

Capsid Specific Antibody Responses of Domestic Pigs Immunized with Low Virulent African swine fever virus

Priscilla Y. L. Tng ^{1,*}, Laila Al-Adwani ¹, Egle Pauletto ^{1,2}, Joshua Hui ¹, and Christopher L. Netherton ^{1,*}

1 The Pirbright Institute, Ash Road, Pirbright, Woking GU24 0NF, UK

2 The Institute of Medical Sciences, Foresterhill, University of Aberdeen, Aberdeen AB25 2ZD, UK

* Correspondence: priscilla.tng@pirbright.com (P.Y.T.); christopher.netherton@pirbright.ac.uk (C.L.N.)

Supplementary Information

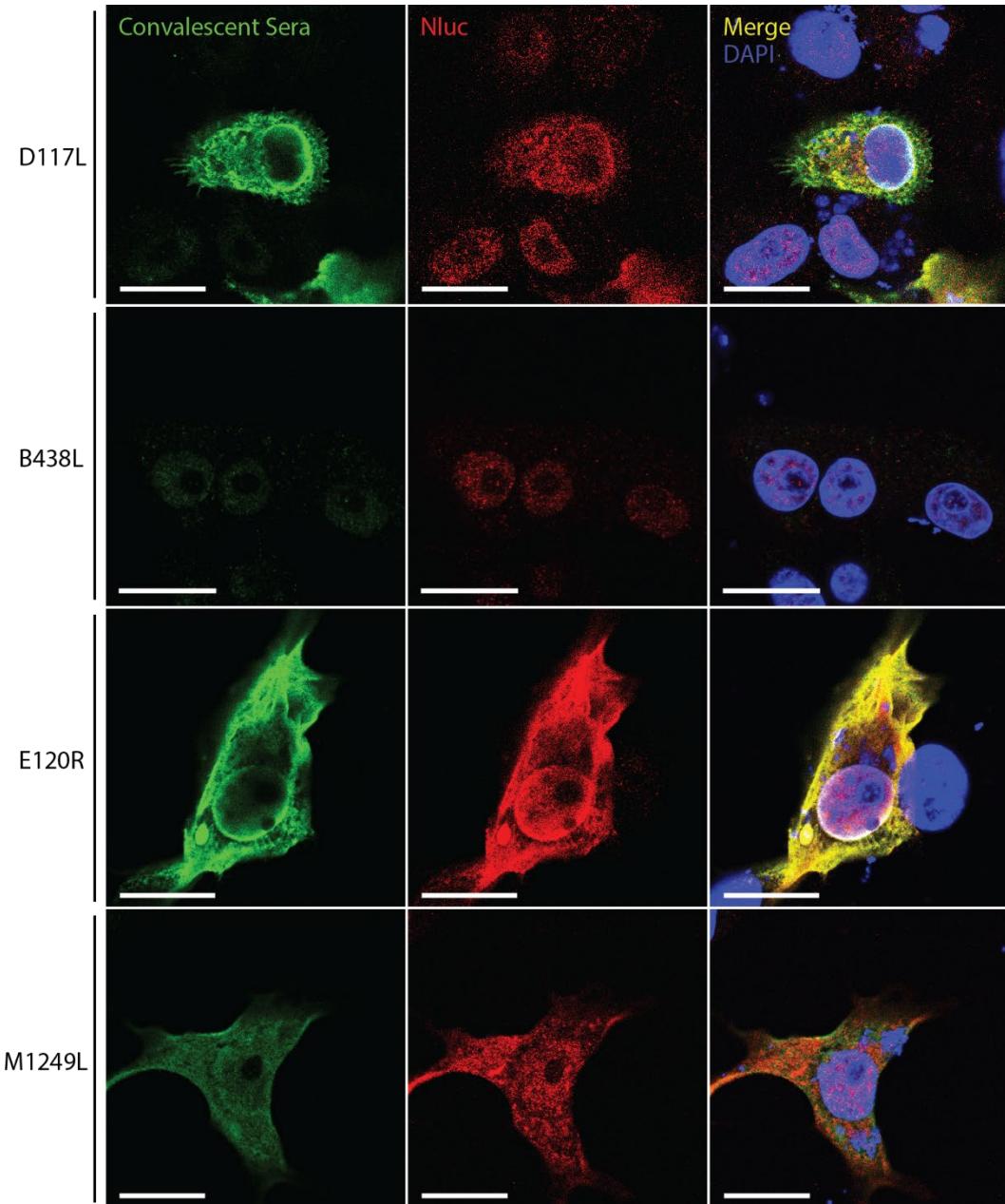


Figure 1. Confocal images of Vero cells expressing recombinant ASFV proteins D117L, B438L, E120R and M1249L. Detection of expression of recombinant nanoluciferase (Nluc)-tagged ASFV proteins in transfected Vero cells was achieved with the monoclonal anti-Nluc antibody (red, Promega) and with convalescent outbred pig sera from our previous study [1] (green). Nuclear DNA was stained with DAPI (blue). White bar denotes 20 μ m.

