

SEQUENCE LISTING

<110> FIT Biotech OYJ

<120> Transreplicase constructs

<130> PD53893PC00

<150> US60/907,446

<151> 2007-04-02

<160> 38

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2432

<212> PRT

<213> Semliki Forest Virus replicase

<400> 1

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

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115	120	125
Ala Glu Ser Pro Thr Phe Cys Leu His Thr Asp Val Thr Cys Arg Thr		
130	135	140
Ala Ala Glu Val Ala Val Tyr Gln Asp Val Tyr Ala Val His Ala Pro		
145	150	155
Thr Ser Leu Tyr His Gln Ala Met Lys Gly Val Arg Thr Ala Tyr Trp		
165	170	175
Ile Gly Phe Asp Thr Thr Pro Phe Met Phe Asp Ala Leu Ala Gly Ala		
180	185	190
Tyr Pro Thr Tyr Ala Thr Asn Trp Ala Asp Glu Gln Val Leu Gln Ala		
195	200	205
Arg Asn Ile Gly Leu Cys Ala Ala Ser Leu Thr Glu Gly Arg Leu Gly		
210	215	220
Lys Leu Ser Ile Leu Arg Lys Lys Gln Leu Lys Pro Cys Asp Thr Val		
225	230	235
Met Phe Ser Val Gly Ser Thr Leu Tyr Thr Glu Ser Arg Lys Leu Leu		
245	250	255
Arg Ser Trp His Leu Pro Ser Val Phe His Leu Lys Gly Lys Gln Ser		
260	265	270
Phe Thr Cys Arg Cys Asp Thr Ile Val Ser Cys Glu Gly Tyr Val Val		
275	280	285
Lys Lys Ile Thr Met Cys Pro Gly Leu Tyr Gly Lys Thr Val Gly Tyr		
290	295	300
Ala Val Thr Tyr His Ala Glu Gly Phe Leu Val Cys Lys Thr Thr Asp		
305	310	315
Thr Val Lys Gly Glu Arg Val Ser Phe Pro Val Cys Thr Tyr Val Pro		
325	330	335
Ser Thr Ile Cys Asp Gln Met Thr Gly Ile Leu Ala Thr Asp Val Thr		
340	345	350
Pro Glu Asp Ala Gln Lys Leu Leu Val Gly Leu Asn Gln Arg Ile Val		
355	360	365
Val Asn Gly Arg Thr Gln Arg Asn Thr Asn Thr Met Lys Asn Tyr Leu		
370	375	380
Leu Pro Ile Val Ala Val Ala Phe Ser Lys Trp Ala Arg Glu Tyr Lys		
385	390	395
Ala Asp Leu Asp Asp Glu Lys Pro Leu Gly Val Arg Glu Arg Ser Leu		
405	410	415
Thr Cys Cys Cys Leu Trp Ala Phe Lys Thr Arg Lys Met His Thr Met		

420	425	430
Tyr Lys Lys Pro Asp Thr Gln Thr Ile Val Lys Val Pro Ser Glu Phe		
435	440	445
Asn Ser Phe Val Ile Pro Ser Leu Trp Ser Thr Gly Leu Ala Ile Pro		
450	455	460
Val Arg Ser Arg Ile Lys Met Leu Leu Ala Lys Lys Thr Lys Arg Glu		
465	470	475
Leu Ile Pro Val Leu Asp Ala Ser Ser Ala Arg Asp Ala Glu Gln Glu		
485	490	495
Glu Lys Glu Arg Leu Glu Ala Glu Leu Thr Arg Glu Ala Leu Pro Pro		
500	505	510
Leu Val Pro Ile Ala Pro Ala Glu Thr Gly Val Val Asp Val Asp Val		
515	520	525
Glu Glu Leu Glu Tyr His Ala Gly Ala Gly Val Val Glu Thr Pro Arg		
530	535	540
Ser Ala Leu Lys Val Thr Ala Gln Pro Asn Asp Val Leu Leu Gly Asn		
545	550	555
Tyr Val Val Leu Ser Pro Gln Thr Val Leu Lys Ser Ser Lys Leu Ala		
565	570	575
Pro Val His Pro Leu Ala Glu Gln Val Lys Ile Ile Thr His Asn Gly		
580	585	590
Arg Ala Gly Arg Tyr Gln Val Asp Gly Tyr Asp Gly Arg Val Leu Leu		
595	600	605
Pro Cys Gly Ser Ala Ile Pro Val Pro Glu Phe Gln Ala Leu Ser Glu		
610	615	620
Ser Ala Thr Met Val Tyr Asn Glu Arg Glu Phe Val Asn Arg Lys Leu		
625	630	635
Tyr His Ile Ala Val His Gly Pro Ser Leu Asn Thr Asp Glu Glu Asn		
645	650	655
Tyr Glu Lys Val Arg Ala Glu Arg Thr Asp Ala Glu Tyr Val Phe Asp		
660	665	670
Val Asp Lys Lys Cys Cys Val Lys Arg Glu Glu Ala Ser Gly Leu Val		
675	680	685
Leu Val Gly Glu Leu Thr Asn Pro Pro Phe His Glu Phe Ala Tyr Glu		
690	695	700
Gly Leu Lys Ile Arg Pro Ser Ala Pro Tyr Lys Thr Thr Val Val Gly		
705	710	715
Val Phe Gly Val Pro Gly Ser Gly Lys Ser Ala Ile Ile Lys Ser Leu		

