

Supplementary Figure 1. MX/Mx wild type and chimerae amino acid sequences.

The sequences of huMX1, huMX2, mmMx1, mmMx2 and Flag tag are shown in red, blue, purple, green and black, respectively. Mutated residues are highlighted in grey.

MX1-Flag

MVVSEVDIAKADPAAASHPLLLNGDATVAQKNPGSVAENNLCSQYEEKVRPCIDLIDSLRALGVEODLA
LPAAVIGDQSSGKSSVLEALSGVALPRGSGIVTRCPLVLKLLKLVNEDKWRGKVSQDYIEIISDASE
VEKEINKAQNAIAGEGMGISHELITLEISSRDVDPDLTLIDLPGITRVAVGNQPADIGYKIKTLIKKYIQ
RQETISLVVVPNSVDIATTEALSMAQEVDPEDGRTIGILTKPDLVDKGTEDKVVDVVRNLVFLKKGYM
IVKCRGQQEIQDQLSLSEALQREKIFFENHPYFRDLLEEGKATVPCLAEKLTSELI THICKSLPLENQ
IKETHQRITTEELQKYGVDIPEDENEKMFFLIDKINAFNQDITALMQGEETVGEEDIRLFTRLRHEFHKW
STIENNFOEGHKILSRKIQKFENQYRGRELPGFVNRYRTFETIVKQQIKALEEPAVDMLHTVTDMLVRLA
FTDVSIGNFEFFNLHRTAKSKIEDIRAEQEREKEKLI RLFHFQMEQIVYCDQVYRGALQKVREKELEE
EKKKSWDFGAFQSSSATDSSMEEIFQHLMAYHQEASKRIS SHIPLIQFFMLQTYGQQLOKAMLQLLQ
DKDQTYSWLLKERSDTS DKRKFLKERLARLTQARRRLAQFPGdykdddk*

MX2-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPFGTVPPQMMFPPNWQGAEKDAAFLAKDFNFLTIN
NQPPPGNRSQPRAMGPENNLYSQYEQVRCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEAL
SGVALPRGSGIVTRCPLVLKLLKQPCAWAGRISYRNTELELQDPGQVEKEIHKANVMAGNNGRIGISHE
LISLEITSPEVPDLTIIDLPGITRVAVDNQPRDIGLQIKALIKKYIQRQQTINLVVVPNSVDIATTEAL
SMAHEVDPEGDRTIGILTKPDLMDRGTEKSVMNVRNLTYPLKKGMIIVKCRGQQEITNRLSLAEATKK
EITFFQTHPYFRVLLEEGSATVPRLAERLTTELIMHIQKSLPLEGQIRESHQKATEELRRCGADIPSQ
EADKMFFLIEKIKMFNQDIEKLVEGEEVRENETRLYNKIREDFKNVWGILATNTQKVKNIIHEEVEKY
EKQYRGKELLGFVNYKTFEIVHQYIQQLVEPALSMLOKAMEIQQAFINVAKKHFGEFFNLNQTVQST
IEDIKVKHTAKAENMIQLQFRMEQMVFCQDQIYSVVLKVVREEIFNPLGTPSQNMKLN SHFPPSNSSVS
SFTEIGIHLNAYFLET SKRLANQIPFIIQYFMLRENGDSLQKAMMQILQEKRNRYSWLLQEQSETATKRR
ILKERIYRLTQARHALCQFSSKEIHdykdddk*

