FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

Genotyping Report

FMDV serotype: O
Country: Vietnam
Year: 2019, 2020
Batch: WRLFMD/2020/00003
No. of sequences: 30
Report date: 9th July 2020
Report generated by: Nick Knowles
Report checked by: Jemma Wadsworth

www: http://www.wrlfmd.org/
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Virus sample name:	VIT/12/2019
Sender reference:	19-5580
Location of origin:	Tien Lanh, Tien Phuoc, Quang Nam
Country of origin:	Vietnam
Date of collection:	26/02/2019
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	24/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 44957, genome 44958, sequence viba_44959, sequencing info 44960

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40632	VIT/20/2018	cattle	99.2	0	O	ME-SA	PanAsia	
viba_40624	VIT/18/2018		99.2	0	O	ME-SA	PanAsia	
viba_40664	VIT/28/2018	porcine	99.2	0	O	ME-SA	PanAsia	
viba_40628	VIT/19/2018	porcine	99.2	0	O	ME-SA	PanAsia	
viba_40692	VIT/35/2018	cattle	98.6	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	98.3	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	98.3	0	O	ME-SA	PanAsia	
viba_37707	LAO/1/2018	cattle	98.1	0	O	ME-SA	PanAsia	
viba_40576	VIT/3/2018	cattle	98.1	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	97.9	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	90.8	0	O	ME-SA	PanAsia	
viba_293	BHU/3/2009	cattle	90.7	0	O	ME-SA	Ind-2001	d
viba_705	KUW/3/97	bovine	90.7	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	90.1	0	O	ME-SA	Ind-2001	c
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_541	OMN/7/2001	bovine	90.0	0	O	ME-SA	Ind-2001	b
viba_359	Manisa/TUR/69		89.9	0	O	ME-SA		
viba_30238	MUR/19/2016	cattle	89.5	0	O	ME-SA	Ind-2001	e
viba_491	TUR/257/2008		89.4	0	O	ME-SA	PanAsia-2	TER-08
viba_766	IRN/31/2009	cattle	89.3	0	O	ME-SA	PanAsia-2	FAR-09

Virus sample name:	VIT/13/2019
Sender reference:	19-5823
Location of origin:	Minh Thanh, Dau Tieng, Binh Duong
Country of origin:	Vietnam
Date of collection:	27/02/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 45001, genome 45005, sequence viba_45006, sequencing info 45007

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_44963	VIT/15/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_44061	VN12/2018		99.7	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_40760	VIT/11/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_44085	VN35/2019		99.7	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	99.7	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.5	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_523	K83/79		83.7	0	O	EA-1		
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/13/2019
Sender reference:	19-5823
Location of origin:	Minh Thanh, Dau Tieng, Binh Duong
Country of origin:	Vietnam
Date of collection:	27/02/2019
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 45001, genome 45002, sequence viba_45003, sequencing info 45004

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45018	VIT/6/2020	cattle	100.0	0	O	ME-SA	Ind-2001	e
viba_45010	VIT/3/2020	cattle	100.0	0	O	ME-SA	Ind-2001	e
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.9	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.9	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.3	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.3	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		87.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_285	UKG/35/2001	porcine	87.7	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	87.3	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.2	0	O	ME-SA		

Virus sample name:	VIT/14/2019
Sender reference:	19-7129-A
Location of origin:	Dak To Kan, Tu Mo Rong, Kon Tum
Country of origin:	Vietnam
Date of collection:	15/03/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020

VIBASys IDs: sample 45039, genome 45040, sequence viba_45041, sequencing info 45042

