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

Genotyping Report

FMDV serotype:	O
Country:	Uganda
Year:	2016, 2017
Batch:	WRLMEG/2020/00003
No. of sequences:	67
Report date:	19th January 2020
Report generated by:	Nick Knowles
Report checked by:	Antonello Di Nardo

www: http://www.wrlfmd.org/
email: reporting@pirbright.ac.uk

Virus sample name:	APA-001-P/UGA/2016
Sender reference:	O/APA-001-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43403, genome 43404, sequence viba_43405, sequencing info 43406	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-002-P/UGA/2016
Sender reference:	O/APA-002-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43407, genome 43408, sequence viba_43409, sequencing info 43410

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-006-P/UGA/2016
Sender reference:	O/APA-006-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43411, genome 43412, sequence viba_43413, sequencing info 43414	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-020-P/UGA/2016
Sender reference:	O/APA-020-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43415, genome 43416, sequence viba_43417, sequencing info 43418	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.9	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.2	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.1	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	APA-037-P/UGA/2016
Sender reference:	O/APA-037-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43419, genome 43420, sequence viba_43421, sequencing info 43422	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-046-P/UGA/2016
Sender reference:	O/APA-046-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43423, genome 43424, sequence viba_43425, sequencing info 43426	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.5	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	APA-067-P/UGA/2016
Sender reference:	O/APA-067-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43427, genome 43428, sequence viba_43429, sequencing info 43430	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43497	APA-262-P/UGA/2016	cattle	99.2	0	O	EA-2		
viba_43505	APA-278-P/UGA/2016	cattle	98.7	0	O	EA-2		
viba_43417	APA-020-P/UGA/2016	cattle	98.6	0	O	EA-2		
viba_43493	APA-254-P/UGA/2016	cattle	98.6	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	98.4	0	O	EA-2		

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_85	UGA/3/2002		90.7	0	O	EA-2		
viba_74	KEN/5/2002	bovine	89.7	0	O	EA-2		
viba_221	MAL/1/98		87.0	0	O	EA-2		
viba_263	TAN/2/2004	bovine	85.9	0	O	EA-2		
viba_576	IND/R2/75		83.9	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	83.8	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	83.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_523	K83/79		83.5	0	O	EA-1		
viba_705	KUW/3/97	bovine	83.2	0	O	ME-SA	Ind-2001	a
viba_30238	MUR/19/2016	cattle	83.2	0	O	ME-SA	Ind-2001	e

Virus sample name:	APA-070-P/UGA/2016
Sender reference:	O/APA-070-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43431, genome 43432, sequence viba_43433, sequencing info 43434

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-081-P/UGA/2016
Sender reference:	O/APA-081-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43435, genome 43436, sequence viba_43437, sequencing info 43438

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-115-P/UGA/2016
Sender reference:	O/APA-115-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43439, genome 43440, sequence viba_43441, sequencing info 43442

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-117-P/UGA/2016
Sender reference:	O/APA-117-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43443, genome 43444, sequence viba_43445, sequencing info 43446

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.6	0	O	EA-2		
viba_221	MAL/1/98		88.2	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.1	0	O	EA-2		
viba_576	IND/R2/75		85.0	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.6	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.4	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.0	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-124-P/UGA/2016
Sender reference:	O/APA-124-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43447, genome 43448, sequence viba_43449, sequencing info 43450

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-128-P/UGA/2016
Sender reference:	O/APA-128-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43451, genome 43452, sequence viba_43453, sequencing info 43454	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-136-P/UGA/2016
Sender reference:	O/APA-136-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43455, genome 43456, sequence viba_43457, sequencing info 43458	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-139-P/UGA/2016
Sender reference:	O/APA-139-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43459, genome 43460, sequence viba_43461, sequencing info 43462	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-144-P/UGA/2016
Sender reference:	O/APA-144-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43463, genome 43464, sequence viba_43465, sequencing info 43466

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-146-P/UGA/2016
Sender reference:	O/APA-146-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43467, genome 43468, sequence viba_43469, sequencing info 43470

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-225-P/UGA/2016
Sender reference:	O/APA-225-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43471, genome 43472, sequence viba_43473, sequencing info 43474

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.5	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	APA-232-P/UGA/2016
Sender reference:	O/APA-232-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43475, genome 43476, sequence viba_43477, sequencing info 43478

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.5	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	APA-241-P/UGA/2016
Sender reference:	O/APA-241-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43479, genome 43480, sequence viba_43481, sequencing info 43482

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.5	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	APA-243-P/UGA/2016
Sender reference:	O/APA-243-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43483, genome 43484, sequence viba_43485, sequencing info 43486