MX2₂₆₋₇₁₅-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPFGTVPPQMMFPPNWQGAEKDAAFLAKDFNFLTIN
NQPPPGNRSQPRAMGPENNLYSQYEQVRCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEAL
SGVALPRGSGIVTRCPLVLKLLKQPCAWAGRISYRNTELELQDPGQVEKEIHKANVMAGNNGRIGISHE
LISLEITSPEVPDLTIIDLPGITRVAVDNQPRDIGLQIKALIKKYIQRQQTINLVVVPNSVDIATTEAL
SMAHEVDPEGDRTIGILTKPDLMDRGTEKSVMNVRNLTYPLKKGMIIVKCRGQQEITNRLSLAEATKK
EITFFQTHPYFRVLLEEGSATVPRLAERLTTELIMHIQKSLPLEGQIRESHQKATEELRRCGADIPSQ
EADKMFFLIEKIKMFNQDIEKLVEGEEVRENETRLYNKIREDFKNVWGILATNTQKVKNIIHEEVEKY
EKQYRGKELLGFVNYKTFEIVHQYIQQLVEPALSMLOKAMEIQQAFINVAKKHFGEFFNLNQTVQST
IEDIKVKHTAKAENMIQLQFRMEQMVFCQDQIYSVVLKVVREEIFNPLGTPSQNMKLN SHFPPSNSSVS
SFTEIGIHLNAYFLET SKRLANQIPFIIQYFMLRENGDSLQKAMMQILQEKRNRYSWLLQEQSETATKRR
ILKERIYRLTQARHALCQFSSKEIHdykdddk*

MX1(L_{4MX2})-Flag

MVVSEVDIAKADPAAASHPLLLNGDATVAQKNPGSVAENNLCSQYEEKVRPCIDLIDSLRALGVEODLA
LPAAVIGDQSSGKSSVLEALSGVALPRGSGIVTRCPLVLKLLKLVNEDKWRGKVSQDYIEIISDASE
VEKEINKAQNAIAGEGMGISHELITLEISSRDVDPDLTLIDLPGITRVAVGNQPADIGYKIKTLIKKYIQ
RQETISLVVVPNSVDIATTEALSMAQEVDPEDGRTIGILTKPDLVDKGTEDKVVDVVRNLVFLKKGYM
IVKCRGQQEIQDQLSLSEALQREKIFFENHPYFRDLLEEGKATVPCLAEKLTSELI THICKSLPLENQ
IKETHQRITTEELQKYGVDIPEDENEKMFFLIDKINAFNQDITALMQGEETVGEEDIRLFTRLRHEFHKW
STIENNFOEGHKILSRKIQKFENQYRGRELPGFVNRYRTFETIVKQQIKALEEPAVDMLHTVTDMLVRLA
FTDVSIGNFEFFNLHRTAKSKIEDIRAEQEREKEKLI RLFHFQMEQIVYCDQIYSVVLKVVREEIFNP
LGTSPSQNMKLN SHFPPSNSSVS MEEIFQHLMAYHQEASKRIS SHIPLIQFFMLQTYGQQLOKAMLQL
LQDKDQTYSWLLKERSDTS DKRKFLKERLARLTQARRRLAQFPGdykdddk*

MX2(L_{MX1})-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPPF^GTVPPQMMFPPNWQGAEKDAAFLAKDFNFLTIN
NQPPPGNRSQPRAMGPENNLYSQYEQKVRPCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEAL
SGVALPRGSGIVTRCPLVLKLLKQPC^EAWAGRISYRNTELELQDPGQVEKEIHK^AQNV^MMAGN^GRGISHE
LISLEITSPEVPDLTIIDLPGITRVAVDN^QPRDIGLQIKALIKKYIQRQQTINLVVPCNVDIATTEAL
SMAHEVDPEGDRITIGILTKPDLMDRGTEK^SVMNVVRNLTYPLKKG^YMI^VKCRGQ^QEITNRLSLAEATKK
EITFFQTHPYFRVLL^EEGSATVPRLAERLTTELIMHIQKSLP^LLEGQIRE^SHQKATEELRRCGADIP^SQ
EADKMFFLIEKIKMFNQDIEKLVEGEEVREN^ETRLYNKIREDFKNVW^GILATNTQKV^KNIIEHEVEKY
EKQYRGKELLGFVNYKTFEIVH^QYIQQLVEPAL^SMLQKAMEIIQQA^FIN^VAKKH^FG^EFFNLNQT^VOST
IEDIKVKHTAKAENMIQLQFRMEQ^MVF^CQDQVYRGALQKVREKELEEEK^KKK^SWDFGAFQSSSATD^SSS^F
TEIGIHLNAYFLET^SKRLANQIPFIQYFMLRENGDSLQKAMMQILQEK^NRYSWLLQEQ^SETATKRRIL
KERIYRLTQARHALCQFSSEIHdykddd^k*

