most closely related to TRN/CAPS. ¹ The mechanism of action of this protein family is currently unknown.	According to our NotI microarray and qPCR data the gene is frequently methylated/deleted and down-regulated in NSCLC, ³ also frequently methylated/deleted in ovarian cancer. ⁴
<i>PRICKLE2</i> 3p14.1	A member of a group of planar cell polarity (PCP) signaling molecules implicated in the regulation of cellular polarity and invasion. ⁵ Generally expressed in postmitotic neurons and promote neurite outgrowth. ⁶	Involved in WNT signaling pathway that is subjected to frequent aberrations in cancer. ⁷ According to our NotI microarray data this gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>ITGA9</i> 3p21.3	Alpha integrin-9, a member of transmembrane glycoprotein receptors responsible for cell-cell and cell-matrix interactions. ^{8, 9} As heterodimer with beta1 subunit - $\alpha9\beta1$ interacts with VCAM1 (vascular cell adhesion molecule 1), fibronectin, osteopontin, VEGF-C, -D and VEGF-A isoforms). Tumor suppressor. ^{3,10}	Chromosomal aberrations in head and neck cancer, ¹¹ methylation in BC ¹² and colorectal cancer, ¹³ deletions in cervical cancer and precancer lesions. ^{14, 15} Fusion of <i>MLH1</i> and <i>ITGA9</i> in hereditary colorectal carcinoma (Lynch syndrome). ¹⁶ Down-regulation in NSCLC, ³ overexpression in SCLC. ¹⁷ According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>LRRC3B</i> 3p24	Leucine rich repeat containing 3B is an evolutionarily highly conserved membrane protein of unknown function. Tumor suppressor candidate. ^{18,19}	Methylation in gastric cancer, ¹⁸ in acute leukemia, ²⁰ in colorectal cancer. ²¹ Down-regulation in colorectal cancer, ²¹ in gastric cancer. ¹⁸ According to our NotI microarray data the gene is frequently methylated/deleted in different cancers. ^{3,4,19}
<i>NKIRAS1</i> 3p24.2	Atypical Ras-like protein that acts as a potent regulator of NF- κ B activity	A member of NF- κ B pathway that is frequently deregulated in cancer. ^{22, 23}

	by preventing the degradation of NF- κ B inhibitor beta (NFKBIB).	Chromosomal aberrations and down-regulation in kidney cancer. ²⁴ Overexpression, associated with poor prognosis in gliomas. ²⁵ According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>RPL15</i> 3p24.2	A ribosomal protein, a component of the large 60S subunit. Belongs to the L15E family of ribosomal proteins.	Overexpression in gastric cancer (both mRNA and protein). ²⁶ Differentially expressed in cutaneous squamous cell carcinoma. ²⁷ According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>VHL</i> 3p25.3	Involved in the ubiquitination and subsequent proteasomal degradation via the von Hippel-Lindau ubiquitination complex, involved in transcriptional repression through interaction with HIF1A, HIF1AN and histone deacetylases. Tumor suppressor. ²⁸	Mutations (both hereditary and somatic) and methylation in kidney cancer. ²⁹⁻³² Deletion and methylation in pancreatic adenomas. ³³ LOH in follicular thyroid cancer. ³⁴ LOH and mutations in hemangioblastomas. ³⁵ mRNA and protein down-regulation in kidney cancer ^{36, 37} and in lung cancer. ^{3,38} According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC. ³
<i>PDZRN3</i> 3p13	E3 ubiquitin-protein ligase plays an important role in regulation of the surface level of MUSK (skeletal muscle-specific tyrosine-protein kinase receptor), might contribute to terminal myogenic differentiation, ³⁹ negatively regulates BMP2-induced osteoblast differentiation through inhibition of WNT signaling pathway. ⁴⁰	Conventional renal cell carcinoma-associated rearrangement breakpoints were localized in 3p12.3 region between <i>PDZRN3</i> and <i>CNTN3</i> genes. ⁴⁰ Germ-line <i>PDZRN3</i> deletions were observed in genomes of patients with strong family history of pancreatic cancer. ⁴¹
<i>IQSEC1</i> 3p25.2	ARF-specific guanine nucleotide exchange factor, a member of a family of small GTPases, mediates internalisation of beta-1 integrin, ⁴² regulates phagocytosis of monocytic phagocytes. ⁴³	Abnormality of EGFR-IQSEC1-ARF6-AMAP1 signalling pathway is essential for BC invasion and metastasis. ^{44,45} According to our NotI microarray and qPCR data the gene is frequently methylated/deleted and down-