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43481	APA-241-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.5	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	APA-253-P/UGA/2016
Sender reference:	O/APA-253-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43487, genome 43488, sequence viba_43489, sequencing info 43490

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.5	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	APA-254-P/UGA/2016
Sender reference:	O/APA-254-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43491, genome 43492, sequence viba_43493, sequencing info 43494

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43501	APA-272-P/UGA/2016	cattle	99.5	0	O	EA-2		
viba_43485	APA-243-P/UGA/2016	cattle	99.4	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	99.4	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	99.4	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	99.4	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	99.4	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	99.4	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	99.4	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.2	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.2	0	O	EA-2		

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_85	UGA/3/2002		91.0	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.3	0	O	EA-2		
viba_221	MAL/1/98		87.9	0	O	EA-2		
viba_263	TAN/2/2004	bovine	86.8	0	O	EA-2		
viba_576	IND/R2/75		84.7	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.0	0	O	ME-SA	Ind-2001	e
viba_491	TUR/257/2008		83.8	0	O	ME-SA	PanAsia-2	TER-08
viba_854	ETH/1/2007	cattle	83.7	0	O	EA-3		

Virus sample name:	APA-262-P/UGA/2016
Sender reference:	O/APA-262-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43495, genome 43496, sequence viba_43497, sequencing info 43498	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43429	APA-067-P/UGA/2016	cattle	99.2	0	O	EA-2		
viba_43493	APA-254-P/UGA/2016	cattle	98.7	0	O	EA-2		
viba_43509	APA-293-P/UGA/2016	cattle	98.6	0	O	EA-2		
viba_43505	APA-278-P/UGA/2016	cattle	98.6	0	O	EA-2		
viba_43485	APA-243-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43417	APA-020-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	98.4	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	98.4	0	O	EA-2		

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_85	UGA/3/2002		90.5	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.0	0	O	EA-2		
viba_221	MAL/1/98		87.3	0	O	EA-2		
viba_263	TAN/2/2004	bovine	86.1	0	O	EA-2		
viba_576	IND/R2/75		84.4	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.0	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	83.8	0	O	ME-SA	PanAsia-2	FAR-09
viba_523	K83/79		83.7	0	O	EA-1		
viba_30238	MUR/19/2016	cattle	83.4	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	83.3	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-272-P/UGA/2016
Sender reference:	O/APA-272-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43499, genome 43500, sequence viba_43501, sequencing info 43502

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.7	0	O	EA-2		

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_85	UGA/3/2002		91.5	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-278-P/UGA/2016
Sender reference:	O/APA-278-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43503, genome 43504, sequence viba_43505, sequencing info 43506

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	99.5	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	99.5	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	99.5	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	99.5	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	99.5	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	99.5	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	99.5	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.4	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.4	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.4	0	O	EA-2		

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_85	UGA/3/2002		91.2	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.4	0	O	EA-2		
viba_221	MAL/1/98		88.1	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.0	0	O	EA-2		
viba_576	IND/R2/75		84.8	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_523	K83/79		84.3	0	O	EA-1		
viba_30238	MUR/19/2016	cattle	84.2	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-293-P/UGA/2016
Sender reference:	O/APA-293-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43507, genome 43508, sequence viba_43509, sequencing info 43510

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.7	0	O	EA-2		

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_85	UGA/3/2002		91.5	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.5	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-298-P/UGA/2016
Sender reference:	O/APA-298-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43511, genome 43512, sequence viba_43513, sequencing info 43514	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.5	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	APA-267-P/UGA/2016
Sender reference:	O/APA-267-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43515, genome 43516, sequence viba_43517, sequencing info 43518

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43485	APA-243-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43481	APA-241-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43425	APA-046-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43489	APA-253-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43477	APA-232-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43473	APA-225-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43513	APA-298-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.7	0	O	EA-2		

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_85	UGA/3/2002		91.5	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_116	SUD/2/86	bovine	84.2	0	O	EA-3		

Virus sample name:	APA-012-P/UGA/2016
Sender reference:	O/APA-012-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43519, genome 43520, sequence viba_43521, sequencing info 43522	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-064-P/UGA/2016
Sender reference:	O/APA-064-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43523, genome 43524, sequence viba_43525, sequencing info 43526

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-135-P/UGA/2016
Sender reference:	O/APA-135-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43527, genome 43528, sequence viba_43529, sequencing info 43530	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-143-P/UGA/2016
Sender reference:	O/APA-143-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43531, genome 43532, sequence viba_43533, sequencing info 43534

