

Sequenced genome segments of subtype 3c strain 14-16753

Sequence Segment	Location (on 14-16753 genome, nested Primer excluded)	First round PCR	Primer Nested PCR	Sequencing
5'n T _{Af} = 68 °C T _{An} = 68 °C	-7 – 483	5'-RACE_s 5'-GS1_as LUP SUP	NUP 5'-GS1n_as	NUP 1_s S_s Sn_s 289_as 393_as 440_as 5'-GS1n_as
Sn T _{Af} = 58 °C T _{An} = 58 °C	132 – 565	S_s S_as	Sn_s Sn_as	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 3_s 2_as_m1 An1_as
2n_7 T _{Af} = 58 °C T _{An} = 58 °C	999 – 2042	2_s 3200_as_m1	3_s 4_as_m1	3_s 4_s 1500s_m1 3_as_m1 1800_as_m1 4_as_m1
A2 T _{Af} = 68 °C T _{An} = 68 °C	1689 – 2117	A_s Aas	An2_s An2_as	An2_s 5_s_m1 1800_as_m1 4_as_m1 An2_as
3n_12 T _{Af} = 58 °C T _{An} = 58 °C	1985 – 2405	1500_s_m1 3200_as_m1	5_s_m1 ins_as	5_s_m1 ins_s_m1 ins_as
4n_12 T _{Af} = 58 °C T _{An} = 58 °C	2254 – 2994	5_s_m1 3800_as_m1	ins_s_m1 3200_as_m1	ins_s_m1 2600s ins_as 3200_as_m1
B1 T _{Af} = 58 °C T _{An} = 58 °C	2750 – 3206	B_s B/Cn1_as	Bn1_s Bn1_as	Bn1_s 3150_s_m1 3200_as_m1

5n_12 T _{Af} = 68 °C T _{An} = 68 °C	2986 – 4118	2600_s 9_as_m1	3150_s_m1 8_as	Bn1_as 3150_s_m1 8_s 3800_as_m1 8_as
B2 T _{Af} = 58 °C T _{An} = 68 °C	3419 – 3872	B_s B/Cn1_as	C/Bn2_s Bn2_as	C/Bn2_s 8_s 3800_as_m1 Bn2_as
C1 T _{Af} = 58 °C T _{An} = 68 °C	3903 – 4340	C/Bn2_s C_as	Cn1_s B/Cn1_as	Cn1_s 9_s_m1 8_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
C2 T _{Af} = 58 °C T _{An} = 58 °C	4416 – 4873	C/Bn2_s C_as	Cn2_s Cn2_as	Cn2_s 10_s_m1 9_as_m1 Cn2_as
7n_12 T _{Af} = 58 °C T _{An} = 58 °C	4604 – 5832	9_s_m1 12_as_m1	10_s_m1 11_as	10s_m1 11_s-neu 10_as 11_as
D1 T _{Af} = 58 °C T _{An} = 68 °C	4983 – 5528	D_s D/En1_as	Dn1_s Dn1_as	Dn1_s 11_s-neu 10_as Dn1_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
D2 T _{Af} = 58 °C T _{An} = 58 °C	5672 – 6126	D_s D/En1_as	E/Dn2_s Dn2_as	E/Dn2_s 12_s 11_as
E1 T _{Af} = 58 °C T _{An} = 68 °C	6076 – 6532	E/Dn2_s E_as	En1_s D/En1_as	En1_s 13_s 12_as_m1 D/En1_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
E2 T _{Af} = 58 °C	6621 – 7067	E/Dn2_s E_as	En2_s En2_as	En2_s 14_s_m1

T _{An} = 68 °C				13_as_m1
				En2_as
9n_12	6822 – 7212	13_s	14_s_m1	14_s_m1
T _{Af} = 58 °C		14_as_m1	14_as_m1	14_as_m1
T _{An} = 58 °C				
3'n	6723 – 7256	3'-GS1_s	3'-GS1n_s	3'-GS1n_s
T _{Af} = 68 °C		3'-RACE_as	NUP	14_s_m1
T _{An} = 68 °C		LUP		13_as_m1
		SUP		14_as_m1

Table S1. Summary of overlapping genome regions sequenced from subtype 3c strain 14-16753. First round PCR primers were added to the RT-mix which was completely 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.