		regulated in NSCLC, ³ also frequently methylated/deleted in ovarian cancer. ⁴
<i>RBPS3/CTDSPL</i> 3p21.3	Belongs to a family of small CTD phosphatases. Negative regulator of the RNA polymerase II (Pol II), preferentially catalyzes serine-5 dephosphorylation in the specific sequence of the Pol II large subunit and in other proteins. Can activate the tumor suppressor RB1 (retinoblastoma 1), that leads to cell cycle arrest at G ₁ /S phases boundary. ⁴⁶ Tumor suppressor. ⁴⁶	Low expression levels in various epithelial tumors because of deletions and methylation, ^{3, 47-49} these aberrations were found in premalignant lesions of head and neck, ¹¹ and cervix. ¹⁴ High mutability of <i>RBSP3</i> was revealed in various primary tumors and cell lines. ^{46, 50} According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>GORASP1</i> 3p22.2	Golgi membrane protein involved in establishing the stacked structure of the Golgi apparatus; a caspase-3 substrate. Its cleavage contributes to Golgi fragmentation in apoptosis.	According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>TTC21A</i> 3p22.2	Putatively involved in stress response.	According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>FOXPI</i> 3p14.1	A transcription factor belongs to the family of Forkhead box proteins. It is involved in the negative regulation of tissue- and cell type-specific gene transcription. ⁵¹	Involved in chromosomal translocation in MALT lymphoma ^{52, 53} and in large B-cell lymphoma. ⁵⁴ RNA and protein down-regulation and deletions in different tumors. ⁵⁵⁻⁵⁸ Overexpressed in a subset of B-cell lymphoma. ⁵⁹ According to our NotI microarray and qPCR data the gene is frequently methylated/deleted and down-regulated in NSCLC, ³ also frequently methylated/deleted in ovarian cancer. ⁴
<i>BHLHE40**</i> 3p26	Basic helix-loop-helix protein is a putative transcription factor widely expressed in various normal tissues. Probably involved in the control of	Overexpression in gastric cell lines ⁶⁰ and hepatocellular carcinomas, ⁶¹ involvement in apoptosis regulation in breast cancer MCF7 cell line, ⁶²

	cell differentiation.	down-regulation associated with poor prognosis in pancreatic ductal adenocarcinoma. ⁶³ According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC. ³
<i>CGGBP1</i> 3p12-p11.1	CGG-triplet repeat binding protein is a transcriptional regulator of some cell cycle regulatory genes (TP53, CDKN1A, GAS1 and ARF). Its expression is important for cell cycle progression through multiple parallel mechanisms. It participates in heat shock and related stress responses.	Decreased mRNA levels in testis cancer and various cancer cell lines. ^{64, 65} Microsatellite instability in ovarian cancer cell line. ⁶⁶ According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3, 4}
<i>EPHB1</i> 3q21-q23	A member of the Eph family of receptor tyrosine kinases that are involved in embryonic nervous and vascular system development. Tumor suppressor candidate. ¹⁰	Epigenetic inactivation in acute lymphoblastic leukemia. ⁶⁷ Under-expressed in poorly differentiated colorectal cancers. ⁶⁸ Down-regulation in gastric carcinoma associated with invasion and metastasis ⁶⁹ but up-regulation in rhabdomyosarcoma ⁷⁰ and ovarian cancer. ⁷¹ According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3, 4}
<i>FGF12</i> 3q28	A member of the fibroblast growth factor family (FGF). The family members possess broad mitogenic and cell survival activities, and are involved in a variety of biological processes, including embryonic development, cell growth, morphogenesis, tissue repair, tumor growth, and invasion. Involved in MAPK signaling pathway.	Significantly methylated in BC ⁷² and colorectal cancer. ⁷³ Some polymorphic alleles of this gene are associated with a high risk of development of esophageal squamous cell carcinoma. ⁷⁴ Deletions in hairy cell leukemia ⁷⁵ but amplifications in lung cancer. ⁷⁶ Some experts reasonably consider <i>FGF12</i> as the oncogene as it is a growth factor participating in the MAPK pathway. ^{76, 77} According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3, 4}
<i>PLCL2</i> 3p24.3	This phospholipase C-like protein may play a role in the regulation of	According to our NotI microarray data this gene is frequently