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-044-P/UGA/2016
Sender reference:	O/APA-044-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43535, genome 43536, sequence viba_43537, sequencing info 43538

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-092-P/UGA/2016
Sender reference:	O/APA-092-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43539, genome 43540, sequence viba_43541, sequencing info 43542	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	APA-099-P/UGA/2016
Sender reference:	O/APA-099-P
Location of origin:	Apac, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43543, genome 43544, sequence viba_43545, sequencing info 43546	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-020-P/UGA/2016
Sender reference:	O/KRD-020-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43547, genome 43548, sequence viba_43549, sequencing info 43550	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-028-P/UGA/2016
Sender reference:	O/KRD-028-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43551, genome 43552, sequence viba_43553, sequencing info 43554	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-014-P/UGA/2016
Sender reference:	O/KRD-014-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43555, genome 43556, sequence viba_43557, sequencing info 43558

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-049-P/UGA/2016
Sender reference:	O/KRD-049-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43559, genome 43560, sequence viba_43561, sequencing info 43562	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.9	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.5	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	KRD-081-P/UGA/2016
Sender reference:	O/KRD-081-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43563, genome 43564, sequence viba_43565, sequencing info 43566	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-194-P/UGA/2016
Sender reference:	O/KRD-194-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43567, genome 43568, sequence viba_43569, sequencing info 43570

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-060-P/UGA/2016
Sender reference:	O/KRD-060-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43571, genome 43572, sequence viba_43573, sequencing info 43574

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-083-P/UGA/2016
Sender reference:	O/KRD-083-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43575, genome 43576, sequence viba_43577, sequencing info 43578	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-189-P/UGA/2016
Sender reference:	O/KRD-189-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43579, genome 43580, sequence viba_43581, sequencing info 43582

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-070-P/UGA/2016
Sender reference:	O/KRD-070-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43583, genome 43584, sequence viba_43585, sequencing info 43586

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-147-P/UGA/2016
Sender reference:	O/KRD-147-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43587, genome 43588, sequence viba_43589, sequencing info 43590

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.9	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.6	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.1	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_354	PAK/16/2010	cattle	84.6	0	O	ME-SA	PanAsia-2	PUN-10
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a
viba_854	ETH/1/2007	cattle	84.1	0	O	EA-3		

Virus sample name:	KRD-184-P/UGA/2016
Sender reference:	O/KRD-184-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43591, genome 43592, sequence viba_43593, sequencing info 43594

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-035-P/UGA/2016
Sender reference:	O/KRD-035-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43595, genome 43596, sequence viba_43597, sequencing info 43598	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-055-P/UGA/2016
Sender reference:	O/KRD-055-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43599, genome 43600, sequence viba_43601, sequencing info 43602

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-042-P/UGA/2016
Sender reference:	O/KRD-042-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43603, genome 43604, sequence viba_43605, sequencing info 43606	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	KRD-156-P/UGA/2016
Sender reference:	O/KRD-156-P
Location of origin:	Kiryandongo, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43607, genome 43608, sequence viba_43609, sequencing info 43610

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	MOY2-018-P/UGA/2016
Sender reference:	O/MOY2-018-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43611, genome 43612, sequence viba_43613, sequencing info 43614

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43625	MOY2-13-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43657	MOY2-015-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43633	MOY2-166-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43621	MOY2-024-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.6	0	O	EA-2		
viba_221	MAL/1/98		88.2	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.1	0	O	EA-2		
viba_576	IND/R2/75		85.0	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.6	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.4	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.0	0	O	ME-SA	Ind-2001	a
viba_523	K83/79		84.0	0	O	EA-1		

Virus sample name:	MOY2-057-P/UGA/2016
Sender reference:	O/MOY2-057-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43615, genome 43616, sequence viba_43617, sequencing info 43618

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	MOY2-024-P/UGA/2016
Sender reference:	O/MOY2-024-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43619, genome 43620, sequence viba_43621, sequencing info 43622	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43625	MOY2-13-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43657	MOY2-015-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43633	MOY2-166-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43613	MOY2-018-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.6	0	O	EA-2		
viba_221	MAL/1/98		88.2	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.1	0	O	EA-2		
viba_576	IND/R2/75		85.0	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.6	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.4	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.0	0	O	ME-SA	Ind-2001	a
viba_523	K83/79		84.0	0	O	EA-1		

Virus sample name:	MOY2-13-P/UGA/2016
Sender reference:	O/MOY2-13-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43623, genome 43624, sequence viba_43625, sequencing info 43626	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43657	MOY2-015-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43633	MOY2-166-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43613	MOY2-018-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43621	MOY2-024-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.6	0	O	EA-2		
viba_221	MAL/1/98		88.2	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.1	0	O	EA-2		
viba_576	IND/R2/75		85.0	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.6	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.4	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.0	0	O	ME-SA	Ind-2001	a
viba_523	K83/79		84.0	0	O	EA-1		

