

## SEQUENCE LISTING

<110> TRANSGENE S.A.  
SILVESTRE Nathalie  
SCHMITT Doris

<120> Vectors for multiple gene expression

<130> TG183 EXT

<150> EP07360019.9

<151> 2007-05-15

<160> 83

<170> PatentIn version 3.3

<210> 1

<211> 649

<212> PRT

<213> Human papillomavirus type 16

<400> 1

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

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      290              295              300
Met Met Ile Glu Pro Pro Lys Leu Arg Ser Thr Ala Ala Ala Leu Tyr
305              310              315              320
Trp Tyr Lys Thr Gly Ile Ser Asn Ile Ser Glu Val Tyr Gly Asp Thr
      325              330              335
Pro Glu Trp Ile Gln Arg Gln Thr Val Leu Gln His Ser Phe Asn Asp
      340              345              350
Cys Thr Phe Glu Leu Ser Gln Met Val Gln Trp Ala Tyr Asp Asn Asp
      355              360              365
Ile Val Asp Asp Ser Glu Ile Ala Tyr Lys Tyr Ala Gln Leu Ala Asp
      370              375              380
Thr Asn Ser Asn Ala Ser Ala Phe Leu Lys Ser Asn Ser Gln Ala Lys
385              390              395              400
Ile Val Lys Asp Cys Ala Thr Met Cys Arg His Tyr Lys Arg Ala Glu
      405              410              415
Lys Lys Gln Met Ser Met Ser Gln Trp Ile Lys Tyr Arg Cys Asp Arg
      420              425              430
Val Asp Asp Gly Gly Asp Trp Lys Gln Ile Val Met Phe Leu Arg Tyr
      435              440              445
Gln Gly Val Glu Phe Met Ser Phe Leu Thr Ala Leu Lys Arg Phe Leu
      450              455              460
Gln Gly Ile Pro Lys Lys Asn Cys Ile Leu Leu Tyr Gly Ala Ala Asn
465              470              475              480
Thr Gly Lys Ser Leu Phe Gly Met Ser Leu Met Lys Phe Leu Gln Gly
      485              490              495
Ser Val Ile Cys Phe Val Asn Ser Lys Ser His Phe Trp Leu Gln Pro
      500              505              510
Leu Ala Asp Ala Lys Ile Gly Met Leu Asp Asp Ala Thr Val Pro Cys
      515              520              525
Trp Asn Tyr Ile Asp Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Leu
      530              535              540
Val Ser Met Asp Val Lys His Arg Pro Leu Val Gln Leu Lys Cys Pro
545              550              555              560
Pro Leu Leu Ile Thr Ser Asn Ile Asn Ala Gly Thr Asp Ser Arg Trp
      565              570              575
Pro Tyr Leu His Asn Arg Leu Val Val Phe Thr Phe Pro Asn Glu Phe
      580              585              590
Pro Phe Asp Glu Asn Gly Asn Pro Val Tyr Glu Leu Asn Asp Lys Asn
      595              600              605
Trp Lys Ser Phe Phe Ser Arg Thr Trp Ser Arg Leu Ser Leu His Glu
      610              615              620
Asp Glu Asp Lys Glu Asn Asp Gly Asp Ser Leu Pro Thr Phe Lys Cys
625              630              635              640
Val Ser Gly Gln Asn Thr Asn Thr Leu
      645

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<210> 2

<211> 365

<212> PRT

<213> Human papillomavirus type 16

<400> 2

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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

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Ser Lys Asn Lys Ala Leu Gln Ala Ile Glu Leu Gln Leu Thr Leu Glu
65      70      75
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
      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> 3

<211> 158

<212> PRT

<213> Human papillomavirus type 16

<400> 3

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Met His Gln Lys Arg Thr Ala Met Phe Gln Asp Pro Gln Glu Arg Pro
1      5      10      15
Arg Lys Leu Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp
      20      25      30
Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu
      35      40      45
Val Tyr Asp Phe Ala Phe Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly
      50      55      60
Asn Pro Tyr Ala Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile
65      70      75      80
Ser Glu Tyr Arg His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu
      85      90      95
Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn
      100      105      110
Cys Gln Lys Pro Leu Cys Pro Glu Glu Lys Gln Arg His Leu Asp Lys

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      115              120              125
Lys Gln Arg Phe His Asn Ile Arg Gly Arg Trp Thr Gly Arg Cys Met
  130              135              140
Ser Cys Cys Arg Ser Ser Arg Thr Arg Arg Glu Thr Gln Leu
  145              150              155

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<210> 4
<211> 98
<212> PRT
<213> Human papillomavirus type 16

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<400> 4
Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
 1      5      10      15
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
      20      25      30
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
 35      40      45
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
 50      55      60
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
 65      70      75      80
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
      85      90      95
Lys Pro

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<210> 5
<211> 737
<212> PRT
<213> artificial sequence

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<220>
<223> HPV-16 membrane-presented and replication-defective E1
      polypeptide

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<400> 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 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

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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				
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															

<210> 6

<211> 746

<212> PRT

<213> artificial sequence

<220>

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

<400> 6

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
				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				

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Trp Gly Val Leu Ile Leu Ala Leu Leu Arg Tyr Lys Cys Gly Lys Ser
305          310
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
          595          600          605
Arg Trp Pro Tyr Leu Glu Ser Arg Ile Thr Val Phe Glu Phe Pro Asn
          610          615          620
Ala Phe Pro Phe Asp Lys Asn Gly Asn Pro Val Tyr Glu Ile Asn Asp
625          630          635          640
Lys Asn Trp Lys Cys Phe Phe Glu Arg Thr Trp Ser Arg Leu Asp Leu
          645          650          655
His Glu Glu Glu Glu Asp Ala Asp Thr Glu Gly Asn Pro Phe Gly Thr
          660          665          670
Phe Lys Leu Arg Ala Gly Gln Asn His Arg Pro Leu Gly Leu Ser Ser
          675          680          685
Thr Ser Ile Val Tyr Ile Leu Ile Ala Val Cys Leu Gly Gly Leu Ile
          690          695          700
Gly Ile Pro Ala Leu Ile Cys Cys Cys Arg Gly Arg Cys Asn Lys Lys
705          710          715          720
Gly Glu Gln Val Gly Met Ser Arg Pro Gly Leu Lys Pro Asp Leu Thr
          725          730          735
Gly Thr Ser Lys Ser Tyr Val Arg Ser Leu
          740          745

