

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

Genotyping Report

FMDV serotype: SAT1
Country: Uganda
Year: 2016
Batch: WRLMEG/2020/00003A
No. of sequences: 14
Report date: 20th 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-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_43317	KYA-055/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43369	NKA-070/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43361	NKA-024/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43365	NKA-012/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	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-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_43273	SEM 030/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43277	SEM-010/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43401	RAK-015/P/UGA/2016	cattle	99.2	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_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
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_43277	SEM-010/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43401	RAK-015/P/UGA/2016	cattle	99.2	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_212	BEC/1/48		73.4	0	SAT1	III		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		
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_43273	SEM 030/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43269	SEM-034/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43317	KYA-055/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43401	RAK-015/P/UGA/2016	cattle	99.1	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:	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_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		
viba_43385	ISI-093/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43369	NKA-070/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43361	NKA-024/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43365	NKA-012/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	89.7	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_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		

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_43317	KYA-055/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43369	NKA-070/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43361	NKA-024/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43365	NKA-012/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	89.7	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_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		

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_43313	KYA-099/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	100.0	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43369	NKA-070/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43361	NKA-024/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43365	NKA-012/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	89.7	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_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		

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_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_43317	KYA-055/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.1	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_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_43317	KYA-055/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.1	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_16635	MOZ/P13/2010 BUF B16	African buffalo	75.0	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.0	0	SAT1	III		
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_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_43317	KYA-055/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.2	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_43317	KYA-055/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43269	SEM-034/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43401	RAK-015/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43369	NKA-070/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	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_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		

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_43317	KYA-055/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43369	NKA-070/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43361	NKA-024/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43365	NKA-012/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	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_16635	MOZ/P13/2010 BUF B16	African buffalo	75.3	0	SAT1	XIII		
viba_495	BOT/1/68	bovine	75.3	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_212	BEC/1/48		73.4	0	SAT1	III		
viba_514	UGA-BUFF/21/70	African buffalo	73.4	0	SAT1	IV		
viba_30769	MOZ/1/75	cattle	73.4	0	SAT1	XIII		

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_43317	KYA-055/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.8	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.7	0	SAT1	I		
viba_43369	NKA-070/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.5	0	SAT1	I		
viba_43361	NKA-024/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43365	NKA-012/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	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:	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_43317	KYA-055/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43313	KYA-099/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43377	MUK-025/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43309	KYA-046/P/UGA/2016	cattle	99.4	0	SAT1	I		
viba_43385	ISI-093/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43389	ISI-046/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43273	SEM 030/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43269	SEM-034/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43229	ISI-084/P/UGA/2016	cattle	99.2	0	SAT1	I		
viba_43369	NKA-070/P/UGA/2016	cattle	99.1	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/2020/00003A



*, not a WRLFMD Reference Number

Analysis Parameters

VP1 subsequence extractor: vp1_SAT1
 Query sequence set: WRLMEG/2020/00003A-Uganda-SAT1 (14 sequences)
 Sequence database set: allseqs_SAT1 (717 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-010/P/UGA/2016*	MH367403	cattle	PIADC	Uganda	I
SEM-034/P/UGA/2016*	MH367401	cattle	PIADC	Uganda	I
SEM 030/P/UGA/2016*	MH367402	cattle	PIADC	Uganda	I
NKA-012/P/UGA/2016*	MH367425	cattle	PIADC	Uganda	I
NKA-024/P/UGA/2016*	MH367424	cattle	PIADC	Uganda	I
NKA-070/P/UGA/2016*	MH367426	cattle	PIADC	Uganda	I
ISI-084/P/UGA/2016*	MH367391	cattle	PIADC	Uganda	I
KYA-099/P/UGA/2016*	MH367412	cattle	PIADC	Uganda	I
KYA-055/P/UGA/2016*	MH367413	cattle	PIADC	Uganda	I
KYA-046/P/UGA/2016*	MH367411	cattle	PIADC	Uganda	I
ISI-093/P/UGA/2016*	MH367430	cattle	PIADC	Uganda	I
ISI-046/P/UGA/2016*	MH367431	cattle	PIADC	Uganda	I
MUK-025/P/UGA/2016*	MH367428	cattle	PIADC	Uganda	I
TAN/11/2014	MF592672	bovine	WRLFMD	Tanzania	I
TAN/12/2014	MF592673	bovine	WRLFMD	Tanzania	I
TAN/13/2014	MF592674	bovine	WRLFMD	Tanzania	I
TAN/20/2014	MF592680	bovine	WRLFMD	Tanzania	I
TAN/41/2014	MF592696	bovine	WRLFMD	Tanzania	I
TAN/30/2014	MF592688	bovine	WRLFMD	Tanzania	I
TAN/31/2014	n/a	bovine	WRLFMD	Tanzania	I
TAN/32/2014	MF592689	bovine	WRLFMD	Tanzania	I
TAN/29/2014	MF592687	bovine	WRLFMD	Tanzania	I
TAN/17/2014	MF592677	bovine	WRLFMD	Tanzania	I
TAN/18/2014	MF592678	bovine	WRLFMD	Tanzania	I
TAN/21/2014	MF592681	bovine	WRLFMD	Tanzania	I
TAN/23/2014	n/a	bovine	WRLFMD	Tanzania	I
TAN/22/2014	MF592682	bovine	WRLFMD	Tanzania	I
TAN/24/2014	MF592683	bovine	WRLFMD	Tanzania	I
TAN/26/2014	MF592685	bovine	WRLFMD	Tanzania	I
TAN/27/2014	n/a	bovine	WRLFMD	Tanzania	I
TAN/25/2014	MF592684	bovine	WRLFMD	Tanzania	I
TAN/28/2014	MF592686	bovine	WRLFMD	Tanzania	I
TAN/33/2014	MF592690	bovine	WRLFMD	Tanzania	I
TAN/34/2014	MF592691	bovine	WRLFMD	Tanzania	I
TAN/35/2014	MF592692	bovine	WRLFMD	Tanzania	I