Virus sample name:	MOY2-128-P/UGA/2016
Sender reference:	O/MOY2-128-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43627, genome 43628, sequence viba_43629, sequencing info 43630	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	MOY2-166-P/UGA/2016
Sender reference:	O/MOY2-166-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43631, genome 43632, sequence viba_43633, sequencing info 43634

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43625	MOY2-13-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43657	MOY2-015-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43613	MOY2-018-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43621	MOY2-024-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.6	0	O	EA-2		
viba_221	MAL/1/98		88.2	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.1	0	O	EA-2		
viba_576	IND/R2/75		85.0	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.6	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.4	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.0	0	O	ME-SA	Ind-2001	a
viba_523	K83/79		84.0	0	O	EA-1		

Virus sample name:	MOY2-109-P/UGA/2016
Sender reference:	O/MOY2-109-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43635, genome 43636, sequence viba_43637, sequencing info 43638

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	MOY2-099-P/UGA/2016
Sender reference:	O/MOY2-099-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43639, genome 43640, sequence viba_43641, sequencing info 43642	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.9	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.9	0	O	EA-2		
viba_221	MAL/1/98		88.6	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.5	0	O	EA-2		
viba_576	IND/R2/75		85.3	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.7	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.3	0	O	ME-SA	Ind-2001	a
viba_491	TUR/257/2008		84.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	MOY2-126-P/UGA/2016
Sender reference:	O/MOY2-126-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43643, genome 43644, sequence viba_43645, sequencing info 43646

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43461	APA-139-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	MOY2-182-P/UGA/2016
Sender reference:	O/MOY2-182-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43647, genome 43648, sequence viba_43649, sequencing info 43650

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43625	MOY2-13-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43657	MOY2-015-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43633	MOY2-166-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43613	MOY2-018-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43621	MOY2-024-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.7	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.7	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.0	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.4	0	O	ME-SA	Ind-2001	e
viba_491	TUR/257/2008		84.1	0	O	ME-SA	PanAsia-2	TER-08
viba_705	KUW/3/97	bovine	84.0	0	O	ME-SA	Ind-2001	a

Virus sample name:	MOY2-095-P/UGA/2016
Sender reference:	O/MOY2-095-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43651, genome 43652, sequence viba_43653, sequencing info 43654

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43453	APA-128-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43557	KRD-014-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43537	APA-044-P/UGA/2016	cattle	100.0	0	O	EA-2		

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_85	UGA/3/2002		91.8	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.8	0	O	EA-2		
viba_221	MAL/1/98		88.4	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.3	0	O	EA-2		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.7	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.5	0	O	ME-SA	Ind-2001	e
viba_523	K83/79		84.2	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.1	0	O	ME-SA	Ind-2001	a

Virus sample name:	MOY2-015-P/UGA/2016
Sender reference:	O/MOY2-015-P
Location of origin:	Moyo, Northern Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020
VIBASys IDs: sample 43655, genome 43656, sequence viba_43657, sequencing info 43658	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43625	MOY2-13-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43633	MOY2-166-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43613	MOY2-018-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43621	MOY2-024-P/UGA/2016	cattle	100.0	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	99.8	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	99.8	0	O	EA-2		

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_85	UGA/3/2002		91.6	0	O	EA-2		
viba_74	KEN/5/2002	bovine	90.6	0	O	EA-2		
viba_221	MAL/1/98		88.2	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.1	0	O	EA-2		
viba_576	IND/R2/75		85.0	0	O	ME-SA		
viba_354	PAK/16/2010	cattle	84.6	0	O	ME-SA	PanAsia-2	PUN-10
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_30238	MUR/19/2016	cattle	84.4	0	O	ME-SA	Ind-2001	e
viba_705	KUW/3/97	bovine	84.0	0	O	ME-SA	Ind-2001	a
viba_523	K83/79		84.0	0	O	EA-1		

Virus sample name:	LUW-037-P/UGA/2016
Sender reference:	O/LUW-037-P
Location of origin:	Luwero, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	O
Topotype:	EA-2
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43659, genome 43660, sequence viba_43661, sequencing info 43662

