

Supplementary Table 1 : The filename, LRI cutoff value, and physical position in samples used for InDel analysis in this study

Filename	LRI cutoff	InDel Type	Location	Variation Position
001-Del-1	2.69	1bp Delete	gi 224589801 chr10	24884787
002-Del-1	2.65	1bp Delete	gi 224589801 chr10	24884787
003-Del-1	1.98	1bp Delete	gi 224589803 chr12	51442577
004-Del-1	2.72	1bp Delete	gi 224589803 chr12	48237736
005-Del-1	1.94	1bp Delete	gi 224589803 chr12	48237736
006-Del-1	2.50	1bp Delete	gi 224589801 chr10	24884787
007-Del-1	1.93	1bp Delete	gi 224589803 chr12	51442577
008-Del-1	3.00	1bp Delete	gi 224589822 chrX	69176881
009-Del-1	3.20	1bp Delete	gi 224589822 chrX	69176881
010-Del-1	3.86	1bp Delete	gi 224589801 chr10	24884787
011-Del-1	3.85	1bp Delete	gi 224589801 chr10	24884787
013-Ins-9	3.76	9bp Insert	gi 224589819 chr7	55249011
016-Ins-6	3.43	6bp Insert	gi 224589819 chr7	55249013
017-Ins-6	3.58	6bp Insert	gi 224589819 chr7	55249013

Supplementary Table 2 : The filename, LRI cutoff value and repeat structure in samples used for microsatellite analysis in this study

Filename	Lri cutoff	Repeat Structure	
126-uSat -CA	<b>3.02</b>	[CA] <sub>16</sub>	[CA] <sub>15</sub>
127-uSat -AC	<b>2.00</b>	[AC] <sub>24</sub>	[CA] <sub>22</sub>
151-uSat -TG	2.00	[TG] <sub>23</sub>	[TG] <sub>22</sub>
158-uSat -TG	2.00	[TG] <sub>18</sub>	[TG] <sub>17</sub>
159-uSat -TG	2.00	[TG] <sub>18</sub>	[TG] <sub>17</sub>
161-uSat -CA	<b>3.28</b>	[CA] <sub>18</sub>	[CA] <sub>17</sub>
162-uSat -CA	<b>3.13</b>	[CA] <sub>18</sub>	[CA] <sub>17</sub>
163-uSat -TG	2.00	[TG] <sub>18</sub>	[TG] <sub>17</sub>
183-uSat -TG	2.00	[TG] <sub>18</sub>	[TG] <sub>17</sub>
187-uSat -TG	2.00	[TG] <sub>18</sub>	[TG] <sub>17</sub>
188-uSat -CA	2.00	[CA] <sub>18</sub>	[CA] <sub>17</sub>
192-uSat -CA	2.00	[CA] <sub>18</sub>	[CA] <sub>17</sub>
194-uSat -CA	2.00	[CA] <sub>23</sub>	[CA] <sub>22</sub>

Supplementary Table 3 : The primer paris designed for amplification of 10 CODIS locus in this study

Name	primer_F	primer_R	Product Size
msTH01	CTAGTCAGCACCCCAACCAG	TCCCTGAGAAGGTACCTGGA	434 bp
msCSF1PO	GGAACATATGCAAGGCTCAAA	CAGACTCTTCCACACACCACTG	600 bp
msTPOX	CACTGCTCTGTCGTGACTCC	GAGGAAGGGCTGTGTTTCAG	387 bp
msD13S317	TTTGGGTAGGAAAAAGAGTGGA	TTGATGTATTGCAAGCACTTAGTT	482 bp
msD16S539	CAAGCGAAAGTGATGCCATA	ATCTGCCCTCATCAGTGGAC	573 bp
msD5S818	TTTTGAAAATACATGGGAGAAAA	CCATCTGGATAGTGGACCTCA	454 bp
msD3S1358	CAGCGAGACCCCATCTCTTA	AGCTGCCAGGGCACTGCT	391 bp
msD8S1179	CACAGCTATTATCAAAAACCCAGA	GCTGAGTCTGAAGTAAGTAAAAACATTG	500 bp
msFGA	TGAAATGCAATCAAACCAACT	GCCTTCCTTTCCCTCTACTC	600 bp
msD21S11	TGTCTGGCACCCAGTAAAAA	CTTTGGCCTCAAACCTGAAGG	486 bp

