

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

Genotyping Report

FMDV serotype: SAT1
Country: Uganda
Year: 2016
Batch: WRLMEG/2020/00003
No. of sequences: 54
Report date: 19th January 2020
Report generated by: Nick Knowles
Report checked by: Antonello Di Nardo



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www: <http://www.wrlfmd.org/>

email: reporting@pirbright.ac.uk

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Virus sample name:	ISI-002/P/UGA/2016
Sender reference:	SAT1/ISI-002/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43187, genome 43188, sequence viba_43189, sequencing info 43190	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-006/P/UGA/2016
Sender reference:	SAT1/ISI-006/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43191, genome 43192, sequence viba_43193, sequencing info 43194	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-017/P/UGA/2016
Sender reference:	SAT1/ISI-017/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43195, genome 43196, sequence viba_43197, sequencing info 43198	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43397	ISI-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43249	ISI-112/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43381	ISI-099/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.8	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.3	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	ISI-019/P/UGA/2016
Sender reference:	SAT1/ISI-019/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43199, genome 43200, sequence viba_43201, sequencing info 43202	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-022/P/UGA/2016
Sender reference:	SAT1/ISI-022/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43203, genome 43204, sequence viba_43205, sequencing info 43206	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-026/P/UGA/2016
Sender reference:	SAT1/ISI-026/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43207, genome 43208, sequence viba_43209, sequencing info 43210	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-032/P/UGA/2016
Sender reference:	SAT1/ISI-032/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43211, genome 43212, sequence viba_43213, sequencing info 43214	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	ISI-041/P/UGA/2016
Sender reference:	SAT1/ISI-041/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43215, genome 43216, sequence viba_43217, sequencing info 43218	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-047/P/UGA/2016
Sender reference:	SAT1/ISI-047/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43219, genome 43220, sequence viba_43221, sequencing info 43222	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-048/P/UGA/2016
Sender reference:	SAT1/ISI-048/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43223, genome 43224, sequence viba_43225, sequencing info 43226	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-084/P/UGA/2016
Sender reference:	SAT1/ISI-084/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43227, genome 43228, sequence viba_43229, sequencing info 43230	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-090/P/UGA/2016
Sender reference:	SAT1/ISI-090/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43231, genome 43232, sequence viba_43233, sequencing info 43234	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-094/P/UGA/2016
Sender reference:	SAT1/ISI-094/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43235, genome 43236, sequence viba_43237, sequencing info 43238	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-100/P/UGA/2016
Sender reference:	SAT1/ISI-100/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43239, genome 43240, sequence viba_43241, sequencing info 43242	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.4	0	SAT1	I		
viba_243	ZIM/23/2003		79.6	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.0	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.0	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.0	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	73.9	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.6	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.5	0	SAT1	II		
viba_212	BEC/1/48		73.2	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.1	0	SAT1	XIII		

Virus sample name:	ISI-102/P/UGA/2016
Sender reference:	SAT1/ISI-102/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43243, genome 43244, sequence viba_43245, sequencing info 43246	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43253	ISI-126/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	ISI-112/P/UGA/2016
Sender reference:	SAT1/ISI-112/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43247, genome 43248, sequence viba_43249, sequencing info 43250	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43397	ISI-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43197	ISI-017/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43381	ISI-099/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.8	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.3	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	ISI-126/P/UGA/2016
Sender reference:	SAT1/ISI-126/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43251, genome 43252, sequence viba_43253, sequencing info 43254	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43229	ISI-084/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43225	ISI-048/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43221	ISI-047/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43233	ISI-090/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43245	ISI-102/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43237	ISI-094/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43201	ISI-019/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43217	ISI-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43193	ISI-006/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43209	ISI-026/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.7	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	72.3	0	SAT1	XIII		

