

<170> PatentIn version 3.3

<400>	1															
Met	Glu	Thr	Leu	Cys	Gln	Arg	Leu	Asn	Val	Cys	Gln	Asp	Lys	Ile	Leu	
1				5					10					15		
Thr	His	Tyr	Glu	Asn	Asp	Ser	Thr	Asp	Leu	Arg	Asp	His	Ile	Asp	Tyr	
			20					25					30			
Trp	Lys	His	Met	Arg	Leu	Glu	Cys	Ala	Ile	Tyr	Tyr	Lys	Ala	Arg	Glu	
		35					40					45				
Met	Gly	Phe	Lys	His	Ile	Asn	His	Gln	Val	Val	Pro	Thr	Leu	Ala	Val	
	50					55					60					
Ser	Lys	Asn	Lys	Ala	Leu	Gln	Ala	Ile	Glu	Leu	Gln	Leu	Thr	Leu	Glu	
65					70					75					80	
Thr	Ile	Tyr	Asn	Ser	Gln	Tyr	Ser	Asn	Glu	Lys	Trp	Thr	Leu	Gln	Asp	
			85						90					95		
Val	Ser	Leu	Glu	Val	Tyr	Leu	Thr	Ala	Pro	Thr	Gly	Cys	Ile	Lys	Lys	
			100					105					110			
His	Gly	Tyr	Thr	Val	Glu	Val	Gln	Phe	Asp	Gly	Asp	Ile	Cys	Asn	Thr	
		115					120					125				
Met	His	Tyr	Thr	Asn	Trp	Thr	His	Ile	Tyr	Ile	Cys	Glu	Glu	Ala	Ser	
	130					135					140					
Val	Thr	Val	Val	Glu	Gly	Gln	Val	Asp	Tyr	Tyr	Gly	Leu	Tyr	Tyr	Val	
145					150						155				160	
His	Glu	Gly	Ile	Arg	Thr	Tyr	Phe	Val	Gln	Phe	Lys	Asp	Asp	Ala	Glu	
			165						170					175		
Lys	Tyr	Ser	Lys	Asn	Lys	Val	Trp	Glu	Val	His	Ala	Gly	Gly	Gln	Val	
			180					185					190			
Ile	Leu	Cys	Pro	Thr	Ser	Val	Phe	Ser	Ser	Asn	Glu	Val	Ser	Ser	Pro	
		195					200					205				
Glu	Ile	Ile	Arg	Gln	His	Leu	Ala	Asn	His	Pro	Ala	Ala	Thr	His	Thr	
	210					215					220					
Lys	Ala	Val	Ala	Leu	Gly	Thr	Glu	Glu	Thr	Gln	Thr	Thr	Ile	Gln	Arg	
225					230						235				240	
Pro	Arg	Ser	Glu	Pro	Asp	Thr	Gly	Asn	Pro	Cys	His	Thr	Thr	Lys	Leu	
				245					250					255		
Leu	His	Arg	Asp	Ser	Val	Asp	Ser	Ala	Pro	Ile	Leu	Thr	Ala	Phe	Asn	

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                260                265                270
Ser Ser His Lys Gly Arg Ile Asn Cys Asn Ser Asn Thr Thr Pro Ile
      275                280                285
Val His Leu Lys Gly Asp Ala Asn Thr Leu Lys Cys Leu Arg Tyr Arg
      290                295                300
Phe Lys Lys His Cys Thr Leu Tyr Thr Ala Val Ser Ser Thr Trp His
305                310                315                320
Trp Thr Gly His Asn Val Lys His Lys Ser Ala Ile Val Thr Leu Thr
      325                330                335
Tyr Asp Ser Glu Trp Gln Arg Asp Gln Phe Leu Ser Gln Val Lys Ile
      340                345                350
Pro Lys Thr Ile Thr Val Ser Thr Gly Phe Met Ser Ile
      355                360                365

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<210> 2

<211> 453

<212> PRT

<213> artificial sequence

<220>

<223> membrane presented and defective HPV-16 E2 variant

<400> 2

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Met Val Pro Gln Ala Leu Leu Leu Val Pro Leu Leu Gly Phe Ser Leu
1      5      10      15
Cys Phe Gly Lys Phe Pro Ile Glu Thr Leu Cys Gln Arg Leu Asn Val
      20      25      30
Cys Gln Asp Lys Ile Leu Thr His Tyr Glu Asn Asp Ser Thr Asp Leu
      35      40      45
Arg Asp His Ile Asp Tyr Trp Lys His Met Arg Leu Ala Cys Ala Ile
      50      55      60
Tyr Tyr Lys Ala Arg Glu Met Gly Phe Lys His Ile Asn His Gln Val
      65      70      75      80
Val Pro Thr Leu Ala Val Ser Lys Asn Lys Ala Leu Gln Ala Ala Glu
      85      90      95
Leu Gln Leu Thr Leu Glu Thr Ile Tyr Asn Ser Gln Tyr Ser Asn Glu
      100     105     110
Lys Trp Thr Leu Gln Asp Val Ser Leu Glu Val Tyr Leu Thr Ala Pro
      115     120     125
Thr Gly Cys Ile Lys Lys His Gly Tyr Thr Val Glu Val Gln Phe Asp
      130     135     140
Gly Asp Ile Cys Asn Thr Met His Tyr Thr Asn Trp Thr His Ile Tyr
      145     150     155     160
Ile Cys Glu Glu Ala Ser Val Thr Val Val Glu Gly Gln Val Asp Tyr
      165     170     175
Tyr Gly Leu Tyr Tyr Val His Glu Gly Ile Arg Thr Tyr Phe Val Gln
      180     185     190
Phe Lys Asp Asp Ala Glu Lys Tyr Ser Lys Asn Lys Val Trp Glu Val
      195     200     205
His Ala Gly Gly Gln Val Ile Leu Cys Pro Thr Ser Val Phe Ser Ser
      210     215     220
Asn Glu Val Ser Ser Pro Glu Ile Ile Arg Gln His Leu Ala Asn His
      225     230     235     240
Pro Ala Ala Thr His Thr Lys Ala Val Ala Leu Gly Thr Glu Glu Thr
      245     250     255
Gln Thr Thr Ile Gln Arg Pro Arg Ser Glu Pro Asp Thr Gly Asn Pro
      260     265     270
Cys His Thr Thr Lys Leu Leu His Arg Asp Ser Val Asp Ser Ala Pro
      275     280     285
Ile Leu Thr Ala Phe Asn Ser Ser His Lys Gly Arg Ile Asn Cys Asn

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      290              295              300
Ser Asn Thr Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr Leu
305              310              315              320
Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr Ala
              325              330              335
Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys Ser
              340              345              350
Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln Phe
              355              360              365
Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly Phe
              370              375              380
Met Ser Ile Tyr Val Leu Leu Ser Ala Gly Thr Leu Ile Ala Leu Met
385              390              395              400
Leu Ile Ile Phe Leu Ile Thr Cys Cys Lys Arg Val Asp Arg Pro Glu
              405              410              415
Ser Thr Gln Arg Ser Leu Arg Gly Thr Gly Arg Asn Val Ser Val Thr
              420              425              430
Ser Gln Ser Gly Lys Phe Ile Ser Ser Trp Glu Ser His Lys Ser Gly
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Gly Glu Thr Arg Leu
450

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<210> 3

<211> 737

<212> PRT

<213> artificial sequence

<220>

<223> membrane-presented and replication-defective HPV-16 E1  
variant

<400> 3

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Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1              5              10              15
Cys Phe Gly Lys Phe Pro Ile Ala Asp Pro Ala Gly Thr Asn Gly Glu
              20              25              30
Glu Gly Thr Gly Cys Asn Gly Trp Phe Tyr Val Glu Ala Val Val Glu
              35              40              45
Lys Lys Thr Gly Asp Ala Ile Ser Asp Asp Glu Asn Glu Asn Asp Ser
              50              55              60
Asp Thr Gly Glu Asp Leu Val Asp Phe Ile Val Asn Asp Asn Asp Tyr
65              70              75              80
Leu Thr Gln Ala Glu Thr Glu Thr Ala His Ala Leu Phe Thr Ala Gln
              85              90              95
Glu Ala Lys Gln His Arg Asp Ala Val Gln Val Leu Lys Arg Lys Tyr
              100              105              110
Leu Gly Ser Pro Leu Ser Asp Ile Ser Gly Cys Val Asp Asn Asn Ile
              115              120              125
Ser Pro Arg Leu Lys Ala Ile Cys Ile Glu Lys Gln Ser Arg Ala Ala
              130              135              140
Lys Arg Arg Leu Phe Glu Ser Glu Asp Ser Gly Tyr Gly Asn Thr Glu
145              150              155              160
Val Glu Thr Gln Gln Met Leu Gln Val Glu Gly Arg His Glu Thr Glu
              165              170              175
Thr Pro Cys Ser Gln Tyr Ser Gly Gly Ser Gly Gly Gly Cys Ser Gln
              180              185              190
Tyr Ser Ser Gly Ser Gly Gly Glu Gly Val Ser Glu Arg His Thr Ile
              195              200              205
Cys Gln Thr Pro Leu Thr Asn Ile Leu Asn Val Leu Lys Thr Ser Asn
210              215              220

