

Serotype: SAT2	Report date: 15/09/2008
WRL Ref No: NMB/2/2008	Reported by: N.J. Knowles
Sender Ref: NAM 02/08 Ref 88/08	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: NMB08-02.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;	Min. no. of nt for comparison: 300
SAT2-P1-1223F/SAT-2B208R	Total turn-around time: 45 days
No. of Nt determined: 648	Sequencing time: 11 days
No. of ambiguities: 0	
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/NMB/3/2008	NMB08-03	648	647	0	99.85	0.15
2	SAT2/NMB/4/2008	NMB08-04	648	647	0	99.85	0.15
3	SAT2/NMB/1/2008	NMB08-01	648	645	0	99.54	0.46
4	SAT2/NMB/4/2007	NMB07-04	648	642	0	99.07	0.93
5	SAT2/ZAM/1/2007	ZAM07-01	648	642	0	99.07	0.93
6	SAT2/ZAM/3/2007	ZAM07-03	648	642	0	99.07	0.93
7	SAT2/NMB/1/2007	NMB07-01	648	641	0	98.92	1.08
8	SAT2/ZAM/2/2007	ZAM07-02	648	641	0	98.92	1.08
9	SAT2/ZAM/8/2008	ZAM08-08	648	637	0	98.3	1.7
10	SAT2/BOT/14/2008	BOT08-14	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	547	0	84.41	15.59
2	SAT2/K52/84 (Kenya)	KEN84K52	648	521	0	80.4	19.6
3	SAT2/K183/74 (Kenya)	KEN74183	648	511	0	78.86	21.14
4	SAT2/SA/106/59 (AY593848)	RSA59--A	648	507	0	78.24	21.76
5	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	492	0	75.93	24.07
6	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	483	0	74.54	25.46
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	466	1	72.02	27.98
10	SAT2/GAM/8/79 [AF479410]	GAM79-08	648	466	0	71.91	28.09

nt, nucleotides

*, not a WRLFMD reference number

Serotype: SAT2	Report date: 15/09/2008
WRL Ref No: NMB/3/2008	Reported by: N.J. Knowles
Sender Ref: NAM 03/08 Ref 88/08	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: NMB08-03.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/NMB/4/2008	NMB08-04	648	648	0	100	0
2	SAT2/NMB/2/2008	NMB08-02	648	647	0	99.85	0.15
3	SAT2/NMB/1/2008	NMB08-01	648	646	0	99.69	0.31
4	SAT2/NMB/4/2007	NMB07-04	648	643	0	99.23	0.77
5	SAT2/ZAM/1/2007	ZAM07-01	648	643	0	99.23	0.77
6	SAT2/ZAM/3/2007	ZAM07-03	648	643	0	99.23	0.77
7	SAT2/NMB/1/2007	NMB07-01	648	642	0	99.07	0.93
8	SAT2/ZAM/2/2007	ZAM07-02	648	642	0	99.07	0.93
9	SAT2/ZAM/8/2008	ZAM08-08	648	638	0	98.46	1.54
10	SAT2/BOT/14/2008	BOT08-14	648	633	0	97.69	2.31

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	548	0	84.57	15.43
2	SAT2/K52/84 (Kenya)	KEN84K52	648	520	0	80.25	19.75
3	SAT2/K183/74 (Kenya)	KEN74183	648	510	0	78.7	21.3
4	SAT2/SA/106/59 (AY593848)	RSA59--A	648	506	0	78.09	21.91
5	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	491	0	75.77	24.23
6	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	484	0	74.69	25.31
7	SAT2/KEN/3/57	KEN57-03	648	476	0	73.46	26.54
8	SAT2/ANG/4/74 [AF479417]	ANG74-04	648	475	0	73.3	26.7
9	SAT2/SAU/6/2000 [AF367135]	SAU00A06	647	467	1	72.18	27.82
10	SAT2/GAM/8/79 [AF479410]	GAM79-08	648	465	0	71.76	28.24

nt, nucleotides

*, not a WRLFMD reference number

Serotype: SAT2	Report date: 15/09/2008
WRL Ref No: NMB/4/2008	Reported by: N.J. Knowles
Sender Ref: NAM 04/08 Ref 88/08	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: NMB08-04.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