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43641	MOY2-099-P/UGA/2016	cattle	98.9	0	O	EA-2		
viba_43417	APA-020-P/UGA/2016	cattle	98.9	0	O	EA-2		
viba_43453	APA-128-P/UGA/2016	cattle	98.7	0	O	EA-2		
viba_43581	KRD-189-P/UGA/2016	cattle	98.7	0	O	EA-2		
viba_43549	KRD-020-P/UGA/2016	cattle	98.7	0	O	EA-2		
viba_43609	KRD-156-P/UGA/2016	cattle	98.7	0	O	EA-2		
viba_43645	MOY2-126-P/UGA/2016	cattle	98.7	0	O	EA-2		
viba_43541	APA-092-P/UGA/2016	cattle	98.7	0	O	EA-2		
viba_43573	KRD-060-P/UGA/2016	cattle	98.7	0	O	EA-2		
viba_43569	KRD-194-P/UGA/2016	cattle	98.7	0	O	EA-2		

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_74	KEN/5/2002	bovine	91.6	0	O	EA-2		
viba_85	UGA/3/2002		91.5	0	O	EA-2		
viba_221	MAL/1/98		88.9	0	O	EA-2		
viba_263	TAN/2/2004	bovine	87.8	0	O	EA-2		
viba_576	IND/R2/75		85.9	0	O	ME-SA		
viba_359	Manisa/TUR/69		85.1	0	O	ME-SA		
viba_523	K83/79		85.0	0	O	EA-1		
viba_705	KUW/3/97	bovine	84.7	0	O	ME-SA	Ind-2001	a
viba_285	UKG/35/2001	porcine	84.6	0	O	ME-SA	PanAsia	
viba_354	PAK/16/2010	cattle	84.5	0	O	ME-SA	PanAsia-2	PUN-10

Virus sample name:	ADJ-309-P/UGA/2017
Sender reference:	O/ADJ-309-P
Location of origin:	Adjumani, Northern Region
Country of origin:	Uganda
Date of collection:	2017
Host species:	cattle
Serotype:	O
Topotype:	EA-4
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43663, genome 43664, sequence viba_43665, sequencing info 43666

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43669	AMU-200-P/UGA/2017	cattle	97.9	0	O	EA-4		
viba_15517	KEN/100/2010	cattle	92.0	0	O	EA-4		
viba_33499	ETH/13/2016	cattle	90.3	0	O	EA-4		
viba_33463	ETH/2/2016	cattle	90.1	0	O	EA-4		
viba_33852	ETH/48/2016	bovine	90.1	0	O	EA-4		
viba_33848	ETH/37/2016	bovine	90.1	0	O	EA-4		
viba_33820	ETH/25/2016	bovine	90.1	0	O	EA-4		
viba_33475	ETH/6/2016	cattle	90.1	0	O	EA-4		
viba_33511	ETH/22/2016	cattle	89.9	0	O	EA-4		
viba_33487	ETH/9/2016	cattle	89.8	0	O	EA-4		

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_50	UGA/17/98		87.8	0	O	EA-4		
viba_621	ETH/58/2005	bovine	87.1	0	O	EA-4		
viba_523	K83/79		87.0	0	O	EA-1		
viba_116	SUD/2/86	bovine	86.7	0	O	EA-3		
viba_359	Manisa/TUR/69		85.2	0	O	ME-SA		
viba_576	IND/R2/75		85.2	0	O	ME-SA		
viba_30238	MUR/19/2016	cattle	85.0	0	O	ME-SA	Ind-2001	e
viba_541	OMN/7/2001	bovine	84.8	0	O	ME-SA	Ind-2001	b
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_854	ETH/1/2007	cattle	84.5	0	O	EA-3		

Virus sample name:	AMU-200-P/UGA/2017
Sender reference:	O/AMU-200-P
Location of origin:	Amuru, Northern Region
Country of origin:	Uganda
Date of collection:	2017
Host species:	cattle
Serotype:	O
Topotype:	EA-4
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	18/01/2020
Last updated:	18/01/2020

VIBASys IDs: sample 43667, genome 43668, sequence viba_43669, sequencing info 43670

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43665	ADJ-309-P/UGA/2017	cattle	97.9	0	O	EA-4		
viba_15517	KEN/100/2010	cattle	93.4	0	O	EA-4		
viba_33499	ETH/13/2016	cattle	91.5	0	O	EA-4		
viba_33463	ETH/2/2016	cattle	91.4	0	O	EA-4		
viba_33852	ETH/48/2016	bovine	91.4	0	O	EA-4		
viba_33848	ETH/37/2016	bovine	91.4	0	O	EA-4		
viba_33820	ETH/25/2016	bovine	91.4	0	O	EA-4		
viba_33475	ETH/6/2016	cattle	91.4	0	O	EA-4		
viba_33511	ETH/22/2016	cattle	91.2	0	O	EA-4		
viba_33487	ETH/9/2016	cattle	91.0	0	O	EA-4		