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Ala	Lys	Ala	Ala	Met	Leu	Ala	Lys	Phe	Lys	Glu	Leu	Tyr	Gly	Val	Ser
225					230					235					240
Phe	Ser	Glu	Leu	Val	Arg	Pro	Phe	Lys	Ser	Asn	Lys	Ser	Thr	Cys	Cys
				245					250					255	
Asp	Trp	Cys	Ile	Ala	Ala	Phe	Gly	Leu	Thr	Pro	Ser	Ile	Ala	Asp	Ser
			260					265					270		
Ile	Lys	Thr	Leu	Leu	Gln	Gln	Tyr	Cys	Leu	Tyr	Leu	His	Ile	Gln	Ser
		275					280					285			
Leu	Ala	Cys	Ser	Trp	Gly	Met	Val	Val	Leu	Leu	Leu	Val	Arg	Tyr	Lys
	290					295					300				
Cys	Gly	Lys	Asn	Arg	Glu	Thr	Ile	Glu	Lys	Leu	Leu	Ser	Lys	Leu	Leu
305					310					315					320
Cys	Val	Ser	Pro	Met	Cys	Met	Met	Ile	Glu	Pro	Pro	Lys	Leu	Arg	Ser
				325					330					335	
Thr	Ala	Ala	Ala	Leu	Tyr	Trp	Tyr	Lys	Thr	Gly	Ile	Ser	Asn	Ile	Ser
			340					345					350		
Glu	Val	Tyr	Gly	Asp	Thr	Pro	Glu	Trp	Ile	Gln	Arg	Gln	Thr	Val	Leu
		355					360					365			
Gln	His	Ser	Phe	Asn	Asp	Cys	Thr	Phe	Glu	Leu	Ser	Gln	Met	Val	Gln
	370					375					380				
Trp	Ala	Tyr	Asp	Asn	Asp	Ile	Val	Asp	Asp	Ser	Glu	Ile	Ala	Tyr	Lys
385					390					395					400
Tyr	Ala	Gln	Leu	Ala	Asp	Thr	Asn	Ser	Asn	Ala	Ser	Ala	Phe	Leu	Lys
				405					410					415	
Ser	Asn	Ser	Gln	Ala	Lys	Ile	Val	Lys	Asp	Cys	Ala	Thr	Met	Cys	Arg
			420					425					430		
His	Tyr	Lys	Arg	Ala	Glu	Lys	Lys	Gln	Met	Ser	Met	Ser	Gln	Trp	Ile
		435					440					445			
Lys	Tyr	Arg	Cys	Asp	Arg	Val	Asp	Asp	Gly	Gly	Asp	Trp	Lys	Gln	Ile
	450					455					460				
Val	Met	Phe	Leu	Arg	Tyr	Gln	Gly	Val	Glu	Phe	Met	Ser	Phe	Leu	Thr
465					470					475					480
Ala	Leu	Lys	Arg	Phe	Leu	Gln	Gly	Ile	Pro	Lys	Lys	Asn	Cys	Ile	Leu
				485					490					495	
Leu	Tyr	Gly	Ala	Ala	Asn	Thr	Asp	Lys	Ser	Leu	Phe	Gly	Met	Ser	Leu
			500					505					510		
Met	Lys	Phe	Leu	Gln	Gly	Ser	Val	Ile	Cys	Phe	Val	Asn	Ser	Lys	Ser
		515					520					525			
His	Phe	Trp	Leu	Gln	Pro	Leu	Ala	Asp	Ala	Lys	Ile	Gly	Met	Leu	Asp
	530					535					540				
Asp	Ala	Thr	Val	Pro	Cys	Trp	Asn	Tyr	Ile	Asp	Asp	Asn	Leu	Arg	Asn
545					550					555					560
Ala	Leu	Asp	Gly	Asn	Leu	Val	Ser	Met	Asp	Val	Lys	His	Arg	Pro	Leu
				565					570					575	
Val	Gln	Leu	Lys	Cys	Pro	Pro	Leu	Leu	Ile	Thr	Ser	Asn	Ile	Asn	Ala
				580					585				590		
Gly	Thr	Asp	Ser	Arg	Trp	Pro	Tyr	Leu	His	Asn	Arg	Leu	Val	Val	Phe
		595					600					605			
Thr	Phe	Pro	Asn	Glu	Phe	Pro	Phe	Asp	Glu	Asn	Gly	Asn	Pro	Val	Tyr
	610					615					620				
Glu	Leu	Asn	Asp	Lys	Asn	Trp	Lys	Ser	Phe	Phe	Ser	Arg	Thr	Trp	Ser
625					630					635					640
Arg	Leu	Ser	Leu	His	Glu	Asp	Glu	Asp	Lys	Glu	Asn	Asp	Gly	Asp	Ser
				645					650					655	
Leu	Pro	Thr	Phe	Lys	Cys	Val	Ser	Gly	Gln	Asn	Thr	Asn	Thr	Leu	Tyr
			660					665					670		
Val	Leu	Leu	Ser	Ala	Gly	Thr	Leu	Ile	Ala	Leu	Met	Leu	Ile	Ile	Phe
		675					680					685			
Leu	Ile	Thr	Cys	Cys	Lys	Arg	Val	Asp	Arg	Pro	Glu	Ser	Thr	Gln	Arg
	690					695					700				
Ser	Leu	Arg	Gly	Thr	Gly	Arg	Asn	Val	Ser	Val	Thr	Ser	Gln	Ser	Gly

705		710		715		720									
Lys	Phe	Ile	Ser	Ser	Trp	Glu	Ser	His	Lys	Ser	Gly	Gly	Glu	Thr	Arg
			725						730						735
Leu															

&lt;210&gt; 4

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; membrane-presented and non oncogenic HPV-16 E6 variant

&lt;400&gt; 4

Met	Gly	Leu	Lys	Val	Asn	Val	Ser	Ala	Ile	Phe	Met	Ala	Val	Leu	Leu
1				5					10					15	
Thr	Leu	Gln	Thr	Pro	Thr	Gly	Gln	Ile	His	Trp	Gly	Met	His	Gln	Lys
			20					25					30		
Arg	Thr	Ala	Met	Phe	Gln	Asp	Pro	Gln	Glu	Arg	Pro	Arg	Lys	Leu	Pro
		35				40					45				
Gln	Leu	Cys	Thr	Glu	Leu	Gln	Thr	Thr	Ile	His	Asp	Ile	Ile	Leu	Glu
	50					55					60				
Cys	Val	Tyr	Cys	Lys	Gln	Gln	Leu	Leu	Arg	Arg	Glu	Val	Tyr	Asp	Phe
65				70					75					80	
Ala	Phe	Arg	Asp	Leu	Cys	Ile	Val	Tyr	Arg	Asp	Gly	Asn	Pro	Tyr	Ala
				85				90						95	
Val	Cys	Asp	Lys	Cys	Leu	Lys	Phe	Tyr	Ser	Lys	Ile	Ser	Glu	Tyr	Arg
			100					105					110		
His	Tyr	Cys	Tyr	Ser	Leu	Tyr	Gly	Thr	Thr	Leu	Glu	Gln	Gln	Tyr	Asn
		115					120					125			
Lys	Pro	Leu	Cys	Asp	Leu	Leu	Ile	Arg	Cys	Ile	Asn	Cys	Gln	Lys	Pro
	130					135					140				
Leu	Gln	Arg	His	Leu	Asp	Lys	Lys	Gln	Arg	Phe	His	Asn	Ile	Arg	Gly
145					150					155					160
Arg	Trp	Thr	Gly	Arg	Cys	Met	Ser	Cys	Cys	Arg	Ser	Ser	Arg	Thr	Arg
				165				170						175	
Arg	Glu	Thr	Gln	Leu	Gly	Leu	Ser	Ser	Thr	Ser	Ile	Val	Tyr	Ile	Leu
			180					185					190		
Ile	Ala	Val	Cys	Leu	Gly	Gly	Leu	Ile	Gly	Ile	Pro	Ala	Leu	Ile	Cys
		195					200					205			
Cys	Cys	Arg	Gly	Arg	Cys	Asn	Lys	Lys	Gly	Glu	Gln	Val	Gly	Met	Ser
	210					215					220				
Arg	Pro	Gly	Leu	Lys	Pro	Asp	Leu	Thr	Gly	Thr	Ser	Lys	Ser	Tyr	Val
225					230					235					240
Arg	Ser	Leu													

&lt;210&gt; 5

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; membrane-presented and non oncogenic HPV-16 E7 variant

&lt;400&gt; 5

Met	Val	Pro	Gln	Ala	Leu	Leu	Phe	Val	Pro	Leu	Leu	Val	Phe	Pro	Leu
1				5					10					15	