725	730	735
Val Thr Lys His Asp Leu Val Thr Ser Gly Lys Lys Glu Asn Cys Gln		
740	745	750
Glu Ile Val Asn Asp Val Lys Lys His Arg Gly Leu Asp Ile Gln Ala		
755	760	765
Lys Thr Val Asp Ser Ile Leu Leu Asn Gly Cys Arg Arg Ala Val Asp		
770	775	780
Ile Leu Tyr Val Asp Glu Ala Phe Ala Cys His Ser Gly Thr Leu Leu		
785	790	795
Ala Leu Ile Ala Leu Val Lys Pro Arg Ser Lys Val Val Leu Cys Gly		
805	810	815
Asp Pro Lys Gln Cys Gly Phe Phe Asn Met Met Gln Leu Lys Val Asn		
820	825	830
Phe Asn His Asn Ile Cys Thr Glu Val Cys His Lys Ser Ile Ser Arg		
835	840	845
Arg Cys Thr Arg Pro Val Thr Ala Ile Val Ser Thr Leu His Tyr Gly		
850	855	860
Gly Lys Met Arg Thr Thr Asn Pro Cys Asn Lys Pro Ile Ile Ile Asp		
865	870	875
Thr Thr Gly Gln Thr Lys Pro Lys Pro Gly Asp Ile Val Leu Thr Cys		
885	890	895
Phe Arg Gly Trp Val Lys Gln Leu Gln Leu Asp Tyr Arg Gly His Glu		
900	905	910
Val Met Thr Ala Ala Ala Ser Gln Gly Leu Thr Arg Lys Gly Val Tyr		
915	920	925
Ala Val Arg Gln Lys Val Asn Glu Asn Pro Leu Tyr Ala Pro Ala Ser		
930	935	940
Glu His Val Asn Val Leu Leu Thr Arg Thr Glu Asp Arg Leu Val Trp		
945	950	955
Lys Thr Leu Ala Gly Asp Pro Trp Ile Lys Val Leu Ser Asn Ile Pro		
965	970	975
Gln Gly Asn Phe Thr Ala Thr Leu Glu Glu Trp Gln Glu Glu His Asp		
980	985	990
Lys Ile Met Lys Val Ile Glu Gly Pro Ala Ala Pro Val Asp Ala Phe		
995	1000	1005
Gln Asn Lys Ala Asn Val Cys Trp Ala Lys Ser Leu Val Pro Val Leu		
1010	1015	1020
Asp Thr Ala Gly Ile Arg Leu Thr Ala Glu Glu Trp Ser Thr Ile Ile		