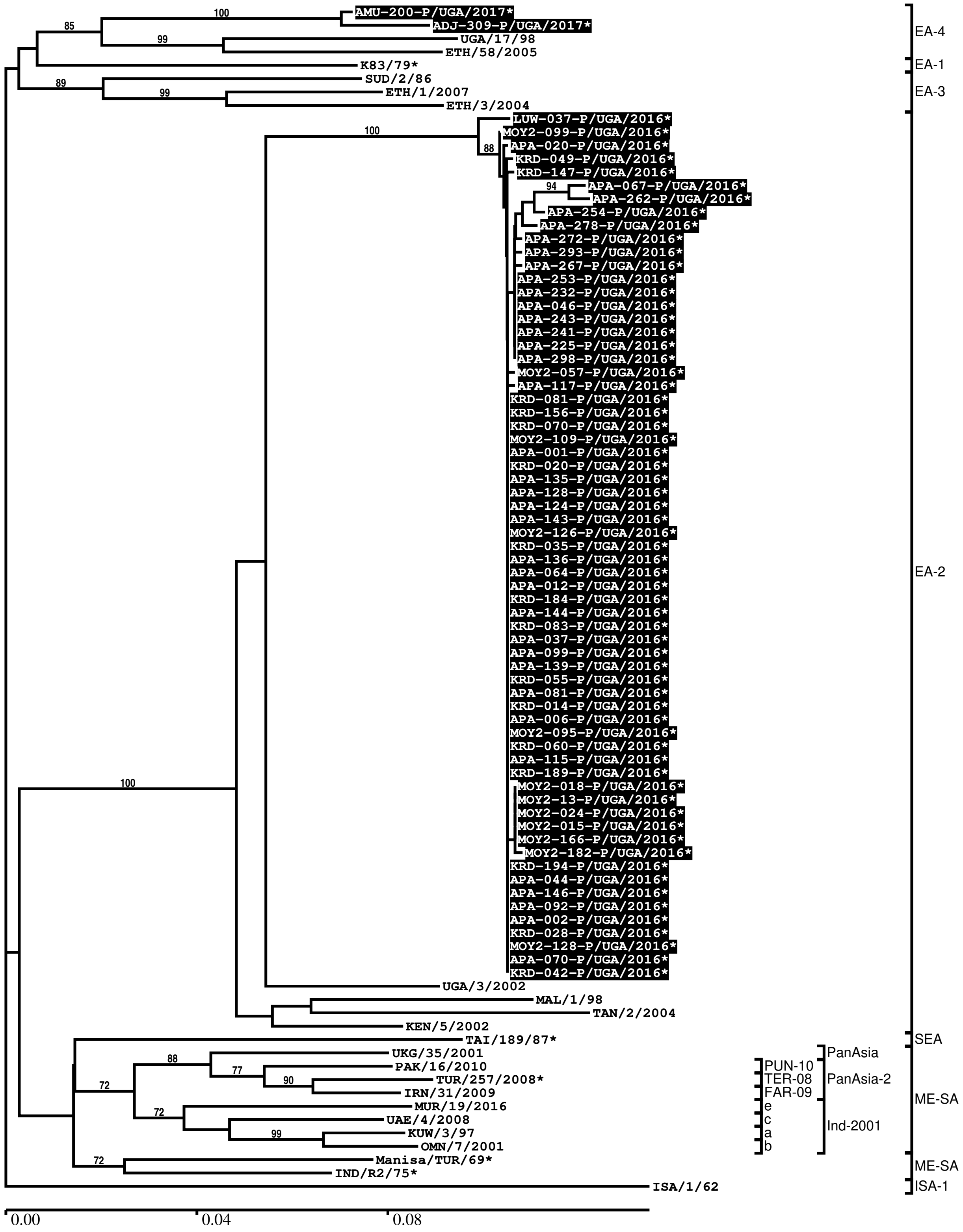
Most Closely Related Prototype Sequences

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

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_50	UGA/17/98		87.9	0	O	EA-4		
viba_523	K83/79		87.5	0	O	EA-1		
viba_116	SUD/2/86	bovine	87.4	0	O	EA-3		
viba_621	ETH/58/2005	bovine	87.1	0	O	EA-4		
viba_85	UGA/3/2002		86.0	0	O	EA-2		
viba_854	ETH/1/2007	cattle	85.8	0	O	EA-3		
viba_221	MAL/1/98		85.8	0	O	EA-2		
viba_408	ETH/3/2004	cattle	85.5	0	O	EA-3		
viba_397	UAE/4/2008	gazelle	85.5	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	85.5	0	O	ME-SA	PanAsia-2	FAR-09