	Ins(1,4,5)P3 around the endoplasmic reticulum.	methylated/deleted in NSCLC. ³
<i>ABHD5</i> 3p21	Lysophosphatidic acid acyltransferase which functions in phosphatidic acid biosynthesis. May regulate the cellular storage of triacylglycerol through activation of the phospholipase PNPLA2. Involved in keratinocyte differentiation.	According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>C3orf77</i> <i>/TOPAZ1</i> 3p21.31	Function is unknown. May play an important role in germ cell development. ⁷⁸	According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>ZIC4</i> 3q24	Member of the ZIC family of C2H2-type zinc finger proteins, was shown to suppress β -catenin-mediated transcriptional activation within the Wnt/ β -catenin signaling pathway (in <i>Xenopus laevis</i>). ⁷⁹	Methylated CpG islands in bladder cancer; associated with high extent of progression and invasive character of bladder tumors. ⁸⁰ Its expression is highly selective for medulloblastomas. ⁸¹ Up-regulation in desmoid tumors. ⁸² Its aberrations are associated with SCLC small-cell lung cancer. ^{83,84} According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>WNT7A</i> 3p25	A member of the WNT family secreted signaling proteins. These proteins are implicated in several developmental processes, including regulation of cell fate and patterning during embryogenesis.	Down-regulation in lung cancer, ^{85,86} in uterine leiomyoma, ⁸⁷ over-expression in thyroid cancer, ⁸⁸ in ovarian cancer, associated with poor prognosis. ^{89,90} Down-regulation, associated with poor prognosis in head and neck squamous cell carcinoma. ⁹¹ According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>UBE2E2</i> 3p24.2	Accepts ubiquitin from the E1 complex and catalyzes its covalent attachment to other proteins.	According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC. ³
<i>THRB</i> 3p24.2	Nuclear hormone receptor for triiodothyronine; may regulate cell proliferation, differentiation, and	In mouse models, a truncated THRB gene leads to thyroid cancer. ⁹² Aberrant methylation in tissue and

	apoptosis. ⁹² Tumor suppressor. ⁹³	plasma of BC patients. ⁹⁴ Low frequency of methylation in prostate cancer, ⁹⁵ but high frequency of LOH in prostate, ^{96, 97} esophageal cancer, ⁹⁸ endocrine tumors of the cervix, ⁹⁹ head and neck cancer. ¹⁰⁰ Mutation of this gene in mice predisposes to the development of mammary tumors. ¹⁰¹ Reduced expression in clear cell renal cell cancer. ⁹³ According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>ALDH1L1</i> 3q21.3	Catalyzes the conversion of 10-formyltetrahydrofolate, NADP, and water to tetrahydrofolate, NADPH, and carbon dioxide. Belongs to the aldehyde dehydrogenase family and is responsible for formate oxidation <i>in vivo</i> . Tumor suppressor candidate. ¹⁰²⁻¹⁰⁴	Down-regulation at the mRNA and protein levels in hepatocellular carcinoma, pilocytic astrocytoma, liver cancer, cancer cell lines (A549, HepG2, 293A, Du-145, PC-3). ^{102, 105, 106} Epigenetic silencing in lung adenocarcinoma, spleen cancer, liver cancer, hemangioma, hepatocellular carcinoma and cancer cell lines (A549, HepG2, HCT116). ¹⁰⁷ Suppresses cell motility in NSCLC cell line A549. ¹⁰⁸ According to our NotI microarray and qPCR data the gene is frequently methylated/deleted and down-regulated in NSCLC. ³
<i>RPL32</i> 3p25-p24	A ribosomal protein, a component of the 60S subunit. It belongs to the L32E family of ribosomal proteins.	According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC. ³
<i>LOC285375</i> <i>/LINC00620</i> 3p25.1	Predicted hypothetical gene (not included in current genome annotation). Probable product is long non-coding RNA.	According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>FGD5</i> 3p25.1	May activate CDC42, a member of the Ras-like family of Rho- and Rac proteins, by exchanging bound GDP for free GTP. May play a role in regulating the actin cytoskeleton and cell shape.	According to our NotI microarray and qPCR data the gene is frequently methylated/deleted and down-regulated in NSCLC. ³
<i>PPP2R3A</i> 3q22.1	A protein of alpha subfamily of regulatory subunit B of the protein	Methylated in childhood acute lymphoblastic leukemia. ¹⁰⁹