1025	1030	1035	1040
Thr Ala Phe Lys Glu Asp Arg Ala Tyr Ser Pro Val Val Ala Leu Asn			
	1045	1050	1055
Glu Ile Cys Thr Lys Tyr Tyr Gly Val Asp Leu Asp Ser Gly Leu Phe			
	1060	1065	1070
Ser Ala Pro Lys Val Ser Leu Tyr Tyr Glu Asn Asn His Trp Asp Asn			
	1075	1080	1085
Arg Pro Gly Gly Arg Met Tyr Gly Phe Asn Ala Ala Thr Ala Ala Arg			
	1090	1095	1100
Leu Glu Ala Arg His Thr Phe Leu Lys Gly Gln Trp His Thr Gly Lys			
1105	1110	1115	1120
Gln Ala Val Ile Ala Glu Arg Lys Ile Gln Pro Leu Ser Val Leu Asp			
	1125	1130	1135
Asn Val Ile Pro Ile Asn Arg Arg Leu Pro His Ala Leu Val Ala Glu			
	1140	1145	1150
Tyr Lys Thr Val Lys Gly Ser Arg Val Glu Trp Leu Val Asn Lys Val			
	1155	1160	1165
Arg Gly Tyr His Val Leu Leu Val Ser Glu Tyr Asn Leu Ala Leu Pro			
	1170	1175	1180
Arg Arg Arg Val Thr Trp Leu Ser Pro Leu Asn Val Thr Gly Ala Asp			
1185	1190	1195	1200
Arg Cys Tyr Asp Leu Ser Leu Gly Leu Pro Ala Asp Ala Gly Arg Phe			
	1205	1210	1215
Asp Leu Val Phe Val Asn Ile His Thr Glu Phe Arg Ile His His Tyr			
	1220	1225	1230
Gln Gln Cys Val Asp His Ala Met Lys Leu Gln Met Leu Gly Gly Asp			
	1235	1240	1245
Ala Leu Arg Leu Leu Lys Pro Gly Gly Ser Leu Leu Met Arg Ala Tyr			
	1250	1255	1260
Gly Tyr Ala Asp Lys Ile Ser Glu Ala Val Val Ser Ser Leu Ser Arg			
1265	1270	1275	1280
Lys Phe Ser Ser Ala Arg Val Leu Arg Pro Asp Cys Val Thr Ser Asn			
	1285	1290	1295
Thr Glu Val Phe Leu Leu Phe Ser Asn Phe Asp Asn Gly Lys Arg Pro			
	1300	1305	1310
Ser Thr Leu His Gln Met Asn Thr Lys Leu Ser Ala Val Tyr Ala Gly			
	1315	1320	1325
Glu Ala Met His Thr Ala Gly Cys Ala Pro Ser Tyr Arg Val Lys Arg			

1330	1335	1340
Ala Asp Ile Ala Thr Cys Thr Glu Ala Ala Val Val Asn Ala Ala Asn		
1345	1350	1355
Ala Arg Gly Thr Val Gly Asp Gly Val Cys Arg Ala Val Ala Lys Lys		1360
1365	1370	1375
Trp Pro Ser Ala Phe Lys Gly Glu Ala Thr Pro Val Gly Thr Ile Lys		
1380	1385	1390
Thr Val Met Cys Gly Ser Tyr Pro Val Ile His Ala Val Ala Pro Asn		
1395	1400	1405
Phe Ser Ala Thr Thr Glu Ala Glu Gly Asp Arg Glu Leu Ala Ala Val		
1410	1415	1420
Tyr Arg Ala Val Ala Ala Glu Val Asn Arg Leu Ser Leu Ser Ser Val		
1425	1430	1435
Ala Ile Pro Leu Leu Ser Thr Gly Val Phe Ser Gly Gly Arg Asp Arg		1440
1445	1450	1455
Leu Gln Gln Ser Leu Asn His Leu Phe Thr Ala Met Asp Ala Thr Asp		
1460	1465	1470
Ala Asp Val Thr Ile Tyr Cys Arg Asp Lys Ser Trp Glu Lys Lys Ile		
1475	1480	1485
Gln Glu Ala Ile Asp Met Arg Thr Ala Val Glu Leu Leu Asn Asp Asp		
1490	1495	1500
Val Glu Leu Thr Thr Asp Leu Val Arg Val His Pro Asp Ser Ser Leu		
1505	1510	1515
Val Gly Arg Lys Gly Tyr Ser Thr Thr Asp Gly Ser Leu Tyr Ser Tyr		
1525	1530	1535
Phe Glu Gly Thr Lys Phe Asn Gln Ala Ala Ile Asp Met Ala Glu Ile		
1540	1545	1550
Leu Thr Leu Trp Pro Arg Leu Gln Glu Ala Asn Glu Gln Ile Cys Leu		
1555	1560	1565
Tyr Ala Leu Gly Glu Thr Met Asp Asn Ile Arg Ser Lys Cys Pro Val		
1570	1575	1580
Asn Asp Ser Asp Ser Ser Thr Pro Pro Arg Thr Val Pro Cys Leu Cys		
1585	1590	1595
Arg Tyr Ala Met Thr Ala Glu Arg Ile Ala Arg Leu Arg Ser His Gln		1600
1605	1610	1615
Val Lys Ser Met Val Val Cys Ser Ser Phe Pro Leu Pro Lys Tyr His		
1620	1625	1630
Val Asp Gly Val Gln Lys Val Lys Cys Glu Lys Val Leu Leu Phe Asp		