Virus sample name:	SEM-027/P/UGA/2016
Sender reference:	SAT1/SEM-027/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43255, genome 43256, sequence viba_43257, sequencing info 43258	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43277	SEM-010/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43269	SEM-034/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.4	0	SAT1	I		
viba_243	ZIM/23/2003		80.4	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.0	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	76.1	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	74.5	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.7	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.6	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	73.5	0	SAT1	III		
viba_212	BEC/1/48		73.0	0	SAT1	III		

Virus sample name:	SEM-032/P/UGA/2016
Sender reference:	SAT1/SEM-032/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43259, genome 43260, sequence viba_43261, sequencing info 43262	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43269	SEM-034/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43305	SEM-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.2	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		

Virus sample name:	SEM-008/P/UGA/2016
Sender reference:	SAT1/SEM-008/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43263, genome 43264, sequence viba_43265, sequencing info 43266	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43269	SEM-034/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43305	SEM-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.2	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		

Virus sample name:	SEM-034/P/UGA/2016
Sender reference:	SAT1/SEM-034/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43267, genome 43268, sequence viba_43269, sequencing info 43270	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43297	SEM-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43305	SEM-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.2	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		

Virus sample name:	SEM 030/P/UGA/2016
Sender reference:	SAT1/SEM_030/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43271, genome 43272, sequence viba_43273, sequencing info 43274	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43269	SEM-034/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43305	SEM-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.2	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		

Virus sample name:	SEM-010/P/UGA/2016
Sender reference:	SAT1/SEM-010/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43275, genome 43276, sequence viba_43277, sequencing info 43278	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43257	SEM-027/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43269	SEM-034/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.4	0	SAT1	I		
viba_243	ZIM/23/2003		80.4	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.0	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	76.1	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.0	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	74.5	0	SAT1	IV		
viba_709	RHO/5/66	bovine	73.7	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.6	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	73.5	0	SAT1	III		
viba_212	BEC/1/48		73.0	0	SAT1	III		

Virus sample name:	SEM-023/P/UGA/2016
Sender reference:	SAT1/SEM-023/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43279, genome 43280, sequence viba_43281, sequencing info 43282	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43269	SEM-034/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43305	SEM-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.2	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		

Virus sample name:	SEM-037/P/UGA/2016
Sender reference:	SAT1/SEM-037/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43283, genome 43284, sequence viba_43285, sequencing info 43286	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43269	SEM-034/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43305	SEM-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.2	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		

Virus sample name:	SEM-041/P/UGA/2016
Sender reference:	SAT1/SEM-041/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43287, genome 43288, sequence viba_43289, sequencing info 43290	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43269	SEM-034/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43305	SEM-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.2	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		

Virus sample name:	SEM-036/P/UGA/2016
Sender reference:	SAT1/SEM_/036/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43291, genome 43292, sequence viba_43293, sequencing info 43294	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43269	SEM-034/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43305	SEM-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.2	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		

Virus sample name:	SEM-049/P/UGA/2016
Sender reference:	SAT1/SEM-049/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43295, genome 43296, sequence viba_43297, sequencing info 43298	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43269	SEM-034/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43305	SEM-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.2	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		

Virus sample name:	SEM-014/P/UGA/2016
Sender reference:	SAT1/SEM-014/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43299, genome 43300, sequence viba_43301, sequencing info 43302	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.8	0	SAT1	I		
viba_243	ZIM/23/2003		80.1	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.5	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.4	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.3	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.2	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.9	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.6	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.6	0	SAT1	XIII		
viba_212	BEC/1/48		73.5	0	SAT1	III		

Virus sample name:	SEM-024/P/UGA/2016
Sender reference:	SAT1/SEM-024/P
Location of origin:	Sembabule, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43303, genome 43304, sequence viba_43305, sequencing info 43306	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43269	SEM-034/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43297	SEM-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43293	SEM-036/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43261	SEM-032/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43281	SEM-023/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43265	SEM-008/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43285	SEM-037/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43289	SEM-041/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43257	SEM-027/P/UGA/2016	cattle	99.7	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.0	0	SAT1	I		
viba_462	RV/11/37	greater kudu	76.4	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.0	0	SAT1	III		
viba_509	BOT/1/77	bovine	73.9	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.6	0	SAT1	XIII		
viba_212	BEC/1/48		73.5	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.1	0	SAT1	IV		

