

Serotype: SAT2	Report date: 15/09/2008						
WRL Ref No: BOT/12/2008	Reported by: N.J. Knowles						
Sender Ref: BOT 16/08	Checked by: D.P. King						
Date collected: 2008							
Date received by WRLFMD: 01/08/2008	Topotype: none defined						
Date received for sequencing: 04/09/2008	Genotype/strain: none designated						
Species: Cattle	Sequence filename: BOT08-12.SEQ						
Material used: BTy1	Date sequence last updated: 13/09/2008						
Region sequenced: VP1	Total no. of comparisons: 442						
RT-PCR primers: SAT2-1C445F/SAT-2B208R; SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 300						
No. of Nt determined: 648	Total turn-around time: 45 days						
No. of ambiguities: 0	Sequencing time: 11 days						
Gene length: 648							
Comments:							
Ten Most Closely Related Viruses							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/BOT/13/2008	BOT08-13	648	648	0	100	0
2	SAT2/NAM/304/98* (AF367129) (buffalo)	NAM98-AC	647	614	1	94.9	5.1
3	SAT2/ZIM 4/02/2 (OVI)	ZIM02-AD	416	354	0	85.1	14.9
4	SAT2/ZIM 5/02/2 (OVI)	ZIM02-AE	419	355	0	84.73	15.27
5	SAT2/ZIM 6/02/2 (OVI)	ZIM02-AF	416	352	0	84.62	15.38
6	SAT2/ZIM 8/02/2 (OVI)	ZIM02-AH	390	330	0	84.62	15.38
7	SAT2/ZIM 7/02/2 (OVI)	ZIM02-AG	414	350	0	84.54	15.46
8	SAT2/ZIM/P45/91 MT12 buffalo	ZIM91B74	563	474	1	84.19	15.81
9	SAT2/ZIM/14/89 (buffalo)	ZIM89B14	648	545	0	84.1	15.9
10	SAT2/ZIM/23/89 (buffalo)	ZIM89B23	647	544	1	84.08	15.92
Relationships to Reference Virus Strains							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	541	0	83.49	16.51
2	SAT2/K52/84 (Kenya)	KEN84K52	648	498	0	76.85	23.15
3	SAT2/RHO/1/48 [AJ251475]	ZAM48A01	648	498	0	76.85	23.15
4	SAT2/K183/74 (Kenya)	KEN74183	648	496	0	76.54	23.46
5	SAT2/SA/106/59 (AY593848)	RSA59--A	648	485	0	74.85	25.15
6	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	477	0	73.61	26.39
7	SAT2/ANG/4/74 [AF479417]	ANG74-04	648	463	0	71.45	28.55
8	SAT2/SAU/6/2000 [AF367135]	SAU00A06	647	462	1	71.41	28.59
9	SAT2/GAM/8/79 [AF479410]	GAM79-08	648	460	0	70.99	29.01
10	SAT2/KEN/3/57	KEN57-03	648	460	0	70.99	29.01
nt, nucleotides							
*, not a WRLFMD reference number							

Serotype: SAT2	Report date: 15/09/2008
WRL Ref No: BOT/14/2008	Reported by: N.J. Knowles
Sender Ref: BOT 18/08	Checked by: D.P. King
Date collected: 2008	
Date received by WRLFMD: 01/08/2008	Topotype: none defined
Date received for sequencing: 04/09/2008	Genotype/strain: none designated
Species: Cattle	Sequence filename: BOT08-14.SEQ
Material used: BTy1	Date sequence last updated: 13/09/2008
Region sequenced: VP1	Total no. of comparisons: 442
RT-PCR primers: SAT2-1C445F/SAT-2B208R; SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 300
No. of Nt determined: 648	Total turn-around time: 45 days
No. of ambiguities: 0	Sequencing time: 11 days
Gene length: 648	

Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/BOT/15/2008	BOT08-15	648	648	0	100	0
2	SAT2/NMB/4/2007	NMB07-04	648	636	0	98.15	1.85
3	SAT2/NMB/1/2007	NMB07-01	648	635	0	97.99	2.01
4	SAT2/ZAM/8/2008	ZAM08-08	648	635	0	97.99	2.01
5	SAT2/ZAM/1/2007	ZAM07-01	648	634	0	97.84	2.16
6	SAT2/ZAM/3/2007	ZAM07-03	648	634	0	97.84	2.16
7	SAT2/NMB/3/2008	NMB08-03	648	633	0	97.69	2.31
8	SAT2/NMB/4/2008	NMB08-04	648	633	0	97.69	2.31
9	SAT2/ZAM/2/2007	ZAM07-02	648	633	0	97.69	2.31
10	SAT2/NMB/2/2008	NMB08-02	648	632	0	97.53	2.47

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/RHO/1/48 [AJ251475]	ZAM48A01	648	543	0	83.8	16.2
2	SAT2/K52/84 (Kenya)	KEN84K52	648	519	0	80.09	19.91
3	SAT2/K183/74 (Kenya)	KEN74183	648	507	0	78.24	21.76
4	SAT2/SA/106/59 (AY593848)	RSA59--A	648	506	0	78.09	21.91
5	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	489	0	75.46	24.54
6	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	484	0	74.69	25.31
7	SAT2/KEN/3/57	KEN57-03	648	477	0	73.61	26.39
8	SAT2/ANG/4/74 [AF479417]	ANG74-04	648	476	0	73.46	26.54
9	SAT2/SAU/6/2000 [AF367135]	SAU00A06	647	472	1	72.95	27.05
10	SAT2/GAM/8/79 [AF479410]	GAM79-08	648	463	0	71.45	28.55

nt, nucleotides

*, not a WRLFMD reference number

Serotype: SAT2	Report date: 15/09/2008
WRL Ref No: BOT/15/2008	Reported by: N.J. Knowles
Sender Ref: BOT 19/08	Checked by: D.P. King
Date collected: 2008	
Date received by WRLFMD: 01/08/2008	Topotype: none defined
Date received for sequencing: 04/09/2008	Genotype/strain: none designated
Species: Cattle	Sequence filename: BOT08-15.SEQ
Material used: BTy1	Date sequence last updated: 13/09/2008
Region sequenced: VP1	Total no. of comparisons: 442
RT-PCR primers: SAT2-1C445F/SAT-2B208R; SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 300
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Ten Most Closely Related Viruses

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2	SAT2/NMB/4/2007	NMB07-04	648	636	0	98.15	1.85
3	SAT2/NMB/1/2007	NMB07-01	648	635	0	97.99	2.01
4	SAT2/ZAM/8/2008	ZAM08-08	648	635	0	97.99	2.01
5	SAT2/ZAM/1/2007	ZAM07-01	648	634	0	97.84	2.16
6	SAT2/ZAM/3/2007	ZAM07-03	648	634	0	97.84	2.16
7	SAT2/NMB/3/2008	NMB08-03	648	633	0	97.69	2.31
8	SAT2/NMB/4/2008	NMB08-04	648	633	0	97.69	2.31
9	SAT2/ZAM/2/2007	ZAM07-02	648	633	0	97.69	2.31
10	SAT2/NMB/2/2008	NMB08-02	648	632	0	97.53	2.47

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3	SAT2/K183/74 (Kenya)	KEN74183	648	507	0	78.24	21.76
4	SAT2/SA/106/59 (AY593848)	RSA59--A	648	506	0	78.09	21.91
5	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	489	0	75.46	24.54
6	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	484	0	74.69	25.31
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10	SAT2/GAM/8/79 [AF479410]	GAM79-08	648	463	0	71.45	28.55

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV SAT 2 viruses from Botswana & Namibia in 2008