1635	1640	1645
Pro Thr Val	Pro Ser Val Val Ser	Pro Arg Lys Tyr Ala Ala Ser Thr
1650	1655	1660
Thr Asp His	Ser Asp Arg Ser Leu Arg Gly Phe Asp	Leu Asp Trp Thr
1665	1670	1675
Thr Asp Ser	Ser Ser Thr Ala Ser Asp Thr Met Ser	Leu Pro Ser Leu
	1685	1690
Gln Ser Cys	Asp Ile Asp Ser Ile Tyr Glu Pro Met	Ala Pro Ile Val
1700	1705	1710
Val Thr Ala	Asp Val His Pro Glu Pro Ala Gly Ile	Ala Asp Leu Ala
1715	1720	1725
Ala Asp Val	His Pro Glu Pro Ala Asp His Val Asp	Leu Glu Asn Pro
1730	1735	1740
Ile Pro Pro	Pro Arg Pro Lys Arg Ala Ala Tyr Leu	Ala Ser Arg Ala
1745	1750	1755
Ala Glu Arg	Pro Val Pro Ala Pro Arg Lys Pro Thr	Pro Ala Pro Arg
	1765	1770
Thr Ala Phe	Arg Asn Lys Leu Pro Leu Thr Phe Gly	Asp Phe Asp Glu
1780	1785	1790
His Glu Val	Asp Ala Leu Ala Ser Gly Ile Thr Phe Gly	Asp Phe Asp
1795	1800	1805
Asp Val Leu	Arg Leu Gly Arg Ala Gly Ala Tyr Ile	Phe Ser Ser Asp
1810	1815	1820
Thr Gly Ser	Gly His Leu Gln Gln Lys Ser Val Arg	Gln His Asn Leu
1825	1830	1835
Gln Cys Ala	Gln Leu Asp Ala Val Glu Glu Glu Lys	Met Tyr Pro Pro
	1845	1850
Lys Leu Asp	Thr Glu Arg Glu Lys Leu Leu Leu Lys	Met Gln Met
1860	1865	1870
His Pro Ser	Glu Ala Asn Lys Ser Arg Tyr Gln Ser	Arg Lys Val Glu
1875	1880	1885
Asn Met Lys	Ala Thr Val Val Asp Arg Leu Thr Ser	Gly Ala Arg Leu
1890	1895	1900
Tyr Thr Gly	Ala Asp Val Gly Arg Ile Pro Thr Tyr	Ala Val Arg Tyr
1905	1910	1915
Pro Arg Pro	Val Tyr Ser Pro Thr Val Ile Glu Arg	Phe Ser Ser Pro
	1925	1930
Asp Val Ala	Ile Ala Ala Cys Asn Glu Tyr Leu Ser	Arg Asn Tyr Pro

1940	1945	1950
Thr Val Ala Ser Tyr Gln Ile Thr Asp Glu Tyr Asp Ala Tyr Leu Asp		
1955	1960	1965
Met Val Asp Gly Ser Asp Ser Cys Leu Asp Arg Ala Thr Phe Cys Pro		
1970	1975	1980
Ala Lys Leu Arg Cys Tyr Pro Lys His His Ala Tyr His Gln Pro Thr		
1985	1990	1995
2000		
Val Arg Ser Ala Val Pro Ser Pro Phe Gln Asn Thr Leu Gln Asn Val		
2005	2010	2015
Leu Ala Ala Ala Thr Lys Arg Asn Cys Asn Val Thr Gln Met Arg Glu		
2020	2025	2030
Leu Pro Thr Met Asp Ser Ala Val Phe Asn Val Glu Cys Phe Lys Arg		
2035	2040	2045
Tyr Ala Cys Ser Gly Glu Tyr Trp Glu Glu Tyr Ala Lys Gln Pro Ile		
2050	2055	2060
Arg Ile Thr Thr Glu Asn Ile Thr Thr Tyr Val Thr Lys Leu Lys Gly		
2065	2070	2075
2080		
Pro Lys Ala Ala Ala Leu Phe Ala Lys Thr His Asn Leu Val Pro Leu		
2085	2090	2095
Gln Glu Val Pro Met Asp Arg Phe Thr Val Asp Met Lys Arg Asp Val		
2100	2105	2110
Lys Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro Lys Val Gln		
2115	2120	2125
Val Ile Gln Ala Ala Glu Pro Leu Ala Thr Ala Tyr Leu Cys Gly Ile		
2130	2135	2140
His Arg Glu Leu Val Arg Arg Leu Asn Ala Val Leu Arg Pro Asn Val		
2145	2150	2155
2160		
His Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala Ile Ile Ala		
2165	2170	2175
Ser His Phe His Pro Gly Asp Pro Val Leu Glu Thr Asp Ile Ala Ser		
2180	2185	2190
Phe Asp Lys Ser Gln Asp Asp Ser Leu Ala Leu Thr Gly Leu Met Ile		
2195	2200	2205
Leu Glu Asp Leu Gly Val Asp Gln Tyr Leu Leu Asp Leu Ile Glu Ala		
2210	2215	2220
Ala Phe Gly Glu Ile Ser Ser Cys His Leu Pro Thr Gly Thr Arg Phe		
2225	2230	2235
2240		
Lys Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr Leu Phe Ile		