MX1(Stalk_{MX2})-Flag

MVVSEVDIAKADPAAASHPLLLNGDATVAQKNPGSVAENNLCSQYEEKVRPCIDLIDSLRALGVEQDLA
LP^AIAVIGDQSSGKSSVLEALSGVALPRGSGIVTRCPLVLKLLKLVNEDKWRGK^VS^YQDY^EIEISDASE
VEKEINKAQNAIAGEGMGISHELITL^EISSRDV^PDLTLIDLPGITRVA^VGNQPADIGYKIK^TL^IKKYIQ
RQETISLVVPSNVDIATTEALSMAQ^EVDPEGDRITIGILTKPDLV^DKGTE^DKVVDVVRNLV^FH^LKKG^YM
IVKCRGQ^QEIQDQLSLSEALQREKIFFENHPYFRD^LLEEGKATVPC^LAEKLTSELITHICKSLP^LLENQ
IKETHQRITEELQKYGV^DIP^EQ^EADKMFFLIEKIKMFNQDIEKLVEGEEVREN^ETRLYNKIREDFKNW
VGILATNTQKV^KNIIEHEVEKEYEKQYRGKELLGFVNYKTFEIVH^QYIQQLVEPAL^SMLQKAMEIIQQA
FIN^VAKKH^FG^EFFNLNQT^VOSTIEDIKVKHTAKAENMIQLQFRMEQ^MVF^CQDQIYSV^VLK^KVREEIFNP
LGT^PSQNMKLN^SH^FPSNESSVSS^FTEIGIHLNAYFLET^SKRLANQIPFIQYFMLRENGDSLQKAMMQI
LQEK^NRYSWLLQ^RSD^TSD^KRK^FLKERL^ARLTQARRRLAQ^FPGdykddd^k*

MX2(Stalk_{MX1})-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPPF^GTVPPQMMFPPNWQGAEKDAAFLAKDFNFLTIN
NQPPPGNRSQPRAMGPENNLYSQYEQKVRPCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEAL
SGVALPRGSGIVTRCPLVLKLLKQPC^EAWAGRISYRNTELELQDPGQVEKEIHK^AQNV^MMAGN^GRGISHE
LISLEITSPEVPDLTIIDLPGITRVAVDN^QPRDIGLQIKALIKKYIQRQQTINLVVPCNVDIATTEAL
SMAHEVDPEGDRITIGILTKPDLMDRGTEK^SVMNVVRNLTYPLKKG^YMI^VKCRGQ^QEITNRLSLAEATKK
EITFFQTHPYFRVLL^EEGSATVPRLAERLTTELIMHIQKSLP^LLEGQIRE^SHQKATEELRRCGADIP^SD
ENEKMFFLIDKINAFNQDITALMQG^EETVGEEDIRL^FTRLRHE^FHKWSTIIEN^NFQEGHKILSRKI^QK^F
ENQYRGRELPGFVNYRTFETIVK^QQIKALEEPAVDMLHTV^TDMVRLA^FTDVSIKNFEEFFNLHRTAK^SK
IEDIRAEQEREGEKLI^RLHFQMEQIVYCQDQVYRGALQKVREKELEEEK^KKK^SWDFGAFQSSSATD^SSM
E^EIFQHLMAYHQEASKRIS^SSHIP^LIIQFFMLQTYGQQLQKAMLQ^LLQDKD^TYSWLLKEQ^SETATKRRIL
KERIYRLTQARHALCQFSSEIHdykddd^k*

