

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

## Genotyping Report

FMDV serotype: O  
Country: Mauritania  
Year: 2018  
Batch: WRLMEG/2018/00039  
No. of sequences: 7  
Report date: 2nd November 2018  
Report generated by: Nick Knowles  
Report checked by: Jemma Wadsworth

This report is prepared on behalf of the FAO Reference Centre & OIE Reference Laboratory for Foot-and-Mouth Disease chez Agence nationale de sécurité sanitaire – Anses, Maisons-Alfort, Île-de-France, France and covers VP1 sequences submitted to the WRLFMD on 29/10/2018.



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

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Virus sample name:	MAU/18Z007127/18
Sender reference:	18Z007127
Location of origin:	Hodh Ech Chargui
Country of origin:	Mauritania
Date of collection:	07/2018
Host species:	
Serotype:	O
Topotype:	EA-3
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	02/11/2018
Last updated:	02/11/2018
VIBASys IDs: sample 37524, genome 37525, sequence viba_37526, sequencing info 37527	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_37538	MAU/18Z007130/18		100.0	0	O	EA-3		
viba_37534	MAU/18Z007129/18		100.0	0	O	EA-3		
viba_36938	ALG/1/2018	cattle	99.8	0	O	EA-3		
viba_37530	MAU/18Z007128/18		99.8	0	O	EA-3		
viba_37252	GNA/18Z005583/18		99.7	0	O	EA-3		
viba_36947	ALG/2/2018	cattle	99.7	0	O	EA-3		
viba_37256	GNA/18Z005587/18		99.7	0	O	EA-3		
viba_37260	GNA/18Z005588/18		99.5	0	O	EA-3		
viba_37542	MAU/18Z007167/18		99.2	0	O	EA-3		
viba_37248	GNA/18Z005582/18		99.2	0	O	EA-3		

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_116	SUD/2/86	bovine	89.3	0	O	EA-3		
viba_854	ETH/1/2007	cattle	86.1	0	O	EA-3		
viba_408	ETH/3/2004	cattle	86.0	0	O	EA-3		
viba_30238	MUR/19/2016	cattle	85.6	0	O	ME-SA	Ind-2001	e
viba_50	UGA/17/98		85.1	0	O	EA-4		
viba_285	UKG/35/2001	porcine	84.6	0	O	ME-SA	PanAsia	
viba_85	UGA/3/2002		84.5	0	O	EA-2		
viba_523	K83/79		84.2	0	O	EA-1		
viba_104	GHA/5/93	bovine	84.2	0	O	WA		
viba_576	IND/R2/75		84.2	0	O	ME-SA		

Virus sample name:	MAU/18Z007128/18
Sender reference:	18Z007128
Location of origin:	Hodh Ech Chargui
Country of origin:	Mauritania
Date of collection:	07/2018
Host species:	
Serotype:	O
Topotype:	EA-3
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	02/11/2018
Last updated:	02/11/2018
VIBASys IDs: sample 37528, genome 37529, sequence viba_37530, sequencing info 37531	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36938	ALG/1/2018	cattle	100.0	0	O	EA-3		
viba_37252	GNA/18Z005583/18		99.8	0	O	EA-3		
viba_36947	ALG/2/2018	cattle	99.8	0	O	EA-3		
viba_37538	MAU/18Z007130/18		99.8	0	O	EA-3		
viba_37526	MAU/18Z007127/18		99.8	0	O	EA-3		
viba_37256	GNA/18Z005587/18		99.8	0	O	EA-3		
viba_37534	MAU/18Z007129/18		99.8	0	O	EA-3		
viba_37260	GNA/18Z005588/18		99.7	0	O	EA-3		
viba_37542	MAU/18Z007167/18		99.4	0	O	EA-3		
viba_37248	GNA/18Z005582/18		99.4	0	O	EA-3		