Virus sample name:	KYA-046/P/UGA/2016
Sender reference:	SAT1/KYA-046/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43307, genome 43308, sequence viba_43309, sequencing info 43310	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-099/P/UGA/2016
Sender reference:	SAT1/KYA-099/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43311, genome 43312, sequence viba_43313, sequencing info 43314	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-055/P/UGA/2016
Sender reference:	SAT1/KYA-055/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43315, genome 43316, sequence viba_43317, sequencing info 43318	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-056/P/UGA/2016
Sender reference:	SAT1/KYA-056/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43319, genome 43320, sequence viba_43321, sequencing info 43322	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-083/P/UGA/2016
Sender reference:	SAT1/KYA-083/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43323, genome 43324, sequence viba_43325, sequencing info 43326	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-111/P/UGA/2016
Sender reference:	SAT1/KYA-111/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43327, genome 43328, sequence viba_43329, sequencing info 43330	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-097/P/UGA/2016
Sender reference:	SAT1/KYA-097/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43331, genome 43332, sequence viba_43333, sequencing info 43334	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-92/P/UGA/2016
Sender reference:	SAT1/KYA-92/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43335, genome 43336, sequence viba_43337, sequencing info 43338	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-030/P/UGA/2016
Sender reference:	SAT1/KYA-030/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43339, genome 43340, sequence viba_43341, sequencing info 43342	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-049/P/UGA/2016
Sender reference:	SAT1/KYA-049/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43343, genome 43344, sequence viba_43345, sequencing info 43346	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-042/P/UGA/2016
Sender reference:	SAT1/KYA-042/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43347, genome 43348, sequence viba_43349, sequencing info 43350	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-035/P/UGA/2016
Sender reference:	SAT1/KYA-035/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43351, genome 43352, sequence viba_43353, sequencing info 43354	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	KYA-022/P/UGA/2016
Sender reference:	SAT1/KYA-022/P
Location of origin:	Kyankwanzi, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43355, genome 43356, sequence viba_43357, sequencing info 43358	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.5	0	SAT1	I		
viba_243	ZIM/23/2003		80.1	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.0	0	SAT1	III		
viba_509	BOT/1/77	bovine	73.9	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.3	0	SAT1	XIII		
viba_212	BEC/1/48		73.2	0	SAT1	III		

Virus sample name:	NKA-024/P/UGA/2016
Sender reference:	SAT1/NKA-024/P
Location of origin:	Nakasongola, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43359, genome 43360, sequence viba_43361, sequencing info 43362	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43373	NKA-042/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43369	NKA-070/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43365	NKA-012/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	99.5	0	SAT1	I		

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_466	T155/71	cattle	89.2	0	SAT1	I		
viba_243	ZIM/23/2003		79.8	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.0	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	73.7	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.3	0	SAT1	XIII		
viba_212	BEC/1/48		73.1	0	SAT1	III		

Virus sample name:	NKA-012/P/UGA/2016
Sender reference:	SAT1/NKA-012/P
Location of origin:	Nakasongola, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43363, genome 43364, sequence viba_43365, sequencing info 43366	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43373	NKA-042/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43369	NKA-070/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43361	NKA-024/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	99.5	0	SAT1	I		

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_466	T155/71	cattle	89.2	0	SAT1	I		
viba_243	ZIM/23/2003		80.1	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.2	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.0	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.0	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	73.7	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.3	0	SAT1	XIII		
viba_514	UGA-BUFF/21/70	African buffalo	73.1	0	SAT1	IV		
viba_212	BEC/1/48		73.0	0	SAT1	III		