MX1(G_{MX2})-Flag

MVVSEVDIAKADPAAASHPLLLNGDATVAQKNPGSVAENNLCSQYEEKVRPCIDLIDSLRALGVEQDLA
LP^AIAVIGDQSSGKSSVLEALSGVALPRGSGIVTRCPLVLKLLKQPC^EAWAGRISYRNTELELQDPGQV
EKEIHK^AQNV^MMAGN^GRGISHELISLEITSPEVPDLTIIDLPGITRVAVDN^QPRDIGLQIKALIKKYIQR
QQTINLVVPCNVDIATTEALSMAHEVDPEGDRITIGILTKPDLMDRGTEK^SVMNVVRNLTYPLKKG^YMI
VKCRGQ^QEITNRLSLAEATKKEITFFQTHPYFRVLL^EEGSATVPRLAERLTTELIMHIQKSLP^LLENQI
KETHQRITEELQKYGV^DIPEDENEKMFFLIDKINAFNQDITALMQG^EETVGEEDIRL^FTRLRHE^FHKWS
TIIEN^NFQEGHKILSRKI^QK^FENQYRGRELPGFVNYRTFETIVK^QQIKALEEPAVDMLHTV^TDMVRLA^F
TDVSIKNFEEFFNLHRTAKSKIEDIRAEQEREGEKLI^RLHFQMEQIVYCQDQVYRGALQKVREKELEEE
K^KKK^SWDFGAFQSSSATDSSMEEIFQHLMAYHQEASKRIS^SSHIP^LIIQFFMLQTYGQQLQKAMLQ^LLQD
K^DTYSWLLKERSD^TSD^KRK^FLKERL^ARLTQARRRLAQ^FPGdykddd^k*

MX2(G_{MX1})-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPPF^GTVPPQMMFPPNWQGAEKDAAFLAKDFNFLT^N
NQPPPGNRSQPRAMGPENNL^SQYEQV^RPCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEAL
SGVALPRGSGIVTRCPLVLK^LKLKLVNEDKWRGKVS^YQDY^EEIEISDASEVEKEINKAQNAIAGEGMGISH
ELITTLEISSRDV^PDLT^LIDLPGITR^VAVGNQ^PADIGYKIK^TLK^KYIQ^RQ^ETISL^VVV^PSNVDIATTEA
LSMAQ^EVDPEGDRTIGILTKPDLVDKGTEDKVV^DVVRN^LVFHLKKG^YMI^VKCRGQ^QEIQDQ^LSLSEALQ
REKIFFENHPYFRDLLEEGKATV^PCLAEKLTSELITHICKSLP^LLEGGQIRESHQKATEELRRCGADIPS
Q^EADKMFFLIEKIKMF^NQDIEK^LVEGEEV^VREN^ETRLYNKI^REDFK^NWVGILATNTQ^KV^KNI^IHEEVEK
YEKQYRGKELLGFV^NYKTFE^IIVH^QYIQ^QLVEPAL^SMLQ^KAMEIQ^QAFINVAKKH^FGEFFNL^NQ^TV^QS
TIEDIKV^KH^TA^KENMIQ^LQ^RMEQ^MV^FCQ^DQ^IYSV^VLK^KV^REEIFN^PLG^TPSQ^NM^KL^NSH^FPS^NESS^V
SS^FTEIGIHLNAY^FLETSKRLANQ^IPFIIQ^YFMLRENGDSLQ^KAMM^QILQ^EKNRY^SWLLQ^EQ^SETAT^KR
RILKERIYRLTQARHALCQFSSKEIHdykddd*