Supplementary Table 4 : The filename, LRI cutoff value and repeat structure in samples analyzing CODIS pattern in this study

Filename	Lri cutoff	Repeat Structure	Note
200-CODIS-CSF1PO-1	1.64	[AGAT] <sub>10</sub> [AGAT] <sub>13</sub>	
201-CODIS-CSF1PO-2	2.00	[AGAT] <sub>12</sub> [AGAT] <sub>12</sub>	
202-CODIS-CSF1PO-3	2.00	[AGAT] <sub>12</sub> [AGAT] <sub>12</sub>	
203-CODIS-D13S317-1	1.58	[TATC] <sub>9</sub> [TATC] <sub>11</sub>	
204-CODIS-D13S317-2	3.27	[TATC] <sub>8</sub> [TATC] <sub>11</sub>	
205-CODIS-D13S317-3	2.20	[TATC] <sub>8</sub> [TATC] <sub>9</sub>	
206-CODIS-D16S539-1	2.00	[GATA] <sub>11</sub> [GATA] <sub>11</sub>	
207-CODIS-D16S539-2	3.79	[GATA] <sub>9</sub> [GATA] <sub>12</sub>	
208-CODIS-D16S539-3	3.13	[GATA] <sub>11</sub> [GATA] <sub>12</sub>	
209-CODIS-D21S11-1	2.50	[TCTA] <sub>6</sub> [TCTG] <sub>6</sub> [TCTA] <sub>3</sub> TA[TCTA] <sub>3</sub> TCA[TCTA] <sub>2</sub> TCCA TA [TCTA] <sub>10</sub> [TCTA] <sub>6</sub> [TCTG] <sub>6</sub> [TCTA] <sub>3</sub> TA[TCTA] <sub>3</sub> TCA[TCTA] <sub>2</sub> TCCA TA[TCTA] <sub>12</sub> TA TCTA	
210-CODIS-D21S11-2	2.67	[TCTA] <sub>5</sub> [TCTG] <sub>6</sub> [TCTA] <sub>3</sub> TA[TCTA] <sub>3</sub> TCA[TCTA] <sub>2</sub> TCCA TA [TCTA] <sub>13</sub> [TCTA] <sub>4</sub> [TCTG] <sub>6</sub> [TCTA] <sub>3</sub> TA[TCTA] <sub>3</sub> TCA[TCTA] <sub>2</sub> TCCA TA [TCTA] <sub>12</sub>	
211-CODIS-D21S11-3	3.45	[TCTA] <sub>6</sub> [TCTG] <sub>5</sub> [TCTA] <sub>3</sub> TA[TCTA] <sub>3</sub> TCA[TCTA] <sub>2</sub> TCCA TA [TCTA] <sub>10</sub> [TCTA] <sub>5</sub> [TCTG] <sub>6</sub> [TCTA] <sub>3</sub> TA[TCTA] <sub>3</sub> TCA[TCTA] <sub>2</sub> TCCA TA [TCTA] <sub>11</sub>	
212-CODIS-D3S1358-1	2.00	TCTA[TCTG] <sub>2</sub> [TCTA] <sub>12</sub> TCTA[TCTG] <sub>2</sub> [TCTA] <sub>12</sub>	