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2	SAT2/NMB/2/2008	NMB08-02	648	647	0	99.85	0.15
3	SAT2/NMB/1/2008	NMB08-01	648	646	0	99.69	0.31
4	SAT2/NMB/4/2007	NMB07-04	648	643	0	99.23	0.77
5	SAT2/ZAM/1/2007	ZAM07-01	648	643	0	99.23	0.77
6	SAT2/ZAM/3/2007	ZAM07-03	648	643	0	99.23	0.77
7	SAT2/NMB/1/2007	NMB07-01	648	642	0	99.07	0.93
8	SAT2/ZAM/2/2007	ZAM07-02	648	642	0	99.07	0.93
9	SAT2/ZAM/8/2008	ZAM08-08	648	638	0	98.46	1.54
10	SAT2/BOT/14/2008	BOT08-14	648	633	0	97.69	2.31

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2	SAT2/K52/84 (Kenya)	KEN84K52	648	520	0	80.25	19.75
3	SAT2/K183/74 (Kenya)	KEN74183	648	510	0	78.7	21.3
4	SAT2/SA/106/59 (AY593848)	RSA59--A	648	506	0	78.09	21.91
5	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	491	0	75.77	24.23
6	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	484	0	74.69	25.31
7	SAT2/KEN/3/57	KEN57-03	648	476	0	73.46	26.54
8	SAT2/ANG/4/74 [AF479417]	ANG74-04	648	475	0	73.3	26.7
9	SAT2/SAU/6/2000 [AF367135]	SAU00A06	647	467	1	72.18	27.82
10	SAT2/GAM/8/79 [AF479410]	GAM79-08	648	465	0	71.76	28.24