Cys	Phe	Gly	Lys	Phe	Pro	Ile	Gly	Ser	Met	His	Gly	Asp	Thr	Pro	Thr
		20						25					30		
Leu	His	Glu	Tyr	Met	Leu	Asp	Leu	Gln	Pro	Glu	Thr	Thr	Gln	Leu	Asn
		35					40					45			
Asp	Ser	Ser	Glu	Glu	Glu	Asp	Glu	Ile	Asp	Gly	Pro	Ala	Gly	Gln	Ala
	50					55					60				
Glu	Pro	Asp	Arg	Ala	His	Tyr	Asn	Ile	Val	Thr	Phe	Cys	Cys	Lys	Cys
65					70					75				80	
Asp	Ser	Thr	Leu	Arg	Leu	Cys	Val	Gln	Ser	Thr	His	Val	Asp	Ile	Arg
				85				90						95	
Thr	Leu	Glu	Asp	Leu	Leu	Met	Gly	Thr	Leu	Gly	Ile	Val	Cys	Pro	Ile
			100					105					110		
Cys	Ser	Gln	Lys	Pro	Arg	Ser	Tyr	Val	Leu	Leu	Ser	Ala	Gly	Ala	Leu
		115					120					125			
Thr	Ala	Leu	Met	Leu	Ile	Ile	Phe	Leu	Met	Thr	Cys	Cys	Arg	Arg	Val
	130					135					140				
Asn	Arg	Ser	Glu	Pro	Thr	Gln	His	Asn	Leu	Arg	Gly	Thr	Gly	Arg	Glu
145					150					155					160
Val	Ser	Val	Thr	Pro	Gln	Ser	Gly	Lys	Ile	Ile	Ser	Ser	Trp	Glu	Ser
				165				170						175	
His	Lys	Ser	Gly	Gly	Glu	Thr	Arg	Leu							
			180					185							

&lt;210&gt; 6

&lt;211&gt; 59

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

<223> portion of 59 nt of HPV-16 E1-encoding sequence degenerated  
to decrease homology with the overlapping HPV-16  
E2-encoding sequence

&lt;400&gt; 6

atggtgattc attacctaca ttcaagtgcg tatctggtca gaacacaaat actttgtga 59

&lt;210&gt; 7

&lt;211&gt; 2214

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

<223> sequence encoding a membrane-addressed and defective  
HPV-16 E1 polypeptide which includes the 59nt degenerated  
sequence

&lt;400&gt; 7

atggtaccgc	aagccctgct	attcgtagct	ttattggtct	ttcccctctg	tttcggtgtaag	60
tttcctatag	ctgatcctgc	aggtaccaat	ggggaagagg	gtacgggatg	taatggatgg	120
ttttatgtag	aggctgtagt	ggaaaaaaaa	acaggggatg	ctatatcaga	tgacgagaac	180
gaaaatgaca	gtgatacagg	tgaagatttg	gtagatttta	tagtaaatga	taatgattat	240
ttaacacagg	cagaaacaga	gacagcacat	gcggtgttta	ctgcacagga	agcaaaacaa	300
catagagatg	cagtacaggt	tctaaaacga	aagtatttgg	gtagtccact	tagtgatatt	360
agtggtatgt	tagacaataa	tattagtcct	agattaaaag	ctatatgtat	agaaaaacaa	420
agtagagctg	caaaaaggag	attatttgaa	agcgaagaca	gcggttatgg	caatactgaa	480
gtggaaactc	agcagatggt	acaggtagaa	gggcgcgatg	agactgaaac	accatgtagt	540
cagtatagtg	gtggaagtgg	gggtggttgc	agtcagtaca	gtagtgggaag	tgggggagag	600
ggtgttagtg	aaagacacac	tatatgccaa	acaccactta	caaatatatt	aaatgtacta	660
aaaactagta	atgcaaaggc	agcaatgtta	gcaaaattta	aagagttata	cggggtgagt	720

ttttcagaat	tagtaagacc	atttaaaagt	aataaatcaa	cgtgttgcca	ttggtgtatt	780
gctgcatttg	gacttacacc	cagtatagct	gacagtataa	aaacactatt	acaacaatat	840
tgtttatatt	tacacattca	aagtttagca	tgttcatggg	gaatggttgt	gttactatta	900
gtaagatata	aatgtggaaa	aaatagagaa	acaattgaaa	aattgctgtc	taaactatta	960
tgtgtgtctc	caatgtgtat	gatgatagag	cctccaaaat	tgcgtagtac	agcagcagca	1020
ttatattggt	ataaaacagg	tatatcaaat	attagtgaag	tgtatggaga	cacgccagaa	1080
tggaatacaa	gacaaacagt	attacaacat	agttttaatg	attgtacatt	tgaattatca	1140
cagatggtac	aatgggccta	cgataatgac	atagtagacg	atagtgaat	tgcatataaa	1200
tatgcacaat	tgccagacac	taatagtaat	gcaagtgcct	ttctaaaaag	taattcacag	1260
gcaaaaattg	taaaggattg	tgcaacaatg	tgtagacatt	ataaacgagc	agaaaaaaaa	1320
caaatgagta	tgagtcaatg	gataaaatat	agatgtgata	gggtagatga	tgagggtgat	1380
tggaagcaaa	ttgttatggt	tttaaggtag	caagggtgtag	agtttatgtc	atttttaact	1440
gcattaaaaa	gattttttgca	aggcatacct	aaaaaaaaat	gcatattact	atatggtgca	1500
gctaacacag	ataaatcatt	atttggtatg	agtttaatga	aatttctgca	agggctctgta	1560
atatgttttg	taaattctaa	aagccatttt	tggttacaac	cattagcaga	tgccaaaata	1620
ggatgtttag	atgatgtctac	agtgcctgt	tggaactata	tagatgacaa	tttaagaaat	1680
gcattggatg	gaaatttagt	ttctatggat	gtaaagcata	gaccattggt	acaactaaaa	1740
tgccctccat	tattaattac	atctaacatt	aatgctggta	cagattctag	gtggccttat	1800
ttacataata	gattggtggt	gtttacattt	cctaattgagt	ttccatttga	cgaaaacgga	1860
aatccagtgt	atgagcttaa	tgataagaac	tggaatcct	ttttctcaag	gacgtggtcc	1920
agattaagtt	tgccagagga	cgaggacaag	gaaaacgatg	gtgattcatt	acctacattc	1980
aagtgcgtat	ctggtcagaa	cacaaatact	ttgtacgtac	tgctatcggc	aggcacgttg	2040
atcgactaa	tgcttatcat	cttcctaata	acctgctgca	agcgggttga	taggcccga	2100
agtacccaaa	ggtccttgag	aggtaccgga	cgcaacgtat	cggtaacgtc	gcaaagcggc	2160
aagttcatta	gcagttggga	gtcgcacaaa	tcagggtggag	agacccgcct	gtga	2214

<210> 8

<211> 1362

<212> DNA

<213> artificial sequence

<220>

<223> nt sequence encoding the membrane-addressed and defective  
HPV-16 E2 polypeptide

<400> 8

atggtaccac	aagcgtgtgt	acttgtccca	ctgcttggtt	tctctttatg	ttttggaaaa	60
ttcccaatag	agactccttg	ccaacgttta	aatgtgtgtc	aggacaaaat	actaacacat	120
tatgaaaatg	atagtacaga	cctacgtgac	catatagact	attggaaaca	catgcgcta	180
gcattgtgcta	tttattacaa	ggccagagaa	atgggattta	aacatattaa	ccaccaggtg	240
gtgccaacgc	tggtgtgtatc	aaagaataaa	gcattacaag	cagctgaact	gcaactaacg	300
ttagaacaa	tatataactc	acaatatagt	aatgaaaagt	ggacattaca	agacgttagc	360
cttgaagtgt	atttaactgc	accaacagga	tgtataaaaa	aacatggata	tacagtggaa	420
gtgcagtttg	atggagacat	atgcaatata	atgcattata	caaactggac	acatatatat	480
atgtgtgaag	aagcatcagt	aactgtggta	gaggggtcaag	ttgactatta	tggtttatat	540
tatgttcatg	aaggaatacg	aacatatatt	gtgcagttta	aagatgatgc	agaaaaatat	600
agtaaaaaata	aagtatggga	agttcatgcg	ggtggtcagg	taatattatg	tcctacatct	660
gtgttttagca	gcaacgaagt	atcctctcct	gaaattatta	ggcagcaact	ggccaaccac	720
cccgccgcga	cccataccaa	agccgtcgcc	ttgggcaccg	aagaaacaca	gacgactatc	780
cagcgacca	gatcagagcc	agacaccgga	aaccctgcc	acaccactaa	gttgttgac	840
agagactcag	tggaacagtgc	tccaatcctc	actgcattta	acagctcaca	caaaggacgg	900
attaactgta	atagtaacac	tacaccata	gtacattttaa	aaggtgatgc	taatacttta	960
aaatgtttta	gatatagatt	taaaaagcat	tgtacattgt	atactgcagt	gtcgtctaca	1020
tggtattgga	caggacataa	tgtaaaacat	aaaagtgcaa	ttgttacact	tacatatgat	1080
agtgaatggc	aacgtgacca	atttttgtct	caagttaaaa	tacaaaaaac	tattacagtg	1140
tctactggat	ttatgtctat	atatgttctt	ctctctgctg	gaactttaat	agctttaatg	1200
ttaataatat	tcttaataac	gtgctgtaaa	agggtagacc	gtccagagtc	aactcagcgc	1260
agccttaggg	gtactgggag	aaatgtttcc	gtgacatcac	agagtggaaa	atztatctcg	1320
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<210> 9  
 <211> 34  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> sens primer  
  
 <400> 9  
 aaacccggat ccatggagac tctttgcaa cgtt 34  
  
 <210> 10  
 <211> 49  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> antisense primer  
  
 <400> 10  
 aaacccgaat tcaagcttag atcttcatat agacataaat ccagtagac 49  
  
 <210> 11  
 <211> 33  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> sens primer  
  
 <400> 11  
 aaacccggat ccatgggtacc acaagcgctg tta 33  
  
 <210> 12  
 <211> 53  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> sens primer  
  
 <400> 12  
 tctctttatg ttttggaata ttccaatag agactctttg ccaacgttta aat 53  
  
 <210> 13  
 <211> 53  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> antisense primer  
  