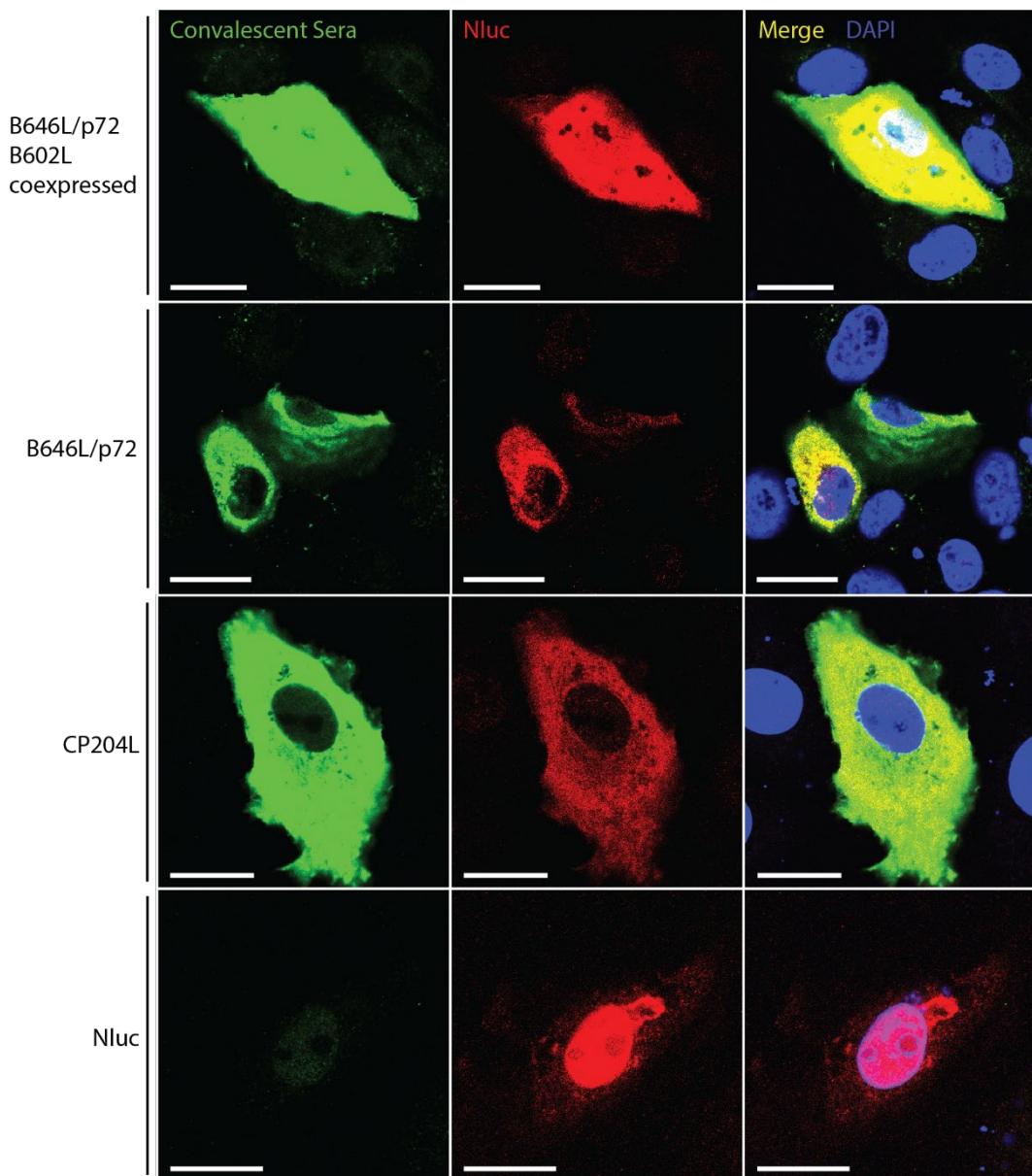


Figure 2. Confocal images of Vero cells expressing recombinant ASFV proteins B646L/p72, B602L, CP204L/p30 and Nluc. B646L/p72 was expressed alone or with chaperone B602L. Detection of expression of recombinant nanoluciferase (Nluc)-tagged ASFV proteins in transfected Vero cells was achieved with the monoclonal anti-Nluc antibody (red, Promega) and with convalescent outbred pig sera from our previous study [1] (green). Nuclear DNA was stained with DAPI (blue). White bar denotes 20 μ m.

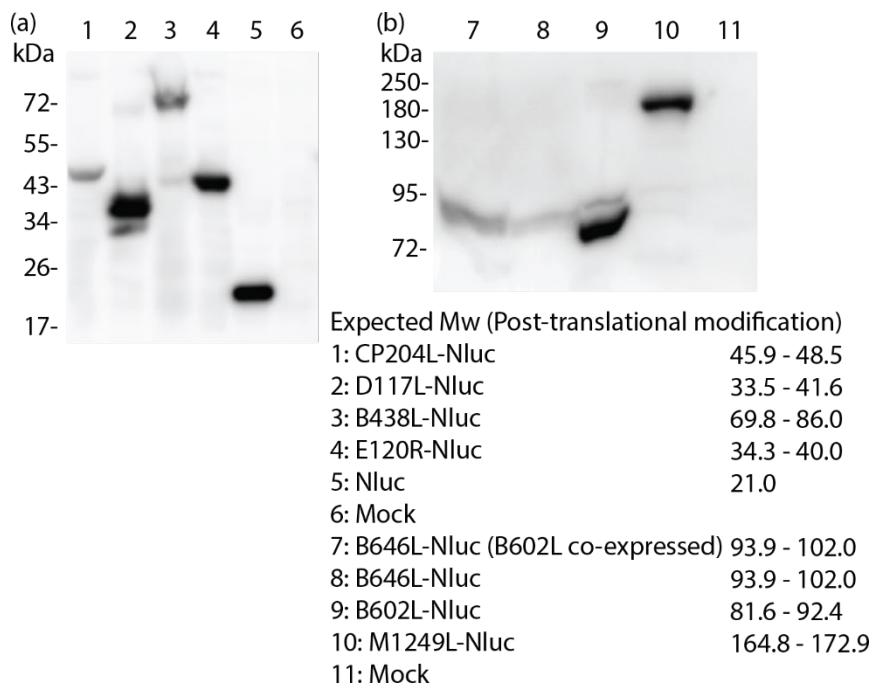


Figure 3. Western blot detection of recombinant Nluc-tagged ASFV proteins. Nluc-tagged ASFV proteins from transfected HEK293T cell lysates were detected with the monoclonal anti-Nluc antibody (Promega). The expected protein molecular weights (Mw) are listed as a range that takes post-translational modifications into account.