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&lt;210&gt; 7

&lt;211&gt; 453

&lt;212&gt; PRT

<213> artificial sequence

<220>

<223> HPV-16 membrane-anchored and replication-defective E2 polypeptide

<400> 7

Met	Val	Pro	Leu	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	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 His Ser Trp Glu Ser Tyr Lys Ser Gly  
 435 440 445  
 Gly Glu Thr Gly Leu  
 450

<210> 8

<211> 453

<212> PRT

<213> artificial sequence

<220>

<223> HPV-18 membrane-anchored and replication-defective E2  
 polypeptide

<400> 8

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 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> 9  
 <211> 59  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> portion of 59 nucleotides of HPV-16 E1-encoding sequences  
 degenerated to decrease homology with the overlapping  
 portion in HPV-16 E2-encoding sequences

<400> 9  
 atggtgattc attacctaca ttcaagtgcg tatctgggtca gaacacaaat actttgtga 59

<210> 10  
 <211> 2214  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> Nucleotide sequence encoding a membrane-anchored and  
 replication-defective HPV-16 E1 polypeptide degenerated  
 in the 59 nucleotides portion overlapping with the native  
 HPV-16 E2-encoding sequence.

<400> 10  
 atggtaccgc aagccctgct attcgtacct ttattgggtct ttccctctctg tttcggtaag 60  
 tttcctatag ctgatoctgc aggtaccaat ggggaagagg gtacgggatg taatggatgg 120  
 ttttatgtag aggctgtagt ggaaaaaaaa acaggggatg ctatatcaga tgacgagaac 180  
 gaaaatgaca gtgatacagg tgaagatttg gtagatttta tagtaaataa taatgattat 240  
 ttaacacagg cagaaacaga gacagacat gcgttggtta ctgcacagga agcaaaacaa 300  
 catagagatg cagtacaggt tctaaaacga aagtatttgg gtagtccact tagtgatatt 360  
 agtggatgtg tagacaataa tattagtcct agattaaaag ctatatgtat agaaaaacaa 420  
 agtagagctg caaaaaggag attatttgaa agcgaagaca gcgggatg caatactgaa 480  
 gtggaaatc agcagatggt acaggtagaa gggcgccatg agactgaaac accatgtagt 540  
 cagtatatgt gtggaagtgg ggggtggtgc agtcagtaca gtagtggaag tgggggagag 600  
 ggtgttagtg aaagacacac tatatgcaa acaccactta caaatatttt 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 tgttcattgg gaatgggtgt gttactatta 900  
 gtaagatata aatgtggaaa aaatagagaa acaattgaaa aattgctgtc taaactatta 960  
 tgtgtgtctc caatgtgtat gatgatagag cctccaaaat tgcgtagtac agcagcagca 1020  
 ttatattggt ataaaacagg tatatcaaat attagtgaag tgtatggaga cacgccagaa 1080  
 tggatacaaa gacaaacagt attacaacat agttttaatg attgtacatt tgaattatca 1140  
 cagatggtac aatgggccta cgataatgac atagtagacg atagtgaat tgcatataaa 1200

tatgcacaat	tggcagacac	taatagtaat	gcaagtgccct	ttctaaaaag	taattcacag	1260
gcaaaaattg	taaaggattg	tgcaacaatg	tgtagacatt	ataaacgagc	agaaaaaaaa	1320
caaatgagta	tgagtcaatg	gataaaatat	agatgtgata	gggtagatga	tggagggtgat	1380
tggaagcaaa	ttgttatggt	tttaaggtat	caaggtgtag	agtttatgtc	atttttaact	1440
gcattaaaaa	gatttttgca	aggcatacct	aaaaaaaaatt	gcatattact	atatgggtgca	1500
gctaacacag	ataaatcatt	atltggatatg	agtttaatga	aattttctgca	agggtctgta	1560
atatgttttg	taaattctaa	aagccatttt	tggttacaac	cattagcaga	tgccaaaata	1620
ggatatgttag	atgatgctac	agtgccctgt	tggaaactata	tagatgacaa	tttaagaaat	1680
gcattggatg	gaaatttagt	ttctatggat	gtaaagcata	gaccattggg	acaactaaaa	1740
tgccctccat	tattaattac	atctaacatt	aatgctggta	cagattctag	gtggccttat	1800
ttacataata	gattgggtgg	gtttacattt	cctaattgag	ttccatttga	cgaaaacgga	1860
aatccagtg	atgagcttaa	tgataagaac	tggaaatcct	ttttctcaag	gacgtggtcc	1920
agattaagtt	tgacagagga	cgaggacaag	gaaaacgatg	gtgattcatt	acctacattc	1980
aagtgcgtat	ctggtcagaa	cacaaatact	ttgtacgtac	tgctatcggc	aggcacgttg	2040
atcgactaa	tgcttatcat	cttcctaata	acctgctgca	agcgggttga	taggcccgaa	2100
agtacccaaa	ggtccttgag	aggtaccgga	cgcaacgtat	cggtaacgtc	gcaaagcggc	2160
aagttcatta	gcagttggga	gtcgcacaaa	tcaggtggag	agacccgcct	gtga	2214

&lt;210&gt; 11

&lt;211&gt; 2241

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

<223> nucleotide sequence encoding a membrane-anchored and  
 replication-defective HPV-18 E1 polypeptide degenerated to  
 decrease homology with E1-encoding HPV-16 sequence