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

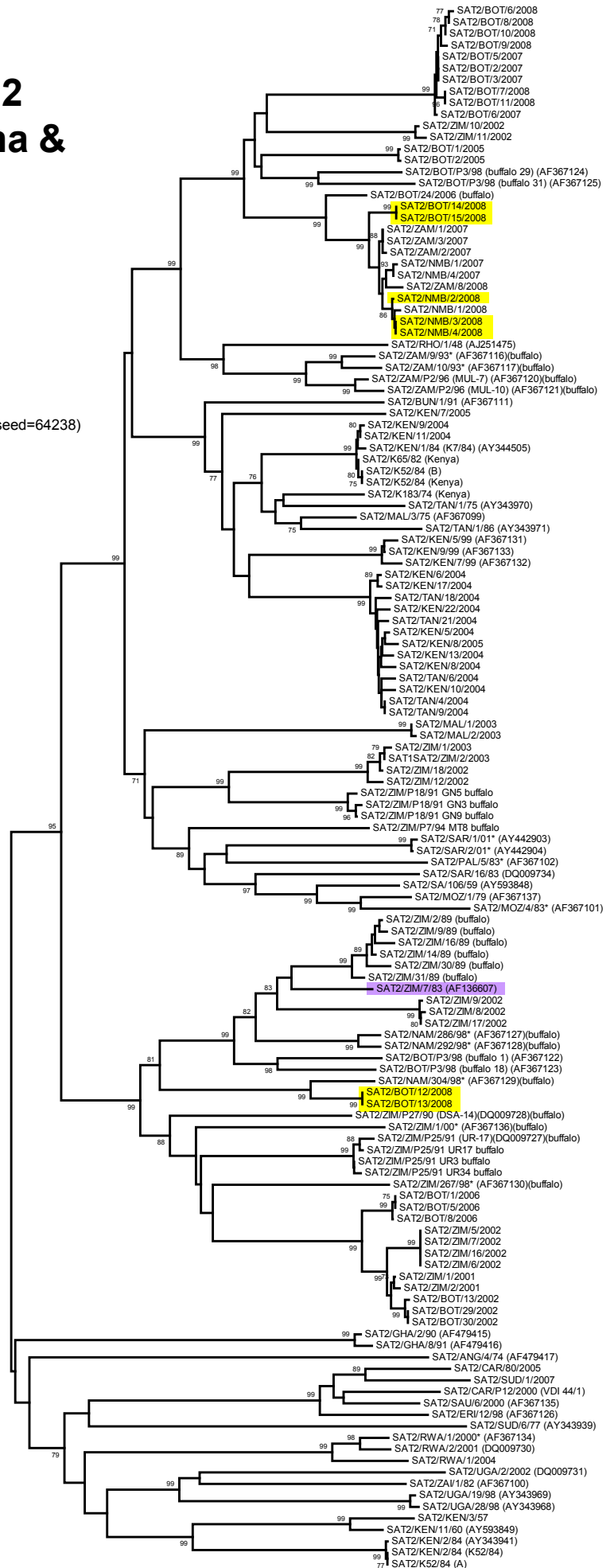
No. of Sites : 648

No Of Bootstrap Reps = 1000

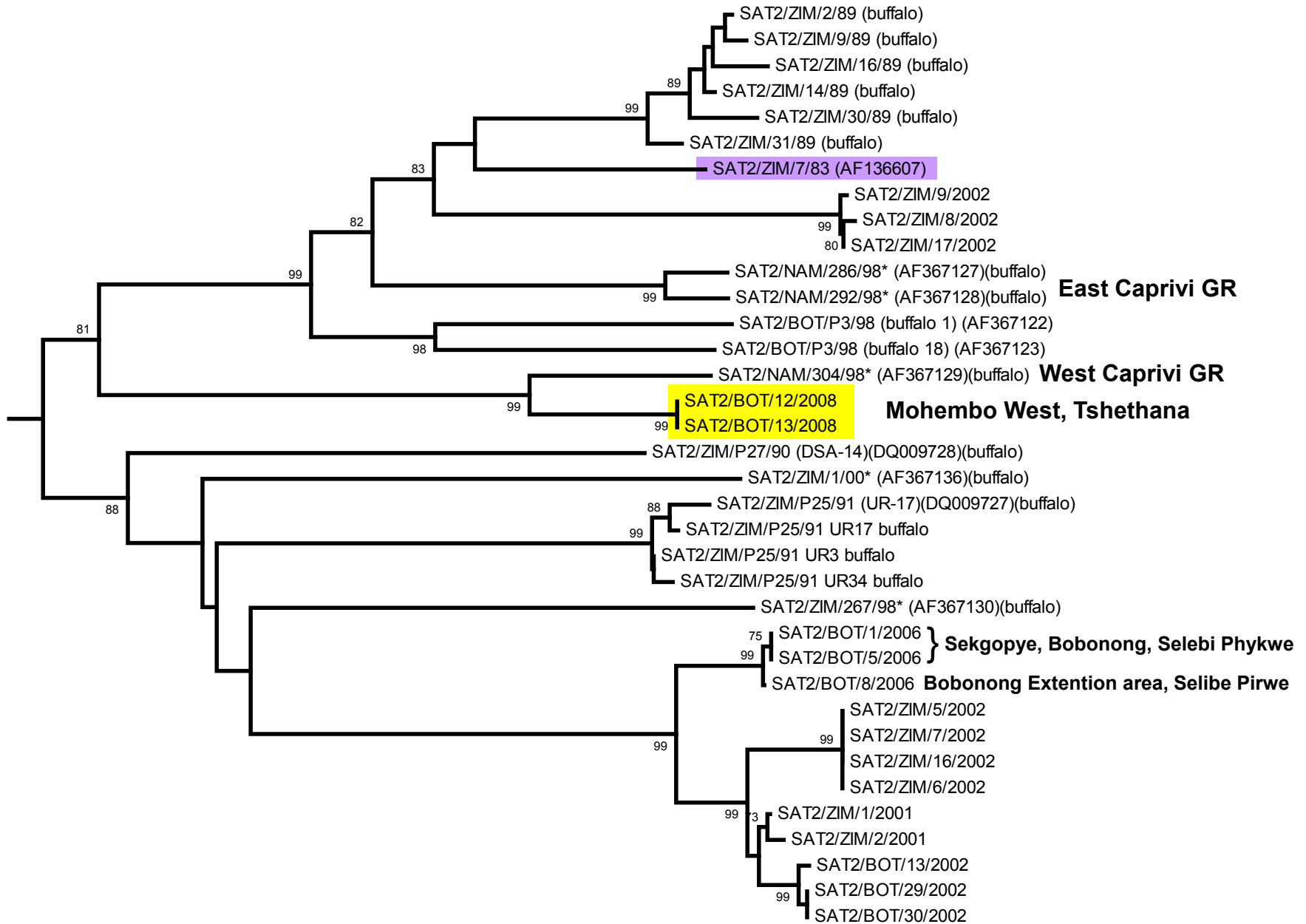
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