Virus sample name:	NKA-070/P/UGA/2016
Sender reference:	SAT1/NKA-070/P
Location of origin:	Nakasongola, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43367, genome 43368, sequence viba_43369, sequencing info 43370	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43373	NKA-042/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43361	NKA-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43365	NKA-012/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	99.7	0	SAT1	I		

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_466	T155/71	cattle	89.4	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.0	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	73.7	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.3	0	SAT1	XIII		
viba_212	BEC/1/48		73.1	0	SAT1	III		

Virus sample name:	NKA-042/P/UGA/2016
Sender reference:	SAT1/NKA-042/P
Location of origin:	Nakasongola, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43371, genome 43372, sequence viba_43373, sequencing info 43374	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43369	NKA-070/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43361	NKA-024/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43365	NKA-012/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	99.7	0	SAT1	I		

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_466	T155/71	cattle	89.4	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.0	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.1	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	73.7	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.6	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.3	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.3	0	SAT1	XIII		
viba_212	BEC/1/48		73.1	0	SAT1	III		

Virus sample name:	MUK-025/P/UGA/2016
Sender reference:	SAT1/MUK-025/P
Location of origin:	Mukono, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43375, genome 43376, sequence viba_43377, sequencing info 43378	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43301	SEM-014/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	99.7	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.3	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_30769	MOZ/1/75	cattle	73.7	0	SAT1	XIII		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	ISI-099/P/UGA/2016
Sender reference:	SAT1/ISI-099/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43379, genome 43380, sequence viba_43381, sequencing info 43382	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43397	ISI-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43197	ISI-017/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43249	ISI-112/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.8	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.3	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	ISI-093/P/UGA/2016
Sender reference:	SAT1/ISI-093/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43383, genome 43384, sequence viba_43385, sequencing info 43386	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43397	ISI-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43197	ISI-017/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43249	ISI-112/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43381	ISI-099/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.8	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.3	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	ISI-046/P/UGA/2016
Sender reference:	SAT1/ISI-046/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43387, genome 43388, sequence viba_43389, sequencing info 43390	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.8	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.4	0	SAT1	II		
viba_509	BOT/1/77	bovine	75.6	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.4	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.3	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.6	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.6	0	SAT1	XIII		
viba_212	BEC/1/48		73.5	0	SAT1	III		

Virus sample name:	ISI-055/P/UGA/2016
Sender reference:	SAT1/ISI-055/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43391, genome 43392, sequence viba_43393, sequencing info 43394	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43333	KYA-097/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		

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_466	T155/71	cattle	89.7	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.2	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	ISI-056/P/UGA/2016
Sender reference:	SAT1/ISI-056/P
Location of origin:	Insingiro, Western Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43395, genome 43396, sequence viba_43397, sequencing info 43398	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43197	ISI-017/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43249	ISI-112/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43381	ISI-099/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.8	0	SAT1	I		

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_466	T155/71	cattle	89.8	0	SAT1	I		
viba_243	ZIM/23/2003		79.9	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.3	0	SAT1	II		
viba_495	BOT/1/68	bovine	75.3	0	SAT1	III		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_509	BOT/1/77	bovine	74.0	0	SAT1	III		
viba_709	RHO/5/66	bovine	73.8	0	SAT1	II		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
viba_212	BEC/1/48		73.4	0	SAT1	III		

Virus sample name:	RAK-015/P/UGA/2016
Sender reference:	SAT1/RAK-015/P
Location of origin:	Rakai, Central Region
Country of origin:	Uganda
Date of collection:	2016
Host species:	cattle
Serotype:	SAT1
Topotype:	I
Lineage:	
Sublineage:	
Sequence length:	657
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 43399, genome 43400, sequence viba_43401, sequencing info 43402	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_43301	SEM-014/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43333	KYA-097/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43345	KYA-049/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43325	KYA-083/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43353	KYA-035/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43321	KYA-056/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43393	ISI-055/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43213	ISI-032/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43341	KYA-030/P/UGA/2016	cattle	99.4	0	SAT1	I		