&lt;400&gt; 11

atgggtctca	agggtgaacgt	ctctgccata	ttcatggcag	tactgttaac	tctccaaaca	60
cccaccggtc	aaatccattg	ggg'gcgagac	ccagaaggca	cagacggaga	aggcacgggt	120
tgcaacggct	ggttctacgt	acaagctatt	gtagacaaga	agaccggaga	tgtaatttct	180
gacgatgagg	acgagaatgc	aacagacaca	gggtcggata	tggttgactt	cattgataca	240
caaggaacat	tttgtgaaca	agccgagcta	gaaactgctc	aggcattggt	ccatgcgcag	300
gaggtccaca	atgatgcaca	agtgttgcat	gttttaaaag	ggaagtttgc	aggaggcagc	360
acagaaaaca	gtccattagg	ggagcggctg	gaggtggata	cagagttaag	cccacggtta	420
caagaaatat	ctttaaatat	tgggcagaaa	aaggctaaga	ggcggctggt	tacaatatca	480
gatagtggct	acggctgttc	tgaggtggaa	gcaacacaga	ttcaggtaac	tacaaatggc	540
gaacatggcg	gcaatgtatg	cagtggcggc	agtacggagg	ctatagacaa	cggaggcaca	600
gagggcaaca	acagcagtg	agacggtaca	agcgacaata	gcaatataga	aaatgtaaat	660
ccacaatgta	ccatagcaca	attaaaagac	ttgttaaaaag	taaaacaataa	acaaggagct	720
atgcttgacg	tattcaagga	cacatatggg	ctatcattta	cagatttagt	tagaaatttc	780
aagagtgaca	aaaccacatg	tacagactgg	gttacagcta	tattcggagt	aaacccaaca	840
atcgacaga	gatttaagac	tctaatacag	ccattttatat	tgtatgcca	tatacaatgt	900
ctagactgta	agtgggggtg	attaatatta	gccctgttgc	gttacaagtg	cggttaagagt	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
agcaacgcga	ctgcattttt	aaagagcaat	tgccaagcta	aataatttaa	agactgtgcc	1320
actatgtgca	aacactatag	gcgtgccag	aaacgacaga	tgaatatgtc	acagtggatt	1380
cgatttaggt	gttcaaaaat	agacgaagg	ggagactgga	gaccaatagt	gcaattcctg	1440
cgataccaac	aaatagaatt	cataacattc	ttaggagcct	tgaaatcatt	cttaaaagga	1500
acccccaaga	agaactgttt	agtattttgt	ggaccagcaa	atactgacaa	gtcatatttc	1560
ggaatgagct	ttatacactt	tatacaagga	gcagttatat	cattcgtgaa	ctccactagt	1620
cacttctggc	tggaaaccgt	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 agtgttttctt tgaaagaaca tgggtcaaggt tagattttaca tgaagaagaa 1980
gaagatgctg atacagaggg taatccattt ggtactttca aattacgagc tggacagaat 2040
cacaggcctc ttggtttatc gagcactagc atagtctaca tcctgattgc agtgtgtctt 2100
ggaggggttg tagggatccc cgctttaata tgttgctgca gggggcggtg taacaaaaaag 2160
ggagaacaag ttggtatgtc aagaccaggc ctaaagcctg atcttacggg aacatcaaaa 2220
tcctatgtaa ggtcgctctg a 2241

```

<210> 12

<211> 1362

<212> DNA

<213> artificial sequence

<220>

<223> nucleotide sequence encoding a membrane-anchored and replication-defective HPV-16 E2 polypeptide

<400> 12

```

atggtaccac aagcgtgtgt acttgtccca ctgcttggtt tctctttatg ttttgaaaa 60
ttcccaatag agactctttg ccaacgttta aatgtgtgtc aggacaaaat actaacacat 120
tatgaaaatg atagtacaga cctacgtgac catatagact attggaaaca catgcgccta 180
gcatgtgcta tttattacaa ggccagagaa atgggattta aacatattaa ccaccagggtg 240
gtgccaacgc tggctgtatc aaagaataaa gcattacaag cagctgaact gcaactaacg 300
ttagaaacaa tatataactc acaatatagt aatgaaaagt ggacattaca agacgttagc 360
cttgaagtgt atttaactgc accaacagga tgtataaaaa aacatggata tacagtggaa 420
gtgcagtttg atggagacat atgcaatata atgcattata caaactggac acatatatat 480
atttgtgaag aagcatcagt aactgtggta gaggggtcaag ttgactatta tggttttatat 540
tatgttcagt aaggaatacg aacatatttt gtgcagttta aagatgatgc agaaaaatat 600
agtaaaaata aagtatggga agttcatgcg ggtggtcagg taatattatg tcctacatct 660
gtgttttagc gcaacgaagt atcctctcct gaaattatta ggcagcaact ggccaaccac 720
cccgccgcga cccataccaa agccgtcgcc ttgggcaccg aagaaacaca gacgactatc 780
cagcgaccaa gatcagagcc agacaccgga aaccctgcc acaccactaa gttgttgac 840
agagactcag tggacagtgc tccaatcctc actgcattta acagctcaca caaaggacgg 900
attaactgta atagtaacac tacaccata gtacatttaa aaggatgatgc taatacttta 960
aaatgtttta gatatagatt taaaaagcat tgtacattgt atactgcagt gtcgtctaca 1020
tggcattgga caggacataa tgtaaaacat aaaagtgcaa ttgttacact tacatatgat 1080
agtgaatggc aacgtgacca atttttgtct caagttaaaa taccaaaaac tattacagt 1140
tctactggat ttatgtctat atatgttctt ctctctgctg gaactttaat agctttaatg 1200
ttaataatat tcttaataac gtgctgtaaa agggtagacc gtccagagtc aactcagcgc 1260
agccttaggg gtactgggag aaatgtttcc gtgacatcac agagtggaaa atttatctcg 1320
tcttgggaat ctcataagag tggaggcgaa acacgtcttt ga 1362

```

<210> 13

<211> 1362

<212> DNA

<213> artificial sequence

<220>

<223> nucleotide sequence encoding a membrane-anchored and replication-defective HPV-18 E2 polypeptide degeneratde to reduce homology with native HPV-16 E2-encoding sequence

<400> 13

```

atggttccctc aggtctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggaaa 60
ttccctattc agacaccgaa ggaaccctt tcggaacgat taagttgcgt gcaagataag 120
atcatagacc actacgagaa cgacagtaaa gacatagaca gccaaatata gtactggcaa 180
ctaatacgtt gggcaaattg aatattcttt gcagcaaggg aacatggcat acagacatta 240
aatcatcagg tagtcccagc ctataacatt tcgaaaagta aggcacataa agctgccgag 300
ctccaaatgg ccctacaagg ccttgcaaaa agtcgatata aaaccgagga ttggactctg 360

```