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_116	SUD/2/86	bovine	89.1	0	O	EA-3		
viba_854	ETH/1/2007	cattle	86.0	0	O	EA-3		
viba_408	ETH/3/2004	cattle	85.8	0	O	EA-3		
viba_30238	MUR/19/2016	cattle	85.5	0	O	ME-SA	Ind-2001	e
viba_50	UGA/17/98		85.2	0	O	EA-4		
viba_85	UGA/3/2002		84.4	0	O	EA-2		
viba_285	UKG/35/2001	porcine	84.4	0	O	ME-SA	PanAsia	
viba_104	GHA/5/93	bovine	84.1	0	O	WA		
viba_576	IND/R2/75		84.1	0	O	ME-SA		
viba_766	IRN/31/2009	cattle	84.0	0	O	ME-SA	PanAsia-2	FAR-09

Virus sample name:	MAU/18Z007129/18
Sender reference:	18Z007129
Location of origin:	Hodh Ech Chargui
Country of origin:	Mauritania
Date of collection:	07/2018
Host species:	
Serotype:	O
Topotype:	EA-3
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	02/11/2018
Last updated:	02/11/2018
VIBASys IDs: sample 37532, genome 37533, sequence viba_37534, sequencing info 37535	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_37538	MAU/18Z007130/18		100.0	0	O	EA-3		
viba_37526	MAU/18Z007127/18		100.0	0	O	EA-3		
viba_36938	ALG/1/2018	cattle	99.8	0	O	EA-3		
viba_37530	MAU/18Z007128/18		99.8	0	O	EA-3		
viba_37252	GNA/18Z005583/18		99.7	0	O	EA-3		
viba_36947	ALG/2/2018	cattle	99.7	0	O	EA-3		
viba_37256	GNA/18Z005587/18		99.7	0	O	EA-3		
viba_37260	GNA/18Z005588/18		99.5	0	O	EA-3		
viba_37542	MAU/18Z007167/18		99.2	0	O	EA-3		
viba_37248	GNA/18Z005582/18		99.2	0	O	EA-3		

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_116	SUD/2/86	bovine	89.3	0	O	EA-3		
viba_854	ETH/1/2007	cattle	86.1	0	O	EA-3		
viba_408	ETH/3/2004	cattle	86.0	0	O	EA-3		
viba_30238	MUR/19/2016	cattle	85.6	0	O	ME-SA	Ind-2001	e
viba_50	UGA/17/98		85.1	0	O	EA-4		
viba_285	UKG/35/2001	porcine	84.6	0	O	ME-SA	PanAsia	
viba_85	UGA/3/2002		84.5	0	O	EA-2		
viba_523	K83/79		84.2	0	O	EA-1		
viba_104	GHA/5/93	bovine	84.2	0	O	WA		
viba_576	IND/R2/75		84.2	0	O	ME-SA		

Virus sample name:	MAU/18Z007130/18
Sender reference:	18Z007130
Location of origin:	Hodh Ech Chargui
Country of origin:	Mauritania
Date of collection:	07/2018
Host species:	
Serotype:	O
Topotype:	EA-3
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	02/11/2018
Last updated:	02/11/2018
VIBASys IDs: sample 37536, genome 37537, sequence viba_37538, sequencing info 37539	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_37526	MAU/18Z007127/18		100.0	0	O	EA-3		
viba_37534	MAU/18Z007129/18		100.0	0	O	EA-3		
viba_36938	ALG/1/2018	cattle	99.8	0	O	EA-3		
viba_37530	MAU/18Z007128/18		99.8	0	O	EA-3		
viba_37252	GNA/18Z005583/18		99.7	0	O	EA-3		
viba_36947	ALG/2/2018	cattle	99.7	0	O	EA-3		
viba_37256	GNA/18Z005587/18		99.7	0	O	EA-3		
viba_37260	GNA/18Z005588/18		99.5	0	O	EA-3		
viba_37542	MAU/18Z007167/18		99.2	0	O	EA-3		
viba_37248	GNA/18Z005582/18		99.2	0	O	EA-3		