2245	2250	2255
Asn Thr Val Leu Asn Ile Thr Ile Ala Ser Arg Val Leu Glu Gln Arg		
2260	2265	2270
Leu Thr Asp Ser Ala Cys Ala Ala Phe Ile Gly Asp Asp Asn Ile Val		
2275	2280	2285
His Gly Val Ile Ser Asp Lys Leu Met Ala Glu Arg Cys Ala Ser Trp		
2290	2295	2300
Val Asn Met Glu Val Lys Ile Ile Asp Ala Val Met Gly Glu Lys Pro		
2305	2310	2315
Pro Tyr Phe Cys Gly Gly Phe Ile Val Phe Asp Ser Val Thr Gln Thr		
2325	2330	2335
Ala Cys Arg Val Ser Asp Pro Leu Lys Arg Leu Phe Lys Leu Gly Lys		
2340	2345	2350
Pro Leu Thr Ala Glu Asp Lys Gln Asp Glu Asp Arg Arg Arg Ala Leu		
2355	2360	2365
Ser Asp Glu Val Ser Lys Trp Phe Arg Thr Gly Leu Gly Ala Glu Leu		
2370	2375	2380
Glu Val Ala Leu Thr Ser Arg Tyr Glu Val Glu Gly Cys Lys Ser Ile		
2385	2390	2395
Leu Ile Ala Met Ala Thr Leu Ala Arg Asp Ile Lys Ala Phe Lys Lys		
2405	2410	2415
Leu Arg Gly Pro Val Ile His Leu Tyr Gly Gly Pro Arg Leu Val Arg		
2420	2425	2430

<210> 2

<211> 871

<212> DNA

<213> Artificial Sequence

<220>

<223> CMV promoter precisely fused with 5'-end of SFV

<400> 2

gagctcttaa ttaatagtta ttaatagtaa tcaattacgg ggtcattagt tcatagccca 60
tatatggagt tccgcgttac ataacttacg gtaaattggcc cgcttggtg accgcccaac 120
gacccccgcc cattgacgtc aataatgacg tatgttccca tagtaacgcc aatagggact 180
ttccattgac gtcaatgggt ggagtattta cggtaaactg cccacttggc agtacatcaa 240

gtgtatcata tgccaagtac gccccctatt gacgtcaatg acggtaaatg gcccgccctgg 300
 cattatgccc agtacatgac cttatgggac tttcctactt ggcagtacat ctacgtatta 360
 gtcacgcgta ttaccatggg gatgcgggtt tggcagtaca tcaatgggag tggatagcgg 420
 tttgactcac ggggatttcc aagtctccac cccattgacg tcaatgggag tttgttttgg 480
 caccaaaatc aacgggactt tocaaaatgt cgtaacaact ccgccccatt gacgcaaagt 540
 ggcggtaggc gtgtacggtg ggaggtctat ataagcagag ctggtttagt gaaccgtatg 600
 gcggatgtgt gacatacacg acgcaaaaag attttgttcc agctcctgcc acctccgcta 660
 cgcgagagat taaccaccca cgatggccgc caaagtgcac gttgatattg aggctgacag 720
 cccattcatc aagtctttgc agaaggcatt tccgtcgttc gaggtggagt cattgcaggt 780
 cacaccaa at gaccatgcaa atgccagagc attttcgcac ctggctacca aattgatcga 840
 gcaggagact gacaaagaca cactcatctt g 871

<210> 3

<211> 618

<212> DNA

<213> Artificial Sequence

<220>

<223> Intron flanked with short fragments of SFV
 ns-region

<400> 3

gatatcgcca gtgcgccttc aaggtaggtt tggggaccct tgattgttct tcttttttcg 60
 ctattgtaaa attcatgtta tatggagggg gcaaagtttt cagggtgttg tttagaatgg 120
 gaagatgtcc cttgtatcac catggaccct catgataatt ttgtttcttt cactttctac 180
 tctgttgaca accattgtct cctcttattt tcttttcatt ttctgtaact ttttcgttaa 240
 acttttagctt gcatttgtaa cgaattttta aattcacttt tgtttatttg tcagattgta 300
 agtactttct ctaatcactt ttttttcaag gcaatcaggg tatattatat tgtacttcag 360
 cacagtttta gagaacaatt gttataatta aatgataagg tagaatattt ctgcatataa 420
 attctggctg gcgtggaaat attcttattg gtagaaacaa ctacaccctg gtcacatcc 480
 tgccctttct tttatggtta caatgatata cactgtttga gatgaggata aaatactctg 540
 agtccaaacc gggccctctt gctaaccatg ttcatgcctt cttctttttc ctacaggaga 600
 atgatgtaat aactcgag 618

