

Supplemental figure 1.

For QProbe RT-LAMP

N	Primer sequence (5'-3', EMC, JX869059.2)	Position
N-F3	GCTCCCAGGTGGTACTTCT	28848-28866
N-B3	cagtcctccatgtggaag	29061-29042
N-FIP	tcatggacccaaacgatgccatACTGGAAGTGGACCCGAAG	28939-28918 + 28872-28890
N-BIP	GCTCCTTCAACTTTTGGGACGtagtaccgggcgcaatt	28956-28977 + 29028-29011
N-LF	cggaatgggagtgctg	28906-28891
N-LB	GGAACCCTAACAATGATTGAGCT	28978-29000
N-QP3G (Qprobe)	GGAACCCTAACAATGATTGAGCTATTGTTACAC	28978-29010

ORF1a	Primer sequence (5'-3', EMC, JX869059.2)	Position
ORF1a-F3	GCCTACTTTGGATGTGAGG	1572-1590
ORF1a-B3	acaacgaactctccaca	1753-1736
ORF1a-FIP	taaagatggagctccaatcctgaAAGGTACTATGTACTTTGTGCC	1656-1632 + 1591-1612
ORF1a-BIP	GTACTGGCTCTTGGACAAGGagttaagggaatgctgagt	1663-1683 + 1734-1716
ORF1a-LF	acaacagacttagctctag	1612-1630
ORF1a-LB	GGTCACTCAAATTGCTAACATG	1682-1703
ORF1a-QP3G (Qprobe)	GGTCACTCAAATTGCTAACATGTTCTTGGAACAGAC	1682-1717

For real-time RT-PCR

upE	Primer sequence (5'-3', EMC, JX869059.2)	Position
upE-Forward	GCAACGCGCGATTTCAGTT	27458-27475
upE-Reverse	GCCTCTACACGGGACCCATA	27549-27530
upE-Probe (FAM-TAMRA)	CTCTTCACATAATCGCCCCGAGCTCG	27477-27502

upE	Primer sequence (5'-3', EMC, JX869059.2)	Position
ORF1a-Forward	CCACTACTCCCATTTTCGTCAG	11197-11217
ORF1a-Reverse	CAGTATGTGTAGTGCATATAAGCA	11255-11280
ORF1a-Probe (FAM-TAMRA)	TTGCAAATTGGCTTGCCCCCACT	11230-11252

Supplemental figure 1. Primer and Probe sequences used for QProbe RT-LAMP and real-time RT-PCR were listed. The references were as follows: QProbe RT-LAMP, Shirato, K et al., *J Virol Methods* 258, 41-48; real-time RT-PCR, Corman, V et al., (2012). *Euro Surveill* 17, 20285 and 20334.

Alignment of S protein (amino acids)