Software: MEGA 4.0

No. of Taxa : 136

Data File : n:\evd\meg\db\fmv\sat2\NMB2008b.meg

Data Title : SAT2 2008

Data Type : Nucleotide (Coding)

Analysis : Phylogeny reconstruction

Tree Inference : =====

->Method : Neighbor-Joining

->Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)

Include Sites : =====

->Gaps/Missing Data : Pairwise Deletion

->Codon Positions : 1st+2nd+3rd+Noncoding

Substitution Model : =====

->Model : Nucleotide: Kimura 2-parameter

->Substitutions to Include : d: Transitions + Transversions

->Pattern among Lineages : Same (Homogeneous)

->Rates among sites : Uniform rates

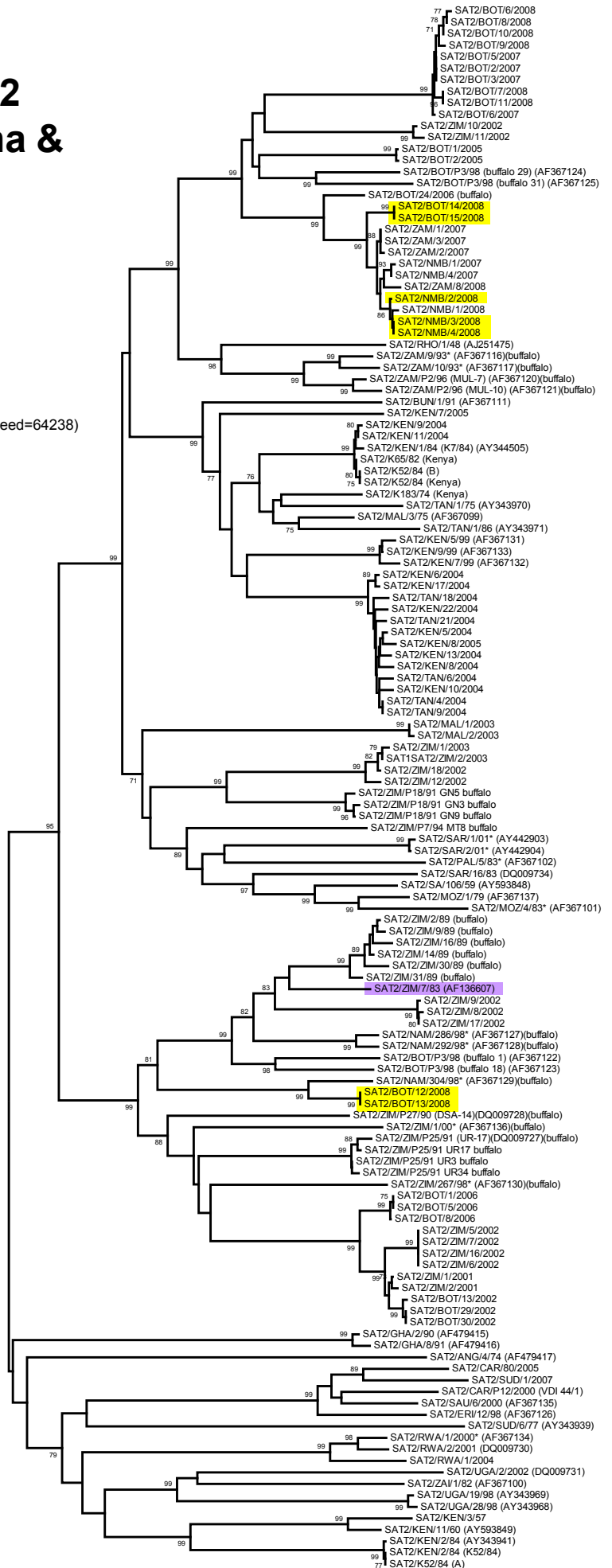
No. of Sites : 648

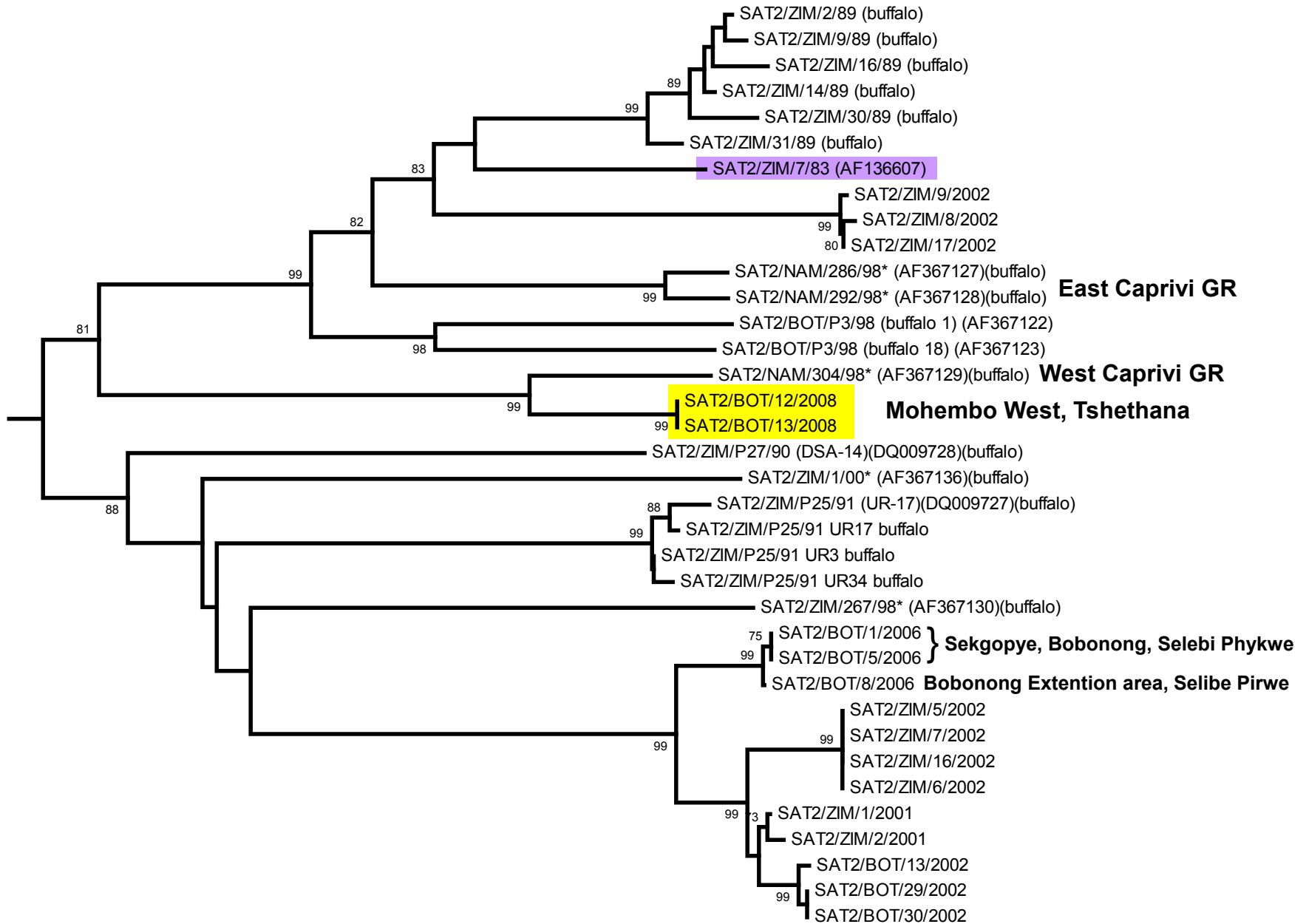
No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