213-CODIS-D3S1358-2	2.00	TCTA[TCTG] <sub>2</sub> [TCTA] <sub>11</sub> TCTA[TCTG] <sub>2</sub> [TCTA] <sub>12</sub>	skip tail 100bp
214-CODIS-D3S1358-3	1.74	TCTA[TCTG] <sub>2</sub> [TCTA] <sub>13</sub> TCTA[TCTG] <sub>3</sub> [TCTA] <sub>13</sub>	skip tail 100bp
215-CODIS-D5S818-1	2.25	[AGAT] <sub>10</sub> [AGAT] <sub>11</sub>	
216-CODIS-D5S818-2	2.43	[AGAT] <sub>10</sub> [AGAT] <sub>14</sub>	
217-CODIS-D5S818-3	2.37	[AGAT] <sub>11</sub> [AGAT] <sub>12</sub>	
218-CODIS-D8S1179-1	1.97	[TCTA] <sub>11</sub> [TCTA] <sub>1</sub> [TCTG] <sub>1</sub> [TCTA] <sub>12</sub>	
220-CODIS-D8S1179-3	2.35	[TCTA] <sub>11</sub> [TCTA] <sub>1</sub> [TCTG] <sub>1</sub> [TCTA] <sub>13</sub>	
221-CODIS-FGA-1	4.44	[TTTC] <sub>3</sub> TTTT TTCT[CTTT] <sub>15</sub> CTCC[TTCC] <sub>2</sub> [TTTC] <sub>3</sub> TTTT TTCT[CTTT] <sub>15</sub> CTCC[TTCC] <sub>2</sub>	
222-CODIS-FGA-2	2.00	[TTTC] <sub>3</sub> TTTT TTCT[CTTT] <sub>13</sub> CTCC[TTCC] <sub>2</sub> [TTTC] <sub>3</sub> TTTT TTCT[CTTT] <sub>13</sub> CTCC[TTCC] <sub>2</sub>	
223-CODIS-FGA-3	2.00	[TTTC] <sub>3</sub> TTTT TTCT[CTTT] <sub>14</sub> CTCC[TTCC] <sub>2</sub> [TTTC] <sub>3</sub> TTTT TTCT[CTTT] <sub>17</sub> CTCC[TTCC] <sub>2</sub>	
224-CODIS-TH01-1	1.71	[AATG] <sub>7</sub> [AATG] <sub>10</sub>	
225-CODIS-TH01-2	1.36	[AATG] <sub>7</sub> [AATG] <sub>9</sub>	
226-CODIS-TH01-3	2.01	[AATG] <sub>6</sub> [AATG] <sub>9</sub>	
227-CODIS-TPOX-1	2.02	[AATG] <sub>8</sub> [AATG] <sub>11</sub>	skip head 100bp

228-CODIS-TPOX-2	2.00	[AATG] <sub>8</sub> [AATG] <sub>8</sub>	
229-CODIS-TPOX-3	3.94	[AATG] <sub>8</sub> [AATG] <sub>8</sub>	

Supplementary Table 5 : The filename, LRI cutoff value, and HPV genotype in dual infection cervical cancers samples in this study

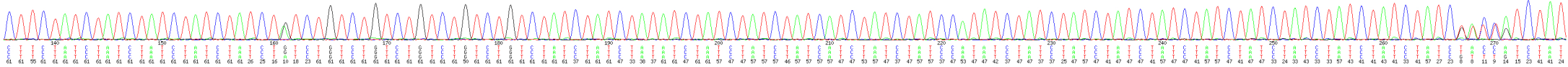
Filename	LRI cutoff	HPV type
300-HPV-33-81	<b>4.71</b>	HPV 33/81
301-HPV-42-71	2.00	HPV 42/71
302-HPV-52-18	<b>4.50</b>	HPV 52/18
303-HPV-54-67	<b>3.66</b>	HPV 54/67
304-HPV-6-53	5.45	HPV 6/53
305-HPV-53-52	<b>3.56</b>	HPV 53/52
306-HPV-52-70	<b>2.00</b>	HPV 52/70