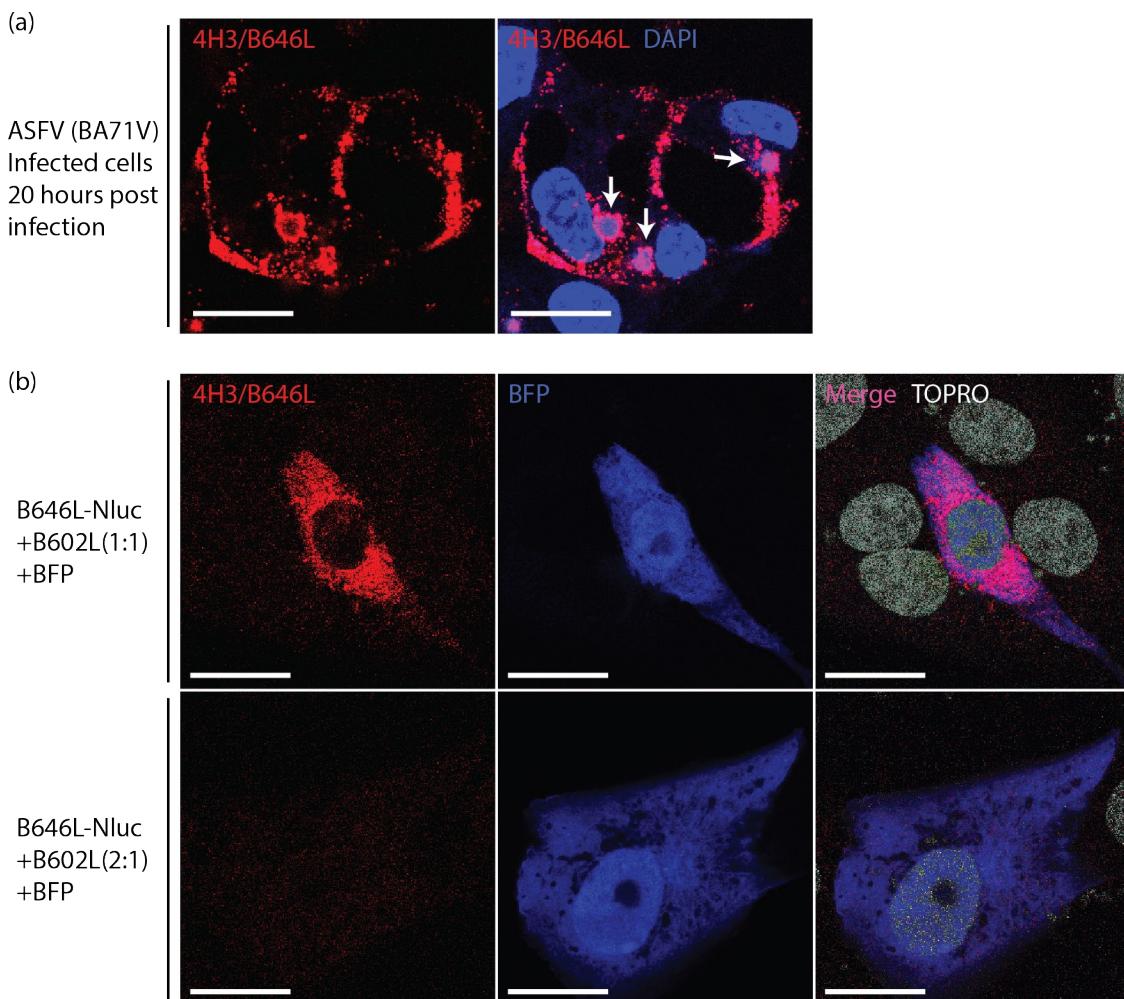


Figure 4. Determination of B646L/p72 and chaperone B602L transfection ratio. (a) ASFV (BA71V) infected Vero cells were used as a positive control for the 4H3 antibody that binds to a conformational epitope on B646L/p72 (red). Nuclear and viral DNA were

stained with DAPI (blue). White arrows indicate ASFV viral factories. (b) Representative confocal images of Vero cells transfected with different ratios of Nluc-tagged B646L/p72 to the chaperone B602L. The amount of B646L-Nluc expressing plasmid was held constant and different amounts of B602L-expressing plasmid were used. A blue fluorescent protein (BFP, blue) was used to detect expression of recombinant Nluc-tagged B646L/p72 with its native conformation. Nuclear DNA was stained with TOPRO (white). White bar denotes 20 μ m.

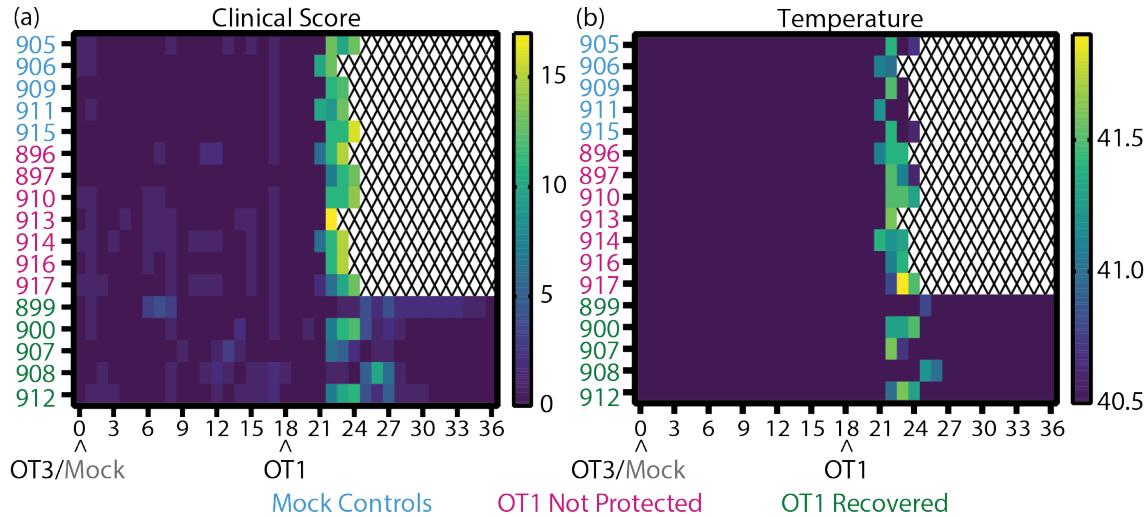


Figure 5. Heatmaps of (a) clinical scores and (b) temperatures of inbred Babraham animals. Data was obtained from our previous study [1]. (b) Data plotted as °C. The negative cutoff for temperature was set at 40.5°C as this is highest value that does not count towards a humane endpoint [1]. Each row denotes the responses of a single animal. Crosses indicate data that were not available for analysis. Arrowheads denote the immunization and ASFV challenge time points. Blue, Mock: mock control animals immunized with PBS, Pink, NP: OURT88/3 immunized animals that were not protected from OURT88/1, Green, R: OURT88/3 immunized animals that recovered from OURT88/1.