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_116	SUD/2/86	bovine	89.3	0	O	EA-3		
viba_854	ETH/1/2007	cattle	86.1	0	O	EA-3		
viba_408	ETH/3/2004	cattle	86.0	0	O	EA-3		
viba_30238	MUR/19/2016	cattle	85.6	0	O	ME-SA	Ind-2001	e
viba_50	UGA/17/98		85.1	0	O	EA-4		
viba_285	UKG/35/2001	porcine	84.6	0	O	ME-SA	PanAsia	
viba_85	UGA/3/2002		84.5	0	O	EA-2		
viba_523	K83/79		84.2	0	O	EA-1		
viba_104	GHA/5/93	bovine	84.2	0	O	WA		
viba_576	IND/R2/75		84.2	0	O	ME-SA		

Virus sample name:	MAU/18Z007167/18
Sender reference:	18Z007167
Location of origin:	Hodh Ech Chargui
Country of origin:	Mauritania
Date of collection:	07/2018
Host species:	
Serotype:	O
Topotype:	EA-3
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	02/11/2018
Last updated:	02/11/2018
VIBASys IDs: sample 37540, genome 37541, sequence viba_37542, sequencing info 37543	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_37550	MAU/18Z007170/18		100.0	0	O	EA-3		
viba_37546	MAU/18Z007168/18		100.0	0	O	EA-3		
viba_36938	ALG/1/2018	cattle	99.4	0	O	EA-3		
viba_37530	MAU/18Z007128/18		99.4	0	O	EA-3		
viba_37252	GNA/18Z005583/18		99.2	0	O	EA-3		
viba_36947	ALG/2/2018	cattle	99.2	0	O	EA-3		
viba_37538	MAU/18Z007130/18		99.2	0	O	EA-3		
viba_37526	MAU/18Z007127/18		99.2	0	O	EA-3		
viba_37256	GNA/18Z005587/18		99.2	0	O	EA-3		
viba_37534	MAU/18Z007129/18		99.2	0	O	EA-3		

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_116	SUD/2/86	bovine	88.8	0	O	EA-3		
viba_854	ETH/1/2007	cattle	85.6	0	O	EA-3		
viba_408	ETH/3/2004	cattle	85.3	0	O	EA-3		
viba_30238	MUR/19/2016	cattle	85.2	0	O	ME-SA	Ind-2001	e
viba_50	UGA/17/98		84.8	0	O	EA-4		
viba_293	BHU/3/2009	cattle	84.4	0	O	ME-SA	Ind-2001	d
viba_285	UKG/35/2001	porcine	84.1	0	O	ME-SA	PanAsia	
viba_576	IND/R2/75		84.1	0	O	ME-SA		
viba_766	IRN/31/2009	cattle	84.0	0	O	ME-SA	PanAsia-2	FAR-09
viba_85	UGA/3/2002		84.0	0	O	EA-2		

Virus sample name:	MAU/18Z007168/18
Sender reference:	18Z007168
Location of origin:	Hodh Ech Chargui
Country of origin:	Mauritania
Date of collection:	07/2018
Host species:	
Serotype:	O
Topotype:	EA-3
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	02/11/2018
Last updated:	02/11/2018
VIBASys IDs: sample 37544, genome 37545, sequence viba_37546, sequencing info 37547	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_37542	MAU/18Z007167/18		100.0	0	O	EA-3		
viba_37550	MAU/18Z007170/18		100.0	0	O	EA-3		
viba_36938	ALG/1/2018	cattle	99.4	0	O	EA-3		
viba_37530	MAU/18Z007128/18		99.4	0	O	EA-3		
viba_37252	GNA/18Z005583/18		99.2	0	O	EA-3		
viba_36947	ALG/2/2018	cattle	99.2	0	O	EA-3		
viba_37538	MAU/18Z007130/18		99.2	0	O	EA-3		
viba_37526	MAU/18Z007127/18		99.2	0	O	EA-3		
viba_37256	GNA/18Z005587/18		99.2	0	O	EA-3		
viba_37534	MAU/18Z007129/18		99.2	0	O	EA-3		

