

1 95

NAH7 -----MVDDEGEVRALVQPTQR-----GTWVQTERA

pM3 -----MANDKNEIRAYAQPAQR-----GTWVQTERA

pG0X5 -----MKSQVGLTTAPN-----GTWVQVERA

pJK21 -----MKPKHVGLTTAPN-----GTWVQVERA

pAM10.6 -----MFTIPHGYVHLKQIKKDP-----ADFAMLTRG

pHW104 -----MAHDENTDELVERNK-RLNELQLNTAAQLQEERRLNLTKNRVT-----GGYYMMSRA

pVCG1.2 -----MSDDKNKIETLEQQLSQARALLSHTVDLTQEERRLAAATKNRVT-----GGYYMMSRA

pXCV19 -----MSLPVPSPSKKR-----IEYVQLYRS

pBMBt_2 -----MFKIYERSKNKTMKNENETDIKISKEEFMKIIELTGLPISHIQKLIDLEKAEQEEAKRKELEKKN-----PPFVQLYKS

pONE429 -----MKNLSDAQKIIAQGNREETKEERLQRLEEEERAEIKQAEAGAKKSPYFNFQVQNQA

pJW1 -----MENLDTKVIPLPTERECTVVLGADGEVKGYINKPRFNKLGREYFVGFKS

pSN2 -----MKERYGTVYKGSQRLIDEESGEVIEVDKLYRKQ-----TSGNFVKAY

pIM13 -----MKERYGTVYKGSQRLIDEESGEVIEVDKLYRKQ-----TSGNFVKAY

pOM1 -----LAKNELSQHVTTKKVKAIGTETYINVTATGEAEFQVTKIE-----RDFNFTKVV

pONE430 -----MDKKPVTTTRKKVKVTGTETYINQSTGEIKEHVIDIDIE-----RDFNFHKVV

pHW126 -----MNIQQILNDSLNIISYENFNDYLNQYDLSPEEKVAAFTFYHENVKQKKAITISAEKTNNYKSIAADV-----EYVHLFPKN

pIGKR -----MDIGNILNESLSIDYEKLDLFLEKYDLTPSEQVAVYEFHAKAYKKNKTLVISETKENFKYSIEGV-----EYVHLFPKN

pIGMS31 MKKNKLVNKENYSILETLPEDPLFENKSTLEIDLNQDFLNRIANETVEELIIKEVNDPNDRSDKSNGVNLNAKYVVEKEKKTSLKKQYVITFVD

pRA01 -----MDISVNVARQRIKPDQEFIFYFLTN

Consensus -----V F V

96 190

NAH7 GHEAWAALIAQAPRAAGOLMHIIIVQHMOK-SGALIVSQSTLAKMMDTSIAITKRAISVIAKHNIQOTISVGQORGGLTAYVVSRIAWADKREN-L

pM3 GHEAWAALIAQAPRAAGOLMHIIIVQHMOK-QGALIIISQATLAKLMETSVAITTKRAIAITTKHNWIQOTISVGQORGGLTAYVVSRIAWADKRDN-L

pG0X5 AMERWSKLAVSNPRAAAVMMLMTSQMGR-NNALVASQATLAKMAGCGLNTLKRALSVERGNWIEVRQIG-PTGTACAYVVDRAVWSGNRDG-I

pJK21 AMERWSKLAVSNPRAAAVMMLMTSQMGR-NNALVASQATLAKMAGCGLNTLKRALSVERGNWIEVRQIG-PTGTACAYVVDRAVWSGNRDG-I

pAM10.6 YIRDLRELRRSPSAFQVFMILLTERMNK-TNAIVISQSTLCQILSYGRTAIHNAIRLIESERWLQIVKIG-----TANGVIVNSKVVDHDSGK--

pHW104 AEKNLRALQKENATAALVFSVIRENMQIGTNAVITISNPVLAKILGKSARTVARATKHIAQHAYVQIVKVG-----NTNTYIVNEQVAFAGSVG--Q

pVCG1.2 AEKNLRALQKENATAALVFSVIRENMQIGTNAVITISNPVLAKILGKSARTVARATKHIAQHAYVQIVKVG-----TTNTYIVNEQVAFAGSVG--Q

pXCV19 SMKALROLALEAPTAAHVLVYLMERINE-RNALVASQATLAKLTGKSRAITITRALAEIRTRNYTEMVKAG-----NVSVIVNVKRWAWATETALRG

pBMBt_2 HMKEIRWLITNHHLSNNILFFLENNMN-RNVIVCSQQLMEQFNKGRITIHNAIKTKEHGFISVAKIG-----NANAYIINPEIAFQDSRDK-I

pONE429 NYKAEDWLMRESPPAYRLRFLIAQNMN-NYALMCSYKVFQESLYGRATIAARAVLLKEKNFTRIAKSG-----TANILVNMKQLYWHSYGTN-Y

pJW1 GLEGLASMDLTGEQYKVLMYLFSRLDFD--NFLKVPQKEISEKLNHLKSNVSKAIKKLAELDVAVGPMAG--HSKTYRLNPRIAHRGLRITTKK