 <400> 13  
 atttaaacgt tggcaaagag tctctattgg gaattttcca aaacataaag aga 53



<210> 14  
 <211> 49  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sens primer

<400> 14  
 cagtgtctac tggatttatg tctatatatg ttcttctctc tgctggaac 49

<210> 15  
 <211> 49  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisense primer

<400> 15  
 gttccagcag agagaagaac atatatagac ataaatccag tagacactg 49

<210> 16  
 <211> 44  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sens primer

<400> 16  
 aaaccagat cttcaaagac gtgtttcgcc tccactctta tgag 44

<210> 17  
 <211> 34  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sens primer

<400> 17  
 aaaccggat ccatggctga tcctgcaggt acca 34

<210> 18  
 <211> 34  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisense primer

<400> 18  
 aaaccgaat tccattatcg taggccatt gtac 34

<210> 19

<211> 32  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sens primer

<400> 19  
 aaaccgcat ccgagacacg ccagaatgga ta 32

<210> 20  
 <211> 50  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisense primer

<400> 20  
 aaaccgaat tcaagcttag atcttcataa tgtgttagta tttgtcctg 50

<210> 21  
 <211> 88  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisense primer

<400> 21  
 aaaccagat cttcaciaaag tatttgtgtt ctgaccagat acgcacttga atgtaggtaa 60  
 tgaatcacca tcgttttcct tgcctcgt 88

<210> 22  
 <211> 21  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sens primer

<400> 22  
 gatgctacag tgccctgttg g 21

<210> 23  
 <211> 35  
 <212> DNA  
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<220>  
 <223> sens primer

<400> 23  
 aaaccgaag atccatggta ccgaagccc tgcta 35

<210> 24  
 <211> 52

<212> DNA  
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<220>  
 <223> sens primer

<400> 24  
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<210> 25  
 <211> 52  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisens primer

<400> 25  
 ccattggtac ctgcaggatc agctatagga aacttaccga aacagagggg aa 52

<210> 26  
 <211> 50  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sens primer

<400> 26  
 tatctggtca gaacacaaat actttgtacg tactgctatc ggcaggcacg 50

<210> 27  
 <211> 50  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisense primer

<400> 27  
 cgtgcctgcc gatagcagta cgtacaaagt atttgtgttc tgaccagata 50

<210> 28  
 <211> 42  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisens primer

<400> 28  
 aaacccaaag atcttcacag gcgggtctct ccacctgatt tg 42

<210> 29  
 <211> 453  
 <212> PRT  
 <213> artificial sequence

&lt;220&gt;

&lt;223&gt; HPV-18 membrane-presented and replication-defective E2 polypeptide (SS-18 E2\*-TMR)

&lt;400&gt; 29

Met	Val	Pro	Gln	Ala	Leu	Leu	Phe	Val	Pro	Leu	Leu	Val	Phe	Pro	Leu
1				5					10					15	
Cys	Phe	Gly	Lys	Phe	Pro	Ile	Gln	Thr	Pro	Lys	Glu	Thr	Leu	Ser	Glu
			20					25					30		
Arg	Leu	Ser	Cys	Val	Gln	Asp	Lys	Ile	Ile	Asp	His	Tyr	Glu	Asn	Asp
		35					40					45			
Ser	Lys	Asp	Ile	Asp	Ser	Gln	Ile	Gln	Tyr	Trp	Gln	Leu	Ile	Arg	Trp
	50					55					60				
Ala	Asn	Ala	Ile	Phe	Phe	Ala	Ala	Arg	Glu	His	Gly	Ile	Gln	Thr	Leu
65					70					75					80
Asn	His	Gln	Val	Val	Pro	Ala	Tyr	Asn	Ile	Ser	Lys	Ser	Lys	Ala	His
			85						90					95	
Lys	Ala	Ala	Glu	Leu	Gln	Met	Ala	Leu	Gln	Gly	Leu	Ala	Gln	Ser	Arg
			100					105					110		
Tyr	Lys	Thr	Glu	Asp	Trp	Thr	Leu	Gln	Asp	Thr	Cys	Glu	Glu	Leu	Trp
		115					120					125			
Asn	Thr	Glu	Pro	Thr	His	Cys	Phe	Lys	Lys	Gly	Gly	Gln	Thr	Val	Gln
	130					135						140			
Val	Tyr	Phe	Asp	Gly	Asn	Lys	Asp	Asn	Cys	Met	Thr	Tyr	Val	Ala	Trp
145					150					155					160
Asp	Ser	Val	Tyr	Tyr	Met	Thr	Asp	Ala	Gly	Thr	Trp	Asp	Lys	Thr	Ala
			165					170						175	
Thr	Cys	Val	Ser	His	Arg	Gly	Leu	Tyr	Tyr	Val	Lys	Glu	Gly	Tyr	Asn
			180					185					190		
Thr	Phe	Tyr	Ile	Glu	Phe	Lys	Ser	Glu	Cys	Glu	Lys	Tyr	Gly	Asn	Thr
		195					200					205			
Gly	Thr	Trp	Glu	Val	His	Phe	Gly	Asn	Asn	Val	Ile	Asp	Cys	Asn	Asp
	210					215					220				
Ser	Met	Cys	Ser	Thr	Ser	Asp	Asp	Thr	Val	Ser	Ala	Thr	Gln	Leu	Val
225					230					235					240
Lys	Gln	Leu	Gln	His	Thr	Pro	Ser	Pro	Tyr	Ser	Ser	Thr	Val	Ser	Val
			245						250					255	
Gly	Thr	Ala	Lys	Thr	Tyr	Gly	Gln	Thr	Ser	Ala	Ala	Thr	Arg	Pro	Gly
		260						265					270		
His	Cys	Gly	Leu	Ala	Glu	Lys	Gln	His	Cys	Gly	Pro	Val	Asn	Pro	Leu
		275					280					285			
Leu	Gly	Ala	Ala	Thr	Pro	Thr	Gly	Asn	Asn	Lys	Arg	Arg	Lys	Leu	Cys
	290					295					300				
Ser	Gly	Asn	Thr	Thr	Pro	Ile	Ile	His	Leu	Lys	Gly	Asp	Arg	Asn	Ser
305					310					315					320
Leu	Lys	Cys	Leu	Arg	Tyr	Arg	Leu	Arg	Lys	His	Ser	Asp	His	Tyr	Arg
			325						330					335	
Asp	Ile	Ser	Ser	Thr	Trp	His	Trp	Thr	Gly	Ala	Gly	Asn	Glu	Lys	Thr
			340					345					350		
Gly	Ile	Leu	Thr	Val	Thr	Tyr	His	Ser	Glu	Thr	Gln	Arg	Thr	Lys	Phe
	355						360					365			
Leu	Asn	Thr	Val	Ala	Ile	Pro	Asp	Ser	Val	Gln	Ile	Leu	Val	Gly	Tyr
	370					375					380				
Met	Thr	Met	Tyr	Val	Leu	Leu	Ser	Ala	Gly	Ala	Leu	Thr	Ala	Leu	Met
385					390					395					400
Leu	Ile	Ile	Phe	Leu	Met	Thr	Cys	Cys	Arg	Arg	Val	Asn	Arg	Ser	Glu
			405						410					415	
Pro	Thr	Gln	His	Asn	Leu	Arg	Gly	Thr	Gly	Arg	Glu	Val	Ser	Val	Thr
			420					425					430		
Pro	Gln	Ser	Gly	Lys	Ile	Ile	Ser	Ser	Trp	Glu	Ser	His	Lys	Ser	Gly
	435						440					445			

Gly Glu Thr Arg Leu  
450

<210> 30

<211> 441

<212> PRT

<213> artificial sequence

<220>

<223> HPV-33 membrane-presented and replication-defective E2  
polypeptide (SS-33 E2\*-TMR)