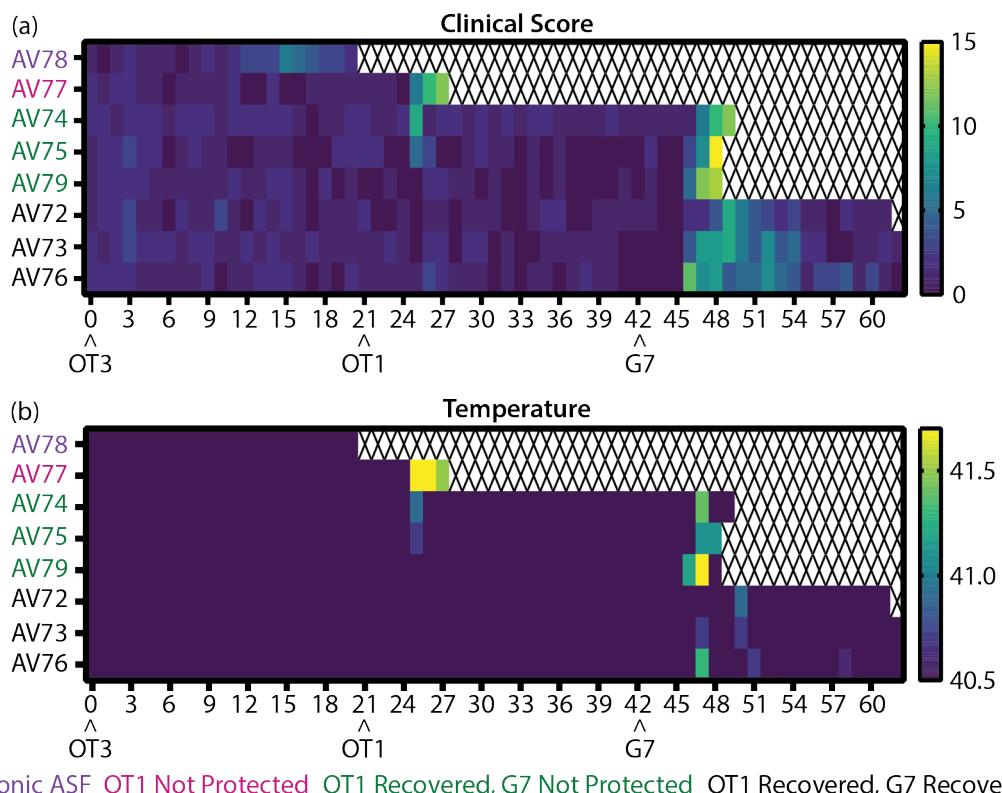


Figure 6. Heatmaps of (a) clinical scores and (b) temperatures of outbred domestic pigs. Data was obtained from our previous study [1]. (b) Data plotted as °C. The negative cutoff for temperature was set at 40.5°C as this is highest value that does not count

towards a humane endpoint [1]. Each row denotes the responses of a single animal. Crosses indicate data that were not available for analysis. Arrowheads denote the immunization and ASFV challenge time points. Purple: OURT88/3 immunized animal that suffered from chronic ASF, Pink: OURT88/3 immunized animal that was not protected from OURT88/1, Green: OURT88/3 immunized animals that recovered from OURT88/1, but were not protected from Georgia 2007/1, Black: OURT88/3 immunized animals that recovered from OURT88/1 and Georgia 2007/1.

B646L_Georgia2007_1 (NC_044959)	MASGGAFCLIANDGKADKIIILAQDLLNSRISNIKNVNKSY	40
B646L_OURT88_3 (NC_044957)	MASGGAFCLIANDGKADKIIILAQDLLNSRISNIKNVNKSY	40
B646L_Georgia2007_1 (NC_044959)	GKPDPEPTLSQIEETHLVHFNAHKPYVPVGFEYNKVRPH	80
B646L_OURT88_3 (NC_044957)	GKPDPEPTLSQIEETHLVHFNAHKPYVPVGFEYNKVRPH	80
B646L_Georgia2007_1 (NC_044959)	TGTPTLGNKLTFGIPQYGDFFHDMVGHHILGACHSSWQDA	120
B646L_OURT88_3 (NC_044957)	TGTPTLGNKLTFGIPQYGDFFHDMVGHHILGACHSSWQDA	120
B646L_Georgia2007_1 (NC_044959)	PIQGT[SQMGAHGQLQTFRNNGYDWDNQTPLEGAVYTLVDP	160
B646L_OURT88_3 (NC_044957)	PIQGT[AQMGAHGQLQTFRNNGYDWDNQTPLEGAVYTLVDP	160
B646L_Georgia2007_1 (NC_044959)	FGRPIVPGTKNAYRNLVYYCEYPGERLYENVRFDVNGNSL	200
B646L_OURT88_3 (NC_044957)	FGRPIVPGTKNAYRNLVYYCEYPGERLYENVRFDVNGNSL	200
B646L_Georgia2007_1 (NC_044959)	DEYSSDVTTLVRKFCIPGDKMTGYKHLVGQEVSVEGTSGP	240
B646L_OURT88_3 (NC_044957)	DEYSSDVTTLVRKFCIPGDKMTGYKHLVGQEVSVEGTSGP	240
B646L_Georgia2007_1 (NC_044959)	LLCNIHDLHKPHQSKEPILTENDTQRTCSHTNPKFLSQHF	280
B646L_OURT88_3 (NC_044957)	LLCNIHDLHKPHQSKEPILTENDTQRTCSHTNPKFLSQHF	280
B646L_Georgia2007_1 (NC_044959)	PENSHNIQTAGKQDITPITDATYLDIRRNVHYSCNGPQTP	320
B646L_OURT88_3 (NC_044957)	PENSHNIQTAGKQDITPITDATYLDIRRNVHYSCNGPQTP	320
B646L_Georgia2007_1 (NC_044959)	KYYQPPLALWIKLRFWFNENVNLAIIPSVSIPFGERFITIK	360
B646L_OURT88_3 (NC_044957)	KYYQPPLALWIKLRFWFNENVNLAIIPSVSIPFGERFITIK	360
B646L_Georgia2007_1 (NC_044959)	LASQKDLVNEFPGLFVRQSRFIAGRPSRRNIRFKPWFIPG	400
B646L_OURT88_3 (NC_044957)	LASQKDLVNEFPGLFIRQSRFIAGRPSRRNIRFKPWFIPG	400
B646L_Georgia2007_1 (NC_044959)	VINEISLTNNELYINNLFVTPEIHNLFVKVRVFSLIRVHK	440
B646L_OURT88_3 (NC_044957)	VINEISLTNNELYINNLFVTPEIHNLFVKVRVFSLIRVHK	440
B646L_Georgia2007_1 (NC_044959)	TQVTHTNNNHDEKLMSALKWPIEYMFIGLKPTWNISDQN	480
B646L_OURT88_3 (NC_044957)	TQVTHTNNNHDEKLMSALKWPIEYMFIGLKPTWNISDQN	480
B646L_Georgia2007_1 (NC_044959)	PHQHRDWHKFGHVNVNAIMQPTHAAEISFQDRDTALPDACS	520
B646L_OURT88_3 (NC_044957)	PHQHRDWHKFGHVNVNAIMQPTHAAEISFQDRDTALPDACS	520
B646L_Georgia2007_1 (NC_044959)	SISDISPVTVPIILPIIKNISVTAHGINLIDKFPSKFCSS	560
B646L_OURT88_3 (NC_044957)	SISDISPVTVPIILPIIKNISVTAHGINLIDKFPSKFCSS	560
B646L_Georgia2007_1 (NC_044959)	YIPFHGGNAIKTPDDPGAMMITFALKPREEYQPSGHINV	600
B646L_OURT88_3 (NC_044957)	YIPFHGGNAIKTPDDPGAMMITFALKPREEYQPSGHINV	600
B646L_Georgia2007_1 (NC_044959)	SRAREFYISWDTDYVGSITTADLVSASAINFLLQNGSA	640
B646L_OURT88_3 (NC_044957)	SRAREFYISWDTDYVGSITTADLVSASAINFLLQNGSA	640
B646L_Georgia2007_1 (NC_044959)	VLRYST	646
B646L_OURT88_3 (NC_044957)	VLRYST	646