MX2(G_{MX1 T103A})-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPPF^GTVPPQMMFPPNWQGAEKDAAFLAKDFNFLT^N
NQPPPGNRSQPRAMGPENNL^SQYEQV^RPCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEAL
SGVALPRGSGIVAR^CPLVLK^LKLKLVNEDKWRGKVS^YQDY^EEIEISDASEVEKEINKAQNAIAGEGMGISH
ELITTLEISSRDV^PDLT^LIDLPGITR^VAVGNQ^PADIGYKIK^TLK^KYIQ^RQ^ETISL^VVV^PSNVDIATTEA
LSMAQ^EVDPEGDRTIGILTKPDLVDKGTEDKVV^DVVRN^LVFHLKKG^YMI^VKCRGQ^QEIQDQ^LSLSEALQ
REKIFFENHPYFRDLLEEGKATV^PCLAEKLTSELITHICKSLP^LLEGGQIRESHQKATEELRRCGADIPS
Q^EADKMFFLIEKIKMF^NQDIEK^LVEGEEV^VREN^ETRLYNKI^REDFK^NWVGILATNTQ^KV^KNI^IHEEVEK
YEKQYRGKELLGFV^NYKTFE^IIVH^QYIQ^QLVEPAL^SMLQ^KAMEIQ^QAFINVAKKH^FGEFFNL^NQ^TV^QS
TIEDIKV^KH^TA^KENMIQ^LQ^RMEQ^MV^FCQ^DQ^IYSV^VLK^KV^REEIFN^PLG^TPSQ^NM^KL^NSH^FPS^NESS^V
SS^FTEIGIHLNAY^FLETSKRLANQ^IPFIIQ^YFMLRENGDSLQ^KAMM^QILQ^EKNRY^SWLLQ^EQ^SETAT^KR
RILKERIYRLTQARHALCQFSSKEIHdykddd*

MX1(G Stalk_{MX2})-Flag

MVVSEVDIAKADPAAASHPLLLNGDATVAQKNPGSVAENNLCSQYEEKV^RPCIDLIDSLRALGVEQDLA
LPAIAVIGDQSSGKSSVLEALSGVALPRGSGIVTRCPLVLK^LKKQ^PCEAWAGRI^SYRNTELELQDPGQV
EKEI^HKAQ^NVMAGN^RGISHELISLEITSPEVPDLT^IIDLPGITR^VAVDNQ^PRDIGLQ^IKALIK^KYIQ^R
QQTINLVVPC^NVDIATTEALSMAHEVDPEGDRTIGILTKPDLMDRGTEK^SVMNV^VRN^LTYPLK^KGYMI
VKCRGQ^QEITNRLSLAEATKKEITFFQ^THPYFRV^LLEEGSATV^PRLAERLTTELIMHI^QKSLP^LLENQ^I
KETHQ^RITEELQ^KYGV^DIP^EQ^EADKMFFLIEKIKMF^NQDIEK^LVEGEEV^VREN^ETRLYNKI^REDFK^NWV
GILATNTQ^KV^KNI^IHEEVEKYEKQYRGKELLGFV^NYKTFE^IIVH^QYIQ^QLVEPAL^SMLQ^KAMEIQ^QAF
INVAKKH^FGEFFNL^NQ^TV^QSTIEDIKV^KH^TA^KENMIQ^LQ^RMEQ^MV^FCQ^DQ^IYSV^VLK^KV^REEIFN^PL
G^TPSQ^NM^KL^NSH^FPS^NESS^VSS^FTEIGIHLNAY^FLETSKRLANQ^IPFIIQ^YFMLRENGDSLQ^KAMM^QIL
Q^EKNRY^SWLLQ^ERS^DTSD^KRK^FLKERL^ARLTQARRRLA^QFP^Gdykddd*

MX2(G Stalk_{MX1})-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPPF^GTVPPQMMFPPNWQGAEKDAAFLAKDFNFLT^N
NQPPPGNRSQPRAMGPENNL^SQYEQV^RPCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEAL
SGVALPRGSGIVTRCPLVLK^LKLKLVNEDKWRGKVS^YQDY^EEIEISDASEVEKEINKAQNAIAGEGMGISH
ELITTLEISSRDV^PDLT^LIDLPGITR^VAVGNQ^PADIGYKIK^TLK^KYIQ^RQ^ETISL^VVV^PSNVDIATTEA
LSMAQ^EVDPEGDRTIGILTKPDLVDKGTEDKVV^DVVRN^LVFHLKKG^YMI^VKCRGQ^QEIQDQ^LSLSEALQ
REKIFFENHPYFRDLLEEGKATV^PCLAEKLTSELITHICKSLP^LLEGGQIRESHQKATEELRRCGADIPS
DENEKMF^LIDKINAF^NQDIT^ALMQ^GEETV^GEEDIRL^FTRLRHE^FHK^WSTI^IENNF^QEGH^KILSR^KIQ^K
FENQYRGRELPGFV^NYRTFETIV^KQ^QIKALEEP^AVDMLHTV^TDMV^RLAFT^DV^SIKNFEE^FFN^LHRT^AK^S
KIEDIRAEQERE^GEKLIRLHFQ^MEIQ^VYCDQ^VYRGALQ^KVREKELEEEK^KKS^WDFGAFQ^SSSAT^DSS
MEEIFQ^HLMA^YHQ^EASKRIS^SHIPLIIQ^FFMLQ^TY^GQ^QLQ^KAMLQ^LLQ^DKD^TYSWLL^LKEQ^SETAT^KRRI
LKERIYRLTQARHALCQFSSKEIHdykddd*