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_116	SUD/2/86	bovine	88.8	0	O	EA-3		
viba_854	ETH/1/2007	cattle	85.6	0	O	EA-3		
viba_408	ETH/3/2004	cattle	85.3	0	O	EA-3		
viba_30238	MUR/19/2016	cattle	85.2	0	O	ME-SA	Ind-2001	e
viba_50	UGA/17/98		84.8	0	O	EA-4		
viba_293	BHU/3/2009	cattle	84.4	0	O	ME-SA	Ind-2001	d
viba_285	UKG/35/2001	porcine	84.1	0	O	ME-SA	PanAsia	
viba_576	IND/R2/75		84.1	0	O	ME-SA		
viba_766	IRN/31/2009	cattle	84.0	0	O	ME-SA	PanAsia-2	FAR-09
viba_85	UGA/3/2002		84.0	0	O	EA-2		

Virus sample name:	MAU/18Z007170/18
Sender reference:	18Z007170
Location of origin:	Hodh Ech Chargui
Country of origin:	Mauritania
Date of collection:	07/2018
Host species:	
Serotype:	O
Topotype:	EA-3
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	n/a
Harvest date of material:	n/a
Primers:	n/a
Received for sequencing:	n/a
Created:	02/11/2018
Last updated:	02/11/2018
VIBASys IDs: sample 37548, genome 37549, sequence viba_37550, sequencing info 37551	

#### Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_37542	MAU/18Z007167/18		100.0	0	O	EA-3		
viba_37546	MAU/18Z007168/18		100.0	0	O	EA-3		
viba_36938	ALG/1/2018	cattle	99.4	0	O	EA-3		
viba_37530	MAU/18Z007128/18		99.4	0	O	EA-3		
viba_37252	GNA/18Z005583/18		99.2	0	O	EA-3		
viba_36947	ALG/2/2018	cattle	99.2	0	O	EA-3		
viba_37538	MAU/18Z007130/18		99.2	0	O	EA-3		
viba_37526	MAU/18Z007127/18		99.2	0	O	EA-3		
viba_37256	GNA/18Z005587/18		99.2	0	O	EA-3		
viba_37534	MAU/18Z007129/18		99.2	0	O	EA-3		

#### Most Closely Related Prototype Sequences

see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_116	SUD/2/86	bovine	88.8	0	O	EA-3		
viba_854	ETH/1/2007	cattle	85.6	0	O	EA-3		
viba_408	ETH/3/2004	cattle	85.3	0	O	EA-3		
viba_30238	MUR/19/2016	cattle	85.2	0	O	ME-SA	Ind-2001	e
viba_50	UGA/17/98		84.8	0	O	EA-4		
viba_293	BHU/3/2009	cattle	84.4	0	O	ME-SA	Ind-2001	d
viba_285	UKG/35/2001	porcine	84.1	0	O	ME-SA	PanAsia	
viba_576	IND/R2/75		84.1	0	O	ME-SA		
viba_766	IRN/31/2009	cattle	84.0	0	O	ME-SA	PanAsia-2	FAR-09
viba_85	UGA/3/2002		84.0	0	O	EA-2		



Report on FMDV O in Mauritania in 2018

Batch: WRLMEG/2018/00039



\*, not a WRLFMD Reference Number

## Analysis Parameters

VP1 subsequence extractor: vp1\_O  
 Query sequence set: WRLMEG/2018/00039-Mauritania-O (7 sequences)  
 Sequence database set: allseqs\_O (3896 sequences)  
 Prototype sequence set: !prototypes\_O (49 sequences)  
 Number of related sequences reported: 10  
 Minimal VP1 subsequence match length: 600  
 Sequence alignment method: muscle (default parameters)  
 Sequence alignment length: 636  
 Phylogeny reconstruction method: fdnadist, fneighbor  
 Number of bootstrap samples: 1000  
 Random seed for bootstrapping: 1  
 Displaying bootstrap values above: 70.0%  
 Number of sequences in tree capped at: 100  
 Number of prototype sequences in tree: 12  
 VIBASys version: reflabs-1.1.2

