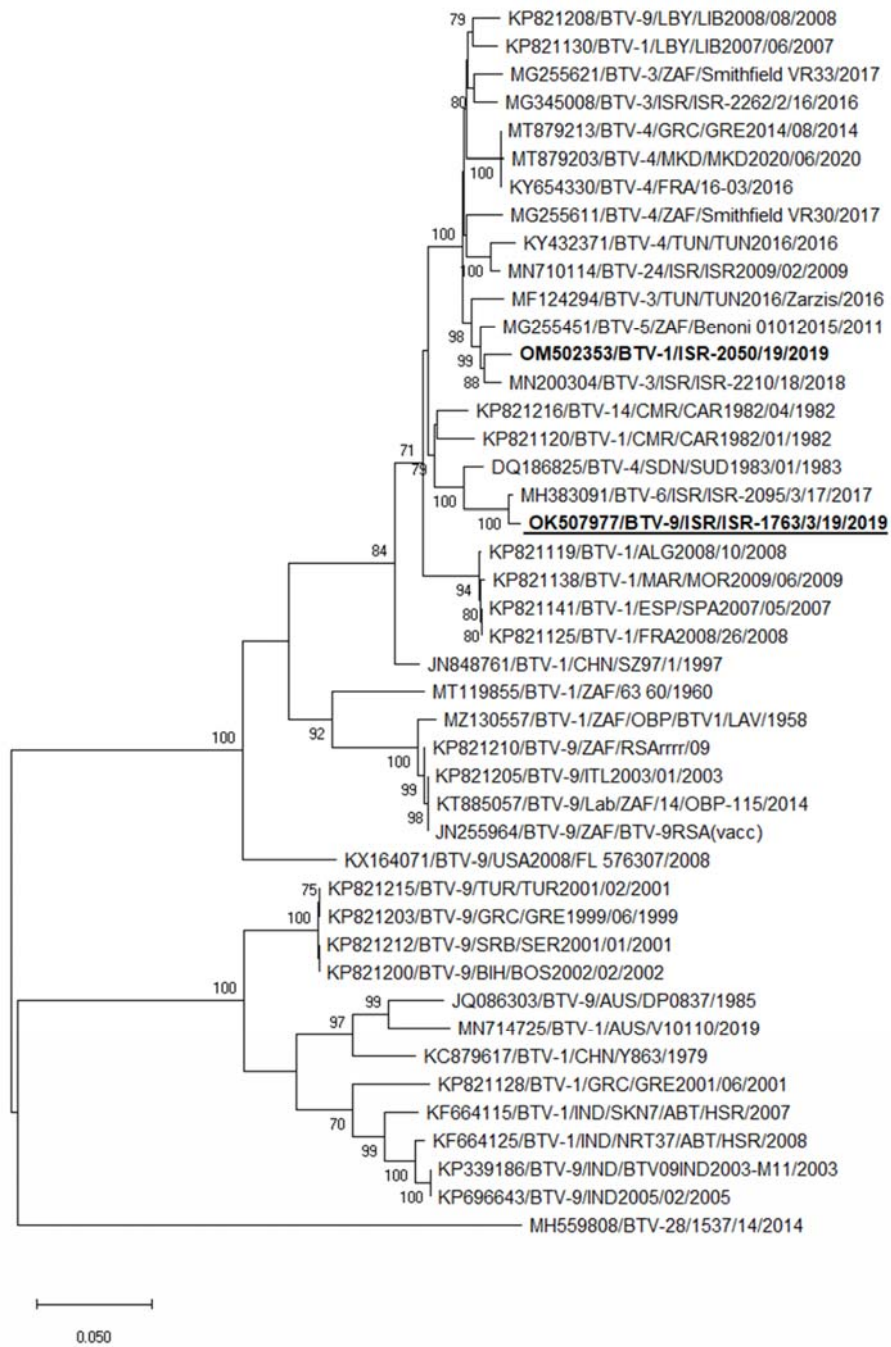
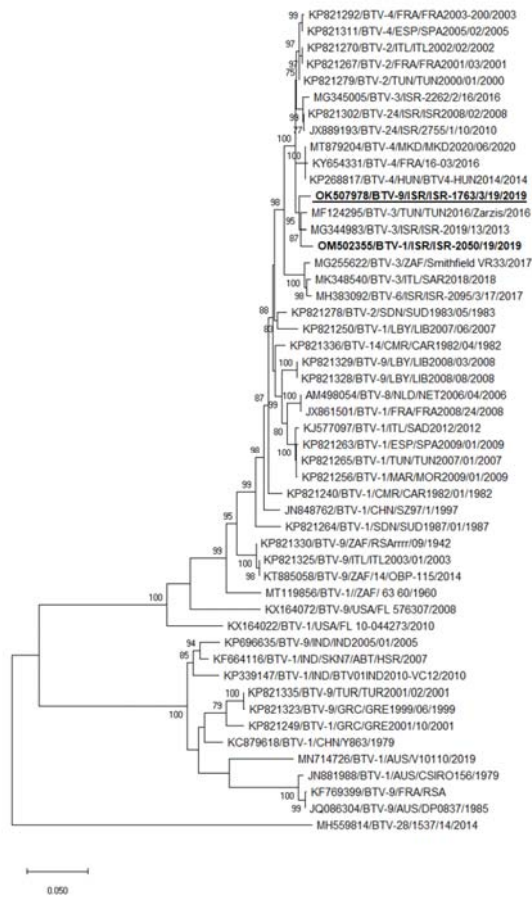