pSN2 IVQLISMLDMIGGKKLIVNYILDNVHLSNMTMIATVREIAEGTNTSTKVNTTLKIEEG-NIIKRRTG-----ALMLNPELLMRGDDQK-Q

pIM13 IVQLISMLDMIGGKKLIVNYILDNVHLSNMTMIATVREIAEGTNTSTKVNTTLKIEEG-NIIKRRTG-----VLMLNPELLMRGDDQK-Q

pOM1 IRNFVATLDLVGNQKTRLVYIIDLNNHNN-QLICTNRLMAEETGISLATVSVTMKAAQDANFLKKQANG-----VYVINPDILFKGTQKA-R

pONE430 LEHIHSMDLIGNQKTRLAFLWLNLLNRDN-VLIMTORKIAEKTGISLETVROTMKAMESGFLIKINSG-----AYCVMPDAVFKGKTD-R

pHW126 LKKIKEYNLTSNELLVTMEILDSMESHGNMLINFSGARCELTINKSTMSKVFKSRAKKVLIENENG-----NLYINSVFMKG-LPH-K

pIGKR LKILIKKYGLNTNELLVLTEIMESMLSHGNLLINFSGARCELTINKSTMCCKFTKQKQCLIE-KNG-----HIYLSVIFMKG-LPH-K

pIGMS31 NLEALAKNLKPNFEFRIIVEIVKVMYEG--NLINLSQSTIAKNLNLAKSNVSYFKNKKK-NILVEKDG-----HVFMSNIFSKQLAHR--

pRA01 MDLSLSDPDITKQDIAVLMKYAAKMQYG--NQISIAQADIAEDLGIDKSNVSKSVRKITQKGVFLKRRS-----LVNMWKYLAKGNLTDFI

Consensus IA L L A LM II NM N LI SQ LA L G SKATV RAIK L E WI V K G YVNV I WKG

191 279

NAH7 QYARFNARVLISSEDDADLGSD---KLKQLPTMSDGEIQLPAGPGMEPPAQESLDGVDLPDMPSIPHHGKNDV-----

pM3 QFALFNARVLVSTEDDADLGDA---KLKQLPTMEDGDIQLPAGPGMDPPAQESLEG-MLPDMPSIPHGN-----

pG0X5 RYSLFASVLLADNEQPDKDEIGLQPSLHPVDPDLYPGEKQLPTGPGLPSPSFPDG-MEPDLPATEK-----

pJK21 RYSLFASVLLADNEQPDKTEIGAQPPLQAITPDLYPGEKQLPTGPGLPSPSFPDG-MEPDLPATEK-----

pAM10.6 RYASFYAEVVVSESDDGRPVEDWDNIELRHVPVLHAGESVVDGAEPLPPDQDQLLPPPEHPFRTSATHEPQAVADTRAPPTRTSTGRPR

pHW104 RKAVFSATVVAHECEDDEGWDQVK--KLKATPIIFDDERPLLSEEVLPDPPDQDLDLN-----

pVCG1.2 RKAVFSATVVAHECEDDEGWDQVK--KLKAVPVYEDERPIILGCEDELPPDQDLDLN-----

pXCV19 KLVFSDARVIVSEEDDEPERLGKEPDLVRLPPVLPPEMATMLEDEDDGQGDQLL-----

pBMBt_2 KYVSFEGKILINKNENEELFKHKFENLVKDEKK-----

pONE429 ARAEFAGAKIIVTADDEPEPDRKQIEFDVKRQKILDVKETTCEEPEPNLFTNEQLQAI-----

pJW1 PLFSMTH-----

pSN2 KYLLLEFGNFEQEDDQKQENALSEYYSFKE-----

pIM13 KYLLLEFGNFEQANEID-----

pOM1 LNLINQFSELGAEPQLSDEQKIQNTITKIAQLSKQLEALQSKSSVDTEIEGQYTLPLDGSIVQKAVNKKKE-----

pONE430 LNLVLIQYRKSEQE--NKTSEPTSEKDEPSLFNNEQLKAM-----

pHW126 LFIQYREHFLKSIYKLTTEENFDQVDAEFIKTYESNIKKIKDKKELEQKKKDKTLKSFNETLKTTELKEAT---EENFDLIFEQNL-

pIGKR LFMQERDHFLLNSISYKLDDEEFKVFDDNFIAKAYENKLEIKKKKQIKEKKISKALDNFEKEISKWEKFKDEEENFEFGFSEI-

pIGMS31 -LDEEKRKNLKSQVEDDNFKNSF-----

pRA01 KADKENSKLSKFQLEDEE-----

Consensus KY LF A VL S EQ D L L

Additional file 2: Alignment of replication proteins. Identical amino acids are shown red, conserved green (present in at least 50% of the sequences) and amino acids with similar properties are highlighted in yellow.