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40744	VIT/4/2019	porcine	99.2	0	O	SEA	Mya-98	
viba_40644	VIT/23/2018	porcine	99.1	0	O	SEA	Mya-98	
viba_40736	VIT/1/2019	porcine	99.1	0	O	SEA	Mya-98	
viba_40700	VIT/37/2018	porcine	98.9	0	O	SEA	Mya-98	
viba_44963	VIT/15/2019	porcine	98.9	0	O	SEA	Mya-98	
viba_44061	VN12/2018		98.9	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	98.9	0	O	SEA	Mya-98	
viba_40760	VIT/11/2019	porcine	98.9	0	O	SEA	Mya-98	
viba_44085	VN35/2019		98.9	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	98.9	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	89.6	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	86.4	0	O	SEA		
viba_766	IRN/31/2009	cattle	83.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_576	IND/R2/75		83.5	0	O	ME-SA		
viba_850	NEP/1/2015	cattle	83.5	1	O	ME-SA	PanAsia-2	KAT-15
viba_523	K83/79		83.5	0	O	EA-1		
viba_354	PAK/16/2010	cattle	83.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_666	IRN/18/2010	cattle	83.3	0	O	ME-SA	PanAsia-2	BAL-09
viba_650	IRN/8/2005	ovine	83.0	0	O	ME-SA	PanAsia-2	
viba_285	UKG/35/2001	porcine	82.9	0	O	ME-SA	PanAsia	

Virus sample name:	VIT/15/2019
Sender reference:	19-38698/19-035
Location of origin:	Tan Loc, Thoi Binh, Ca Mau
Country of origin:	Vietnam
Date of collection:	19/03/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	26/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 44961, genome 44962, sequence viba_44963, sequencing info 44964

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_44061	VN12/2018		100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40760	VIT/11/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_44085	VN35/2019		100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_523	K83/79		83.7	0	O	EA-1		
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/16/2019
Sender reference:	19-38698/19-051
Location of origin:	Tan Phu Thanh, Chau Thanh, Hau Giang
Country of origin:	Vietnam
Date of collection:	31/03/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020

VIBASys IDs: sample 45043, genome 45044, sequence viba_45045, sequencing info 45046

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40732	VIT/46/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_44963	VIT/15/2019	porcine	99.5	0	O	SEA	Mya-98	
viba_44061	VN12/2018		99.5	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.5	0	O	SEA	Mya-98	
viba_40760	VIT/11/2019	porcine	99.5	0	O	SEA	Mya-98	
viba_44085	VN35/2019		99.5	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.5	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		83.4	0	O	ME-SA	PanAsia-2	ANT-10

Virus sample name:	VIT/17/2019
Sender reference:	19-11868
Location of origin:	Khanh Binh, Khanh Vinh, Khanh Hoa
Country of origin:	Vietnam
Date of collection:	20/05/2019
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 44965, genome 44966, sequence viba_44967, sequencing info 44968

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	100.0	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	100.0	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.8	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45069	VIT/34/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	96.1	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	94.0	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.2	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		88.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.4	0	O	ME-SA		

Virus sample name:	VIT/18/2019
Sender reference:	19-38698/19-1755
Location of origin:	Phuong 1, Nga Nam, Soc Trang
Country of origin:	Vietnam
Date of collection:	26/07/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020

VIBASys IDs: sample 45047, genome 45048, sequence viba_45049, sequencing info 45050

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_44963	VIT/15/2019	porcine	99.5	0	O	SEA	Mya-98	
viba_44061	VN12/2018		99.5	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.5	0	O	SEA	Mya-98	
viba_40760	VIT/11/2019	porcine	99.5	0	O	SEA	Mya-98	
viba_44085	VN35/2019		99.5	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	99.5	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.2	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.4	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_666	IRN/18/2010	cattle	84.0	0	O	ME-SA	PanAsia-2	BAL-09
viba_354	PAK/16/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_523	K83/79		83.9	0	O	EA-1		
viba_285	UKG/35/2001	porcine	83.6	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	83.5	0	O	ME-SA	PanAsia-2	
viba_694	CAM/3/98	bovine	83.4	0	O	SEA	Cam-94	