Report on FMDV O in Uganda in 2016, 2017

Batch: WRLMEG/2020/00003



*, not a WRLFMD Reference Number

Analysis Parameters

VP1 subsequence extractor:	vp1_O
Query sequence set:	WRLMEG/2020/00003-Uganda-O (67 sequences)
Sequence database set:	allseqs_O (4688 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
AMU-200-P/UGA/2017*	MH367380	cattle	PIADC	Uganda	EA-4
ADJ-309-P/UGA/2017*	MH367379	cattle	PIADC	Uganda	EA-4
UGA/17/98	HM211075	n/a	WRLFMD	Uganda	EA-4
ETH/58/2005	FJ798141	bovine	WRLFMD	Ethiopia	EA-4
K83/79*	AJ303511	n/a	WRLFMD	Kenya	EA-1
SUD/2/86	DQ165075	bovine	WRLFMD	Sudan	EA-3
ETH/1/2007	FJ798137	cattle	WRLFMD	Ethiopia	EA-3
ETH/3/2004	FJ798109	cattle	WRLFMD	Ethiopia	EA-3
LUW-037-P/UGA/2016*	MH367378	cattle	PIADC	Uganda	EA-2
MOY2-099-P/UGA/2016*	MH367373	cattle	PIADC	Uganda	EA-2
APA-020-P/UGA/2016*	MH367317	cattle	PIADC	Uganda	EA-2
KRD-049-P/UGA/2016*	MH367353	cattle	PIADC	Uganda	EA-2
KRD-147-P/UGA/2016*	MH367360	cattle	PIADC	Uganda	EA-2
APA-067-P/UGA/2016*	MH367320	cattle	PIADC	Uganda	EA-2
APA-262-P/UGA/2016*	MH367337	cattle	PIADC	Uganda	EA-2
APA-254-P/UGA/2016*	MH367336	cattle	PIADC	Uganda	EA-2
APA-278-P/UGA/2016*	MH367339	cattle	PIADC	Uganda	EA-2
APA-272-P/UGA/2016*	MH367338	cattle	PIADC	Uganda	EA-2
APA-293-P/UGA/2016*	MH367340	cattle	PIADC	Uganda	EA-2
APA-267-P/UGA/2016*	MH367342	cattle	PIADC	Uganda	EA-2
APA-253-P/UGA/2016*	MH367335	cattle	PIADC	Uganda	EA-2
APA-232-P/UGA/2016*	MH367332	cattle	PIADC	Uganda	EA-2
APA-046-P/UGA/2016*	MH367319	cattle	PIADC	Uganda	EA-2
APA-243-P/UGA/2016*	MH367334	cattle	PIADC	Uganda	EA-2
APA-241-P/UGA/2016*	MH367333	cattle	PIADC	Uganda	EA-2
APA-225-P/UGA/2016*	MH367331	cattle	PIADC	Uganda	EA-2
APA-298-P/UGA/2016*	MH367341	cattle	PIADC	Uganda	EA-2
MOY2-057-P/UGA/2016*	MH367367	cattle	PIADC	Uganda	EA-2
APA-117-P/UGA/2016*	MH367324	cattle	PIADC	Uganda	EA-2
KRD-081-P/UGA/2016*	MH367354	cattle	PIADC	Uganda	EA-2
KRD-156-P/UGA/2016*	MH367365	cattle	PIADC	Uganda	EA-2
KRD-070-P/UGA/2016*	MH367359	cattle	PIADC	Uganda	EA-2
MOY2-109-P/UGA/2016*	MH367372	cattle	PIADC	Uganda	EA-2
APA-001-P/UGA/2016*	MH367314	cattle	PIADC	Uganda	EA-2
KRD-020-P/UGA/2016*	MH367350	cattle	PIADC	Uganda	EA-2
APA-135-P/UGA/2016*	MH367345	cattle	PIADC	Uganda	EA-2