Figure 7. Multiple sequence alignment of B646L/p72 amino acid sequences from Georgia2007/1 and OURT88/3. These sequences have 99.5% identity.

B602L_Georgia2007_1 (NC_044959)	MAEFNIDELLKNVLEDPSTEISEETLKQLYQRTNPYKQFK	40
B602L_OURT88_3 (NC_044957)	MAEFNIDELLKNVLEDPSTEISEETLKQLYQRTNPYKQFK	40
B602L_Georgia2007_1 (NC_044959)	NDSRVAFCSTNLREQYIRRLIMTSFIGYVFKALQEWMPS	80
B602L_OURT88_3 (NC_044957)	NDSRVAFCSTNLREQYIRRLIMTSFIGYVFKALQEWMPS	80
B602L_Georgia2007_1 (NC_044959)	YSKPTHTTKTLLSELITLVDTLKQETNDVPSESVVNTILS	120
B602L_OURT88_3 (NC_044957)	YSKPTHTTKTLLSELITLVDTLKQETNDVPSESVVNTILS	120
B602L_Georgia2007_1 (NC_044959)	IADSCKTQTQKSKEAKTTIDSFLREHFVFDPNLHAQSAY-	159
B602L_OURT88_3 (NC_044957)	IADSCKTQTQKSKEAKTTIDSFLREHFVFDPNLHAQSAYT	160
B602L_Georgia2007_1 (NC_044959)	-----	159
B602L_OURT88_3 (NC_044957)	CASTCADTNVDTCASTCASTCASTCASTCASTCASTCAST	200
B602L_Georgia2007_1 (NC_044959)	-----	159
B602L_OURT88_3 (NC_044957)	CASTCASTCASTCASTCASTGASTGASTCASTCADTNVDT	240
B602L_Georgia2007_1 (NC_044959)	-----	159
B602L_OURT88_3 (NC_044957)	CASTCADTNVDTCASTCASTCASTCASTGASTCASTCADT	280
B602L_Georgia2007_1 (NC_044959)	-----TCADTNVDTCASMCADTNVDT	180
B602L_OURT88_3 (NC_044957)	NVDTCASTCADTNVDTCASTTCADTNVDTCASTCADTNVNT	320
B602L_Georgia2007_1 (NC_044959)	CASMCADTNVDTCAS-----TCTSTEYTDLADPERIPLHIM	216
B602L_OURT88_3 (NC_044957)	CASMCADTNVDTCASTCANTCASTEYTDLADPERIPLHIM	360
B602L_Georgia2007_1 (NC_044959)	QKTLNVPNELQADIDAITQTQPQGYRAAAHILQNIELHQSI	256
B602L_OURT88_3 (NC_044957)	QKTLNVPNELQADIDAITQTQPQGYRAAAHILQNIELHQSI	400
B602L_Georgia2007_1 (NC_044959)	KHMLENPRAFKPILFNTKITRYLSQHIPQDTFYKWNYYI	296
B602L_OURT88_3 (NC_044957)	KHMLENPRAFKPILFNTKITRYLSQHIPQDTFYKWNYYI	440
B602L_Georgia2007_1 (NC_044959)	EDNYEELRAATESIYPEKPDLEFAFIIFYDVVDSSNQQKVD	336
B602L_OURT88_3 (NC_044957)	EDNYEELRAATESIYPEKPDLEFAFIIFYDVVDSSNQQKVD	480
B602L_Georgia2007_1 (NC_044959)	EFYYKYKDQIFSEVSSIQLGNWTLLGSFKANRERYNYFNQ	376
B602L_OURT88_3 (NC_044957)	EFYYKYKDQIFSEVSSIQLGNWTLLGSFKANRERYNYFNQ	520
B602L_Georgia2007_1 (NC_044959)	NNEIIKRILDRHEEDLKIGKEILRNTIYHKKAKNIQETGP	416
B602L_OURT88_3 (NC_044957)	NNEIIKRILDRHEEDLKIGKEILRNTIYHKKAKNIQETGP	560
B602L_Georgia2007_1 (NC_044959)	DAPGLSIYNSTFHDSGIKGLLSFKELKNLEKASGNIKKA	456
B602L_OURT88_3 (NC_044957)	DAPGLSIYNSTFHDSGIKGLLSFKELKNLEKASGNIKKA	600
B602L_Georgia2007_1 (NC_044959)	REYDFIDDCEEKIKQLLSKENLTPDEESELIKTKQLDNA	496
B602L_OURT88_3 (NC_044957)	REYDFIDDCEEKIKQLLSKENLTPDEESELIKTKQLNNNA	640
B602L_Georgia2007_1 (NC_044959)	LEMLNVPPDDTIRVDMWVNNNNKLEKEILYTKAEL	530
B602L_OURT88_3 (NC_044957)	LEMLNVPPDDTIRVDMWVNNNNKLEKEILYTKAEL	674

Figure 8. Multiple sequence alignment of B602L amino acid sequences from Georgia2007/1 and OURT88/3. These sequences have 78.0% identity.