MX1(N_{MX2})-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPPF^GTVPPQMMFPPNWQGAEKDAAFLAKDFNFLT^N
NQPPPGNRSQPRAMGPEN^NLYSQYEEKVRPCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEAL
SGVALPRGSGIVTRCPLVLK^KLVNEDKWRGKVSQDYEIEISDASEVEKEINKAQNAIAGEGMGISH
ELITTLEISSRDV^PDLT^LIDLPGITRVA^VGNQPADIGYKIK^TLK^KYIQRQETISL^VVVPSNVDIATEAL
SMAQEVDPEDRTIGILTKPDLVDKGTEDKVV^DVVRNLV^FH^LKKGYMIVKCRGQ^QEIQDQ^LSLSEALQ^R
EKIFFENHPYFRDLLEEGKATVPC^LAEKLTSELITHICKSLP^LLENQIKETHQRITEELQKYGV^DIPED
ENEKMF^FLIDKINAF^NQDIT^ALMQGEETVGEEDIRL^FTRLRHEFH^KWSTI^IENNFQEGHKILSRKI^QK^F
ENQYRGRELPGFVNYRTFETIVK^QQIKALEEPAVDMLHTV^TDMVRLA^FTDVSIKNFEEFFNLHRTAK^S
IEDIRAEQEREGEK^LIRLHFQMEQIVYCQDQVYRGALQKVREKELEEEK^KKK^KSWDFGAFQSSSATD^SSM
EEIFQHLMAYHQEASKRIS^SHIPLIIQFFMLQTYGQQLQKAMLQ^LLQDKDTYSWLLKERSDTSD^KRRK^F
KERLARLTQARRRLAQFPGdykddd^k*

MX1_{K83A}(N_{MX2})-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPPF^GTVPPQMMFPPNWQGAEKDAAFLAKDFNFLT^N
NQPPPGNRSQPRAMGPEN^NLYSQYEEKVRPCIDLIDSLRALGVEQDLALPAIAVIGDQSSG^ASSVLEAL
SGVALPRGSGIVTRCPLVLK^KLVNEDKWRGKVSQDYEIEISDASEVEKEINKAQNAIAGEGMGISH
ELITTLEISSRDV^PDLT^LIDLPGITRVA^VGNQPADIGYKIK^TLK^KYIQRQETISL^VVVPSNVDIATEAL
SMAQEVDPEDRTIGILTKPDLVDKGTEDKVV^DVVRNLV^FH^LKKGYMIVKCRGQ^QEIQDQ^LSLSEALQ^R
EKIFFENHPYFRDLLEEGKATVPC^LAEKLTSELITHICKSLP^LLENQIKETHQRITEELQKYGV^DIPED
ENEKMF^FLIDKINAF^NQDIT^ALMQGEETVGEEDIRL^FTRLRHEFH^KWSTI^IENNFQEGHKILSRKI^QK^F
ENQYRGRELPGFVNYRTFETIVK^QQIKALEEPAVDMLHTV^TDMVRLA^FTDVSIKNFEEFFNLHRTAK^S
IEDIRAEQEREGEK^LIRLHFQMEQIVYCQDQVYRGALQKVREKELEEEK^KKK^KSWDFGAFQSSSATD^SSM
EEIFQHLMAYHQEASKRIS^SHIPLIIQFFMLQTYGQQLQKAMLQ^LLQDKDTYSWLLKERSDTSD^KRRK^F
KERLARLTQARRRLAQFPGdykddd^k*