		*	20	*	40	*	60	*	
EMC :	MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTFFDKTWPRPIDVSKADGIIYPQGR	TYSNITITYQGLFPYQ	:	78					
118 :	MIHSVFLLMFLLTPTESYVDVGPDSAKSACIEVDIQQTFFDKTWPRPIDVSKADGIIYPQGR	TYSNITITYQGLFPYQ	:	78					
126 :	MIHSVFLLMFLLTPTESYVDVGPDSAKSACIEVDIQQTFFDKTWPRPIDVSKADGIIYPQGR	TYSNITITYQGLFPYQ	:	78					
	MIHSVFLLMFLLTPTESYVDVGPDSaKSACIEVDIQQTFFDKTWPRPIDVSKADGIIYPQGR	TYSNITITYQGLFPYQ							
	80	*	100	*	120	*	140	*	
EMC :	GDHGDMYVYSAGHATGTTTPQKLFVANYSQDVKQFANGFVVRIGAAANSTGTVIISPSTSAI	IRKIYPAFMLGSSVGNF	:	156					
118 :	GDHGDMYVYSAGHATGTTTPQKLFVANYSQDVKQFANGFVVRIGAAANSTGTVIISPSTSAI	IRKIYPAFMLGSSVGNF	:	156					
126 :	GDHGDMYVYSAGHATGTTTPQKLFVANYSQDVKQFANGFVVRIGAAANSTGTVIISPSTSAI	IRKIYPAFMLGSSVGNF	:	156					
	GDHGDMYVYSAGHATGTTTPQKLFVANYSQDVKQFANGFVVRIGAAANSTGTVIISPSTSAI	IRKIYPAFMLGSSVGNF							
	160	*	180	*	200	*	220	*	
EMC :	SDGKMGRFFNHTLVLLPDGCGTLLRAFYCILEPRSGNH	CPAGNSYTSFATYHTPATDCSDGNYNRNASLNSFKEYFNL	:	234					
118 :	SYGKMGRFFNHTLVLLPDGCGTLLRAFYCILEPRSGNY	CPAGNSYTSFATYHTPATDCSDGNYNRNASLNSFKEYFNL	:	234					
126 :	SYGKMGRFFNHTLVLLPDGCGTLLRAFYCILEPRSGNY	CPAGNSYTSFATYHTPATDCSDGNYNRNASLNSFKEYFNL	:	234					
	SyGKMGRFFNHTLVLLPDGCGTLLRAFYCILEPRSGNy	CPAGNSYTSFATYHTPATDCSDGNYNRNASLNSFKEYFNL							
	240	*	260	*	280	*	300	*	
EMC :	RNCTFMYTYNITEDEILEWFGITQTAQGVHLFSSRYVDLYGGNMFQFATLPVYDTIKYYSIIPH	SIRSIQSDRKAWAA	:	312					
118 :	RNCTFMYTYNITEDEILEWFGITQTAQGVHLFSSRYVDLYGGNMFQFATLPVYDTIKYYSIIPH	SIRSIQSDRKAWAA	:	312					
126 :	RNCTFMYTYNITEDEILEWFGITQTAQGVHLFSSRYVDLYGGNMFQFATLPVYDTIKYYSIIPH	SIRSIQSDRKAWAA	:	312					
	RNCTFMYTYNITEDEILEWFGITQTAQGVHLFSSRYVDLYGGNMFQFATLPVYDTIKYYSIIPH	SIRSIQSDRKAWAA							
	320	*	340	*	360	*	380	*	
EMC :	FYVYKLQPLTFLLDFSVDGYIRRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQAEGVECDFSP	LLS	:	390					
118 :	FYVYKLQPLTFLLDFSVDGYIRRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQAEGVECDFSP	LLF	:	390					
126 :	FYVYKLQPLTFLLDFSVDGYIRRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQAEGVECDFSP	LLF	:	390					
	FYVYKLQPLTFLLDFSVDGYIRRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQAEGVECDFSP	LLf							