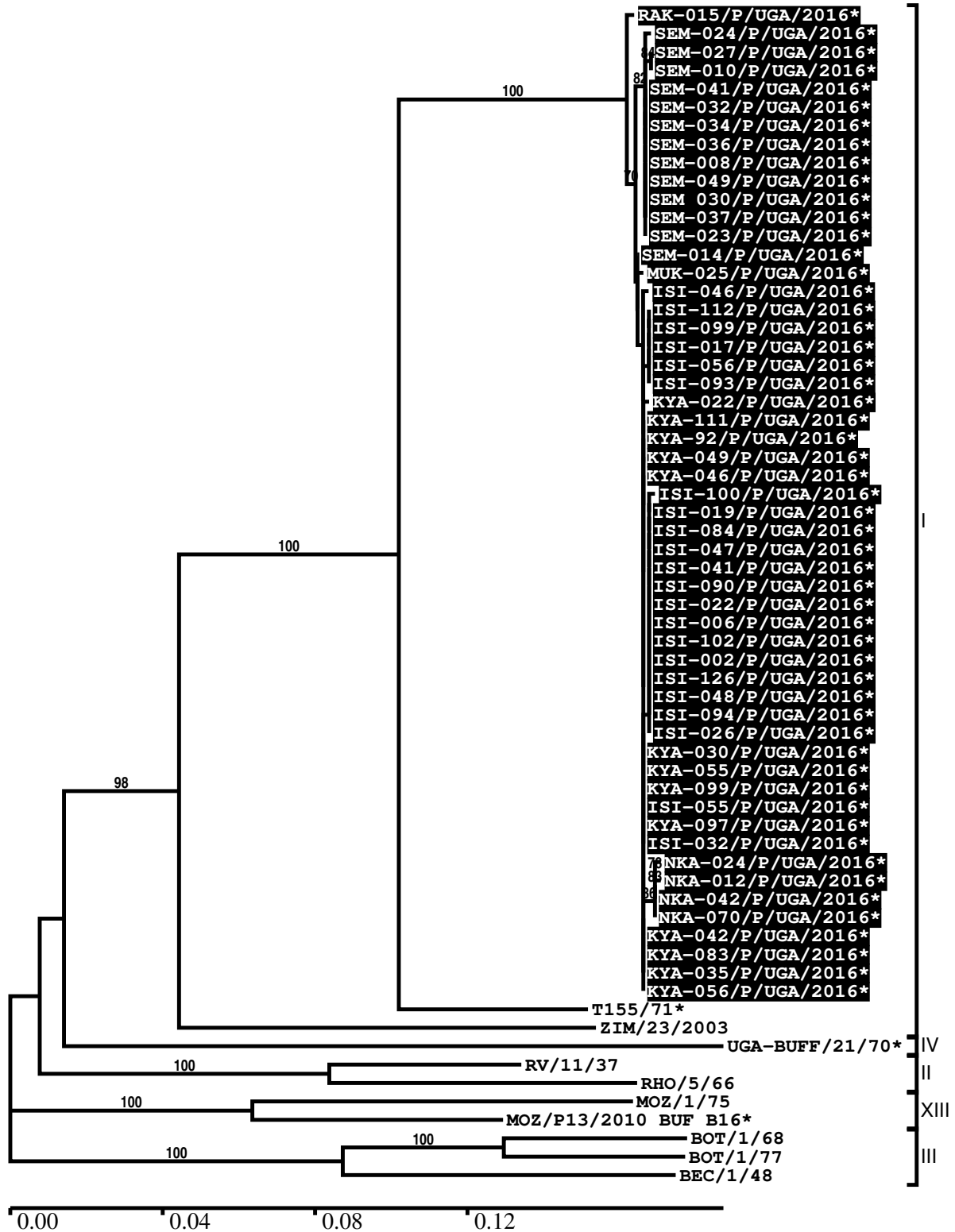
Most Closely Related Prototype Sequences