continued on next page

label	accession	host(s)	lab	country	taxonomic information
TAN/19/2014	MF592679	bovine	WRLFMD	Tanzania	I
TAN/38/2014	MF592695	bovine	WRLFMD	Tanzania	I
TAN/36/2014	MF592693	bovine	WRLFMD	Tanzania	I
TAN/16/2014	MF592676	bovine	WRLFMD	Tanzania	I
TAN/15/2014	n/a	bovine	WRLFMD	Tanzania	I
TAN/14/2014	MF592675	bovine	WRLFMD	Tanzania	I
TAN/37/2014	MF592694	bovine	WRLFMD	Tanzania	I
TAN/29/2013	MF592662	cattle	WRLFMD	Tanzania	I
TAN/27/2013	MF592661	cattle	WRLFMD	Tanzania	I
TAN/22/2013	MF592656	cattle	WRLFMD	Tanzania	I
TAN/25/2013	MF592659	cattle	WRLFMD	Tanzania	I
TAN/21/2013	n/a	cattle	WRLFMD	Tanzania	I
TAN/20/2013	MF592655	cattle	WRLFMD	Tanzania	I
TAN/31/2013	MF592664	cattle	WRLFMD	Tanzania	I
TAN/32/2013	n/a	cattle	WRLFMD	Tanzania	I
TAN/30/2013	MF592663	cattle	WRLFMD	Tanzania	I
TAN/23/2013	MF592657	cattle	WRLFMD	Tanzania	I
TAN/24/2013	MF592658	cattle	WRLFMD	Tanzania	I
KEN/PRB28/2016 pro*	MH882588	African buffalo	PIADC	Kenya	I
KEN/PRB31/2016 pro*	MH882591	African buffalo	PIADC	Kenya	I
KEN/93/2010	KR188475	cattle	WRLFMD	Kenya	I
KEN/120/2010	KR188497	cattle	WRLFMD	Kenya	I
TAN/27/2012	MF592644	cattle	WRLFMD	Tanzania	I
TAN/25/2012	MF592618	cattle	n/a	Tanzania	I
KEN/23/2008	n/a	cattle	WRLFMD	Kenya	I
KEN/26/2008	n/a	cattle	WRLFMD	Kenya	I
KEN/34/2008	n/a	cattle	WRLFMD	Kenya	I
KEN/35/2008	n/a	cattle	WRLFMD	Kenya	I
K114/99*	HQ267524	n/a	n/a	Kenya	I
TAN/51/99	AY442004	cattle	OVI	Tanzania	I
TAN/51/99	KF561720	cattle	WRLFMD	Tanzania	I
K96/99*	HQ267523	n/a	n/a	Kenya	I
BUN/1/99	n/a	cattle	WRLFMD	Burundi	I
BUN/2/99	n/a	cattle	WRLFMD	Burundi	I
BUN/5/99	n/a	cattle	WRLFMD	Burundi	I
TAN/60/99	KF561721	wildebeest	WRLFMD	Tanzania	I
TAN/26/99	KF561717	cattle	WRLFMD	Tanzania	I
TAN/21/99	KF561715	cattle	WRLFMD	Tanzania	I
TAN/19/99	KF561714	cattle	WRLFMD	Tanzania	I
TAN/25/99	KF561716	cattle	WRLFMD	Tanzania	I
KEN/PRB36/2016 pro*	MH882593	African buffalo	PIADC	Kenya	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
RHO/5/66	AY593846	bovine	PIADC	Rhodesia	II
RV/11/37	AY593839	greater kudu	PIADC	Rhodesia (RV)	II
MOZ/P13/2010 BUF B16*	KF219691	African buffalo	WRLFMD	Mozambique	XIII
MOZ/1/75	MG972461	cattle	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