Supplementary Table 6 : The copy number ratio of DEFB4/HSPDP3 predicted by MSR program and T/A cloning experiment

Sample	T/A Cloning		MSR Result		T/A Cloning		MSR Result	
	HSPDP3	DEFB4	HSPDP3	DEFB4	Log2(DEFB4/HSPDP3*2)	Log2(DEFB4/HSPDP3*2)	Log2(DEFB4/HSPDP3*2)	Log2(DEFB4/HSPDP3*2)
629	3	5	2	3	2	2	2	2
654	3	11	2	6	3	3	3	3
658	5	5	2	3	1	1	1	1
718	3	14	2	8	3	3	3	3
728	3	3	2	3	1	1	1	1



(A)

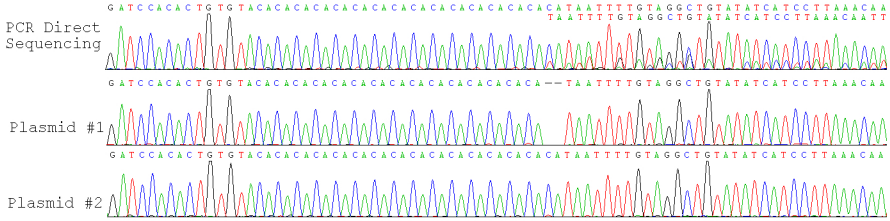


(B)

$\overbrace{CTTCTATCTATCTATCTATCTA}^1 \text{----} \overbrace{TCTGTCTGTCTGTCTGTCTGTCTGTCTATCTA}^1 \overbrace{TCTATCTA}^2 \overbrace{TCTATCTA}^3 \overbrace{TCTATCTA}^4 \overbrace{TCTATCTA}^5 \overbrace{TCTATCTA}^6 \text{----} \overbrace{TATCTATCTATCTATCATCTATCTATCCATA}^1 \overbrace{TCTATCTA}^2 \overbrace{TCTATCTA}^3 \overbrace{TCTATCTA}^4 \overbrace{TCTATCTA}^5 \overbrace{TCTATCTA}^6 \overbrace{TCTATCTA}^7 \overbrace{TCTATCTA}^8 \overbrace{TCTATCTA}^9 \overbrace{TCTATCTA}^{10} \overbrace{TCTATCTATC}^{11} \text{----} \text{GTCTAT}$   
 $\underbrace{CTTCTATCTATCTATCTATCTA}^1 \underbrace{TCTGTCTGTCTGTCTGTCTGTCTGTCTATCTA}^2 \underbrace{TCTATCTA}^3 \underbrace{TCTATCTA}^4 \underbrace{TCTATCTA}^5 \underbrace{TCTATCTA}^6 \underbrace{TCTATCTA}^7 \underbrace{TCTATCTA}^8 \underbrace{TCTATCTA}^9 \underbrace{TCTATCTA}^{10} \underbrace{TCTATCTATC}^{11} \text{----} \text{GTCTAT}$

Supplementary Fig. 1 (A) Chromatography trace of one Indel [CA] STR repeat structure and those of plasmid cloning, (B) MSR analyzed results are shown as the IUPAC code and decomposed sequences

(A)



(B)

chr5:172593038  
 MSR IUPAC GATCCCACTGTGTACACACACACACACACACACACACACAYAWWWTTKTRKRSKSTRATMWMYMYWWAMAMWW  
 MSR Result #1 GATCCCACTGTGTACACACACACACACACACACACACACACA--TAATTTTGTAGGCTGTATATCATCCTTAAACAA  
 MSR Result #2 GATCCCACTGTGTACACACACACACACACACACACACACACACATAAATTTTGTAGGCTGTATATCATCCTTAAACAA

Supplementary Fig. 2 (A) Chromatography trace of a combined two CODIS D21S11 Locus subtype, (B) there were two 4-bp gaps in the alignment of two subtypes in CODIS D21S11 Locus.