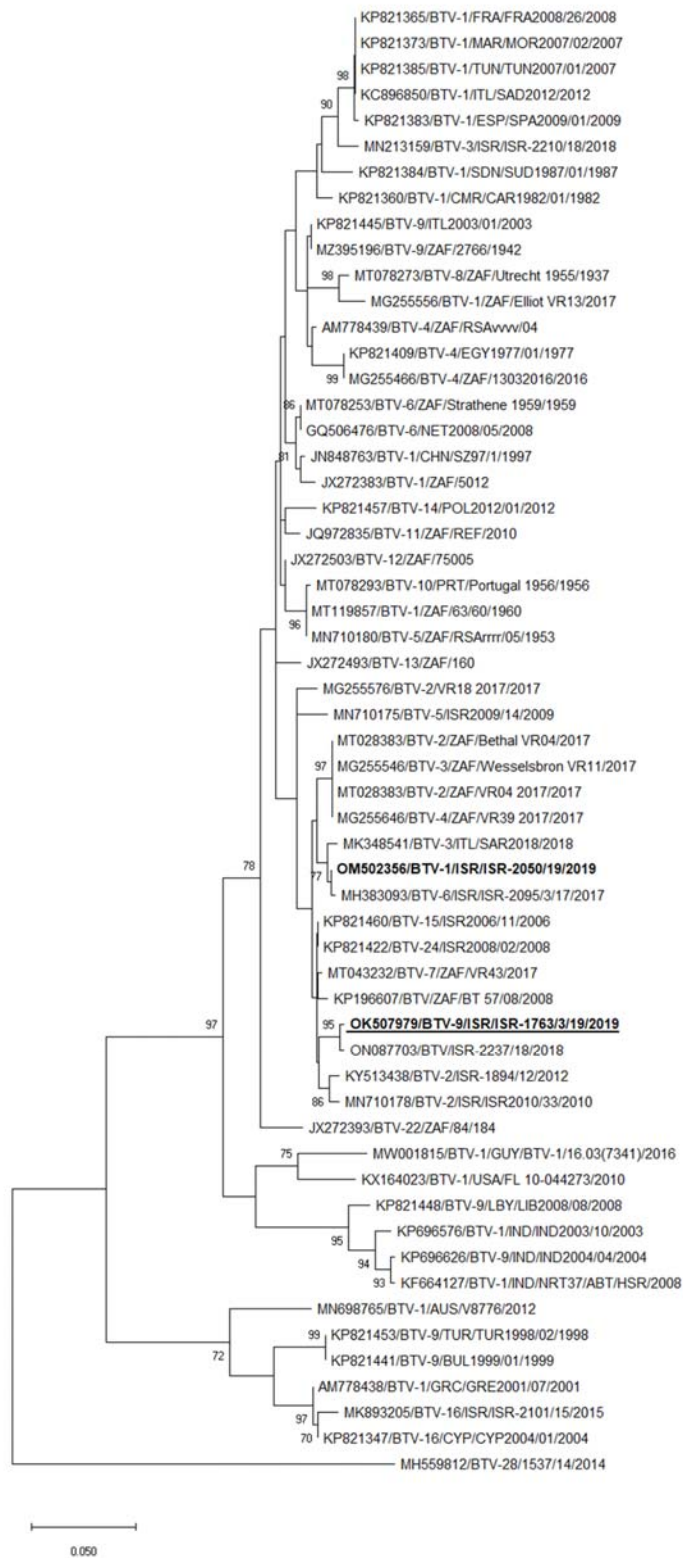
(a)



