

Sequenced genome segments of subtype 3f-like strain 15-22016

Sequence Segment	Location (on 14-16753 genome, nested Primer excluded)	First round PCR	Primer Nested PCR	Sequencing
5'n_5n T _{Af} = 68 °C T _{An} = 58 °C	-7 – 138	5'-RACE_s 5'-GS5_as LUP SUP	NUP 5'-GS5n_as	1_s 5'-GS5n_as
Sn T _{Af} = 58 °C T _{An} = 58 °C	132 – 565	S_s S_as	Sn_s Sn_as	1_as
427n T _{Af} = 68 °C T _{An} = 58 °C	445 – 852	409_s 897_as	427_s 874_as	427_s 560g_s An1_s 874_as
A1 T _{Af} = 58 °C T _{An} = 68 °C	750 – 1198	A_s A_as	An1_s An1_as	An1_s 3_s 2_as_m1 An1_as
902n T _{Af} = 58 °C T _{An} = 58 °C	920 – 1805	560g_s 3034g_as	902g_s 1825g_as	902g_s 3_s 1542g_s 3_as_m1 1825g_as
1542n T _{Af} = 68 °C T _{An} = 68 °C	1560 – 2521	560g_s 3034g_as	1542g_s 2539g_as	1542g_s 1825g_as 2539g_as
2001n T _{Af} = 58 °C T _{An} = 58 °C	2019 – 2968	560g_s 3034g_as	2001g_s 2986g_as	2001g_s 2418g_s 2757g_s 2539g_as
2418n T _{Af} = 68 °C T _{An} = 68 °C	2438 – 3014	2001g_s 4276g_as	2418g_s 3034g_as	2418g_s 2757g_s 2539g_as 2986g_as 3034g_as
2757n T _{Af} = 58 °C T _{An} = 68 °C	2778 – 3682	2001g_s 4276g_as	2757g_s 3700g_as	2757g_s 3150_s_m1 3553g_s 2986g_as 3034g_as 3700g_as
3553n	3571 – 4121	2001g_s	3553g_s	3553g_s

T _{Af} = 68 °C T _{An} = 68 °C			4276g_as	4143g_as	8_as 4143g_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 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 B/Cn1_as 9_as_m1
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 D_s Dn1_s 11_s-neu C_as 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_as_m1
6196n T _{Af} = 58 °C T _{An} = 58 °C	6217 – 6367		6062_s 6525_as	6196_s 6387_as	6196_s 12_as_m1 6387_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
3'n_4 T _{Af} = 58 °C T _{An} = 58 °C	6756 – 7256		3'-GS4_s 3'-RACE_as LUP SUP	3'-GSn4_s NUP	3'-GSn4s 3'-GS3_s 3'-GSn3_s 14_as_m1

Table S3. Summary of overlapping genome regions sequenced from subtype 3f-like strain 15-22016. 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.