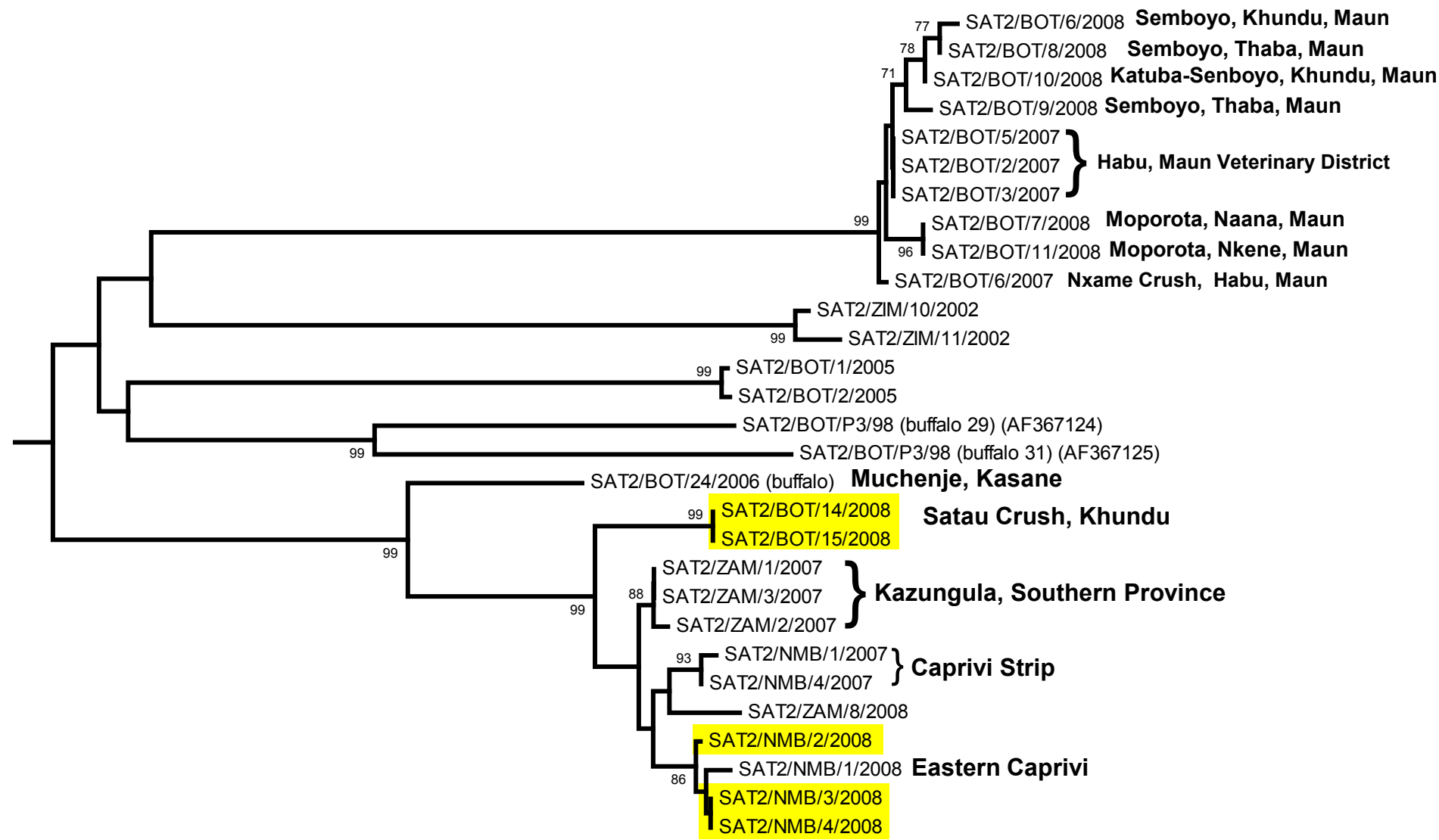
N.J. Knowles, K. Ebert & J. Wadsworth, 14 September 2008



0.05



0.02



0.02