<210> 4

<211> 404

<212> DNA

<213> Artificial Sequence

<220>

<223> -150/+51 subgenomic promoter with SFV capsid
enhancer element, foot and mouth disease 2A
autoprotease sequence and polylinker for the gene
of interest

<400> 4

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cttggggggcc gaactggagg tggcactaac atctaggtat gaggtagagg gctgcaaaaag 60
tattcctcata gccatggcca ccttggcgag ggacattaag gcgtttaaga aattgagagg 120
acctgttata cacctctacg gcggtcctag attggtgcgt taatacacag aattctgatt 180
atagcgcact attatagcac catgaattac atccctacgc aaacgtttta cggccgccgg 240
tggcgcccgcc gcccggcggc ccgtccctgg ccgttgccagg ccactccggg ggctcccgtc 300
gtcaattttg accttcttaa gcttgccgga gacgtcgagt ccaaccctgg gcccgggggt 360
tcgaatagtt taaacataag atctatacta gtatatgcgg ccgc 404
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<210> 5

<211> 246

<212> DNA

<213> Artificial Sequence

<220>

<223> -150/+51 subgenomic promoter (without SFV capsid
enhancer element, foot and mouth disease 2A
autoprotease sequence) and polylinker for the gene
of interest

<400> 5

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cttgaggggcc gaactggagg tggcactaac atctaggtat gaggtagagg gctgcaaaaag 60
tattcctcata gccatggcca ccttggcgag ggacattaag gcgtttaaga aattgagagg 120
acctgttata cacctctacg gcggtcctag attggtgcgt taatacacag aattctgatt 180
atagcgcact attatagcac cttcgaatag tttaaacata agatctatac tagtatatgc 240
ggccgc 246
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<210> 6

<211> 866

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'UTR of SFV with poly(A), HDV ribozyme sequence,
spacer and SV40 terminator signal

<400> 6

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taagttaggg taggcaatgg cattgatata gcaagaaaat tgaaaacaga aaaagttagg 60
gtaagcaatg gcatataacc ataactgtat aacttgtaac aaagcgcaac aagacctgcg 120
caattggccc cgtgggccgc ctcacggaaa ctcggggcaa ctcatattga cacattaatt 180
ggcaataatt ggaagcttac ataagcttaa ttcgacgaat aattggattt ttattttatt 240
ttgcaattgg tttttaatat ttccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 300
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaagggctcg catggcatct ccacctctc 360
gcgggtccgac ctgggcatcc gaaggaggac gcacgtccac tcggatggct aaggagacct 420
gcattcgag aagccgaatt ccagcacact ggcgccggtt actagggccg cgcccttccc 480
aacagttgag cagcctgaat gggaatgga gatccaattt ttaagtgtat aatgtgttaa 540
actactgatt ctaattgttt gtgtatttta gattcacagt cccaaggctc atttcaggcc 600
cctcagtcct cacagtctgt tcatgatcat aatcagccat accacatttg tagaggtttt 660
acttgcttta aaaaacctcc cacacctccc cctgaacctg aaacataaaa tgaatgcaat 720
tgttggtgtt aacttgctta ttgcagctta taatggttac aaataaagca atagcatcac 780
aaatttcaca aataaagcat ttttttctact gcattctagt tgtggtttgt ccaaactcat 840
caatgtatct taggcgcgcc ggtacc                                     866

```

<210> 7

<211> 7299

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of native wild type replicase encoding
region of SFV

<400> 7

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atggccgcca aagtgcattg tgatattgag gctgacagcc cattcatcaa gtctttgcag 60
aaggcatttc cgtcgttcga ggtggagtca ttgcaggtea caccaaatga ccatgcaaatt 120
gccagagcat tttcgcacct ggetaccaa ttgatcgagc aggagactga caaagacaca 180
ctcatottgg atatcggcag tgcgccttcc aggagaatga tgtctacgca caaataccac 240
tgcgtatgcc ctatgcgcag cgcagaagac cccgaaaggc tcgtatgcta cgcaaagaaa 300
ctggcagcgg cctccgggaa ggtgctggat agagagatcg caggaaaaat caccgacctg 360