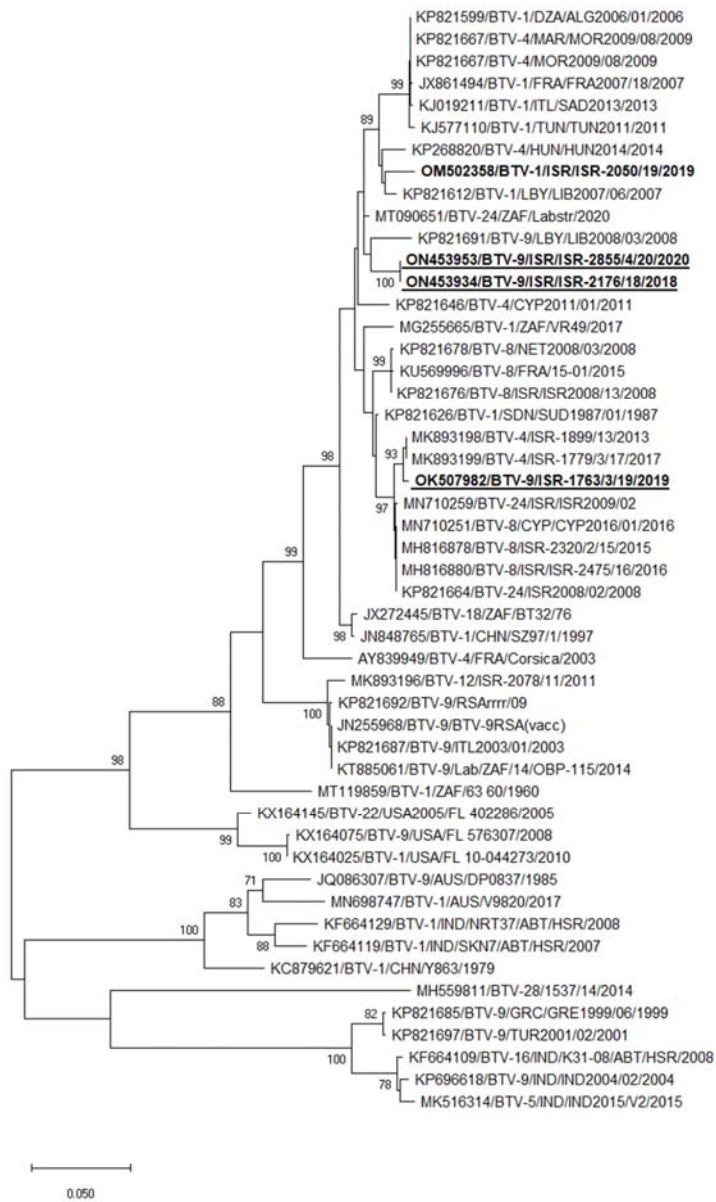
(b)