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

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_466	T155/71	cattle	90.0	0	SAT1	I		
viba_243	ZIM/23/2003		79.1	0	SAT1	I		
viba_462	RV/11/37	greater kudu	77.5	0	SAT1	II		
viba_16635	MOZ/P13/2010 BUF B16	African buffalo	75.8	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.6	0	SAT1	III		
viba_509	BOT/1/77	bovine	74.5	0	SAT1	III		
viba_709	RHO/5/66	bovine	74.2	0	SAT1	II		
viba_212	BEC/1/48		73.8	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	73.7	0	SAT1	XIII		
viba_514	UGA-BUFF/21/70	African buffalo	73.6	0	SAT1	IV		

Report on FMDV SAT1 in Uganda in 2016

Batch: WRLMEG/2020/00003



*, not a WRLFMD Reference Number

Analysis Parameters

VP1 subsequence extractor:	vp1_SAT1
Query sequence set:	WRLMEG/2020/00003-Uganda-SAT1 (54 sequences)
Sequence database set:	allseqs_SAT1 (757 sequences)
Prototype sequence set:	!prototypes_SAT1 (19 sequences)
Number of related sequences reported:	10
Minimal VP1 subsequence match length	600
Sequence alignment method:	muscle (default parameters)
Sequence alignment length:	657
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:	10
VIBASys version:	reflabs-1.1.2

Sequences in the Phylogenetic Tree

All sequences in the tree are in taxonomic group FMDV/SAT1

label	accession	host(s)	lab	country	taxonomic information
RAK-015/P/UGA/2016*	MH367434	cattle	PIADC	Uganda	I
SEM-024/P/UGA/2016*	MH367410	cattle	PIADC	Uganda	I
SEM-027/P/UGA/2016*	MH367398	cattle	PIADC	Uganda	I
SEM-010/P/UGA/2016*	MH367403	cattle	PIADC	Uganda	I
SEM-041/P/UGA/2016*	MH367406	cattle	PIADC	Uganda	I
SEM-032/P/UGA/2016*	MH367399	cattle	PIADC	Uganda	I
SEM-034/P/UGA/2016*	MH367401	cattle	PIADC	Uganda	I
SEM-036/P/UGA/2016*	MH367407	cattle	PIADC	Uganda	I
SEM-008/P/UGA/2016*	MH367400	cattle	PIADC	Uganda	I
SEM-049/P/UGA/2016*	MH367408	cattle	PIADC	Uganda	I
SEM 030/P/UGA/2016*	MH367402	cattle	PIADC	Uganda	I
SEM-037/P/UGA/2016*	MH367405	cattle	PIADC	Uganda	I
SEM-023/P/UGA/2016*	MH367404	cattle	PIADC	Uganda	I
SEM-014/P/UGA/2016*	MH367409	cattle	PIADC	Uganda	I
MUK-025/P/UGA/2016*	MH367428	cattle	PIADC	Uganda	I
ISI-046/P/UGA/2016*	MH367431	cattle	PIADC	Uganda	I
ISI-112/P/UGA/2016*	MH367396	cattle	PIADC	Uganda	I
ISI-099/P/UGA/2016*	MH367429	cattle	PIADC	Uganda	I
ISI-017/P/UGA/2016*	MH367383	cattle	PIADC	Uganda	I
ISI-056/P/UGA/2016*	MH367433	cattle	PIADC	Uganda	I
ISI-093/P/UGA/2016*	MH367430	cattle	PIADC	Uganda	I
KYA-022/P/UGA/2016*	MH367423	cattle	PIADC	Uganda	I
KYA-111/P/UGA/2016*	MH367416	cattle	PIADC	Uganda	I
KYA-92/P/UGA/2016*	MH367418	cattle	PIADC	Uganda	I
KYA-049/P/UGA/2016*	MH367420	cattle	PIADC	Uganda	I
KYA-046/P/UGA/2016*	MH367411	cattle	PIADC	Uganda	I
ISI-100/P/UGA/2016*	MH367394	cattle	PIADC	Uganda	I
ISI-019/P/UGA/2016*	MH367384	cattle	PIADC	Uganda	I
ISI-084/P/UGA/2016*	MH367391	cattle	PIADC	Uganda	I
ISI-047/P/UGA/2016*	MH367389	cattle	PIADC	Uganda	I
ISI-041/P/UGA/2016*	MH367388	cattle	PIADC	Uganda	I
ISI-090/P/UGA/2016*	MH367392	cattle	PIADC	Uganda	I
ISI-022/P/UGA/2016*	MH367385	cattle	PIADC	Uganda	I
ISI-006/P/UGA/2016*	MH367382	cattle	PIADC	Uganda	I
ISI-102/P/UGA/2016*	MH367395	cattle	PIADC	Uganda	I
ISI-002/P/UGA/2016*	MH367381	cattle	PIADC	Uganda	I