Virus sample name:	VIT/19/2019
Sender reference:	19-38731/19-3225-1
Location of origin:	Dap Thanh, Ba Che, Quang Ninh
Country of origin:	Vietnam
Date of collection:	28/08/2019
Host species:	water buffalo
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 44969, genome 44970, sequence viba_44971, sequencing info 44972

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36493	VIT/32/2017	bovine	97.9	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	97.9	0	O	ME-SA	PanAsia	
viba_37688	TAI/3/2018	cattle	97.8	0	O	ME-SA	PanAsia	
viba_37696	TAI/5/2018	cattle	97.8	0	O	ME-SA	PanAsia	
viba_40580	VIT/5/2018	porcine	97.8	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	97.6	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	97.6	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	97.6	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	97.6	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	97.6	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_293	BHU/3/2009	cattle	91.5	0	O	ME-SA	Ind-2001	d
viba_705	KUW/3/97	bovine	91.0	0	O	ME-SA	Ind-2001	a
viba_285	UKG/35/2001	porcine	90.5	0	O	ME-SA	PanAsia	
viba_541	OMN/7/2001	bovine	90.4	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		89.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_397	UAE/4/2008	gazelle	89.3	0	O	ME-SA	Ind-2001	c
viba_30238	MUR/19/2016	cattle	89.3	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.1	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		88.8	0	O	ME-SA		

Virus sample name:	VIT/20/2019
Sender reference:	19-38731/19-4008
Location of origin:	Quang Lac, Lang Son, Lang Son
Country of origin:	Vietnam
Date of collection:	11/11/2019
Host species:	water buffalo
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	24/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 44973, genome 44974, sequence viba_44975, sequencing info 44976

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44991	VIT/29/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.7	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.2	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		88.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.4	0	O	ME-SA		

Virus sample name:	VIT/21/2019
Sender reference:	19-36675
Location of origin:	Cam Hung, Cam Xuyen, Ha Tinh
Country of origin:	Vietnam
Date of collection:	12/11/2019
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020

VIBASys IDs: sample 45051, genome 45052, sequence viba_45053, sequencing info 45054

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.8	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.8	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.8	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.8	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45069	VIT/34/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.9	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.8	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.0	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.7	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.7	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.0	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		87.8	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.7	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.2	0	O	ME-SA		

Virus sample name:	VIT/22/2019
Sender reference:	19-38698/19-4234
Location of origin:	Hoa Tan, Cau Ke, Tra Vinh
Country of origin:	Vietnam
Date of collection:	16/11/2019
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020
VIBASys IDs: sample 45055, genome 45056, sequence viba_45057, sequencing info 45058	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.8	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.8	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.8	0	O	ME-SA	Ind-2001	e
viba_45014	VIT/4/2020	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.8	0	O	ME-SA	Ind-2001	e
viba_44999	VIT/32/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45030	VIT/12/2020	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.9	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.8	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.3	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	91.0	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	90.1	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		88.2	0	O	ME-SA	PanAsia-2	ANT-10
viba_285	UKG/35/2001	porcine	88.2	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	88.0	0	O	ME-SA	PanAsia-2	
viba_666	IRN/18/2010	cattle	87.4	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/23/2019
Sender reference:	20-3829/19F-87
Location of origin:	Quang Chu, Cho Moi, Bac Kan
Country of origin:	Vietnam
Date of collection:	19/11/2019
Host species:	water buffalo
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020

VIBASys IDs: sample 45059, genome 45060, sequence viba_45061, sequencing info 45062

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.8	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.8	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.8	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.8	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45069	VIT/34/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	96.2	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.8	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.3	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	91.0	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	90.1	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.3	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		88.2	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	88.0	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.5	0	O	ME-SA		

