

Sequenced genome segments of subtype 3e strain 14-22707

Sequence Segment	Location (on 14-16753 genome, nested Primer excluded)	First round PCR	Primer Nested PCR	Sequencing
5'n_2n T _{Af} = 68 °C T _{An} = 68 °C	-7 – 315	5'-RACE_s 5'-GS2n_as LUP SUP	NUP 5'-GS4_as	Sn_s 5'-GS4n_as
5'n_4 T _{Af} = 58 °C T _{An} = 58 °C	-7 – 175	5'-RACE_s 5'-GS4_as LUP SUP	NUP 5'-GS4n_as	1_s 5'-GS4n_as
Sn T _{Af} = 58 °C T _{An} = 58 °C	132 – 565	S_s S_as	Sn_s Sn_as	Sn_s 2_s 1_as Sn_as
2n_12 T _{Af} = 58 °C T _{An} = 58 °C	473 – 1031	1_s 3_as_m1	2_s 2_as_m1	2_s 2_as_m1
A1 T _{Af} = 58 °C T _{An} = 58 °C	750 – 1198	A_s A_as	An1_s An1_as	An1_s An1_as
Fn11 T _{Af} = 58 °C T _{An} = 58 °C	1127 – 2065	F1_s F1_as	Fn1_s Fn1_as	Fn1_s Fun2_s 3_as_m1 Fun2_as Fn1_as
Fn22 T _{Af} = 58 °C T _{An} = 58 °C	1164 – 2082	F2_s F2_as	Fn2_s Fn2_as	Fn2_s 4_s 3_as_m1 Fun2_as Fn2_as
3n_12 T _{Af} = 58 °C T _{An} = 58 °C	1985 – 2405	1500_s_m1 3200_as_m1	5_s_m1 ins_as	ins_as
Hn11 T _{Af} = 58 °C T _{An} = 58 °C	2040 – 2346	H1_s H1_as	H1n_s H1n_as	H1n_s F2_as H1n_as
Gn11 T _{Af} = 58 °C T _{An} = 58 °C	2284 – 3939	G1_s G1_as	G2/Gn1_s Gn1_as	G2/Gn1_s Gun2s Gun2_as Bn1_as Gun3_as

Gn22 T _{Af} = 68 °C T _{An} = 68 °C	2326 – 4075	G2/Gn1_s G2_as	Gn2_s Gn2_as	Gn1_as Gn2_s Gun3_s Gun2_as Gun3_as Gun4_as Gn2_as
In11 T _{Af} = 58 °C T _{An} = 58 °C	3484 – 4271	I1_s I1_as	I1n_s I1n_as	I1n_s 8_s 9_s_m1 Gun3_as Gn1_as Gn2_as I1n_as
C1 T _{Af} = 58 °C T _{An} = 68 °C	3903 – 4340	C/Bn2_s C_as	Cn1_s B/Cn1_as	B/Cn1_as
6n_12 T _{Af} = 58 °C T _{An} = 58 °C	4107 – 4628	8_s 10_as	9_s_m1 9_as_m1	9_s_m1 9_as_m1
Jn11 T _{Af} = 58 °C T _{An} = 58 °C	4509 – 4687	J1_s J1_as	J1n_s J1n_as	J1n_s 9_as_m1 J1n_as
7n_12 T _{Af} = 58 °C T _{An} = 58 °C	4604 – 5832	9_s_m1 12_as_m1	10_s_m1 11_as	10_s_m1 Dn1_s 11_s-neu 10_as 11_as
6n_7 T _{Af} = 58 °C T _{An} = 58 °C	5305 – 6333	10_s_m1 13_as_m1	11_s-neu 12_as_m1	11_s-neu 12_s 11_as 12_as_m1
Kn11 T _{Af} = 58 °C T _{An} = 58 °C	5717 – 5923	K1_s K1_as	K1n_s K1n_as	K1n_s 12_s 11_as K1n_as
8n_12 T _{Af} = 58 °C T _{An} = 58 °C	6303 – 6840	12_s 14_as_m1	13_s 13_as_m1	13_s 13_as_m1
9n_12 T _{Af} = 58 °C T _{An} = 58 °C	6822 – 7212	13_s 14_as_m1	14_s_m1 14_as_m1	14s_m1 14_as_m1
3'n_2 T _{Af} = 68 °C	6609 – 7256	3'-GS2_s 3'-RACE_as	3'-GSn2_s NUP	3'-GSn2_s 3'-GS3_s

T _{An} = 68 °C			LUP SUP		3'-GSn3_s
3'n	6723 – 7256		3'-GS1_s	3'-GS1n_s	14_s_m1
T _{Af} = 68 °C			3'-RACE_as	NUP	14_as_m1
T _{An} = 68 °C			LUP SUP		
3'n_3	7079 – 7256		3'-GS3_s	3'-GSn3_s	3'-GSn3_s
T _{Af} = 68 °C			3'-RACE_as	NUP	14_as_m1
T _{An} = 68 °C			LUP SUP		

Table S2. Summary of overlapping genome regions sequenced from subtype 3e strain 14-22707. First round PCR primers were added to the RT-mix which was introduced into the first round PCR-mix after transcription. Smart Primer were added to the smart cDNA-mix which was partly used in the first round PCR-mix after smart cDNA-synthesis. T_{Af}, annealing temperature of first round PCR; T_{An}, annealing temperature of nested PCR.