D117L_Georgia2007_1 (NC_044959)	MDTETSPLLSHNLSTREGIKQSTQGLLAHTIAKYPGTTAI	40
D117L_OURT88_3 (NC_044957)	MDTETSPLLSHNLSTREGIKQSTQGLLAHTIARYPGTTAI	40
D117L_Georgia2007_1 (NC_044959)	LLGILILLTIILIIIVAIIVYYNRITIDCKSSIPKPPPSYYVQ	80
D117L_OURT88_3 (NC_044957)	LLGILILLVIILIIIVAIIVYYNRSVDCKSSMPKPPPSYYVQ	80
D117L_Georgia2007_1 (NC_044959)	QPEPHHHFPVFFRKRNSTSLQSHIPSDQEQLAELAHS	117
D117L_OURT88_3 (NC_044957)	QPEPHHHFPVFFRKRNSTSLQSHIPSDQEQLAELAHS	117

Figure 9. Multiple sequence alignment of D117L/p17 amino acid sequences from Georgia2007/1 and OURT88/3. These sequences have 95.7% identity.

B438L_Georgia2007_1 (NC_044959)	MYHDYASKLLADYRSDPPLWESDLPRLRNRYSDNILNSRYC	40
B438L_OURT88_3 (NC_044957)	MYHDYASKLLADYRSDPPLWESDLPRLRNRYSDNILNSRYC	40
B438L_Georgia2007_1 (NC_044959)	GNKNGAAPVYNEYTN SPEKAEGKLQLSDLRNFSFMLNPQH	80
B438L_OURT88_3 (NC_044957)	GNKNGAAPVYNEYTN SPEKAEGKLQLSDLRNFSFMLNPQH	80
B438L_Georgia2007_1 (NC_044959)	KNIGYGDAQDLEPYSSI PKNKLFNHFKNHRPAFSTHTENL	120
B438L_OURT88_3 (NC_044957)	KNIGYGDAQDLEPYSSI PKNKLFNHFKNHRPAFSTHTENL	120
B438L_Georgia2007_1 (NC_044959)	IIRRNVVRTEKKTFPQVASLKG TQKNCLTQPSSLPSLKNPK	160
B438L_OURT88_3 (NC_044957)	IIRRNVVRTEKKTFPQVASLKG TQKNCLTQPSSLPSLKNPK	160
B438L_Georgia2007_1 (NC_044959)	NSSVPSTRFSEHTKFFSYEDIPKLRTKG TIKHEQHLGDQM	200
B438L_OURT88_3 (NC_044957)	NSSVPSTRFSEHTKFFSYEDIPKLKG TIKHEQHLGDQM	200
B438L_Georgia2007_1 (NC_044959)	PGQHYNGYIPHKD VYNILCLAHNL PASVEKGIA GRGIPLG	240
B438L_OURT88_3 (NC_044957)	PGQHYNGYIPHKD VYNILCLAHNL PASVEKGIA GRGIPLG	240
B438L_Georgia2007_1 (NC_044959)	NPHVKPNIEQELIKSTSTYTIDVPMGLPLPKDSQHGREYQ	280
B438L_OURT88_3 (NC_044957)	NPHVKPNIEQELIKSTSTYTGVPMGLPLPKDSQHGREYQ	280
B438L_Georgia2007_1 (NC_044959)	EFSANRHMLQVS N ILHSV FANHS I K P QILEDIPVLNAQLT	320
B438L_OURT88_3 (NC_044957)	EFSANRHMLQVANILHSV FANHS I K P QILEDIPVLNAQLT	320
B438L_Georgia2007_1 (NC_044959)	SIKPVSPFLNKAYQTHYMENIVTLVPRFKSIANYSSPIPN	360
B438L_OURT88_3 (NC_044957)	SIKPVSPFLNKAYQTHYMENIVTLVPRFKSIANYSSPIPN	360
B438L_Georgia2007_1 (NC_044959)	YSKRNSGQA EYFDTSKQTISRHNNYI PKYTGGIGDSK LDS	400
B438L_OURT88_3 (NC_044957)	YSKRNSGQA EYFDTSKQTISRHNNYI PKYTGGIGDSK LDS	400
B438L_Georgia2007_1 (NC_044959)	TFPKDFNASSVPLTSAEKDHSLRGDNSACCISSISPSL	438
B438L_OURT88_3 (NC_044957)	TFPKDFNASSVPLTSAEKDHSLRGDNSACCISSISPSL	438

Figure 10. Multiple sequence alignment of B438L/p49 amino acid sequences from Georgia2007/1 and OURT88/3. These sequences have 99.1% identity.

E120R_Georgia2007_1 (NC_044959)	MADFNSPIQYLKEDSRDRTSIGSLEYDENADTMIPSFAAG	40
E120R_OURT88_3 (NC_044957)	MADFNSPIQYLKEDSRDRTSIGSLEYDENSDTIPSFAAG	40
E120R_Georgia2007_1 (NC_044959)	LEEFEPPIPDYDPTTSTSLSQLTHNMEKIAEEEDSNFLHD	80
E120R_OURT88_3 (NC_044957)	LEDFEPIP--SPTTSTSLSQLTHNMEKIAEEEDINFLHD	78
E120R_Georgia2007_1 (NC_044959)	TREFTSLVPDEADNKPEDDEESGAKPKKKKHLPFKLSSHK	120
E120R_OURT88_3 (NC_044957)	TREFTSLVPDEADNKPEDDEESGAKPKKKRHLFPKLSSHK	118
E120R_Georgia2007_1 (NC_044959)	SK	122
E120R_OURT88_3 (NC_044957)	SK	120

Figure 11. Multiple sequence alignment of E120R/p14.5 amino acid sequences from Georgia2007/1 and OURT88/3. These sequences have 93.4% identity.