	phosphatase 2, one of the four major Ser/Thr phosphatases is implicated in the negative control of cell growth and division.	According to our NotI microarray data the gene is frequently methylated/deleted in NSCLC and ovarian cancer. ^{3,4}
<i>SOX14</i> 3q22-q23	Member of the SOX (SRY-related HMG-box) family of transcription factors involved in the regulation of embryonic development and in the determination of the cell fate.	Methylated in lymphocytic leukemia. ¹¹⁰

Note: * – GeneCards data portal, available at: <http://www.genecards.org/>. ** – One of the aliases of this gene is similar to official gene name of chromosome 9 gene – DEC1, do not implicate them. Abbreviations: NSCLC – non-small cell lung cancer, SCLC – small cell lung cancer, BC – breast cancer.

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Tables S3-S5. Results of bisulfite genomic sequencing of genes in cervical SCC from NotI-microarray. A. Sequence of a gene. CpG sites are shown in bold and yellow, NotI sites are underlined, primers for bisulfite sequencing are shown in red.

B. Numbers of SCC presented as Figure 2B. Methylated (red “+”) and unmethylated (black “-”) CG sites are shown in sequenced clones (C1 and etc). CpGs in NotI site are shown in red.

S3. *ITGA9*

A.

CCCTGGGGTCCCAGCCCAGAGCGTGGGGGGAGAGC**CG**CTAGAGTTGTCTCCTC**CGCCG**
 CCCAGCTAGACT**CG**GCTTCACTCTCTGAAT**CG**AAAAGTAACTTGGCTCCTCTGCCTC**CG**
 GG**CGGCCG****CG**CTGGCCCAG**CG**AGCCTCCTGAACCT**CG**CAGGGCCTGGAGGAGT**CGG**
 GGC**ACTGGAGCTGCACCCCTCCC****CG**GTTTTGGGGAACCC**CTGAGGAAGGAGTATAGCC**
TCTC

B. Cervical tumor №17

CpG	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16
1	+	+	+	-	-	+	+	+	+	+	+	+	-	-	+	+
2	+	+	+	-	-	+	+	+	+	+	-	+	-	-	+	+
3	+	+	+	-	-	+	+	+	+	+	+	+	-	+	+	+
4	-	+	-	-	-	+	+	+	+	+	+	+	-	-	+	+
5	+	+	+	-	-	-	-	+	+	+	-	+	-	+	-	+
6	+	+	+	-	-	+	+	-	+	+	+	-	-	+	-	+
7	+	-	+	-	-	-	-	+	+	-	-	+	-	+	-	-
8	+	+	+	-	-	+	+	-	+	+	-	+	-	+	+	-
9	+	+	-	-	-	+	+	+	+	+	+	+	-	+	+	+
10	+	+	-	-	-	+	+	+	+	+	-	+	-	-	+	+
11	+	+	-	-	-	+	+	+	+	+	-	+	-	+	+	+
12	+	-	+	-	-	+	+	-	+	+	+	+	-	+	-	-
13	+	+	+	-	-	+	+	-	+	+	+	+	-	+	-	-
14	+	+	+	-	-	+	+	+	+	+	-	+	-	-	-	+

S4. *FGF12*

A.