```

cagacogtca tggctacgcc agacogtgaa tctoctacct tttgcctgca tacagacgtc 420
 acgtgtcgta cggcagccga agtggccgta taccaggacg tgtatgctgt acatgcacca 480
 acatcgctgt accatcaggc gatgaaaggt gtcagaacgg cgtattggat tgggtttgac 540
 accaccccggt ttatgtttga cgcgctagca ggcgcgtatc caacctacgc cacaaactgg 600
 gccgacgagc aggtgttaca ggccaggaac ataggactgt gtgcagcadc cttgactgag 660
 ggaagactcg gcaaactgtc cttctccgc aagaagcaat tgaaaccttg cgacacagtc 720
 atgttctcgg taggatctac attgtacact gagagcagaa agctactgag gagctggcac 780
 ttacctccg tattccacct gaaaggtaaa caatccttta cctgtaggtg cgataccatc 840
 gtatcatgtg aagggtagct agttaagaaa atcactatgt gcccggcct gtacggtaaa 900
 acggtaggggt acgccgtgac gtatcacgcg gagggattcc tagtgtgcaa gaccacagac 960
 actgtcaaag gagaaagagt ctcatccct gtatgcacct acgtcccctc aaccatctgt 1020
 gatcaaatga ctggcatact agcgaccgac gtcacaccgg aggacgcaca gaagttgtta 1080
 gtgggattga atcagaggat agttgtgaac ggaagaacac agcgaacac taacacgatg 1140
 aagaactatc tgctccgat tgtggccgtc gcatttagca agtgggcgag ggaatacaag 1200
 gcagaccttg atgatgaaa acctctgggt gtccgagaga ggtcacttac ttgctgctgc 1260
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 atagtgaagg tgccttcaga gtttaactcg ttcgtcatcc cgagcctatg gtctacaggc 1380
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 ttaataacctg ttctcgacgc gtcgtcagcc agggatgctg aacaagagga gaaggagag 1500
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 acgggagtcg tcgacgtcga cgttgaagaa ctagagtatc acgcaggtgc aggggtcgtg 1620
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<213> Artificial Sequence

<220>

<223> Sequence of the resynthesized sequence, encoding
for wild type SFV replicase with inserted intron

<400> 9

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<213> Artificial Sequence

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<211> 2174

<212> DNA

<213> Artificial Sequence

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<223> Sequence of RT-13P4

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<210> 13

<211> 2016

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of RT-13M4

<400> 13

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<210> 14

<211> 1790

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of the RT-14

<400> 14

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cgcgagagat taaccaccca cgatggcgcg caaagtgcac gttgatattg aggtgacag 720
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<210> 15

<211> 2396

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of the RT-124

<400> 15

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gacccccgcc cattgacgtc aataatgacg tatgttccca tagtaacgcc aatagggact 180
ttccattgac gtcaatgggt ggagtattta cggtaaactg cccacttggc agtacatcaa 240
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<210> 16

<211> 1853

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of the RT-1(2A)4

<400> 16

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aagatctata ctagtatatg cggccgctaa gttagggtag gcaatggcat tgatatagca 1020
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<210> 17

<211> 2465

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of the RT-12(2A)4

<400> 17

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gcaggagact gacaaagaca cactcatctt ggatatcggc agtgccctt caaggtgagt 900

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gtacc 2465

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<210> 18

<211> 2296

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of the RT-1(SL2-PL)24

<400> 18

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<213> Artificial Sequence

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LTR promoter. Heterologous rabbit beta-globin gene
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<213> Artificial Sequence

<220>

<223> pheIF4A1-Nspl234 is 10248bp plasmid vector

expresses codon optimised SFV replicase from human

eIF4A1 promoter promoter. Heterologous rabbit

beta-globin gene derived intron is introduced into

the replicase coding sequence

<400> 21

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<212> DNA

<213> Artificial Sequence

<220>

<223> pHEFlaHTLV-Nspl234 is 10258bp plasmid vector
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```

<210> 28

<211> 85

<212> DNA

<213> Artificial Sequence

<220>

<223> 85bp long cis-sequence of 5' end of the SFV genome

<400> 28

```

atggcgcatg tgtgacatac acgacgcca aagattttgt tccagctcct gccacctccg 60
ctacgcgaga gattaaccac ccacg 85

```

<210> 29

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> 51 b long cis-sequence which may be incorporated

into the replicase template expression unit. For SFV it maps to region of nspl,178-228 b from the 5' end of SFV genome

<400> 29

gcaggtcaca ccaaagacc atgcaaagc cagagcattt tcgacactgg c 51

<210> 30

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' end of the SFV genome

<221> polyA_signal

<222> (62)...(62)

<223> This A is repeated at least 20 times, i.e. the poly A track comprises at least 20 A residues in total

<400> 30

agcttaattc gacgaataat tggattttta ttttattttg caattgggtt ttaatatattc 60
ca 62

<210> 31

<211> 275

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' end region of the SFV genomic RNA