<400> 30

Met	Val	Pro	Gln	Ala	Leu	Leu	Phe	Val	Pro	Leu	Leu	Val	Phe	Pro	Leu	1	5	10	15
Cys	Phe	Gly	Lys	Phe	Pro	Ile	Glu	Glu	Ile	Ser	Ala	Arg	Leu	Asn	Ala	20	25	30	
Val	Gln	Glu	Lys	Ile	Leu	Asp	Leu	Tyr	Glu	Ala	Asp	Lys	Thr	Asp	Leu	35	40	45	
Pro	Ser	Gln	Ile	Glu	His	Trp	Lys	Leu	Ile	Arg	Met	Ala	Cys	Ala	Leu	50	55	60	
Leu	Tyr	Thr	Ala	Lys	Gln	Met	Gly	Phe	Ser	His	Leu	Cys	His	Gln	Val	65	70	75	80
Val	Pro	Ser	Leu	Leu	Ala	Ser	Lys	Thr	Lys	Ala	Phe	Gln	Val	Ala	Glu	85	90	95	
Leu	Gln	Met	Ala	Leu	Glu	Thr	Leu	Ser	Lys	Ser	Gln	Tyr	Ser	Thr	Ser	100	105	110	
Gln	Trp	Thr	Leu	Gln	Gln	Thr	Ser	Leu	Glu	Val	Trp	Leu	Cys	Glu	Pro	115	120	125	
Pro	Lys	Cys	Phe	Lys	Lys	Gln	Gly	Glu	Thr	Val	Thr	Val	Gln	Tyr	Asp	130	135	140	
Asn	Asp	Lys	Lys	Asn	Thr	Met	Asp	Tyr	Thr	Asn	Trp	Gly	Glu	Ile	Tyr	145	150	155	160
Ile	Ile	Glu	Glu	Asp	Thr	Cys	Thr	Met	Val	Thr	Gly	Lys	Val	Asp	Tyr	165	170	175	
Ile	Gly	Met	Tyr	Tyr	Ile	His	Asn	Cys	Glu	Lys	Val	Tyr	Phe	Lys	Tyr	180	185	190	
Phe	Lys	Glu	Asp	Ala	Ala	Lys	Tyr	Ser	Lys	Thr	Gln	Met	Trp	Glu	Val	195	200	205	
His	Val	Gly	Gly	Gln	Val	Ile	Val	Cys	Pro	Thr	Ser	Ile	Ser	Ser	Asn	210	215	220	
Gln	Ile	Ser	Thr	Thr	Glu	Thr	Ala	Asp	Ile	Gln	Thr	Asp	Asn	Asp	Asn	225	230	235	240
Arg	Pro	Pro	Gln	Ala	Ala	Ala	Lys	Arg	Arg	Arg	Pro	Ala	Asp	Thr	Thr	245	250	255	
Asp	Thr	Ala	Gln	Pro	Leu	Thr	Lys	Leu	Phe	Cys	Ala	Asp	Pro	Ala	Leu	260	265	270	
Asp	Asn	Arg	Thr	Ala	Arg	Thr	Ala	Thr	Asn	Cys	Thr	Asn	Lys	Gln	Arg	275	280	285	
Thr	Val	Cys	Ser	Ser	Asn	Val	Ala	Pro	Ile	Val	His	Leu	Lys	Gly	Glu	290	295	300	
Ser	Asn	Ser	Leu	Lys	Cys	Leu	Arg	Tyr	Arg	Leu	Lys	Pro	Tyr	Lys	Glu	305	310	315	320
Leu	Tyr	Ser	Ser	Met	Ser	Ser	Thr	Trp	His	Trp	Thr	Ser	Asp	Asn	Lys	325	330	335	
Asn	Ser	Lys	Asn	Gly	Ile	Val	Thr	Val	Thr	Phe	Val	Thr	Glu	Gln	Gln	340	345	350	
Gln	Gln	Met	Phe	Leu	Gly	Thr	Val	Lys	Ile	Pro	Pro	Thr	Val	Gln	Ile	355	360	365	
Ser	Thr	Gly	Phe	Met	Thr	Leu	Tyr	Val	Leu	Leu	Ser	Ala	Gly	Thr	Leu				

370		375		380
Ile Ala Leu Met Leu Ile	Ile Phe Leu Ile Thr	Cys Cys Lys Arg Val		
385	390	395	400	
Asp Arg Pro Glu Ser Thr	Gln Arg Ser Leu Arg Gly Thr	Gly Arg Asn		
	405	410	415	
Val Ser Val Thr Ser Gln Ser	Gly Lys Phe Ile Ser Ser Trp	Glu Ser		
	420	425	430	
His Lys Ser Gly Gly Glu Thr	Arg Leu			
	435	440		

<210> 31  
 <211> 457  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> HPV-52 membrane-presented and replication-defective E2 polypeptide

<400> 31

Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala Val Leu Leu															
1		5				10			15						
Thr Leu Gln Thr Pro Thr Gly Gln Ile His Trp Gly Glu Ser Ile Pro						20	25		30						
Ala Arg Leu Asn Ala Val Gln Glu Lys Ile Leu Asp Leu Tyr Glu Ala						35	40		45						
Asp Ser Asn Asp Leu Asn Ala Gln Ile Glu His Trp Lys Leu Thr Arg						50	55		60						
Met Ala Cys Val Leu Phe Tyr Lys Ala Lys Glu Leu Gly Ile Thr His						65	70		75						80
Ile Gly His Gln Val Val Pro Pro Met Ala Val Ser Lys Ala Lys Ala							85		90						95
Cys Gln Ala Ala Glu Leu Gln Leu Ala Leu Glu Ala Leu Asn Lys Thr							100		105						110
Gln Tyr Ser Thr Asp Gly Trp Thr Leu Gln Gln Thr Ser Leu Glu Met							115		120						125
Trp Arg Ala Glu Pro Gln Lys Tyr Phe Lys Lys His Gly Tyr Thr Ile							130		135						140
Thr Val Gln Tyr Asp Asn Asp Lys Asn Asn Thr Met Asp Tyr Thr Asn							145		150						155
Trp Lys Glu Ile Tyr Leu Leu Gly Glu Cys Glu Cys Thr Ile Val Glu							160		165						170
Gly Gln Val Asp Tyr Tyr Gly Leu Tyr Tyr Trp Cys Asp Gly Glu Lys							175		180						185
Ile Tyr Phe Val Lys Phe Ser Asn Asp Ala Lys Gln Tyr Cys Val Thr							190		195						200
Gly Val Trp Glu Val His Val Gly Gly Gln Val Ile Val Cys Pro Ala							205		210						215
Ser Val Ser Ser Asn Glu Val Ser Thr Thr Glu Thr Ala Val His Leu							220		225						230
Cys Thr Glu Thr Ser Lys Thr Ser Ala Val Ser Val Gly Ala Lys Asp							235		240						245
Thr His Leu Gln Pro Pro Gln Lys Arg Arg Arg Pro Asp Val Thr Asp							245		250						255
Ser Arg Asn Thr Lys Tyr Pro Asn Asn Leu Leu Arg Gly Gln Gln Ser							260		265						270
Val Asp Ser Thr Thr Arg Gly Leu Val Thr Ala Thr Glu Cys Thr Asn							275		280						285
Lys Gly Arg Val Ala His Thr Thr Cys Thr Ala Pro Ile Ile His Leu							290		295						300
305		310							315						320

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Lys Gly Asp Pro Asn Ser Leu Lys Cys Leu Arg Tyr Arg Val Lys Thr
                325                330                335
His Lys Ser Leu Tyr Val Gln Ile Ser Ser Thr Trp His Trp Thr Ser
                340                345                350
Asn Glu Cys Thr Asn Asn Lys Leu Gly Ile Val Thr Ile Thr Tyr Ser
                355                360                365
Asp Glu Thr Gln Arg Gln Gln Phe Leu Lys Thr Val Lys Ile Pro Asn
                370                375                380
Thr Val Gln Val Ile Gln Gly Val Met Ser Leu Gly Leu Ser Ser Thr
385                390                395                400
Ser Ile Val Tyr Ile Leu Ile Ala Val Cys Leu Gly Gly Leu Ile Gly
                405                410                415
Ile Pro Ala Leu Ile Cys Cys Cys Arg Gly Arg Cys Asn Lys Lys Gly
                420                425                430
Glu Gln Val Gly Met Ser Arg Pro Gly Leu Lys Pro Asp Leu Thr Gly
                435                440                445
Thr Ser Lys Ser Tyr Val Arg Ser Leu
                450                455

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<210> 32

<211> 746

<212> PRT

<213> artificial sequence

<220>

<223> HPV-18 membrane-presented and replication defective E1  
polypeptide

<400> 32

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Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala Val Leu Leu
1                5                10                15
Thr Leu Gln Thr Pro Thr Gly Gln Ile His Trp Gly Ala Asp Pro Glu
                20                25                30
Gly Thr Asp Gly Glu Gly Thr Gly Cys Asn Gly Trp Phe Tyr Val Gln
                35                40                45
Ala Ile Val Asp Lys Lys Thr Gly Asp Val Ile Ser Asp Asp Glu Asp
50                55                60
Glu Asn Ala Thr Asp Thr Gly Ser Asp Met Val Asp Phe Ile Asp Thr
65                70                75                80
Gln Gly Thr Phe Cys Glu Gln Ala Glu Leu Glu Thr Ala Gln Ala Leu
                85                90                95
Phe His Ala Gln Glu Val His Asn Asp Ala Gln Val Leu His Val Leu
                100                105                110
Lys Arg Lys Phe Ala Gly Gly Ser Thr Glu Asn Ser Pro Leu Gly Glu
                115                120                125
Arg Leu Glu Val Asp Thr Glu Leu Ser Pro Arg Leu Gln Glu Ile Ser
130                135                140
Leu Asn Ser Gly Gln Lys Lys Ala Lys Arg Arg Leu Phe Thr Ile Ser
145                150                155                160
Asp Ser Gly Tyr Gly Cys Ser Glu Val Glu Ala Thr Gln Ile Gln Val
                165                170                175
Thr Thr Asn Gly Glu His Gly Gly Asn Val Cys Ser Gly Gly Ser Thr
                180                185                190
Glu Ala Ile Asp Asn Gly Gly Thr Glu Gly Asn Asn Ser Ser Val Asp
                195                200                205
Gly Thr Ser Asp Asn Ser Asn Ile Glu Asn Val Asn Pro Gln Cys Thr
210                215                220
Ile Ala Gln Leu Lys Asp Leu Leu Lys Val Asn Asn Lys Gln Gly Ala
225                230                235                240
Met Leu Ala Val Phe Lys Asp Thr Tyr Gly Leu Ser Phe Thr Asp Leu