Virus sample name:	VIT/25/2019
Sender reference:	19-36995
Location of origin:	Phu Cuong, Cai Lay, Tien Giang
Country of origin:	Vietnam
Date of collection:	26/11/2019
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	25/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020
VIBASys IDs: sample 44977, genome 44978, sequence viba_44979, sequencing info 44980	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	100.0	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	100.0	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.8	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45069	VIT/34/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	96.1	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	94.0	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.2	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		88.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.4	0	O	ME-SA		

Virus sample name:	VIT/27/2019
Sender reference:	19-38316
Location of origin:	My Tan, Cao Lanh, Dong Thap
Country of origin:	Vietnam
Date of collection:	28/11/2019
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020
VIBASys IDs: sample 44981, genome 44982, sequence viba_44983, sequencing info 44984	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	100.0	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.8	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45069	VIT/34/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	96.1	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	94.0	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.2	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		88.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.4	0	O	ME-SA		

Virus sample name:	VIT/28/2019
Sender reference:	19-38379
Location of origin:	Phuoc My, Phuoc Son, Quang Nam
Country of origin:	Vietnam
Date of collection:	30/11/2019
Host species:	water buffalo
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 44985, genome 44986, sequence viba_44987, sequencing info 44988

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	100.0	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.8	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45069	VIT/34/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	96.1	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	94.0	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.2	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		88.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.4	0	O	ME-SA		

Virus sample name:	VIT/29/2019
Sender reference:	19-38731/19-4183-1
Location of origin:	Dan Chu, Hoa An, Cao Bang
Country of origin:	Vietnam
Date of collection:	03/12/2019
Host species:	water buffalo
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	24/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020
VIBASys IDs: sample 44989, genome 44990, sequence viba_44991, sequencing info 44992	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44975	VIT/20/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45030	VIT/12/2020	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.7	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.2	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		88.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.4	0	O	ME-SA		

Virus sample name:	VIT/31/2019
Sender reference:	19-38909
Location of origin:	Thanh Binh, Bu Dop, Binh Phuoc
Country of origin:	Vietnam
Date of collection:	08/12/2019
Host species:	cattle
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	26/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020
VIBASys IDs: sample 44993, genome 44994, sequence viba_44995, sequencing info 44996	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40732	VIT/46/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_44963	VIT/15/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_44061	VN12/2018		99.7	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_40760	VIT/11/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_44085	VN35/2019		99.7	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.7	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_354	PAK/16/2010	cattle	83.8	0	O	ME-SA	PanAsia-2	PUN-10
viba_850	NEP/1/2015	cattle	83.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_576	IND/R2/75		83.4	0	O	ME-SA		
viba_523	K83/79		83.4	0	O	EA-1		
viba_285	UKG/35/2001	porcine	83.4	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	83.3	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/32/2019
Sender reference:	19-39050
Location of origin:	Hoa Loc, Tam B?nh, Vinh Long
Country of origin:	Vietnam
Date of collection:	11/12/2019
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020
VIBASys IDs: sample 44997, genome 44998, sequence viba_44999, sequencing info 45000	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45057	VIT/22/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_45014	VIT/4/2020	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45030	VIT/12/2020	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	96.1	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		88.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_285	UKG/35/2001	porcine	88.0	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_666	IRN/18/2010	cattle	87.2	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/33/2019
Sender reference:	19-39383
Location of origin:	My Binh, Tan Tru, Long An
Country of origin:	Vietnam
Date of collection:	16/12/2019
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020

VIBASys IDs: sample 45063, genome 45064, sequence viba_45065, sequencing info 45066

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45057	VIT/22/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_45014	VIT/4/2020	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44999	VIT/32/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45030	VIT/12/2020	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.7	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	91.2	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		88.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_285	UKG/35/2001	porcine	88.0	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_666	IRN/18/2010	cattle	87.2	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/34/2019
Sender reference:	19-39627
Location of origin:	An Hoa Tay, Ba Tri, Ben Tre
Country of origin:	Vietnam
Date of collection:	19/12/2019
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020
VIBASys IDs: sample 45067, genome 45068, sequence viba_45069, sequencing info 45070	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.7	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	94.0	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.3	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		88.2	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	88.0	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.5	0	O	ME-SA		