TGTAAAAAGAGGAAT**CCTGGTTCCTTC**CAC**CG**GGGGTCC**CG**AGGTGCTTTGAGGAGGGA
 GAAAGGAGGG**CG**TCCCCTCTGGGGAGCCACTCTC**CG**GGCTTCTACTGACCTGGTCTC
CGCCTCAC**CG**GCCTCTTG**CG**GC**CG**CTGCAGAAG**CG**CACTTTGCTGAACACCC**CG**AGGA
CGTGCCTCT**CG**CACAGGGAG**CG**CC**CG**TCTTTGCTGGGGCTGGAG**CGG****CG**CTTGGAGGC
CGACACT**CG**GT**CG**CTGTTGGACTCCCT**CG**CCTGC**CG**CTTCTGC**CG**GATCAAGGAGCTG
 GCTAT**CG****CG**CAGCCATAGCTGCTCAG**CG**AGGGCCTCAGGCCCCAGCCTCTACTG**CG**C
 CCTC**CG**GCTTG**CG**CTC**CG****CG**GGG**CG**AGGGCAGGACCTGGG**CG**GCCAGGGAAAGGGC
 AGT**CGCG**GGGAG**GCAGTGCTAAAATTGAGGAGGCTGCAG**

B. Cervical tumor №42

CpG	C1	C2	C3	C4	C5	C6	C7
1	+	-	-	-	+	-	-
2	+	-	-	-	+	-	-
3	+	+	-	+	+	-	-
4	+	+	+	+	+	-	-
5	+	+	+	+	+	-	-
6	+	+	+	+	+	-	-
7	+	+	+	+	+	-	-
8	+	+	+	+	+	-	-
9	+	+	+	+	+	-	-
10	+	+	+	+	+	-	-
11	+	+	+	+	+	-	-
12	+	+	+	+	+	-	-
13	+	+	+	+	+	-	-
14	+	+	+	+	+	-	-
15	+	+	+	+	+	-	-
16	+	+	+	+	+	-	-
17	+	+	+	+	+	-	-
18	+	+	+	+	+	-	-
19	+	+	+	+	+	-	-
20	+	+	+	+	+	-	-
21	+	+	+	+	-	-	-
22	+	+	+	+	+	-	-
23	+	+	+	+	+	-	-
24	+	+	+	+	+	-	-
25	+	+	+	+	+	-	-
26	+	+	+	+	+	-	-
27	+	+	+	+	+	-	-
28	+	+	+	+	+	-	-
29	+	+	+	+	+	-	-
30	+	+	+	+	+	-	-
31	+	+	+	-	+	-	-
32	+	+	+	+	+	-	-
33	+	+	+	+	+	+	-
34	+	+	+	+	+	-	-

S5. RBSP3

A.

GCCCCTGCACACTCACACTGGCTCAGT CGGCACA CGCACTCTGGCAGCCT CGCTCTCCT
 C CGGGCG CACCCCACACCCACG CACCCTC CGGGCCCTGTGCACCCCTCCCCCAGGCC
 ATGC CGGCGCC CGGCAGTGA ACTCCAG CGG CGCG GGGTGTG CGCT CGCCCCAGCC C
 GCGGCCG CCTGCG CCCCTCCTCACCTTTCT CGCC CGCG CC CGGCAAC CGGCCCT CGTC
 CTCC TTGGGGTTGGTCACCTGGGTGATG

B. Cervical tumor №47

CpG	C1	C2	C3	C4	C5	C6	C7
1	-	-	-	-	-	-	-
2	-	-	-	-	-	-	+
3	-	-	-	-	-	-	-
4	-	+	+	-	-	-	-
5	-	+	+	-	-	-	-
6	+	+	-	-	-	-	-
7	-	-	-	-	-	-	-
8	-	-	-	+	+	-	-
9	-	+	+	+	+	-	-
10	-	+	+	+	+	-	-
11	-	+	+	+	+	-	-
12	+	+	-	+	+	-	-
13	+	+	+	+	+	-	-
14	+	+	+	+	+	-	-
15	+	-	+	+	+	-	-
16	+	+	-	+	+	-	-
17	-	+	+	-	-	-	-
18	+	+	+	+	-	-	+
19	-	+	+	+	+	-	+
20	-	+	-	+	+	-	+
21	+	-	-	+	-	-	-
22	+	-	+	+	+	-	-
23	+	+	+	+	+	-	-