M1249L_Georgia2007_1 (NC_044959)	MEEVITIAQIVHRGTDILSLNNEEIEALVDEIYSTLKGSN	40
M1249L_OURT88_3 (NC_044957)	MEEVITIAQIVHRGTDILSLNNEEIEALVDEIYSTLKGSN	40
M1249L_Georgia2007_1 (NC_044959)	DIKNIRLIDFLTLKDFVNHVRAEQSKLPDLSMP IEAYIR	80
M1249L_OURT88_3 (NC_044957)	DIKNIRLIDFLTLKDFVNHVRAEQSKLPDLSMP MEAYIR	80
M1249L_Georgia2007_1 (NC_044959)	QLLVDPDVVPIVSEKKKELRVRPSTRKEIFLINGTHLAVP	120
M1249L_OURT88_3 (NC_044957)	QLLVDPDVVPIVSEKKKELRVRPSTRKEIFLINGTHLAVP	120
M1249L_Georgia2007_1 (NC_044959)	AEAPIEIYGLKLRLKT FSPQCFCMRMAEIGSFSPETLGYVA	160
M1249L_OURT88_3 (NC_044957)	AEAPIEIYGLKLRLKS FSPQCFCMRMAEIGSFSPETLGYVA	160
M1249L_Georgia2007_1 (NC_044959)	SGANLTNFIRVFMKCVDQETWKKNGEVVVTTKENIIQFT	200
M1249L_OURT88_3 (NC_044957)	SGANLTNFIRVFMKCVDQETWKKNGEVVVTTKENIIQFT	200
M1249L_Georgia2007_1 (NC_044959)	HQYIELYKFLRSGGHSWLINRLAEMVHRKLDREDQGSHI	240
M1249L_OURT88_3 (NC_044957)	HQYIELYKFLRSGGHSWLINRLAEMVHRKLDREDQGSHI	240
M1249L_Georgia2007_1 (NC_044959)	SNIVETEEIEPEENIKRVIFFLKELSTMYSVSPVFTSGYM	280
M1249L_OURT88_3 (NC_044957)	SNIVETEEIEPEENIKRVIFFLKELSTMYSVSPVFTSGYM	280
M1249L_Georgia2007_1 (NC_044959)	PLLYDLYRAGYLEVLWNPNVEQKFLQHAEQREKEQMILQQV	320
M1249L_OURT88_3 (NC_044957)	PLLYDLYRAGYLEVLWNPNVEQKFLQHAEQREKEQMILQQV	320
M1249L_Georgia2007_1 (NC_044959)	DMKLTEVITQARQYFKIMEEKIGRVQSDAIРЕILTMEGKV	360
M1249L_OURT88_3 (NC_044957)	DMKLTEVITQARQYFKIMEEKIGRVQSDAIРЕILTMEGKV	360
M1249L_Georgia2007_1 (NC_044959)	DDPNSILQEVIKACGKQEAEELITTEYLNNIKKQWELQEKN A	400
M1249L_OURT88_3 (NC_044957)	DDPNSILQEVIKACGKQEAEELITTEYLNNIKKQWELQEKN A	400
M1249L_Georgia2007_1 (NC_044959)	CAHLKLVQLRSGLQYAELLKVLESIRVLYKEKNNTTNWN	440
M1249L_OURT88_3 (NC_044957)	CAHLKLVQLRSGLQYAELLKVLESIRVLYKEKNNTTNWN	440
M1249L_Georgia2007_1 (NC_044959)	LCKACGFKLLCPHVDMLIQLQAAEASYDTMRTKLMKFSGI	480
M1249L_OURT88_3 (NC_044957)	LCKACGFKLLCPHVDMLIQLQAAEASYDTMRTKLMKFSGI	480
M1249L_Georgia2007_1 (NC_044959)	NKEKENNQGLIYSYFCKICGEELAHFIQEDRTADVG T IGD	520
M1249L_OURT88_3 (NC_044957)	NKEKENNQGLIYSYFCKICGEELAHFIQEDRTADVG V IGD	520
M1249L_Georgia2007_1 (NC_044959)	LNSKLRVFIWQETMKACTFIHFGKLVDVKQFANIAVN VCL	560
M1249L_OURT88_3 (NC_044957)	LNSKLRVFIWQETMKACTFIHFGKLVDVKQFANIAVN VCL	560
M1249L_Georgia2007_1 (NC_044959)	PLVYSIENIKKEEDYDPLTQLYAVIYIYAYILNLIYSSQK	600
M1249L_OURT88_3 (NC_044957)	PLVYSIENIKKEEDYDPLTQLYAVIYIYAYILNLIYSSQK	600
M1249L_Georgia2007_1 (NC_044959)	NKEFLTITIHGMKADSSLNAYVTFLLEKMMQQYSGIINQL	640
M1249L_OURT88_3 (NC_044957)	NKEFLTITIHGMKADSSLNAYVTFLLEKMMQQYSGIINQL	640
M1249L_Georgia2007_1 (NC_044959)	SEITDQWIANNFREAFKKIIHQNGLQGLSVQDDTKVLLTE	680
M1249L_OURT88_3 (NC_044957)	SEITDQWIANNFREAFKKIIHQNGLQGLSVQDDTKVLLTE	680
M1249L_Georgia2007_1 (NC_044959)	ILLDPMYDYAATVARIDGSIPMHKPRTPK EA EYE F KTVIG	720
M1249L_OURT88_3 (NC_044957)	ILLDPMYDYAATVARIDGSIPMHKPRTPK EA EYE F KTVIG	720

Figure 12. Multiple sequence alignment of M1249L amino acid sequences (1-720) from Georgia2007/1 and OURT88/3. These sequences have 99.4% identity.