```

caggacacat gcgaggaact atggaataca gaacctactc actgctttaa gaaaggtggc 420
caaaccgtac aagtatatatt cgacggcaac aaagacaatt gtatgacctg tgtagcatgg 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 tcagcttggt 720
aaacagctac agcacacccc ctcaccgtat tccagcaccg tgtccgtggg aaccgcaaag 780
acctacggcc agacgtcggc tgctacacga cctggccact gtggactcgc ggagaagcag 840
cattgtggac ctgtcaaccc acttctcgtg 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
ttgggtggat acatgacaat gtatgtatta ctgagtgcag gggccctgac tgccttgatg 1200
ttgataattt tcctgatgac atgttgtaga agagtcaatc gatcagaacc tacgcaacac 1260
aatctcagag ggacagggag ggaggtgtca gtcactcccc aaagcgggaa gatcatatct 1320
tcatgggaat cacacaagag tgggggtgag accagactgt ga 1362

```

<210> 14

<211> 741

<212> DNA

<213> artificial sequence

<220>

<223> Nucleotide sequence encoding a membrane-anchored and non-oncogenic HPV-18 E6 polypeptide degenerated to reduce homology with the native HPV-16 E6-encoding sequence

<400> 14

```

atggtaccgc aagccotgct attcgtacct ttatttgtct ttcccctctg tttcggtaag 60
tttcttatag gatctatggc gcgctttgag gatccaacac ggcgacccta caagctacct 120
gatctgtgca cggaactgaa cacttcactg caagacatag aaataacctg tgtatattgt 180
aagacagtat tggaacttac agaggtattt gaatttgcac ttaaagacct atttgtgggtg 240
tatcgtgaca gtatacccca tgccgcatgc cataagtgtg tagattttta ctctagaatc 300
agagaattaa ggcactattc agactctgtg tacggagaca cattggaaaa actaactaac 360
actgggttat acaatttatt aataagatgc ctgcggtgcc agaaaccgtt gcttagacac 420
cttaatgaaa aacgacgatt tcacaacata gctgggcact atagaggcca gtgccattcg 480
tgctgcaacc gagcacgaca ggaacgactc caacgacgca gggagacaca agtaagatcc 540
tacgtactgc tatcggcagg cacgttgatc gcactaatgc ttatcatctt cctaataacc 600
tgctgcaagc gggttgatag gccgaaagt acccaaagg ccttgagagg taccggacgc 660
aacgtatcgg taacgtcgca aagcggcaag ttcattagca gttgggagtc gcacaaatca 720
ggtggagaga cccgcctgtg a 741

```

<210> 15

<211> 585

<212> DNA

<213> artificial sequence

<220>

<223> Nucleotide sequence encoding a membrane-anchored and non-oncogenic HPV-18 E7 polypeptide degenerated to reduce homology with the native HPV-16 E7-encoding sequence

<400> 15

```

atgggtctca aggtgaacgt ctctgccata ttcattggcag tactgttaac tctccaaaca 60
cccaccggtc aaatccattg gggcagatct atgcacggac ctaaggcaac actgcaagac 120
attgtattgc atttagagcc ccaaaatgaa attccggttg cacagttaag cgactcagag 180
gaagaaaacg acgagattga cggagttaat catcaacatt taccagcccg acgagctgaa 240
ccacaacgtc acacaatggt gtgtatgtgc tgtaaattgcg aagccagaat tgagctggta 300

```

```

gtagagagct cagcagacga ccttcgagca ttccagcagc tatttctgaa caccctgtcc 360
tttgtctgtc cgtggtgtgc atcccagcag ggatctggtt tatcgagcac tagcatagtc 420
tacatcctga ttgcagtgtg tcttgaggag ttgataggga tccccgcttt aatatgttgc 480
tgcagggggc gttgtaacaa aaaggagaa caagttggtg tgtcaagacc aggcctaaag 540
cctgatctta cgggaaacatc aaaatcctat gtaaggtcgc tctga 585

```

<210> 16

<211> 34

<212> DNA

<213> artificial sequence

<220>

<223> sense primer to amplify HPV-16 E2 sequence from CaSki cells

<400> 16

```
aaacccggat ccatggagac tctttgcaa cgtt 34
```

<210> 17

<211> 49

<212> DNA

<213> artificial sequence

<220>

<223> antisense primer to isolate HPV-16 E2 sequence from caSki cells

<400> 17

```
aaacccgaat tcaagcttag atcttcatat agacataaat ccagtagac 49
```

<210> 18

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> primer for reassembling HPV16 SS-E2muté-TMR sequence

<400> 18

```
aaacccggat ccatggtacc acaagcgctg tta 33
```

<210> 19

<211> 53

<212> DNA

<213> artificial sequence

<220>

<223> primer for reassembling HPV-16 SS-E2muté-TMR sequence

<400> 19