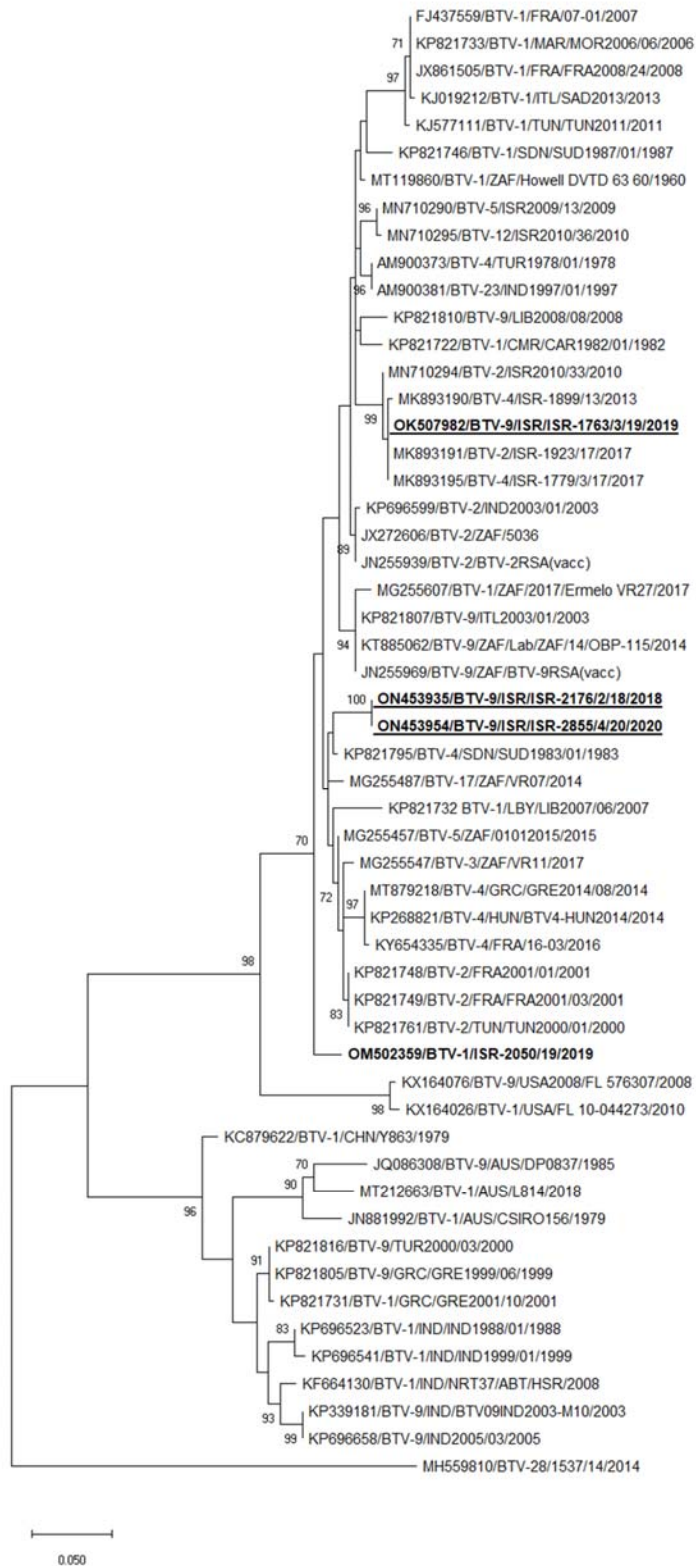
(c)



(d)



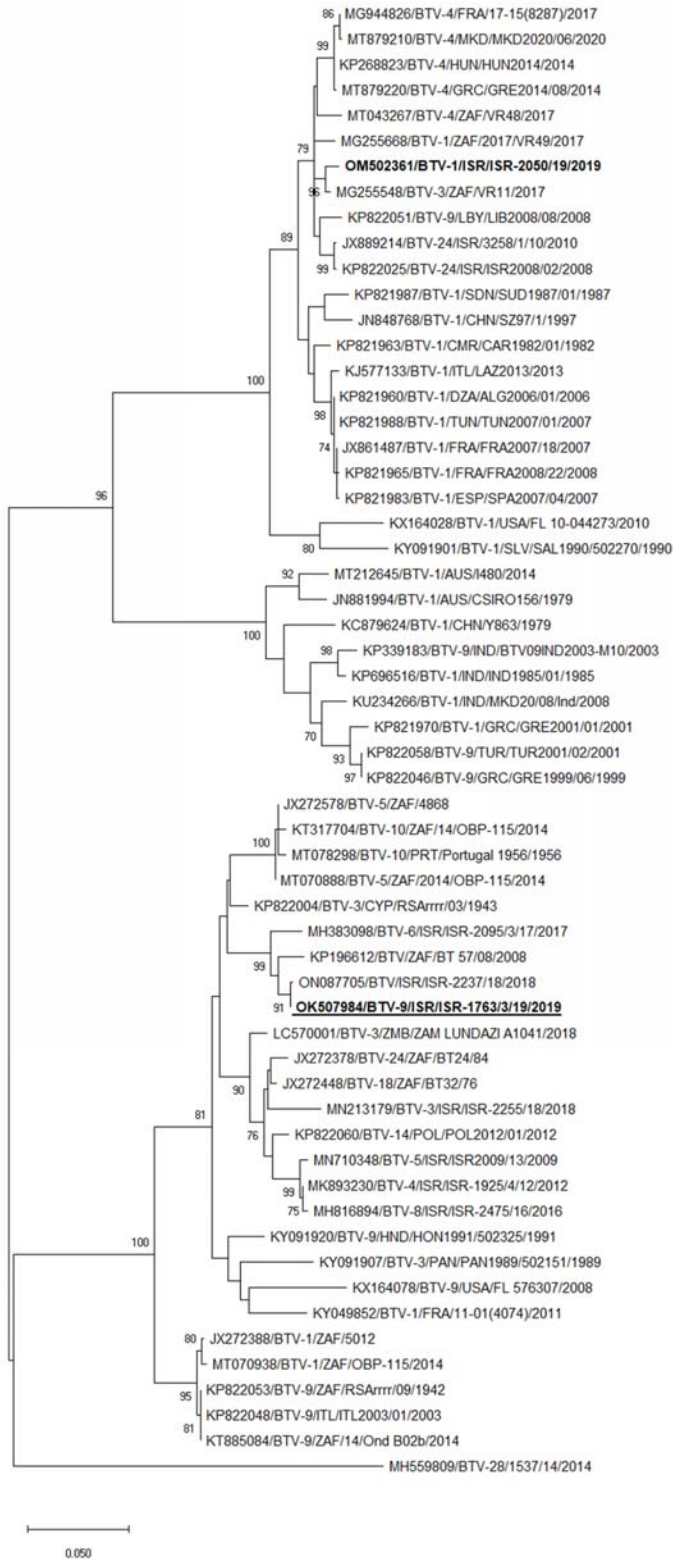
(e)