continued on next page

label	accession	host(s)	lab	country	taxonomic information
ISI-126/P/UGA/2016*	MH367397	cattle	PIADC	Uganda	I
ISI-048/P/UGA/2016*	MH367390	cattle	PIADC	Uganda	I
ISI-094/P/UGA/2016*	MH367393	cattle	PIADC	Uganda	I
ISI-026/P/UGA/2016*	MH367386	cattle	PIADC	Uganda	I
KYA-030/P/UGA/2016*	MH367419	cattle	PIADC	Uganda	I
KYA-055/P/UGA/2016*	MH367413	cattle	PIADC	Uganda	I
KYA-099/P/UGA/2016*	MH367412	cattle	PIADC	Uganda	I
ISI-055/P/UGA/2016*	MH367432	cattle	PIADC	Uganda	I
KYA-097/P/UGA/2016*	MH367417	cattle	PIADC	Uganda	I
ISI-032/P/UGA/2016*	MH367387	cattle	PIADC	Uganda	I
NKA-024/P/UGA/2016*	MH367424	cattle	PIADC	Uganda	I
NKA-012/P/UGA/2016*	MH367425	cattle	PIADC	Uganda	I
NKA-042/P/UGA/2016*	MH367427	cattle	PIADC	Uganda	I
NKA-070/P/UGA/2016*	MH367426	cattle	PIADC	Uganda	I
KYA-042/P/UGA/2016*	MH367421	cattle	PIADC	Uganda	I
KYA-083/P/UGA/2016*	MH367415	cattle	PIADC	Uganda	I
KYA-035/P/UGA/2016*	MH367422	cattle	PIADC	Uganda	I
KYA-056/P/UGA/2016*	MH367414	cattle	PIADC	Uganda	I
T155/71*	KF561706	cattle	WRLFMD	Tanzania	I
ZIM/23/2003	KF219690	n/a	WRLFMD	Zimbabwe	I
UGA-BUFF/21/70*	KF219682	African buffalo	WRLFMD	Uganda	IV
RV/11/37	AY593839	greater kudu	PIADC	Rhodesia (RV)	II
RHO/5/66	AY593846	bovine	PIADC	Rhodesia	II
MOZ/1/75	MG972461	cattle	WRLFMD	Mozambique	XIII
MOZ/P13/2010 BUF B16*	KF219691	African buffalo	WRLFMD	Mozambique	XIII
BOT/1/68	AY593845	bovine	PIADC	Botswana	III
BOT/1/77	KF219686	bovine	WRLFMD	Botswana	III
BEC/1/48	AY593838	n/a	PIADC	Bechuanaland	III

*, not a WRLFMD Reference Number

n/a, not available