## Sequences in the Phylogenetic Tree

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

label	accession	host(s)	lab	country	taxonomic information
MAU/18Z007170/18*	n/a	n/a	ANSES	Mauritania	EA-3
MAU/18Z007167/18*	n/a	n/a	ANSES	Mauritania	EA-3
MAU/18Z007168/18*	n/a	n/a	ANSES	Mauritania	EA-3
ALG/2/2018	n/a	cattle	WRLFMD	Algeria	EA-3
GNA/18Z005588/18*	n/a	n/a	ANSES	Guinea	EA-3
ALG/1/2018	n/a	cattle	WRLFMD	Algeria	EA-3
MAU/18Z007128/18*	n/a	n/a	ANSES	Mauritania	EA-3
GNA/18Z005582/18*	n/a	n/a	ANSES	Guinea	EA-3
GNA/18Z005587/18*	n/a	n/a	ANSES	Guinea	EA-3
GNA/18Z005583/18*	n/a	n/a	ANSES	Guinea	EA-3
MAU/18Z007129/18*	n/a	n/a	ANSES	Mauritania	EA-3
MAU/18Z007130/18*	n/a	n/a	ANSES	Mauritania	EA-3
MAU/18Z007127/18*	n/a	n/a	ANSES	Mauritania	EA-3
NIG/21/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/15/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/16/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/14/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/18/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/10/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/7/2016	n/a	sheep	WRLFMD	Nigeria	EA-3
NIG/11/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/9/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/6/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/19/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/17/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/5/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/12/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/13/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/4/2016	n/a	cattle	WRLFMD	Nigeria	EA-3
NIG/10/14*	KY041874	bovine	CODA-CERVA	Nigeria	EA-3
NIG/4/14*	KY065153	bovine	CODA-CERVA	Nigeria	EA-3
NIG/6/14*	KY065155	bovine	CODA-CERVA	Nigeria	EA-3
NIG/5/14*	KY065154	bovine	CODA-CERVA	Nigeria	EA-3
NIG/7/14*	KY065151	bovine	CODA-CERVA	Nigeria	EA-3
NIG/9/14*	KY065152	bovine	CODA-CERVA	Nigeria	EA-3
NIG/3/14*	KY065150	bovine	CODA-CERVA	Nigeria	EA-3