continued on next page

label	accession	host(s)	lab	country	taxonomic information
APA-128-P/UGA/2016*	MH367326	cattle	PIADC	Uganda	EA-2
APA-124-P/UGA/2016*	MH367325	cattle	PIADC	Uganda	EA-2
APA-143-P/UGA/2016*	MH367346	cattle	PIADC	Uganda	EA-2
MOY2-126-P/UGA/2016*	MH367374	cattle	PIADC	Uganda	EA-2
KRD-035-P/UGA/2016*	MH367362	cattle	PIADC	Uganda	EA-2
APA-136-P/UGA/2016*	MH367327	cattle	PIADC	Uganda	EA-2
APA-064-P/UGA/2016*	MH367344	cattle	PIADC	Uganda	EA-2
APA-012-P/UGA/2016*	MH367343	cattle	PIADC	Uganda	EA-2
KRD-184-P/UGA/2016*	MH367361	cattle	PIADC	Uganda	EA-2
APA-144-P/UGA/2016*	MH367329	cattle	PIADC	Uganda	EA-2
KRD-083-P/UGA/2016*	MH367357	cattle	PIADC	Uganda	EA-2
APA-037-P/UGA/2016*	MH367318	cattle	PIADC	Uganda	EA-2
APA-099-P/UGA/2016*	MH367349	cattle	PIADC	Uganda	EA-2
APA-139-P/UGA/2016*	MH367328	cattle	PIADC	Uganda	EA-2
KRD-055-P/UGA/2016*	MH367363	cattle	PIADC	Uganda	EA-2
APA-081-P/UGA/2016*	MH367322	cattle	PIADC	Uganda	EA-2
KRD-014-P/UGA/2016*	MH367352	cattle	PIADC	Uganda	EA-2
APA-006-P/UGA/2016*	MH367316	cattle	PIADC	Uganda	EA-2
MOY2-095-P/UGA/2016*	MH367376	cattle	PIADC	Uganda	EA-2
KRD-060-P/UGA/2016*	MH367356	cattle	PIADC	Uganda	EA-2
APA-115-P/UGA/2016*	MH367323	cattle	PIADC	Uganda	EA-2
KRD-189-P/UGA/2016*	MH367358	cattle	PIADC	Uganda	EA-2
MOY2-018-P/UGA/2016*	MH367366	cattle	PIADC	Uganda	EA-2
MOY2-13-P/UGA/2016*	MH367369	cattle	PIADC	Uganda	EA-2
MOY2-024-P/UGA/2016*	MH367368	cattle	PIADC	Uganda	EA-2
MOY2-015-P/UGA/2016*	MH367377	cattle	PIADC	Uganda	EA-2
MOY2-166-P/UGA/2016*	MH367371	cattle	PIADC	Uganda	EA-2
MOY2-182-P/UGA/2016*	MH367375	cattle	PIADC	Uganda	EA-2
KRD-194-P/UGA/2016*	MH367355	cattle	PIADC	Uganda	EA-2
APA-044-P/UGA/2016*	MH367347	cattle	PIADC	Uganda	EA-2
APA-146-P/UGA/2016*	MH367330	cattle	PIADC	Uganda	EA-2
APA-092-P/UGA/2016*	MH367348	cattle	PIADC	Uganda	EA-2
APA-002-P/UGA/2016*	MH367315	cattle	PIADC	Uganda	EA-2
KRD-028-P/UGA/2016*	MH367351	cattle	PIADC	Uganda	EA-2
MOY2-128-P/UGA/2016*	MH367370	cattle	PIADC	Uganda	EA-2
APA-070-P/UGA/2016*	MH367321	cattle	PIADC	Uganda	EA-2
KRD-042-P/UGA/2016*	MH367364	cattle	PIADC	Uganda	EA-2
UGA/3/2002	DQ165077	n/a	WRLFMD	Uganda	EA-2
MAL/1/98	DQ165074	n/a	WRLFMD	Malawi	EA-2
TAN/2/2004	KF561679	bovine	WRLFMD	Tanzania	EA-2
KEN/5/2002	DQ165073	bovine	WRLFMD	Kenya	EA-2
TAI/189/87*	KY091288	bovine	TRRL	Thailand	SEA
UKG/35/2001	AJ539141	porcine	PIADC	United Kingdom	ME-SA/PanAsia
PAK/16/2010	KY091285	cattle	WRLFMD	Pakistan	ME-SA/PanAsia-2/PUN-10
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
MUR/19/2016	MG972510	cattle	WRLFMD	Mauritius	ME-SA/Ind-2001/e
UAE/4/2008	KM921876	gazelle	WRLFMD	United Arab Emirates	ME-SA/Ind-2001/c
KUW/3/97	DQ164904	bovine	WRLFMD	Kuwait	ME-SA/Ind-2001/a
OMN/7/2001	DQ164941	bovine	WRLFMD	Oman	ME-SA/Ind-2001/b
Manisa/TUR/69*	AY593823	n/a	PIADC	Turkey	ME-SA
IND/R2/75*	AF204276	n/a	PD-FMD	India	ME-SA
ISA/1/62	AJ303500	n/a	WRLFMD	Indonesia	ISA-1

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