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				245					250					255	
Val	Arg	Asn	Phe	Lys	Ser	Asp	Lys	Thr	Thr	Cys	Thr	Asp	Trp	Val	Thr
			260					265					270		
Ala	Ile	Phe	Gly	Val	Asn	Pro	Thr	Ile	Ala	Glu	Gly	Phe	Lys	Thr	Leu
		275					280					285			
Ile	Gln	Pro	Phe	Ile	Leu	Tyr	Ala	His	Ile	Gln	Cys	Leu	Asp	Cys	Lys
	290					295					300				
Trp	Gly	Val	Leu	Ile	Leu	Ala	Leu	Leu	Arg	Tyr	Lys	Cys	Gly	Lys	Ser
305				310						315					320
Arg	Leu	Thr	Val	Ala	Lys	Gly	Leu	Ser	Thr	Leu	Leu	His	Val	Pro	Glu
			325						330					335	
Thr	Cys	Met	Leu	Ile	Gln	Pro	Pro	Lys	Leu	Arg	Ser	Ser	Val	Ala	Ala
			340					345					350		
Leu	Tyr	Trp	Tyr	Arg	Thr	Gly	Ile	Ser	Asn	Ile	Ser	Glu	Val	Met	Gly
		355				360						365			
Asp	Thr	Pro	Glu	Trp	Ile	Gln	Arg	Leu	Thr	Ile	Ile	Gln	His	Gly	Ile
	370					375					380				
Asp	Asp	Ser	Asn	Phe	Asp	Leu	Ser	Glu	Met	Val	Gln	Trp	Ala	Phe	Asp
385				390						395					400
Asn	Glu	Leu	Thr	Asp	Glu	Ser	Asp	Met	Ala	Phe	Glu	Tyr	Ala	Leu	Leu
			405						410				415		
Ala	Asp	Ser	Asn	Ser	Asn	Ala	Ala	Ala	Phe	Leu	Lys	Ser	Asn	Cys	Gln
			420					425					430		
Ala	Lys	Tyr	Leu	Lys	Asp	Cys	Ala	Thr	Met	Cys	Lys	His	Tyr	Arg	Arg
		435					440					445			
Ala	Gln	Lys	Arg	Gln	Met	Asn	Met	Ser	Gln	Trp	Ile	Arg	Phe	Arg	Cys
	450					455					460				
Ser	Lys	Ile	Asp	Glu	Gly	Gly	Asp	Trp	Arg	Pro	Ile	Val	Gln	Phe	Leu
465				470						475					480
Arg	Tyr	Gln	Gln	Ile	Glu	Phe	Ile	Thr	Phe	Leu	Gly	Ala	Leu	Lys	Ser
			485						490					495	
Phe	Leu	Lys	Gly	Thr	Pro	Lys	Lys	Asn	Cys	Leu	Val	Phe	Cys	Gly	Pro
			500					505					510		
Ala	Asn	Thr	Asp	Lys	Ser	Tyr	Phe	Gly	Met	Ser	Phe	Ile	His	Phe	Ile
		515					520					525			
Gln	Gly	Ala	Val	Ile	Ser	Phe	Val	Asn	Ser	Thr	Ser	His	Phe	Trp	Leu
	530					535					540				
Glu	Pro	Leu	Thr	Asp	Thr	Lys	Val	Ala	Met	Leu	Asp	Asp	Ala	Thr	Thr
545				550						555					560
Thr	Cys	Trp	Thr	Tyr	Phe	Asp	Thr	Tyr	Met	Arg	Asn	Ala	Leu	Asp	Gly
			565						570					575	
Asn	Pro	Ile	Ser	Ile	Asp	Arg	Lys	His	Lys	Pro	Leu	Ile	Gln	Leu	Lys
			580					585					590		
Cys	Pro	Pro	Ile	Leu	Leu	Thr	Thr	Asn	Ile	His	Pro	Ala	Lys	Asp	Asn
		5													



Gly Thr Ser Lys Ser Tyr Val Arg Ser Leu  
740 745

<210> 33  
<211> 1362  
<212> DNA  
<213> artificial sequence

<220>  
<223> nucleotide sequence encoding a membrane-presented and  
replication-defective HPV-18 E2 polypeptide  
(degenerated to reduce homology with HPV-16  
E2-encoding sequence)

<400> 33  
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ttccctattc agacaccgaa ggaaaccctt tcggaacgat taagttgcgt gcaagataag 120  
atcatagacc actacgagaa cgacagtaaa gacatagaca gccaaataca gtactggcaa 180  
ctaatacgtt gggcaaatgc aatattcttt gcagcaaggg aacatggcat acagacatta 240  
aatcatcagg tagtcccagc ctataacatt tcgaaaagta aggcacataa agctgccgag 300  
ctccaaatgg ccctacaagg ccttgacaaa agtcgataca aaaccgagga ttggactctg 360  
caggacacat gcgaggaact atggaataca gaacctactc actgctttaa gaaaggtggc 420  
caaaccgtac aagtatatatt cgacggcaac aaagacaatt gtatgacctg ttagcatggg 480  
gacagtgtgt attatatgac tgatgcagga acatgggaca aaaccgctac ctgtgtaagt 540  
cacaggggat tgtactacgt aaaggagggg tacaacacgt tttatataga attcaaaagt 600  
gaatgtgaga agtatgggaa cacaggtacg tgggaggtac attttgggaa taatgtcatt 660  
gattgtaatg actctatgtg cagtaccagt gacgacacgg tctccgctac tcagcttgtt 720  
aaacagctac agcacacccc ctaccgatat tccagcaccg tgtccgtggg aaccgcaaag 780  
acctacggcc agacgtcggc tgctacacga cctggccact gtggactcgc ggagaagcag 840  
cattgtggac ctgtcaaccc acttctcggg gcagctacac ctacaggcaa caacaagaga 900  
cgaaaactct gcagtggtaa tacgacgcct ataatacact tgaagggaga cagaaacagt 960  
ttgaagtgtc tacggtacag gttgcgaaaa catagcgacc actatagaga tatatcatcc 1020  
acctggcact ggaccggtgc aggcaatgaa aaaacaggaa tactgactgt aacctaccat 1080  
agcgaaacac aaagaacaaa attcttaaat actgttgcaa ttccagatag tgtacaaata 1140  
ttggtgggat acatgacaat gtatgtatta ctgagtgcag gggccctgac tgccttgatg 1200  
ttgataattt tcctgatgac atgtttaga agagtcaatc gatcagaacc tacgcaacac 1260  
aatctcagag ggacagggag ggaggtgtca gtcactcccc aaagcgggaa gatcataatc 1320  
tcatgggaat cacacaagag tgggggtgag accagactgt ga 1362

<210> 34  
<211> 1062  
<212> DNA  
<213> artificial sequence

<220>  
<223> nucleotide sequence encoding a replication-defective  
HPV-33 E2 polypeptide (degenerated sequence)

<400> 34  
atggaggaaa tatcagcacg cttgaatgca gtccaagaga aaattctaga tctttacgaa 60  
gcagataaaa ctgatttacc atctcaaatt gaacactgga aattgatacg catggcctgc 120  
gctttattgt atacagccaa acagatgggc ttttcacatt tatgtcacca agtggtagct 180  
tctttgttag catccaaaac caaagcgttt caagtagcgg aactacagat ggcattagag 240  
acattaagta aatcacagta tagcacaagc caatggacgt tgcaacagac aagcttagag 300  
gtttggcttt gtgaaccacc aaaatgtttt aaaaagcaag gagaacagat aactgtgcaa 360  
tatgacaatg aaaaaaaaaa taccatggac tatactaact ggggtgaaat atacattata 420  
gaggaagata catgtactat gggtacaggg aaagtagatt atataggtat gtattacata 480  
cataactgtg aaaaggtata ctttaaatat ttttaaggagg atgctgccaa atactctaaa 540  
acacaaatgt gggaagtcca tgtaggtggc caggttattg tttgccctac gtctatatct 600

agcaatcaaa	tatccactac	tgagactgct	gacatacaga	cagacaacga	taaccgacca	660
ccacaagcag	cggccaaacg	acgacgacct	gcagacacta	ctgacaccgc	ccagcccctt	720
acaaagctgt	tctgtgcaga	ccccgccttg	gataatagaa	cagcacgtac	agcaactaac	780
tgacaaaata	agcagcggac	tgtgtgtagt	tctaacgttg	caccaatagt	gcatttgaaa	840
ggcgaatcaa	atagcttaaa	gtgtttgaga	tacagattaa	aaccttataa	agagttgtac	900
agttctatgt	cttcaacttg	gcaactggact	agtgacaaca	aaaatagtaa	aaatggcata	960
gtaaccgtga	catttgtaac	tgaacagcaa	caacaaatgt	tcttgggtac	cgtaaagata	1020
cctcctactg	tgacagataag	taccggattc	atgaccttat	aa		1062

&lt;210&gt; 35

&lt;211&gt; 1326

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

<223> nucleotide sequence encoding a membrane-presented and  
replication-defective HPV-33 E2 polypeptide (SS-33E2\*-TMR)  
(degenerated sequence)