*continued on next page*

label	accession	host(s)	lab	country	taxonomic information
NIG/1/14*	KY041876	bovine	CODA-CERVA	Nigeria	EA-3
CAR/A72J180P/2015*	MG873210	cattle	PIADC	Cameroon	EA-3
CAR/A78J360P/2016*	MG873212	cattle	PIADC	Cameroon	EA-3
CAR/A72J270P/2016*	MG873211	cattle	PIADC	Cameroon	EA-3
CAR/C66J270P/2016*	MG873215	cattle	PIADC	Cameroon	EA-3
CAR/C66J180P/2015*	MG873214	cattle	PIADC	Cameroon	EA-3
CAR/C67J270P/2016*	MG873217	cattle	PIADC	Cameroon	EA-3
CAR/C67BSJ90P/2015*	MG873216	cattle	PIADC	Cameroon	EA-3
CAR/B80J270P/2016*	MG873213	cattle	PIADC	Cameroon	EA-3
CAR/A68J270P/2016*	MG873209	cattle	PIADC	Cameroon	EA-3
CAR/A58BSJ90P/2015*	MG873208	cattle	PIADC	Cameroon	EA-3
CAR/D55J270P/2016*	MG873219	cattle	PIADC	Cameroon	EA-3
CAR/D65J270P/2016*	MG873222	cattle	PIADC	Cameroon	EA-3
CAR/D62J270P/2016*	MG873221	cattle	PIADC	Cameroon	EA-3
CAR/D56J360P/2016*	MG873220	cattle	PIADC	Cameroon	EA-3
CAR/D78J270P/2016*	MG873223	cattle	PIADC	Cameroon	EA-3
CAR/D1J270P/2016*	MG873218	cattle	PIADC	Cameroon	EA-3
CAR/G4258/2013*	KY581680	n/a	PIADC	Cameroon	EA-3
CAR/G4260/2013*	KY581679	n/a	PIADC	Cameroon	EA-3
NIG/1/2011	KX258022	bovine	WRLFMD	Nigeria	EA-3
NIG/8/2011	KX258024	bovine	WRLFMD	Nigeria	EA-3
NIG/10/2011	KX258025	bovine	WRLFMD	Nigeria	EA-3
NIG/15/2009	KX258021	cattle	WRLFMD	Nigeria	EA-3
CAR/59/2010*	KU720572	cattle	PIADC	Cameroon	EA-3
CAR/61/2010*	KU720573	cattle	PIADC	Cameroon	EA-3
SUD/11/2011	KX258036	cattle	WRLFMD	Sudan	EA-3
SUD/8/2008	GU566063	cattle	WRLFMD	Sudan	EA-3
SUD/12/2004	GU566049	bovine	WRLFMD	Sudan	EA-3
SUD/16/2004	GU566052	bovine	WRLFMD	Sudan	EA-3
SUD/26/2004	GU566054	bovine	WRLFMD	Sudan	EA-3
SUD/1/2004	GU566045	bovine	WRLFMD	Sudan	EA-3
SUD/3/2004	GU566046	bovine	WRLFMD	Sudan	EA-3
SUD/4/2004	GU566047	bovine	WRLFMD	Sudan	EA-3
SUD/15/2004	GU566051	bovine	WRLFMD	Sudan	EA-3
SUD/14/2004	GU566050	bovine	WRLFMD	Sudan	EA-3
SUD/30/2004	GU566055	bovine	WRLFMD	Sudan	EA-3
SUD/9/2004	GU566048	bovine	WRLFMD	Sudan	EA-3
SUD/25/2004	GU566053	bovine	WRLFMD	Sudan	EA-3
SUD/1/2005	GU566056	cattle	WRLFMD	Sudan	EA-3
SUD/2/2005	GU566057	cattle	WRLFMD	Sudan	EA-3
SUD/3/2005	GU566058	cattle	WRLFMD	Sudan	EA-3
NIG/1/2007	KX258020	cattle	WRLFMD	Nigeria	EA-3
ERI/12/2011	n/a	porcine	WRLFMD	Eritrea	EA-3
SUD/5/2008	GU566061	cattle	WRLFMD	Sudan	EA-3
SUD/6/2008	GU566062	cattle	WRLFMD	Sudan	EA-3
SUD/2/86	DQ165075	bovine	WRLFMD	Sudan	EA-3
GHA/5/93	AJ303488	bovine	WRLFMD	Ghana	WA
UGA/17/98	HM211075	n/a	WRLFMD	Uganda	EA-4
ETH/1/2007	FJ798137	cattle	WRLFMD	Ethiopia	EA-3
ETH/3/2004	FJ798109	cattle	WRLFMD	Ethiopia	EA-3
UGA/3/2002	DQ165077	n/a	WRLFMD	Uganda	EA-2
K83/79*	AJ303511	n/a	WRLFMD	Kenya	EA-1
TAI/189/87*	KY091288	bovine	TRRL	Thailand	SEA
IND/R2/75*	AF204276	n/a	PD-FMD	India	ME-SA
MUR/19/2016	MG972510	cattle	WRLFMD	Mauritius	ME-SA/Ind-2001/e
BHU/3/2009	KM921814	cattle	WRLFMD	Bhutan	ME-SA/Ind-2001/d
IRN/31/2009	KY091284	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/FAR-09
UKG/35/2001	AJ539141	porcine	PIADC	United Kingdom	ME-SA/PanAsia
ISA/1/62	AJ303500	n/a	WRLFMD	Indonesia	ISA-1

\*, not a WRLFMD Reference Number

n/a, not available