Virus sample name:	VIT/35/2019
Sender reference:	20-3829/19F-117
Location of origin:	Nam Lu, Muong Khuong, Lao Cai
Country of origin:	Vietnam
Date of collection:	25/12/2019
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020
VIBASys IDs: sample 45071, genome 45072, sequence viba_45073, sequencing info 45074	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e
viba_45069	VIT/34/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.7	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	94.0	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.9	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.5	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.6	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_285	UKG/35/2001	porcine	87.9	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		87.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_359	Manisa/TUR/69		87.4	0	O	ME-SA		

Virus sample name:	VIT/3/2020
Sender reference:	20-1606
Location of origin:	Pho Thanh, Duc Pho, Quang Ngai
Country of origin:	Vietnam
Date of collection:	15/01/2020
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020
VIBASys IDs: sample 45008, genome 45009, sequence viba_45010, sequencing info 45011	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45018	VIT/6/2020	cattle	100.0	0	O	ME-SA	Ind-2001	e
viba_45003	VIT/13/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.9	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.9	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.3	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.3	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		87.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_285	UKG/35/2001	porcine	87.7	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	87.3	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.2	0	O	ME-SA		

Virus sample name:	VIT/4/2020
Sender reference:	20-1775
Location of origin:	Thanh Tri, Go Cong Tay, Tien Giang
Country of origin:	Vietnam
Date of collection:	20/01/2020
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 45012, genome 45013, sequence viba_45014, sequencing info 45015

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45057	VIT/22/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44999	VIT/32/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45030	VIT/12/2020	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.7	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.8	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		88.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	88.2	0	O	ME-SA	PanAsia-2	
viba_285	UKG/35/2001	porcine	88.0	0	O	ME-SA	PanAsia	
viba_666	IRN/18/2010	cattle	87.5	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/6/2020
Sender reference:	20-2248
Location of origin:	Binh Phu, Binh Son, Quang Ngai
Country of origin:	Vietnam
Date of collection:	22/01/2020
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	25/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020
VIBASys IDs: sample 45016, genome 45017, sequence viba_45018, sequencing info 45019	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45010	VIT/3/2020	cattle	100.0	0	O	ME-SA	Ind-2001	e
viba_45003	VIT/13/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.9	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.9	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.3	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.3	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		87.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_285	UKG/35/2001	porcine	87.7	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	87.3	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.2	0	O	ME-SA		

Virus sample name:	VIT/7/2020
Sender reference:	20-1917
Location of origin:	Thanh Tri, Go Cong Tay, Tien Giang
Country of origin:	Vietnam
Date of collection:	29/01/2020
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	27/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 45020, genome 45021, sequence viba_45022, sequencing info 45023

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_44967	VIT/17/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	100.0	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	100.0	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	100.0	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.8	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.8	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45069	VIT/34/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	96.1	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	94.0	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.2	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.9	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.5	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.2	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		88.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.9	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.4	0	O	ME-SA		

Virus sample name:	VIT/9/2020
Sender reference:	20-2074
Location of origin:	Quang Truc, Tuy Duc, Dak Nong
Country of origin:	Vietnam
Date of collection:	31/01/2020
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	27/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 45024, genome 45025, sequence viba_45026, sequencing info 45027

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.7	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.7	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.7	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.9	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.5	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	87.9	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		87.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.5	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.0	0	O	ME-SA		

Virus sample name:	VIT/12/2020
Sender reference:	20-3243
Location of origin:	Hoai My, Hoai Nhon, Binh Dinh
Country of origin:	Vietnam
Date of collection:	19/02/2020
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 45028, genome 45029, sequence viba_45030, sequencing info 45031