```
tctctttatg ttttgaaaa ttccaatag agactctttg ccaacgttta aat 53
```

<210> 20

<211> 53

<212> DNA

<213> artificial sequence

<220>  
 <223> primer for reassembling HPV-16 SS-E2muté-TMR sequence  
  
 <400> 20  
 atttaaactg tggcaaagag tctctattgg gaattttcca aaacataaag aga 53  
  
 <210> 21  
 <211> 49  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer for reassembling HPV-16 SS-E2muté-TMR sequence  
  
 <400> 21  
 cagtgtctac tggatttatg tctatatatg ttcttctctc tgctggaac 49  
  
 <210> 22  
 <211> 49  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer for reassembling HPV-16 SS-E2muté-TMR sequence  
  
 <400> 22  
 gttccagcag agagaagaac atatataagac ataaatccag tagacactg 49  
  
 <210> 23  
 <211> 44  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer for reassembling HPV-16 SS-E2muté-TMR sequence  
  
 <400> 23  
 aaaccagat cttcaaagac gtgtttcgcc tccactctta tgag 44  
  
 <210> 24  
 <211> 34  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer for isolating HPV-16 E1 sequence from CaSki cells  
  
 <400> 24  
 aaaccgcat ccatggctga tcctgcaggt acca 34  
  
 <210> 25  
 <211> 34  
 <212> DNA  
 <213> artificial sequence  
  
 <220>

<223> primer for isolating HPV-16 E1 sequence from CaSki cells

<400> 25  
aaacccgaat tccattatcg taggccatt gtac 34

<210> 26  
<211> 32  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer for isolating HPV-16 E1 sequence from CaSki cells

<400> 26  
aaacccgat ccgagacacg ccagaatgga ta 32

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

<220>  
<223> primer for isolating HPV-16 E1 sequence from CaSki cells

<400> 27  
aaacccgaat tcaagcttag atcttcataa tgtgttagta tttgtcctg 50

<210> 28  
<211> 88  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer for generating E1 degenerated sequence

<400> 28  
aaaccagat cttcacaaag ttttgtgtt ctgaccagat acgcacttga atgtaggtaa 60  
tgaatcacca tcgttttcct tgcctcg 88

<210> 29  
<211> 21  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer for generating degenerated HPV-16 E1 sequence

<400> 29  
gatgctacag tgccctgttg g 21

<210> 30  
<211> 35  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer for reconstituting sequence encoding



## HPV-16 SS-E1\*deg-TMR

<400> 30  
aaaccaagg atccatggta ccgcaagccc tgcta 35

<210> 31  
<211> 52  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer for reconstituting sequence encoding  
HPV-16 SS-E1\*deg-TMR

<400> 31  
ttcccctctg ttctggtaag ttctctatag ctgacctgc aggtaccaat gg 52

<210> 32  
<211> 52  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer for reconstituting sequence encoding  
HPV-16 SS-E1\*deg-TMR

<400> 32  
ccattggtac ctgcaggatc agctatagga aacttaccga aacagagggg aa 52

<210> 33  
<211> 50  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer oTG17563 for reconstituting sequence encoding  
HPV-16 SS-E1

<400> 33  
tatctgtgta gaacacaaat actttgtacg tactgctatc ggcaggcacg 50

<210> 34  
<211> 50  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer oTG17564 for reconstituting sequence encoding  
HPV-16 SS-E1\*deg-TMR

<400> 34  
cgtgcctgcc gatagcagta cgtacaaagt atttgtgttc tgaccagata 50

<210> 35  
<211> 42  
<212> DNA  
<213> artificial sequence

<220>  
 <223> primer oTG17565 for reconstituting sequence encoding  
         SS-E1\*deg-TMR  
  
 <400> 35  
 aaacccaaag atcttcacag gcgggtctct ccacctgatt tg 42  
  
 <210> 36  
 <211> 33  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG15315 for reconstituting sequence encoding  
         HPV-18 SS6E1\*deg-TMF  
  
 <400> 36  
 ggggagatct atgggtctca aggtgaacgt ctc 33  
  
 <210> 37  
 <211> 39  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG17881 for reconstituting sequence encoding  
         HPV-18 SS-E1\*deg-TMF  
  
 <400> 37  
 gtgccttctg ggtctgcgcc ccaatggatt tgaccggtg 39  
  
 <210> 38  
 <211> 37  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG17882 for reconstituting sequence encoding  
         HPV-18 SS-E1\*deg-TMF  
  
 <400> 38  
 ggtcaaatcc attggggcgc agaccagaa ggcacag 37  
  
 <210> 39  
 <211> 42  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG17883 for reconstituting sequence encoding  
         HPV-18 SS-E1\*deg-TMF  
  
 <400> 39  
 cagaatcaca ggcctcttgg tttatcgagc actagcatag tc 42  
  
 <210> 40

<211> 39  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG17884 for reconstituting sequence encoding  
         HPV-18 SS-E1\*deg-TMF  
  
 <400> 40  
 gctagtgtctc gataaaccaa gaggcctgtg attctgtcc 39  
  
 <210> 41  
 <211> 32  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG17885 for reconstituting sequence encoding HPV-18  
         SS-E1\*deg-TMF  
  
 <400> 41  
 gggggcggcc gctcagagcg accttacata gg 32  
  
 <210> 42  
 <211> 31  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> sense primer oTG17875 for reconstituting sequence  
         encoding HPV-18 SS-E2\*deg-TMR  
  
 <400> 42  
 ggggagatct atgggttcctc aggctctcct g 31  
  
 <210> 43  
 <211> 39  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> sense primer oTG17876 for reconstituting sequence  
         encoding HPV-18 SS-E2\*deg-TMR  
  
 <400> 43  
 gttttgggaa attccctatt cagacaccga aggaaaccc 39  
  
 <210> 44  
 <211> 43  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> antisense primer oTG17877 for reconstituting sequence  
         encoding HPV-18 SS-E2\*deg-TMR  
  
 <400> 44

gtttccttcg gtgtctgaat agggaatttc ccaaaacaca atg 43

<210> 45  
 <211> 39  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sense primer oTG17878 for reconstituting sequence  
 encoding HPV-18 SS-E2\*deg-TMR

<400> 45  
 gtgggataca tgacaatgta tgtattactg agtgcaggg 39

<210> 46  
 <211> 38  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisense primer oTG17879 for reconstituting sequence  
 encoding HPV-18 SS-E2\*deg-TMR

<400> 46  
 ctgcactcag taatacatatc attgtcatgt atcccacc 38

<210> 47  
 <211> 29  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisense primer oTG17880 for reconstituting sequence  
 encoding HPV-18 SS-E2\*deg-TMR

<400> 47  
 gggggcggcc gctcacagtc tggctcac 29

<210> 48  
 <211> 83  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sense primer oTG15174 for reconstituting sequence  
 encoding HPV-18 E6\*deg

<400> 48  
 ggggagatct atggcgcgct ttgaggatcc aacacggcga ccctacaagc tacctgatct 60  
 gtgcacggaa ctgaacactt cac 83

<210> 49  
 <211> 84  
 <212> DNA  
 <213> artificial sequence

<220>

<223> sense primer oTG15175 for reconstituting sequence  
encoding HPV-18 E6\*deg

<400> 49

gtattggaac ttacagaggt atttgaattt gcatttaaag acctatttgt ggtgtatcgt 60  
gacagtatac cccatgccgc atgc 84

<210> 50

<211> 85

<212> DNA

<213> artificial sequence

<220>

<223> sense primer oTG15176 for reconstituting sequence  
encoding HPV-18 E6\*deg

<400> 50

aggcactatt cagactctgt gtacggagac acattggaaa aactaactaa cactgggtta 60  
tacaatttat taataagatg cctgc 85

<210> 51

<211> 72

<212> DNA

<213> artificial sequence

<220>

<223> sense primer oTG15177 for reconstituting sequence  
encoding HPV-18 E6\*deg

<400> 51

ccttaatgaa aaacgacgat ttcacaacat agctgggcac tatagaggcc agtgccattc 60  
gtgctgcaac cg 72

<210> 52

<211> 76

<212> DNA

<213> artificial sequence

<220>

<223> antisense primer oTG15178 for reconstituting sequence  
encoding HPV-18 E2\*deg

<400> 52

ggggagatct tacttgtgtc tccctgcgtc gttggagtcg ttctgtcgt gtcggttgc 60  
agcacgaatg gcactg 76

<210> 53

<211> 78

<212> DNA

<213> artificial sequence

<220>

<223> antisense primer oTG15179 for reconstituting sequence  
encoding HPV-18 E6\*deg

<400> 53

gttgtgaaat cgtcgttttt cattaagggtg tctaagcaac ggtttctggc accgcaggca 60  
tcttattaat aaattgta 78

<210> 54  
<211> 82  
<212> DNA  
<213> artificial sequence

<220>  
<223> antisense primer oTG15180 for reconstituting sequence  
encoding HPV-18 E6\*deg

<400> 54  
cacagagtct gaatagtgcc ttaattctct gattctagag taaaaatcta tacacttatg 60  
gcatgcggca tggggtatac tg 82

<210> 55  
<211> 86  
<212> DNA  
<213> artificial sequence

<220>  
<223> antisense primer oTG15181 for reconstituting sequence  
encoding HPV-18 E6\*deg

<400> 55  
caaatacttc tgtaagttcc aatactgtct tacaatatac acagggttatt tctatgtctt 60  
gcagtgaagt gttcagttcc gtgcac 86

<210> 56  
<211> 70  
<212> DNA  
<213> artificial sequence

<220>  
<223> sense primer oTG14773 for reconstituting sequence  
encoding HPV-18 E7\*deg

<400> 56  
aaaccagat ctatgcacgg acctaaggca aactgcaag acattgtatt gcatttagag 60  
ccccaaaatg 70

<210> 57  
<211> 76  
<212> DNA  
<213> artificial sequence

<220>  
<223> antisense primer oTG14774 for reconstituting sequence  
encoding HPV-18 E7\*deg

<400> 57  
aatctcgtcg ttttcttctt ctgagtcgct taactgtgca accggaattt cattttgggg 60  
ctctaaatgc aataca 76

<210> 58  
<211> 76

<212> DNA  
 <213> artificial sequence

<220>  
 <223> sense primer oTG14775 for reconstituting sequence  
 encoding HPV-18 E7\*deg

<400> 58  
 actcagagga agaaaacgac gagattgacg gagttaatca tcaacattta ccagcccgcac 60  
 gagctgaacc acaacg 76

<210> 59  
 <211> 76  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisense primer oTG14776 for reconstituting sequence  
 encoding HPV-18 E7\*deg

<400> 59  
 ctagctcaat tctggcttcg catttacagc acatacacia cattgtgtga cggtgtggtt 60  
 cagctcgtcg ggctgg 76

<210> 60  
 <211> 76  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sense primer oTG14777 for reconstituting sequence  
 encoding HPV-18 E7\*deg

<400> 60  
 taaatgcgaa gccagaattg agctagtagt agagagctca gcagacgacc ttcgagcatt 60  
 ccagcagcta tttctg 76

<210> 61  
 <211> 79  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> antisense primer oTG14778 for reconstituting sequence  
 encoding HPV-18 E7\*deg

<400> 61  
 aaaccgcat ccctgctggg atgcacacca cggacagaca aaggacaggg tggtcagaaa 60  
 tagctgctgg aatgctcga 79

<210> 62  
 <211> 20  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> primer sens polylinker

<400> 62  
cctgcagaag cttcccggg 20

<210> 63  
<211> 28  
<212> DNA  
<213> artificial sequence

<220>  
<223> anstisense primer polylinker

<400> 63  
gatcccccg gaagcttctg caggagct 28

<210> 64  
<211> 243  
<212> PRT  
<213> artificial sequence

<220>  
<223> HPV-16 membrane-presented and non-oncogenic E6 variant  
(SS-16E6\*-TMF)

<400> 64  
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

<210> 65



<211> 185  
 <212> PRT  
 <213> artificial sequence

<220>

<223> HPV-16 membrane-presented and non-oncogenic E7 variant  
 (SS-16E7\*-TMR)

<400> 65