		400	*	420	*	440	*	460	
EMC :	GTPPQVYNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIASNCYSSLILDYFSYPLSMKSDLSVSSAGPISQFN	:	468						
118 :	GTPPQVYNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIASNCYSSLILDYFSYPLSMKSDLSVSSAGPISQFN	:	468						
126 :	GTPPQVYNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIASNCYSSLILDYFSYPLSMKSDLSVSSAGPISQFN	:	468						
	*	480	*	500	*	520	*	540	
EMC :	YKQSFNPTCLILATVPHNLTTITKPLKYSYINKCSRLLSDDRTEVPQLVNaNQYSPCVSIVPSTVWEDGDYYRKQLS	:	546						
118 :	YKQSFNPTCLILATVPHNLTTITKPLKYSYINKCSRLLSDDRTEVPQLVNaNQYSPCVSIVPSTVWEDGDYYRKQLS	:	546						
126 :	YKQSFNPTCLILATVPHNLTTITKPLKYSYINKCSRLLSDDRTEVPQLVNaNQYSPCVSIVPSTVWEDGDYYRKQLS	:	546						
	*	560	*	580	*	600	*	620	
EMC :	PLEGGGWLVASGSTVAMTEQLQMFGGITVQYGTDTNSVCPKLEFANDTKIASQLGNCVEYSLYGVSGRGVFQNCCTAVG	:	624						
118 :	PLEGGGWLVASGSTVAMTEQLQMFGGITVQYGTDTNSVCPKLEFANDTKIVSQLGNCVEYSLYGVSGRGVFQNCCTAVG	:	624						
126 :	PLEGGGWLVASGSTVAMTEQLQMFGGITVQYGTDTNSVCPKLEFANDTKIVSQLGNCVEYSLYGVSGRGVFQNCCTAVG	:	624						
					Receptor binding domain				
	*	640	*	660	*	680	*	700	
EMC :	VRQQRFFVYDAYQNLVGYYSDDGNYYCLRACVSPVSVIYDKETKTHATLFGSVACEHISSTMSQYSRSTRSMLKRRDS	:	702						
118 :	VPQQRFFVYDAYQNLVGYYSDDGNYYCLRACVSPVSVIYDKETKTHATLFGSVACEHISSTMSQYSRSTRSMLKRRDS	:	702						
126 :	VPQQRFFVYDAYQNLVGYYSDDGNYYCLRACVSPVSVIYDKETKTHATLFGSVACEHISSTMSQYSRSTRSMLKRRDS	:	702						
	*	720	*	740	*	760	*	780	
EMC :	TYGPLQTPVGCVLGLVNSSLFVEDCKLPLGQSLCALPDTTPSTLTTPRSVRSVPGEMRLASIAFNHPIQVDQLNSSYFKL	:	780						
118 :	TYGPLQTPVGCVLGLVNSSLFVEDCKLPLGQSLCALPDTTPSTLTTPRSVRSVPGEMRLASIAFNHPIQVDQLNSSYFKL	:	780						
126 :	TYGPLQTPVGCVLGLVNSSLFVEDCKLPLGQSLCALPDTTPSTLTTPRSVRSVPGEMRLASIAFNHPIQVDQLNSSYFKL	:	780						
					1st Furin site				

	1180	*	1200	*	1220	*	1240	
EMC :	YFIKTNNTRIVDEWSYTGSSFYAPEPITSLNTKYVAPQVTYQNISTNLPPPLLGNSTGIDFQDELDEFFKNVSTSIPN							: 1248
118 :	YFIKTNNTRIVDEWSYTGSSFYAPEPITSLNTKYVAPQVTYQNISTNLPPPLLGNSTGIDFQDELDEFFKNVSTSIPN							: 1248
126 :	YFIKTNNTRIVDEWSYTGSSFYAPEPITSLNTKYVAPQVTYQNISTNLPPPLLGNSTGIDFQDELDEFFKNVSTSIPN							: 1248
	*	1260	*	1280	*	1300	*	1320
EMC :	FGSLTQINTTLLDLTYEMLSLQQVVKALNESYIDLKELGNYTYYNKWPWYIWL							: 1326
118 :	FGSLTQINTTLLDLTYEMLSLQQVVKALNESYIDLKELGNYTYYNKWPWYIWL							: 1326
126 :	FGSLTQINTTLLDLTYEMLSLQQVVKALNESYIDLKELGNYTYYNKWPWYIWL							: 1326
	*	1340	*					
EMC :	CMGKLKCNRCDDRYEEYDLEPHKVHVH							: 1353
118 :	CMGKLKCNRCDDRYEEYDLEPHKVHVH							: 1353
126 :	CMGKLKCNRCDDRYEEYDLEPHKVHVH							: 1353
	CMGKLKCNRCDDRYEEYDLEPHKVHVH							

Supplement figure 2. An alignment of amino acid sequences of Amibara and EMC S proteins. The alignment were constructed using GeneDoc software [Nicholas, Kb & Nicholas, Hb. (1996). GeneDoc: a tool for editing and annotating multiple sequence alignments. Distributed by the authors.]. Two furin recognition sites were enclosed by blue and green lines. The receptor binding domain was enclosed by red line referring following study: Guangwen Lu et al., (2013). Nature. 500: 227–231.