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45057	VIT/22/2019	cattle	99.7	0	O	ME-SA	Ind-2001	e
viba_45022	VIT/7/2020	porcine	99.5	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.5	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_45014	VIT/4/2020	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_44991	VIT/29/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.5	0	O	ME-SA	Ind-2001	e
viba_44999	VIT/32/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.9	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.5	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.6	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	91.3	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	90.2	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		88.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_285	UKG/35/2001	porcine	88.5	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	88.3	0	O	ME-SA	PanAsia-2	
viba_666	IRN/18/2010	cattle	87.7	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/13/2020
Sender reference:	20-3504
Location of origin:	Long Giao, Cam My, Dong Nai
Country of origin:	Vietnam
Date of collection:	25/02/2020
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	26/06/2020
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	05/07/2020
Created:	06/07/2020
Last updated:	06/07/2020

VIBASys IDs: sample 45032, genome 45033, sequence viba_45034, sequencing info 45035

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.5	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.5	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.5	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.4	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.2	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.2	0	O	ME-SA	Ind-2001	e

Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.9	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.8	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.0	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.7	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	90.1	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.0	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.0	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		87.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_359	Manisa/TUR/69		87.5	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	87.4	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/14/2020
Sender reference:	20-3701
Location of origin:	Binh Son, Hiep Duc, Quang Nam
Country of origin:	Vietnam
Date of collection:	27/02/2020
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	10% epi susp
Harvest date of material:	n/a
Primers:	O-1C244F/EUR-2B52R; FMD-3161F/FMD-4303R
Received for sequencing:	07/07/2020
Created:	09/07/2020
Last updated:	09/07/2020
VIBASys IDs: sample 45075, genome 45076, sequence viba_45077, sequencing info 45078	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_45022	VIT/7/2020	porcine	99.5	0	O	ME-SA	Ind-2001	e
viba_44967	VIT/17/2019	porcine	99.5	0	O	ME-SA	Ind-2001	e
viba_44987	VIT/28/2019	water buffalo	99.5	0	O	ME-SA	Ind-2001	e
viba_44979	VIT/25/2019	porcine	99.5	0	O	ME-SA	Ind-2001	e
viba_44983	VIT/27/2019	cattle	99.5	0	O	ME-SA	Ind-2001	e
viba_45057	VIT/22/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e
viba_45061	VIT/23/2019	water buffalo	99.4	0	O	ME-SA	Ind-2001	e
viba_45053	VIT/21/2019	cattle	99.4	0	O	ME-SA	Ind-2001	e
viba_45065	VIT/33/2019	cattle	99.2	0	O	ME-SA	Ind-2001	e
viba_45073	VIT/35/2019	cattle	99.2	0	O	ME-SA	Ind-2001	e