```

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

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<210> 66  
 <211> 1062  
 <212> DNA  
 <213> artificial sequence

<220>

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

<400> 66

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atggaggaaa tatcagcacg cttgaatgca gtccaagaga aaattctaga tctttacgaa      60
gcagataaaa ctgatttacc atctcaaatt gaacactgga aattgatacg catggcctgc      120
gctttattgt atacagccaa acagatgggc ttttcacatt tatgtcacca agtggtacct      180
tctttgttag catccaaaac caaagcgttt caagtagcgg aactacagat ggcattagag      240
acattaagta aatcacagta tagcacaagc caatggacgt tgcaacagac aagcttagag      300
gtttggcttt gtgaaccacc aaaatgtttt aaaaagcaag gagaaacagt aactgtgcaa      360
tatgacaatg acaaaaaaaaa taccatggac tatactaact ggggtgaaat atacattata      420
gaggaagata catgtactat ggttacaggg aaagtagatt atataggat gtattacata      480
cataactgtg aaaagggtata ctttaaatat tttaaggagg atgctgccaa atactctaaa      540
acacaaatgt gggaagtcca tgtaggtggc cagggttattg tttgccctac gtctatatct      600
agcaatcaaa tatccactac tgagactgct gacatacaga cagacaacga taaccgacca      660
ccacaagcag cggccaaacg acgacgacct gcagacacta ctgacaccgc ccagcccctt      720
acaaagctgt tctgtgcaga ccccgcttg gataatagaa cagcacgtac agcaactaac      780
tgcacaaata agcagcggac tgtgtgtagt tctaacgttg caccaatagt gcatttgaaa      840
ggcgaatcaa atagcttaaa gtgtttgaga tacagattaa aaccttataa agagttgtac      900
agttctatgt cttcaacttg gcactggact agtgacaaca aaaaatagtaa aaatggcata      960

```