(f)



(g)



(h)

Figure S1. Phylogenetic trees of Israeli BTV-1 and BTV-9 strains isolated in 2018-2020 and global strains. a) segment 1; b) segment 3; c) segment 4; d) segment 5; e) segment 7; f) segment 8; g) segment 9; e) segment 10. Israeli BTV-1 strain is shown in bold. Israeli BTV-9 strain is shown in bold and is underlined. The phylogeny was inferred using the Maximum Likelihood method and Tamura-Nei model method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. Viruses were identified by accession number/serotype/location/isolate/year.

Table S1. List of primers used for partial sequencing of Israeli bluetongue virus serotype 9

segment	name	sequence	length of product	source
1	UNI-VP1-1-F	GTAAAAATGCAATGGTCGCAAT		this study
	VP1-414R	TAT ATT TGC ATC TCG TTT TTA GC	436	this study
	UNI-VP1-810-R	CCCCACATCTTYACAAACCA	829	this study
	VP1-Uni-2212F	ATA ACA TGG CTA TTG GGA CC		this study
	VP1-Uni-2684R	TCA AAC TTT CTG TCG CGA TAC	493	this study
2	9VP2-1F	GTT AAA AAC GCT GTC CCG AGA		this study
	9VP2-422R	TTC GCA ACM CCA TTC ATA AA	444	this study
	9VP2-950R	TCC GAG AAG AAC ATG GTA TCA	970	this study
	9VP2-150F	AAA GAG CGT AAA GCA ATT GA		this study
	9VP2-507R	CAC ATC TTG TAC CCT GGA ATG	377	this study
3	VP3-Isr-F	GGAGATGTRCTKTCGAGTGATTC		this study
	VP3-Isr-R	CATTAAGYTGTGTGCGGTTGG	958	this study
	BT-S3-F	GTAAATTTCCGTRGCRYATGGC		Sun 2014
	VP3-337R	CCT GCG ACA TCT CTT CAT AGT	352	this study
4	BT-S4-F	GTAAAAACATGCCTGAGCCA		this study
	VP4-281R	ATC TTG ACT TTT TGC GAC TTC C	303	this study
	VP4-516R	TCA GTH GGC TCA TCG TCA AA	536	this study
5	NS1-1191F	TAG TTC GCG ATG AAC AAA TTG G		this study
	uni-NS1-1747R	AAG TTG AAA AGT TCT AGT AGA GTG CT	579	this study
	UNI-NS1-40F	GCGCTTTTTGAGAAAATACAAC		this study
	UNI-NS1-428R	AGAGAATCATCCAATCTAACTCT	411	this study
6	9VP5-1F	GTT AAA AAG CGT ACC CTT AGC		this study
	9VP5-818R	TCA AAT CAA TTC CGC TCA G	836	this study
	9VP5-442R	TTC GCA ACM CCA TTC ATA AA	431	this study
7	VP7-Isr-F	TTTATGTGTTTAGATATGATGCTGT	874	this study
	3VP7-1f-deg	GTAAAAAATHCTAGAGATGGACACT	694	this study
	VP7-Isr-R	TATTCGGCAGTGTAGTTCTGTTTAG		this study