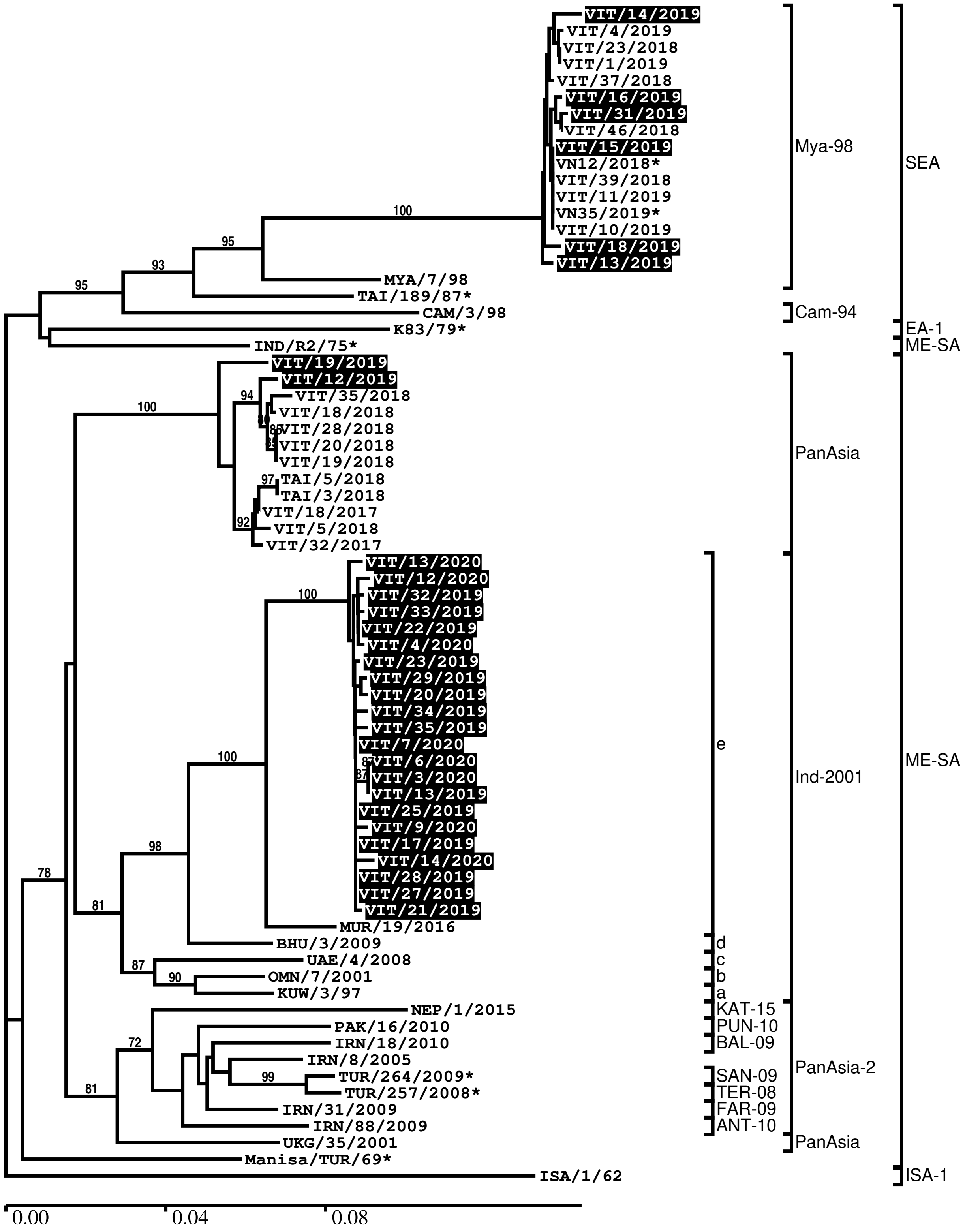
Most Closely Related Prototype Sequences

see `http://www.wrlfmd.org/fmdv-genome/fmd-prototype-strains`

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_30238	MUR/19/2016	cattle	95.6	0	O	ME-SA	Ind-2001	e
viba_293	BHU/3/2009	cattle	93.5	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.7	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	90.4	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.4	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	88.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_285	UKG/35/2001	porcine	88.0	0	O	ME-SA	PanAsia	
viba_719	IRN/88/2009		87.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_650	IRN/8/2005	ovine	87.7	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		86.9	0	O	ME-SA		

Report on FMDV O in Vietnam in 2019, 2020

Batch: WRLFMD/2020/00003



*, not a WRLFMD Reference Number

Analysis Parameters

VP1 subsequence extractor:	vp1_O
Query sequence set:	WRLFMD/2020/00003-Vietnam-O (30 sequences)
Sequence database set:	allseqs_O (4805 sequences)
Prototype sequence set:	!prototypes_O (49 sequences)
Number of related sequences reported:	10
Minimal VP1 subsequence match length	600
Sequence alignment method:	muscle (default parameters)
Sequence alignment length:	636
Phylogeny reconstruction method:	fdnadist, fneighbor
Number of bootstrap samples:	1000
Random seed for bootstrapping:	1
Displaying bootstrap values above:	70.0%
Number of sequences in tree capped at:	100
Number of prototype sequences in tree:	20
VIBASys version:	reflabs-1.1.2