M1249L_Georgia2007_1 (NC_044959)	RTPAELLSQKEFYDKIYTSKYRPDFTQL	TRLNDIYFQEES	760	
M1249L_OURT88_3 (NC_044957)	RTPAELLSQKEFYDKIYTSKYRPDFTQL	ARLNDIYFQEES	760	
M1249L_Georgia2007_1 (NC_044959)	LRVWWGGRDEEKSTLIYLRAYELFLKYLQNAPNFS	ELA	800	
M1249L_OURT88_3 (NC_044957)	LRVWWGGRDEEKSTLIYLRAYELFLKYLQNAPNFS	ELA	800	
M1249L_Georgia2007_1 (NC_044959)	EFKTYENAYGEQKALLAQQGFYNIFDPNTGRADQRTR	LFE	840	
M1249L_OURT88_3 (NC_044957)	EFKTYENAYGEQKALLAQQGFYNIFDPNTGRADQRTR	LFE	840	
M1249L_Georgia2007_1 (NC_044959)	YKRLPISTLYDERGLPHKWTIYVYKAVDSSQKP	AIEVTR	880	
M1249L_OURT88_3 (NC_044957)	YKRLPISTLYDERGLPHKWTIYVYKAVDSSQKP	AIEVTR	880	
M1249L_Georgia2007_1 (NC_044959)	KDVIKKIDNHYALADLRC	SVCVHLQHEVGQLNIKKVQTAL	920	
M1249L_OURT88_3 (NC_044957)	KDVIKKIDNHYALADLRC	SVCVHLQHEVGQLNIKKVQTAL	920	
M1249L_Georgia2007_1 (NC_044959)	KASLEFNTFYAFYESRCPKG	GLHDFQDKKCVKCGLFTYII	960	
M1249L_OURT88_3 (NC_044957)	KASLEFNTFYAFYESRCPKG	GLHDFQDKKCVKCGLFTYII	960	
M1249L_Georgia2007_1 (NC_044959)	YDHLSQPELVHDYNNYKDQYDKEKMSIRSIQIKKDM	TTP	1000	
M1249L_OURT88_3 (NC_044957)	YDHLSQPELVHDYNNYKDQYDKEKMSIRSIQIKKDM	TTP	1000	
M1249L_Georgia2007_1 (NC_044959)	SETQP	KPPQEPWTFDYGKIIKTA	ILDISPAVIEAIGAM	1040
M1249L_OURT88_3 (NC_044957)	SSETQP	KPPQEPWTFDYGKIIKTA	ILDISPAVIEAIGAM	1040
M1249L_Georgia2007_1 (NC_044959)	EGRSYADIREGQGAPP	PPTSMDDPRLMAVDSAVRIFLYNY	1080	
M1249L_OURT88_3 (NC_044957)	EGRSYADIREGQGAPP	PPTSMDDPRLMAVDSAVRIFLYNY	1080	
M1249L_Georgia2007_1 (NC_044959)	NCLRHVSTFNKPPI	HVERLVLKHSYEKE	DLKVLPNVVN	1120
M1249L_OURT88_3 (NC_044957)	NCLRHVSTFNKP	MHVERLVLKHSYEKE	DLKVLPNVVN	1120
M1249L_Georgia2007_1 (NC_044959)	EYHTTFKHLRVTD	PASALLYSIEFLCIS	FLTLYEIKEPSW	1160
M1249L_OURT88_3 (NC_044957)	EYHTTFKHLRVTD	PASALLYSIEFLCV	SFLTLYEIKEPSW	1160
M1249L_Georgia2007_1 (NC_044959)	VVNIVREFALTELNTII	IQSEKLLSKPGAFNFMIFGEDFVC	1200	
M1249L_OURT88_3 (NC_044957)	VVNIVREFALTELNTII	IQSEKLLSKPGAFNFMIFGEDFVC	1200	
M1249L_Georgia2007_1 (NC_044959)	SGEDSSMDDISAYSSPGL	FGEDIIDRLDDPF	SIEDVDISL	1240
M1249L_OURT88_3 (NC_044957)	SGEDSSMDDISAYSSPGL	FGEDIIDRLDDPF	SIEDVDISL	1240
M1249L_Georgia2007_1 (NC_044959)	DVLDNLAPQ			1249
M1249L_OURT88_3 (NC_044957)	DVLDNLAPQ			1249

Figure 13. Multiple sequence alignment of M1249L amino acid sequences (721-1249) from Georgia2007/1 and OURT88/3. These sequences have 99.4% identity.

Supplementary Materials and Methods

Confocal staining and imaging

Vero African green monkey cells were used for confocal imaging as these enable better demarcation of cell morphology and have been used previously in our group (add DOI: 10.1099/jgv.0.001637). Briefly, cells were seeded at a density of 5×10^4 cells before transfection with plasmids and TransIT-LT1. After 24 hours incubation post-transfection, cells were fixed in 4% paraformaldehyde for 20 min before three washes with 1xPBS. For cells that were infected with ASFV (BA71V), cells were infected at an multiplicity of infection of 2, before washing and fixing 20 hours after infection. Cells were permeabilized with 0.2% (v/v) Triton-X in 1x PBS, then blocked with block buffer consisting of 10% (v/v) goat sera, 0.2% (v/v) NaN3 and 0.2% (v/v) fish skin gelatin (Sigma-Aldrich, USA) in 1x PBS. Primary antibodies from pig sera were first pre-adsorbed on untransfected cells that were treated in the same manner. Coverslips were incubated for 1h with the following primary antibodies: pre-adsorbed pig sera (1:800) and mouse anti-nanoluciferase (1:200, Promega, USA) or anti-B646L/p72 (1:10, 4H3, in-house hybridoma supernatant) diluted in block buffer. After 3 washes with 1x PBS, coverslips were incubated with the appropriate secondary antibodies: anti-pig IgG Alexa Flour 488 (1:250, Southern Biotech, USA) and/or anti-mouse IgG Alexa Flour 568 (1:200, Invitrogen, USA) diluted in block buffer. Coverslips were washed another three times with 1x PBS before DNA staining with DAPI or TOPRO. Coverslips were mounted with Vectashield and imaging on a Leica SP8 confocal microscope.

Western blot analysis

Protein expression was confirmed with sodium dodecyl sulfate-polyacrylamide gel electrophoresis and western blot analysis. Human embryonic kidney cells (HEK293T) were used as these have a high transfection efficiency that is suitable for transient expression of exogenous proteins. Briefly, cell lysates from plasmid transfected HEK293T cells were prepared for separation on 4-12% NuPAGE Bis-Tris protein gels (Invitrogen, USA) with NuPAGE LDS sample buffer and reducing agent. Proteins were then transferred onto PVDF membranes (Cyvita, USA). Mouse anti-nanoluciferase antibodies (1:400, Promega, USA) were used for protein detection. Membranes were blocked with 5% skim milk (w/v) in 0.5% (v/v) PBS-Tween20 (PBS-T). Primary antibodies were diluted in 5% bovine serum albumin (BSA, w/v) in PBS-T and incubated with the blocked membranes for 1h with agitation. Membranes were washed three times with PBS-T before detection of primary antibodies with goat anti-mouse IgG HRP-conjugated antibodies (1:2000, BioRad, USA) diluted in 5% BSA in PBS-T. Protein visualization was achieved with SuperSignal West Pico PLUS chemiluminescent substrate (Thermo Scientific, USA) on the G:BOX XX6 (Syngene, USA).

Multiple alignments of ASFV protein sequences

Multiple sequences alignments generated from the selected ASFV capsid protein amino acid sequences derived from Georgia 2007/1 (GenBank No. NC_044959) and OURT88/3 (GenBank No. NC_044957) were aligned with EMBOSS Needle (EMBL-EBI). The FASTA output was shaded with the Multiple Align Show (http://www.bioinformatics.org/SMS/multi_align.html).

References

1. Goatley, L. C.; Nash, R. H.; Andrews, C.; Hargreaves, Z.; Tng, P.; Reis, A. L.; Graham, S. P.; Netherton, C. L., Cellular and Humoral Immune Responses after Immunisation with Low Virulent African Swine Fever Virus in the Large White Inbred Babraham Line and Outbred Domestic Pigs. *Viruses* **2022**, *14*, (7).