&lt;400&gt; 35

atgggtaccgc	aagccctgct	attcgtacct	ttattgggtct	ttcccctctg	tttcggttaag	60
tttcctatag	aggaaatata	agcacgcttg	aatgcagtcc	aagagaaaat	tctagatcct	120
tacgaagcag	ataaaaactga	tttaccatct	caaattgaac	actggaaatt	gatacgcagt	180
gcctgcgctt	tattgtatac	agccaaacag	atgggctttt	cacatttatg	tcaccaagtg	240
gtaccttctt	tgttagcatc	caaaaccaa	gcgtttcaag	tagcggaaact	acagatggca	300
ttagagacat	taagtaaata	acagtatagc	acaagccaat	ggacgttgca	acagacaagc	360
ttagaggttt	ggctttgtga	accaccaaaa	tgttttaaaa	agcaaggaga	aacagtaact	420
gtgcaatatg	acaatgacaa	aaaaaatacc	atggactata	ctaactgggg	tgaaatatac	480
attatagagg	aagatacatg	tactatgggt	acagggaaag	tagattatat	aggtatgtat	540
tacatacata	actgtgaaaa	ggtatacttt	aaatatttta	aggaggatgc	tgccaaatac	600
tctaaaacac	aaatgtggga	agtccatgta	ggtggccagg	ttattgtttg	ccctacgtct	660
atatctagca	atcaaataatc	cactactgag	actgctgaca	tacagacaga	caacgataac	720
cgaccaccac	aagcagcggc	caaacgacga	cgacctgcag	acactactga	caccgcccag	780
ccccttacaa	agctgttctg	tgacagcccc	gccttggtata	atagaacagc	acgtacagca	840
actaactgca	caaataagca	gcggactgtg	tgtagtctta	acgttgccacc	aatagtgcac	900
ttgaaaggcg	aatcaaatag	cttaaagtgt	ttgagataca	gattaaaaac	ttataaagag	960
ttgtacagtt	ctatgtcttc	aacttggcac	tggactagtg	acaacaaaaa	tagtaaaaat	1020
ggcatagtaa	ccgtgacatt	tgttaactgaa	cagcaacaac	aaatgttctt	gggtaccgta	1080
aagataacct	ctactgtgca	gataagtacc	ggattcatga	ccttatacgt	actgctatcg	1140
gcaggcactg	tgatgcgact	aatgcttata	atcttcctaa	taacctgctg	caagcgggtt	1200
gataggcccc	aaagtaccca	aaggtccttg	agaggtaccg	gacgcaacgt	atcggtaacg	1260
tcgcaaagcg	gcaagttcat	tagcagttgg	gagtcgcaca	aatcaggtgg	agagaccgcg	1320
ctgtga						1326

&lt;210&gt; 36

&lt;211&gt; 1107

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

<223> nucleotide sequence encoding a HPV-52 replication-defective E2  
polypeptide ((52degE2\*)) (degenerated sequence)

&lt;400&gt; 36

atggaatcga	taccggcacg	gttaaacgct	gtgcaggaaa	agatactcga	tctatatgag	60
gctgacagca	atgatctaaa	cgcacaaatc	gagcattgga	agttgactcg	aatggcttgt	120
gttttgtttt	ataaagcaaa	ggaactggga	ataactcata	taggccatca	agtagtgcct	180
ccaatggcag	tgtctaaggc	aaaggcctgc	caagccgcag	agcttcaatt	ggctttggag	240
gcattgaaca	aaactcaata	cagtacagat	ggctggacct	tacagcaaac	aagtctagaa	300

atgtggcgtg	cagagccaca	aaaatacttc	aagaagcacg	ggtacacaat	aacagtccaa	360
tacgataatg	ataaaaacaa	cactatggat	tacacaaatt	ggaaggaaat	ttattttactt	420
ggtgagtgtg	aatgcacaat	tgtagaagga	caagtggatt	actatgggtt	atactatttg	480
tgtgatggag	aaaaaatcta	tttcgtaaaa	tttagtaacg	acgcaaagca	atattgtgta	540
acaggagtct	gggaggtgca	cgtgggcggt	caagtaatcg	tgtgtccagc	atcggtatca	600
agtaacgagg	tttctactac	agaaacagct	gtccacctat	gcaccgaaac	ctccaagacc	660
tccgcagtgt	ccgtgggtgc	caaagacaca	cacctacaac	caccacagaa	gcgacgtcga	720
ccagatgtca	cagattccag	aaacaccaag	taccccaaca	accttttgcg	gggacaacaa	780
tccgttgaca	gcactacacg	gggactcgta	actgccactg	agtgcactaa	taaaggctcg	840
gttgcacata	caacttgtac	tgctcctatt	attcacctaa	agggtgaccc	caacagcttg	900
aaatgcctaa	ggtatagggg	aaaaacacat	aaaagtttat	atgttcaa	ttcatctacg	960
tggcattgga	cgagtaatga	atgtacaaa	aataaactag	gtattgtaac	aataacgtac	1020
agtgatgaga	cacagcgtca	acagttttta	aaaactgtca	aaatcccaaa	taccgtccaa	1080
gttatacaag	gtgtcatgtc	attgttaa				1107

&lt;210&gt; 37

&lt;211&gt; 1374

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

<223> nucleotide sequence encoding a membrane-presented and  
 replication defective HPV-52 E2 polypeptide  
 SS-52degE2\*-TMF) (degenrated sequence)

&lt;400&gt; 37

atgggtctca	aggtgaacgt	ctctgccata	ttcatggcag	tactgttaac	tctccaaaca	60
cccaccggtc	aaatccattg	gggcgaatcg	ataccggcac	ggttaaacgc	tgtgcaggaa	120
aagatactcg	atctatatga	ggctgacagc	aatgatctaa	acgcacaaat	cgagcattgg	180
aagttgactc	gaatggcttg	tgttttgttt	tataaagcaa	aggaactggg	aataactcat	240
ataggccatc	aagtagtgcc	tccaatggca	gtgtctaagg	caaaggcctg	ccaagccgca	300
gagcttcaat	tggcttttga	ggcattgaac	aaaactcaat	acagtacaga	tggctggacc	360
ttacagcaaa	caagtctaga	aatgtggcgt	gcagagccac	aaaaatactt	caagaagcac	420
gggtacacaa	taacagtcca	atacgataat	gataaaaaca	acactatgga	ttacacaaat	480
tggaaggaaa	tttattttact	tggtagtgtg	gaatgcacaa	ttgtagaagg	acaagtggat	540
tactatgggt	tatactattg	gtgtgatgga	gaaaaaatct	atttcgtaaa	atttagtaac	600
gacgcaaagc	aatatttgtg	aacaggagtc	tgggaggtgc	acgtgggcgg	tcaagtaatc	660
gtgtgtccag	catcggtatc	aagtaacgag	gtttctacta	cagaaacagc	tgtccaccta	720
tgcaccgaaa	cctccaagac	ctccgcagtg	tccgtgggtg	caaagacac	acacctacaa	780
ccaccacaga	agcgacgtcg	accagatgtc	acagattcca	gaaacaccaa	gtaccccaac	840
aaccttttgc	ggggacaaca	atccgttgac	agcactacac	ggggactcgt	aactgccact	900
gagtgcacta	ataaagggtcg	ggttgacacat	acaacttgta	ctgctcctat	tattcaccta	960
aagggtgacc	ccaacagctt	gaaatgccta	aggtataggg	taaaaacaca	taaaagttta	1020
tatgttcaaa	tttcatctac	gtggcattgg	acgagtaatg	aatgtacaaa	taataaacta	1080
ggtattgtaa	caataacgta	cagtgtgag	acacagcgtc	aacagttttt	aaaaactgtc	1140
aaaatcccaa	ataccgtcca	agttatacaa	ggtgtcatgt	cattgggttt	atcgagcact	1200
agcatagtct	acatcctgat	tgcagtgtgt	cttgagggtg	tgatagggat	ccccgcttta	1260
atatgttgct	gcagggggcg	ttgtaacaaa	aagggagaac	aagttgggat	gtcaagacca	1320
ggcctaaagc	ctgatcttac	gggaacatca	aaatcctatg	taaggtcgct	ctga	1374

&lt;210&gt; 38

&lt;211&gt; 2241

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

<223> nucleotide sequence encoding a membrane-presented and  
 replication-defective HPV-18 E1 (SS-18E1\*-TMF) (degenerated  
 to decrease homology with E1-encoding HPV-16 nucleotide

sequence)