```

gtaaccgtga catttgtaac tgaacagcaa caacaaatgt tcttgggtac cgtaaagata 1020
cctcctactg tgcagataag taccggattc atgaccttat aa 1062

```

<210> 67

<211> 1326

<212> DNA

<213> artificial sequence

<220>

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

<400> 67

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atggtaccgc aagccctgct attcgtacct ttattgggtct ttcccctctg tttcggtaaag 60
tttcctatag aggaaatata agcacgcttg aatgcagtcc aagagaaaat tctagatctt 120
tacgaagcag ataaaactga tttaccatct caaattgaac actggaaatt gatacgcatg 180
gcctgcgctt tattgtatac agccaaacag atgggctttt cacatttatg tcaccaagtg 240
gtaccttctt tgtagcatc caaaaccaa gcggtttcaag tagcggaact acagatggca 300
ttagagacat taagtaaata acagtatagc acaagccaat ggacgttgca acagacaagc 360
ttagagggtt ggctttgtga accacaaaaa tgttttaaaa agcaaggaga aacagtaact 420
gtgcaatatg acaatgacaa aaaaaatacc atggactata ctaactgggg tgaaatatac 480
attatagagg aagatacatg tactatgggt acagggaaaag tagattatat aggtatgtat 540
tacatacata actgtgaaaa ggtatacttt aaatatTTTA aggaggatgc tgccaaatac 600
tctaaaacac aaatgtggga agtccatgta ggtggccagg ttattgtttg ccctacgtct 660
atatctagca atcaaataat cactactgag actgctgaca tacagacaga caacgataac 720
cgaccaccac aagcagcggc caaacgacga cgacctgcag acactactga caccgcccag 780
ccccttacaa agctgttctg tgcagacccc gccttgata atagaacagc acgtacagca 840
actaactgca caaataagca gcggactgtg tgtagtTcta acgttgcaac aatagtgcac 900
ttgaaaggcg aatcaaatag cttaaagtgt ttgagataca gattaaaacc ttataaagag 960
ttgtacagtt ctatgtcttc aacttggcac tggactagtg acaacaaaaa tagtaaaaaa 1020
ggcatagtaa ccgtgacatt tgtaactgaa cagcaacaac aaatgttctt gggtagcgta 1080
aagatacctc ctactgtgca gataagtacc ggattcatga ccttatacgt actgctatcg 1140
gcaggcacgt tgatgcgact aatgcttata atcttcctaa taacctgctg caagcgggtt 1200
gataggcccc aaagtaccca aaggtccttg agaggtaccg gacgcaacgt atcggtaacg 1260
tcgcaaagcg gcaagttcat tagcagttgg gagtcgcaca aatcaggtgg agagaccgcg 1320
ctgtga 1326

```

<210> 68

<211> 1107

<212> DNA

<213> artificial sequence

<220>

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

<400> 68

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atggaatcga taccggcacg gttaaacgct gtgcaggaaa agatactcga tctatatgag 60
gctgacagca atgatctaaa cgacaaaatc 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 ttatttactt 420
ggtagagtgt aatgcacaat tgtagaagga caagtggatt actatgggtt atactattgg 480
tgtgatggag aaaaaatcta tttcgtaaaa tttagtaacg acgcaaagca atattgtgta 540
acaggagtct gggaggtgca cgtgggcggg caagtaatcg tgtgtccagc atcggtatca 600
agtaacgagg tttctactac agaaacagct gtccacctat gcaccgaaac ctccaagacc 660

```