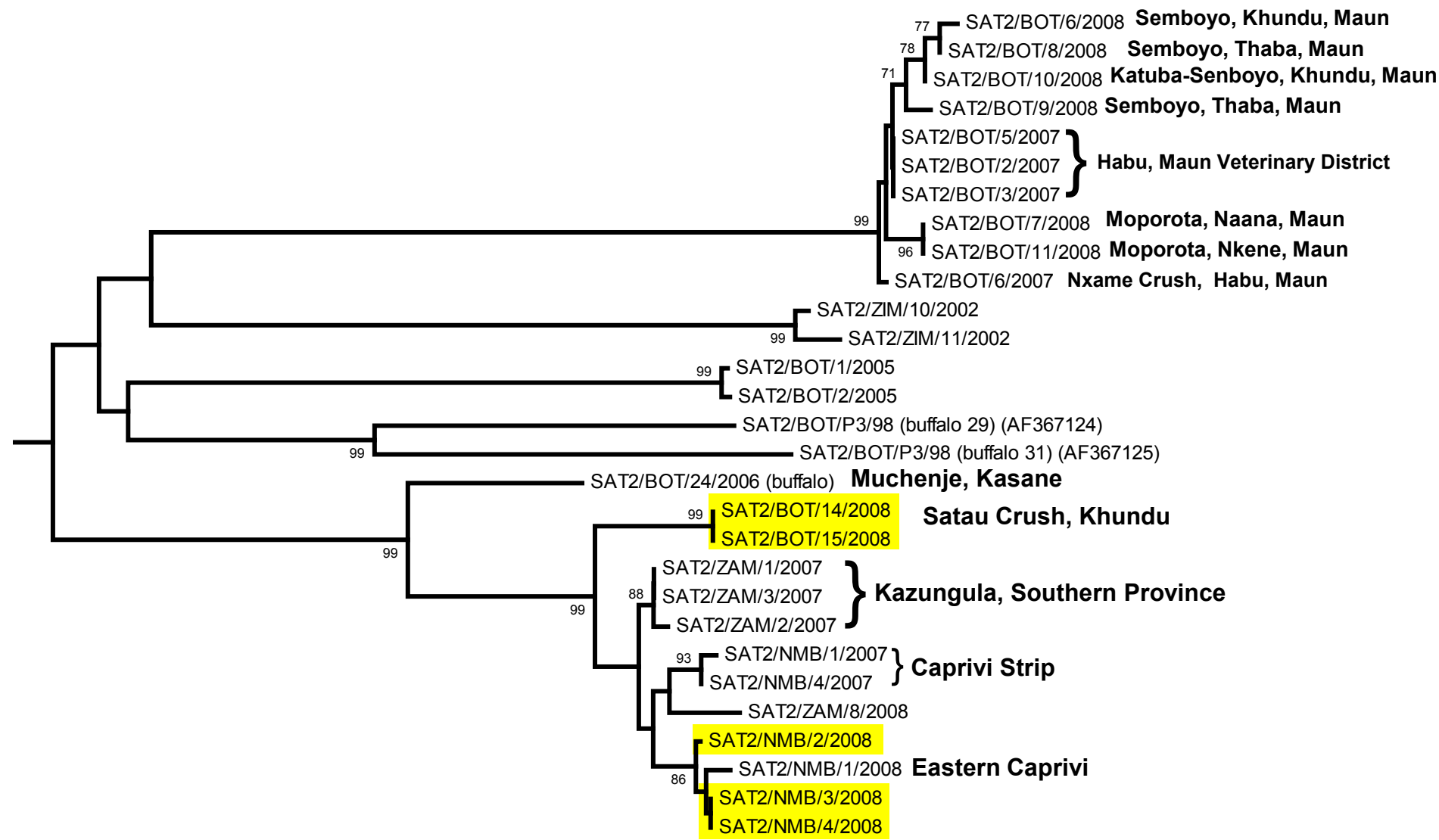
*, not a WRLFMD Ref. No.

N.J. Knowles, K. Ebert & J. Wadsworth, 14 September 2008





0.02



0.02