<400> 31

atggcggatg tgtgacatac acgacgcaa aagattttgt tccagctcct gccacctccg 60
ctacgcgaga gattaaccac ccacgatggc cgccaaagtg catgttgata ttgaggctga 120
cagcccatte atcaagtctt tgcagaaggc attccgtcg ttcgaggtgg agtcattgca 180
ggtcacacca aatgaccatg caaatgccag agcattttcg cacctggcta ccaaattgat 240

cgagcaggag actgacaaaag acacactcat cttgg

275

<210> 32

<211> 280

<212> DNA

<213> Artificial Sequence

<220>

<223> SFV part in fragment 1 (up to EcoRV site used for cloning)

<400> 32

atggcggatg tgtgacatac acgacgccaa aagatTTTgt tccagctcct gccacctccg 60
ctacgcgaga gattaaccac ccacgatggc cgccaaagtg catgttgata ttgaggctga 120
cagccattc atcaagtctt tgcagaaggc atttccgtcg ttcgagggtg agtcattgca 180
ggtcacacca aatgaccatg caaatgccag agcattttcg cacctggcta ccaaattgat 240
cgagcaggag actgacaaaag acacactcat cttggatata 280

<210> 33

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> SFV part surrounding intron

<221> intron

<222> (17)...(18)

<223> Intron is inserted in between bases 17 and 18

<400> 33

ggcagtgcgc cttcaaggag aatgatg

27

<210> 34

<211> 573

<212> DNA

<213> Artificial Sequence

<220>

<223> Intron from rabbit beta globin gene

<221> variation

<222> (118)...(118)

<223> In RT templates this position is C

<400> 34

```
gtgagtttgg ggacccttga ttgttctttc tttttcgcta ttgtaaaatt catgttatat 60
ggaggggggca aagttttcag ggtgttggtt agaatgggaa gatgtccctt gtatcactat 120
ggaccctcat gataattttg tttctttcac tttctactct gttgacaacc attgtctcct 180
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cttattggta gaaacaacta caccctggtc atcatcctgc ctttctcttt atggttacaa 480
tgatatacac tgtttgagat gaggataaaa tactctgagt ccaaaccggg cccctctgct 540
aaccatgttc atgccttctt ctttttcta cag 573
```

<210> 35

<211> 201

<212> DNA

<213> Artificial Sequence

<220>

<223> subgenomic promoter region of SFV

<221> variation

<222> (5)...(5)

<223> In RT templates it is G in this position.

<400> 35

```
cttgagggcc gaactggagg tggcactaac atctaggtat gaggtagagg gctgcaaaag 60
tatcctcata gccatggcca ccttggcgag ggacattaag gcgtttaaga aattgagagg 120
acctgttata cacctctacg gcggtcctag attggtgcgt taatacacag aattctgatt 180
atagcgcact attatagcac c 201
```

<210> 36

<211> 265

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' end of the SFV genome together with a polyA
tail (A)_n is a poly(A) track consisting of at
least 20 A-residues

<221> polyA_signal

<222> (265)...(265)

<223> This A is repeated at least 20 times, i.e. the
poly A track is at least 20 A residues long

<400> 36

```
taagttaggg taggcaatgg cattgatata gcaagaaaat tgaaaacaga aaaagttagg 60
gtaagcaatg gcatataacc ataactgtat aacttgtaac aaagcgcaac aagacctgcg 120
caattggccc cgtgggtccgc ctcacggaaa ctcggggcaa ctcatttga cacattaatt 180
ggcaataatt ggaagcttac ataagcttaa ttcgacgaat aattggattt ttattttatt 240
ctgcaattgg tttttaatat ttcca                                     265
```

<210> 37

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> hepatitis delta virus ribozyme structure

<400> 37

```
gggtcgcat ggcattctcca cctctctcg gtccgacctg ggcattccgaa ggaggacgca 60
cgtccactcg gatggctaag ggag                                     84
```

<210> 38

<211> 307

<212> DNA

<213> Artificial Sequence

<220>

<223> After joining the cloning fragments and splicing of
the intron all sequence gets together into 307 b
sequence of SFV

<221> mutation

<222> (295)...(295)

<223> Point mutation to facilitate splicing

<400> 38

```
atggcggatg tgtgacatac acgacgccaa aagattttgt tccagctcct gccacctccg 60
ctacgcgaga gattaaccac ccacgatggc cgccaaagtg catgttgata ttgaggctga 120
cagcccatc atcaagtctt tgcagaaggc atttcogtcg ttcgaggtgg agtcattgca 180
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cgagcaggag actgacaaaag acacactcat cttggatatc ggcagtgcgc cttcaaggag 300
aatgatg                                           307
```