8	BT-S8-F	GTAAAAAAWCCTTGAGTCATG		Sun 2014
	NS2-331R	TCA ACC ATC ACD CCA TTA TGT T	353	this study
	3NS2-350R	GCA TCA ACC ATC ACA CCA TT	370	this study
	UNI-NS2-17F	ATGGAGCAAAAGCAACG		this study
	UNI-NS2-1026R	AGAGACAAAAGCAACACGCT	1026	this study
9	BT-S9-F	GTAAAAAAATCGCATATGTCTRG		Sun 2014
	VP6-448R	TCA ACT TTC GTA CCG TAT TTA GA	471	this study
10	BTV-NS3-183F	AAATMTTGGAYAAAGCRATGTCAAA		Wernike 2015
	NS3-802r-deg	TAA GTG TGT AGY GYC GCG YA	639	this study
	BT-EHD-S10R	ACCCTCCCCCGYTAKACARC	604	this study

Table S2. List of sequenced Israeli BTV strains used for the present study

host/date of sampling/source	segment/ length serotype /strain	1/3944	2/2926-2939	3/2772	4/1981	5/1774-1776	6/1637-1645	7/1156	8/1125-1131	9/1047-1050	10/822
sheep/2018/ whole blood	9/ISR- 2077/3/18	ON453918 12-436	ON453919 1-574	ON453920 18-357	ON453921 1-535	ON453922 52-435	ON453923 46-790	ON453924 14-526	ON453925 11-354	ON453926 1-470	ON453927 120-783
cattle/2018/ whole blood	9/ISR- 2176/2/18	ON453928 12-436	ON453929 153-518	ON453930 18-357	ON453931 24-286	ON453932 1231-1712	ON453933 2-441	ON453934 214-888	ON453935 1-354	ON453936 22-465	ON453937 1-282
sheep/2019/ VI (Vero cells)	9/ISR- 1763/3/19	OK507975 1-3930	OK507976 10-2893	OK507977 4-2768	OK507978 8-1968	OK507979 1-1754	OK507980 13-1625	OK507981 13-1114	OK507982 1-1112	OK507983 1-1036	OK507984 14-794
sheep/2019/ VI (ECE)	9/ISR-1872/19	-	-	-	-	-	-	ON453957 14-881	ON453958 14-1031	ON453959 3-1018	-
sheep/2019/ VI (ECE)	9/ISR-1915/19	-	-	-	-	-	-	ON453960 15-884	ON453961 11-1017	ON453963 5-1008	-
cattle/2019/ VI (ECE)	9/ISR- 2020/2/19	ON453908 1-817	ON453909 153-949	ON453910 91-1015	ON453911 1-535	ON453912 49-435	ON453913 1-829	ON453914 1-874	ON453915 11-1017	ON453916 1-471	ON453917 200-802
sheep/2019/ VI (ECE)	9/ISR- 2077/4/19	-	-	-	-	-	-	ON453963 16-885	ON453964 42-998	ON453965 49-1012	-
sheep/2020/ whole blood	9/ISR- 2758/1/20	ON453938 1-436	ON453939 153-528	ON453940 2196-2758	ON453941 1-257	ON453942 1235-1713	ON494587 1-441	ON453943 246-884	ON453944 11-354	ON453945 1-470	ON453946 200-783
cattle/2020/	9/ISR- 2855/4/20	ON453947	ON453948	ON453949	ON453950	ON453951	ON453952	ON453953	ON453954	ON453955	ON453956

whole blood		1-817	17-949	18-1015	1-535	52-435	1-441	203-884	11-354	1-470	200-783
		OM50236		OM50235	OM50235			OM50235			OM50236
cattle/2019	1/ISR-2050/19	2	OM502353	4	5	OM502356	OM502357	8	OM502359	OM502360	1
VI (Vero cells)		15-3933	5-2768	5-2768	1-1969	1-1771	11-1631	1-1143	17-1113	1-1044	1-822

Upper rows provide accession numbers of sequenced regions. Lower rows show sequences regions. Source- source or sequencing. VI- virus isolation. ECE- embryonated chicken embryos. Strains ISR-2050/19 and ISR-1763/3/19 were sequenced by NGS technology; the last of the strains were sequenced by Sanger sequencing technology.