<400> 38

atgggtctca	aggatgaacgt	ctctgccata	ttcatggcag	tactgttaac	tctccaaaca	60
cccaccgggtc	aaatccattg	gggcgcagac	ccagaaggca	cagacggaga	aggcacgggt	120
tgcaacggct	ggttctacgt	acaagctatt	gtagacaaga	agaccggaga	tgtaatttct	180
gacgatgagg	acgagaatgc	aacagacaca	gggtcggata	tggttgactt	cattgataca	240
caaggaacat	tttgtgaaca	agccgagcta	gaaactgctc	aggcattgtt	ccatgcgcag	300
gaggtccaca	atgatgcaca	agtgttgcac	gtttttaaagc	ggaagtttgc	aggaggcagc	360
acagaaaaca	gtccattagg	ggagcggctg	gaggtggata	cagagttaag	cccacggtta	420
caagaaatat	ctttaaatat	tgggcagaaa	aaggctaaga	ggcggctgtt	tacaatatca	480
gatagtggct	acggctgttc	tgaggtggaa	gcaacacaga	ttcaggtaac	tacaaatggc	540
gaacatggcg	gcaatgtatg	cagtggcggc	agtacggagg	ctatagacaa	cggaggcaca	600
gagggcaaca	acagcagtgt	agacggtaca	agcgacaata	gcaatataga	aaatgtaaat	660
ccacaatgta	ccatagcaca	attaaaagac	ttgtttaaag	taaacaataa	acaaggagct	720
atgcttgacg	tattcaagga	cacatatggg	ctatcattta	cagatttagt	tagaaatttc	780
aagagtgaca	aaaccacatg	tacagactgg	gttacagcta	tattcggagt	aaaccaaca	840
atcgacagaag	gatttaagac	tctaatacag	ccattttatat	tgtatgcca	tatacaatgt	900
ctagactgta	agtggggtgt	attaatatta	gccctgttgc	gttacaagtg	cggtaagagt	960
agactaacag	ttgctaaagg	tttaagtacg	ttgttacacg	tacctgaaac	ttgcatgtta	1020
attcaaccac	ctaagttacg	aagtagtggt	gctgcactat	actggtacag	aactggaatt	1080
tctaacataa	gcgaggtaat	gggtgacaca	cctgagtggg	ttcagagact	tactattata	1140
cagcatggaa	tagacgatag	caatttcgat	ttgtcagaaa	tggttcagtg	ggcatttgac	1200
aacgagctga	cagatgaaag	cgatatggca	tttgaatacg	ccttatttagc	tgacagcaac	1260
agcaacgcag	ctgcattttt	aaagagcaat	tgccaagcta	aatattttaaa	agactgtgcc	1320
actatgtgca	aacactatag	gcgtgcccag	aaacgacaga	tgaatatgtc	acagtggatt	1380
cgatttaggt	gttcaaaaat	agacgaaggg	ggagactgga	gaccaatagt	gcaattcctg	1440
cgataccaac	aaatagaatt	cataacattc	ttaggagcct	tgaaatcatt	cttaaaaagga	1500
acccccaaga	agaactgttt	agtattttgt	ggaccagcaa	atactgacaa	gtcatatttc	1560
ggaatgagct	ttatacactt	tatacaagga	gcagttatat	cattcgtgaa	ctccactagt	1620
cacttctggc	tggaaccgtt	aacagacact	aagggtggcca	tgctagacga	cgcaacgacc	1680
acgtgctgga	catactttga	tacctatatg	aggaacgcgt	tagacggcaa	tccaataagt	1740
attgatagaa	aacacaaacc	tttaatacag	cttaagtgtc	cgccaatact	actaaccaca	1800
aatatacatc	cagcaaagga	taatagatgg	ccatacttag	aaagtagaat	aacagtattt	1860
gaattcccaa	atgcattccc	gttcgataaa	aatggcaacc	ctgtatacga	aataaacgac	1920
aaaaattgga	agtgtttcct	tgaaagaaca	tggtcaaggt	tagattttaca	tgaagaagaa	1980
gaagatgctg	atacagaggg	taatccattt	ggtactttca	aattacgagc	tggaacagaat	2040
cacaggcctc	ttggttttatc	gagcactagc	atagtctaca	tcctgattgc	agtgtgtcct	2100
ggagggttga	tagggatccc	cgctttaaata	tgttgctgca	gggggcgttg	taacaaaaag	2160
ggagaacaag	ttgggtatgtc	aagaccaggc	ctaaagcctg	atcttacggg	aacatcaaaa	2220
tcctatgtaa	ggtcgctctg	a				2241

<210> 39

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> primer oTG15315 for reconstituting sequence encoding HPV-18  
SS-6E1\*deg-TMF

<400> 39

ggggagatct atgggtctca aggtgaacgt ctc

33

<210> 40

<211> 39

<212> DNA

<213> artificial sequence

<220>  
 <223> primer oTG17881 for reconstituting sequence encoding HPV-18  
 SS-E1\*deg-TMF  
  
 <400> 40  
 gtgccttctg ggtctgcgcc ccaatggatt tgaccggtg 39  
  
 <210> 41  
 <211> 37  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG17882 for reconstituting sequence encoding HPV-18  
 SS-E1\*deg-TMF  
  
 <400> 41  
 ggtcaaatcc attggggcgc agaccagaa ggcacag 37  
  
 <210> 42  
 <211> 42  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG17883 for reconstituting sequence encoding HPV-18  
 SS-E1\*deg-TMF  
  
 <400> 42  
 cagaatcaca ggcctcttgg tttatcgagc actagcatag tc 42  
  
 <210> 43  
 <211> 39  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG17884 for reconstituting sequence encoding HPV-18  
 SS-E1\*deg-TMF  
  
 <400> 43  
 gctagtgtc gataaaccaa gaggcctgtg attctgtcc 39  
  
 <210> 44  
 <211> 32  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG17885 for reconstituting sequence encoding HPV-18  
 SS-E1\*deg-TMF  
  
 <400> 44  
 gggggcggcc gctcagagcg accttacata gg 32  
  
 <210> 45

<211> 31  
 <212> DNA  
 <213> artificial sequence

<220>

<223> sense primer oTG17875 for reconstituting sequence encoding  
 HPV-18 SS-E2\*deg-TMR

<400> 45

ggggagatct atggttcctc aggctctcct g

31

<210> 46

<211> 39

<212> DNA

<213> artificial sequence

<220>

<223> sense primer oTG17876 for reconstituting sequence encoding  
 HPV-18 SS-E2\*deg-TMR

<400> 46

gttttgggaa attccctatt cagacaccga aggaaaccc

39

<210> 47

<211> 43

<212> DNA

<213> artificial sequence

<220>

<223> antisense primer oTG17877 for reconstituting sequence  
 encoding HPV-18 SS-E2\*deg-TMR

<400> 47

gtttccttcg gtgtctgaat agggaatttc ccaaaacaca atg

43

<210> 48

<211> 39

<212> DNA

<213> artificial sequence

<220>

<223> sense primer oTG17878 for reconstituting sequence encoding  
 HPV-18 SS-E2\*deg-TMR

<400> 48

gtgggataca tgacaatgta tgtattactg agtgcaggg

39

<210> 49

<211> 38

<212> DNA

<213> artificial sequence

<220>

<223> antisense primer oTG17879 for reconstituting sequence  
 encoding HPV-18 SS-E2\*deg-TMR

<400> 49

ctgcactcag taatacatac attgtcatgt atcccacc 38

<210> 50

<211> 29

<212> DNA

<213> artificial sequence

<220>

<223> antisense primer oTG17880 for reconstituting sequence  
encoding HPV-18 SS-E2\*deg-TMR

<400> 50

gggggcggcc gctcacagtc tggctcac 29

<210> 51

<211> 36

<212> DNA

<213> artificial sequence

<220>

<223> primer oTG18962 for reconstituting sequence encoding  
SS-33E2\*-TMR

<400> 51

cccaaaggat ccaccatggt accgcaagcc ctgcta 36

<210> 52

<211> 52

<212> DNA

<213> artificial sequence

<220>

<223> primer oTG18963 for reconstituting sequence encoding  
SS-33E2\*-TMR

<400> 52

ttcccctctg ttccggtaag tttcctatag aggaaatc agcacgcttg aa 52

<210> 53

<211> 52

<212> DNA

<213> artificial sequence

<220>

<223> primer oTG18964 for reconstituting sequence encoding  
SS-33E2\*-TMR

<400> 53

ttcaagcgtg ctgatatttc ctctatagga aacttaccga aacagagggg aa 52

<210> 54

<211> 49

<212> DNA

<213> artificial sequence

<220>

<223> primer oTG18965 for reconstituting sequence encoding  
SS-33E2\*-TMR

<400> 54  
gataagtacc ggattcatga ccttatacgt actgctatcg gcaggcacg 49

<210> 55  
<211> 49  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer oTG18966 for reconstituting sequence encoding  
SS-33E2\*-TMR

<400> 55  
cgtgcctgcc gatagcagta cgtataaggt catgaatccg gtacttatac 49

<210> 56  
<211> 56  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer oTG18967 for reconstituting sequence encoding  
SS-33E2\*-TMR

<400> 56  
aaaaccccgcc atgcgcgggcc gcaagctatc acaggcgggt ctctccacct gatttg 56

<210> 57  
<211> 37  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer oTG18968 for reconstituting sequence encoding  
SS-52E2\*-TMF

<400> 57  
aaacccgaga tctacatgg gtctcaaggt gaacgtc 37

<210> 58  
<211> 46  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer oTG18969 for reconstituting sequence encoding  
SS-52E2\*-TMF

<400> 58  
cccaccggtc aaatccattg gggcgaatcg ataccggcac ggttaa 46

<210> 59  
<211> 46



<212> DNA  
 <213> artificial sequence

<220>

<223> primer oTG18970 for reconstituting sequence encoding  
 SS-52E2\*-TMF

<400> 59

ttaaccgtgc cggtatcgat tcgcccgaat ggatttgacc ggtggg

46

<210> 60

<211> 43

<212> DNA

<213> artificial sequence

<220>

<223> primer oTG18971 for reconstituting sequence encoding  
 SS-52E2\*-TMF

<400> 60

gttatacaag gtgtcatgtc attgggttta tcgagcacta gca

43

<210> 61

<211> 43

<212> DNA

<213> artificial sequence

<220>

<223> primer oTG18972 for reconstituting sequence encoding  
 SS-52E2\*-TMF

<400> 61

tgctagtgtc cgataaacc aatgacatga caccttgat aac

43

<210> 62

<211> 53

<212> DNA

<213> artificial sequence

<220>

<223> primer oTG18973 for reconstituting sequence encoding  
 SS-52E2\*-TMF

<400> 62

aagcttgcta gccaccggtg gggccgcggc cgctcagagc gaccttacat agg

53