Sequences in the Phylogenetic Tree

All sequences in the tree are in taxonomic group FMDV/O

label	**accession**	**host(s)**	**lab**	**country**	**taxonomic information**
VIT/14/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/4/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/23/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/1/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/37/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/16/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/31/2019	n/a	cattle	WRLFMD	Vietnam	SEA/Mya-98
VIT/46/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/15/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VN12/2018*	n/a	n/a	APQA	Vietnam	SEA/Mya-98
VIT/39/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/11/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VN35/2019*	n/a	n/a	APQA	Vietnam	SEA/Mya-98
VIT/10/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/18/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/13/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
MYA/7/98	DQ164925	bovine	WRLFMD	Myanmar	SEA/Mya-98
TAI/189/87*	KY091288	bovine	TRRL	Thailand	SEA
CAM/3/98	AJ294910	bovine	WRLFMD	Cambodia	SEA/Cam-94
K83/79*	AJ303511	n/a	WRLFMD	Kenya	EA-1
IND/R2/75*	AF204276	n/a	PD-FMD	India	ME-SA
VIT/19/2019	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/12/2019	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/35/2018	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/18/2018	n/a	n/a	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/28/2018	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/20/2018	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/19/2018	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
TAI/5/2018	n/a	cattle	WRLFMD	Thailand	ME-SA/PanAsia
TAI/3/2018	n/a	cattle	WRLFMD	Thailand	ME-SA/PanAsia
VIT/18/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/5/2018	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/32/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/13/2020	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/12/2020	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/32/2019	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e

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label	accession	host(s)	lab	country	taxonomic information
VIT/33/2019	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/22/2019	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/4/2020	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/23/2019	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/29/2019	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/20/2019	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/34/2019	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/35/2019	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/7/2020	n/a	porcine	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/6/2020	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/3/2020	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/13/2019	n/a	porcine	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/25/2019	n/a	porcine	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/9/2020	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/17/2019	n/a	porcine	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/14/2020	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/28/2019	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/27/2019	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
VIT/21/2019	n/a	cattle	WRLFMD	Vietnam	ME-SA/Ind-2001/e
MUR/19/2016	MG972510	cattle	WRLFMD	Mauritius	ME-SA/Ind-2001/e
BHU/3/2009	KM921814	cattle	WRLFMD	Bhutan	ME-SA/Ind-2001/d
UAE/4/2008	KM921876	gazelle	WRLFMD	United Arab Emirates	ME-SA/Ind-2001/c
OMN/7/2001	DQ164941	bovine	WRLFMD	Oman	ME-SA/Ind-2001/b
KUW/3/97	DQ164904	bovine	WRLFMD	Kuwait	ME-SA/Ind-2001/a
NEP/1/2015	MN276045	cattle	WRLFMD	Nepal	ME-SA/PanAsia-2/KAT-15
PAK/16/2010	KY091285	cattle	WRLFMD	Pakistan	ME-SA/PanAsia-2/PUN-10
IRN/18/2010	KY091283	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/BAL-09
IRN/8/2005	KY091281	ovine	WRLFMD	Iran	ME-SA/PanAsia-2
TUR/264/2009*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/SAN-09
TUR/257/2008*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/TER-08
IRN/31/2009	KY091284	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/FAR-09
IRN/88/2009	KY091282	n/a	WRLFMD	Iran	ME-SA/PanAsia-2/ANT-10
UKG/35/2001	AJ539141	porcine	PIADC	United Kingdom	ME-SA/PanAsia
Manisa/TUR/69*	AY593823	n/a	PIADC	Turkey	ME-SA
ISA/1/62	AJ303500	n/a	WRLFMD	Indonesia	ISA-1

*, not a WRLFMD Reference Number
n/a, not available