```

tccgcagtgt ccggtgggtgc caaagacaca cacctacaac caccacagaa gcgacgtcga 720
ccagatgtca cagattccag aaacaccaag taccccaaca accttttgcg gggacaacaa 780
tccgttgaca gcactacacg gggactcgtg actgccactg agtgcactaa taaaggctcg 840
gttgacata caacttgtag tgctcctatt attcacctaa agggtgacct caacagcttg 900
aaatgcctaa ggtatagggt aaaaacacat aaaagtttat atgttcaaat ttcattctacg 960
tggtattgga cgagtaatga atgtacaaat aataaactag gtattgtaac aataacgtac 1020
agtgatgaga cacagcgtca acagttttta aaaactgtca aaatcccaaa taccgtccaa 1080
gttatacaag gtgtcatgtc attgtaa 1107

```

<210> 69

<211> 1374

<212> DNA

<213> artificial sequence

<220>

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

<400> 69

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atgggtctca aggtgaacgt ctctgccata ttcattggcag tactgttaac tctccaaaca 60
cccaccggtc aaatccattg gggcgaaatcg ataccggcac ggttaaagcg tgtgcaggaa 120
aagatactcg atctatatga ggctgacagc aatgatctaa acgcacaaat cgagcattgg 180
aagttgactc gaatggcttg tgttttgttt tataaagcaa aggaactggg aataactcat 240
ataggccatc aagtagtgcc tccaatggca gtgtctaagg caaaggcctg ccaagccgca 300
gagcttcaat tggctttgga ggcattgaac aaaactcaat acagtacaga tggctggacc 360
ttacagcaaa caagtctaga aatgtggcgt gcagagccac aaaaatactt caagaagcac 420
gggtacacaa taacagtcca atacgataat gataaaaaca acactatgga ttacacaaat 480
tggaaggaaa tttattttact tggtagtgtt gaatgcacaa ttgtagaagg acaagtggat 540
tactatgggt tatactattg gtgtgatgga gaaaaaatct atttcgtaaa atttagtaac 600
gacgcaaagc aatatttgtt aacaggagtc tgggaggtgc acgtgggcgg tcaagtaatc 660
gtgtgtccag catcggtatc aagtaacgag gtttctacta cagaaacagc tgtccaccta 720
tgcaccgaaa cctccaagac ctccgcagtg tccgtgggtg ccaaagacac acacctacaa 780
ccaccacaga agcgacgtcg accagatgtc acagattcca gaaacaccaa gtacccaac 840
aaccttttgc ggggacaaca atccgttgac agcactacac ggggactcgt aactgccact 900
gagtgcacta ataaaggctg ggttgacat acaacttgta ctgctcctat tattcaccta 960
aagggtgacc ccaacagctt gaaatgccta aggtataggg taaaaacaca taaaagttaa 1020
tatgttcaaa tttcatctac gtggcattgg acgagtaatg aatgtacaaa taataaacta 1080
ggattgttaa caataacgta cagtgtgag acacagcgtc aacagttttt aaaaactgtc 1140
aaaatcccaa ataccgtcca agttatacaa ggtgtcatgt cattgggttt atcgagcact 1200
agcatagtct acatcctgat tgcagtgtgt cttggagggt tgatagggat ccccgcttta 1260
atatgttgct gcagggggcg ttgtaacaaa aagggagaac aagttgggat gtcaagacca 1320
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<210> 70

<211> 441

<212> PRT

<213> artificial sequence

<220>

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

<400> 70

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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 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

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[illegible]

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<210> 71
<211> 457
<212> PRT
<213> artificial sequence
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<220>  
<223> membrane-presented and replication-defective HPV-52 E2 polypeptide (SS-52E2\*-TMF)

&lt;400&gt; 71

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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 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     160
Trp Lys Glu Ile Tyr Leu Leu Gly Glu Cys Glu Cys Thr Ile Val Glu
      165     170     175
Gly Gln Val Asp Tyr Tyr Gly Leu Tyr Tyr Trp Cys Asp Gly Glu Lys
      180     185     190
Ile Tyr Phe Val Lys Phe Ser Asn Asp Ala Lys Gln Tyr Cys Val Thr
195     200     205
Gly Val Trp Glu Val His Val Gly Gly Gln Val Ile Val Cys Pro Ala
210     215     220
Ser Val Ser Ser Asn Glu Val Ser Thr Thr Glu Thr Ala Val His Leu
225     230     235     240
Cys Thr Glu Thr Ser Lys Thr Ser Ala Val Ser Val Gly Ala Lys Asp
      245     250     255
Thr His Leu Gln Pro Pro Gln Lys Arg Arg Arg Pro Asp Val Thr Asp
260     265     270
Ser Arg Asn Thr Lys Tyr Pro Asn Asn Leu Leu Arg Gly Gln Gln Ser
275     280     285
Val Asp Ser Thr Thr Arg Gly Leu Val Thr Ala Thr Glu Cys Thr Asn
290     295     300
Lys Gly Arg Val Ala His Thr Thr Cys Thr Ala Pro Ile Ile His Leu
305     310     315     320
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> 72  
 <211> 36  
 <212> DNA  
 <213> artificial sequence  
  
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 <223> priler oTG18962 for reconstituting sequence encoding  
 SS-33E2\*-TMR  
  
 <400> 72  
 cccaaaggat ccaccatggt accgcaagcc ctgcta 36  
  
 <210> 73  
 <211> 52  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer oTG18963 for reconstituting sequence encoding  
 SS-33E2\*-TMR  
  
 <400> 73  
 ttcccctctg ttccggttaag tttcctatag aggaaatattc agcacgcttg aa 52  
  
 <210> 74  
 <211> 52  
 <212> DNA  
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 <223> primer oTG18964 for reconstituting sequence encoding  
 SS-33E2\*-TMR  
  
 <400> 74  
 ttcaagcgtg ctgatatttc ctctatagga aacttaccga aacagagggg aa 52  
  
 <210> 75  
 <211> 49  
 <212> DNA  
 <213> artificial sequence  
  
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 <223> primer oTG18965 for reconstituting sequence encoding  
 SS-33E2\*-TMR  
  
 <400> 75  
 gataagtacc ggattcatga ccttatacgt actgctatcg gcaggcacg 49  
  
 <210> 76  
 <211> 49  
 <212> DNA  
 <213> artificial sequence  
  
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SS-33-E2\*-TMR

<400> 76  
cgtgcctgcc gatagcagta cgtataaggt catgaatccg gtacttatc 49

<210> 77  
<211> 56  
<212> DNA  
<213> artificial sequence

<220>  
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SS-33E2\*-TMR

<400> 77  
aaaaccccgcc atgcgcggcc gcaagctatc acaggcgggt ctctccacct gatttg 56

<210> 78  
<211> 37  
<212> DNA  
<213> artificial sequence

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

<400> 78  
aaacccgaga tctacatgg gtctcaaggt gaacgtc 37

<210> 79  
<211> 46  
<212> DNA  
<213> artificial sequence

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

<400> 79  
cccaccggtc aaatccattg gggcgaatcg ataccggcac ggttaa 46

<210> 80  
<211> 46  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer oTG18970 for reconstituting sequence encoding  
SS-52E2\*-TMF

<400> 80  
ttaaccgtgc cggtatcgat tcgcccgaat ggatttgacc ggtggg 46

<210> 81  
<211> 43  
<212> DNA

<213> artificial sequence

<220>

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

<400> 81

gttatacaag gtgtcatgtc attgggttta tcgagcacta gca

43

<210> 82

<211> 43

<212> DNA

<213> artificial sequence

<220>

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

<400> 82

tgctagtgtc cgataaaccc aatgacatga caccttgtat aac

43

<210> 83

<211> 53

<212> DNA

<213> artificial sequence

<220>

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

<400> 83

aagcttgcta gccaccggtg gggccgcggc cgctcagagc gaccttacat agg

53