MX1_{T103A}(N_{MX2})-Flag

MSKAHKPWPYRRRSQFSSRKYLKEMNSFQQQPPPF^GTVPPQMMFPPNWQGAEKDAAFLAKDFNFLT^N
NQPPPGNRSQPRAMGPEN^NLYSQYEEKVRPCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEAL
SGVALPRGSGIV^ARCPLVLK^KLVNEDKWRGKVSQDYEIEISDASEVEKEINKAQNAIAGEGMGISH
ELITTLEISSRDV^PDLT^LIDLPGITRVA^VGNQPADIGYKIK^TLK^KYIQRQETISL^VVVPSNVDIATEAL
SMAQEVDPEDRTIGILTKPDLVDKGTEDKVV^DVVRNLV^FH^LKKGYMIVKCRGQ^QEIQDQ^LSLSEALQ^R
EKIFFENHPYFRDLLEEGKATVPC^LAEKLTSELITHICKSLP^LLENQIKETHQRITEELQKYGV^DIPED
ENEKMF^FLIDKINAF^NQDIT^ALMQGEETVGEEDIRL^FTRLRHEFH^KWSTI^IENNFQEGHKILSRKI^QK^F
ENQYRGRELPGFVNYRTFETIVK^QQIKALEEPAVDMLHTV^TDMVRLA^FTDVSIKNFEEFFNLHRTAK^S
IEDIRAEQEREGEK^LIRLHFQMEQIVYCQDQVYRGALQKVREKELEEEK^KKK^KSWDFGAFQSSSATD^SSM
EEIFQHLMAYHQEASKRIS^SHIPLIIQFFMLQTYGQQLQKAMLQ^LLQDKDTYSWLLKERSDTSD^KRRK^F
KERLARLTQARRRLAQFPGdykddd^k*

MX2(N_{MX1})-Flag

MVVSEVDIAKADPAAASHPLLLNGDATVAQKNPGSVAENNLCSQYEQKVRPCIDLIDSLRALGVEQDLA
LPAAVIGDQSSGKSSVLEALSGVALPRGSGIVTRCPLVLK^KQPC^EAWAGRI^SYRNTELELQDPGQ^V
EKEI^HKAQNV^MMAGN^RGISHELISLEITSPEV^PDLT^IIDLPGITRVA^VDNQPRD^IGLQIKALIK^KYIQ^R
QQTINLVVPCNVDIATTEAL^SMAHEVDPEGDRTIGILTKPDLMDRGTEK^SVMNVVRNLTYPLK^KGYM^I
VKCRGQ^QEITNRLSLAEATKKEITFFQTHPYFRV^LLEEGSATVPRLAERLTTELIMHIQKSLP^LLEGQ^I
RESHQKATEELRRCGADIPSQ^EEADKMFFLIEKIKMF^NQDIEKLV^EGE^EVVREN^ETRLYNKIRED^FKNW^V
GILATNTQ^KVKNI^IHEEVEKYE^KQYRGKELLGFVNYKTFEIVH^QYIQQLVEPALSM^LQKAMEIIQQA^F
INVAKKHGFEFFNLNQT^VQSTIEDIKVKHTAKAENMIQLQ^FRMEQMVFCDQ^IYSVVLK^KVREEIFN^PL
GTPSQNMKLN^SHP^SNESSVSS^FTEIGIHLNAYFLET^SKRLANQIPFI^IQYFMLRENGDSLQKAMM^QIL
QEK^NRYSWLLQEQSETATKRRILKERIYRLTQARHALCQFSSKEIHdykddd^k*

mmMx1-Flag

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mmMx1(N_{Mx2})-Flag

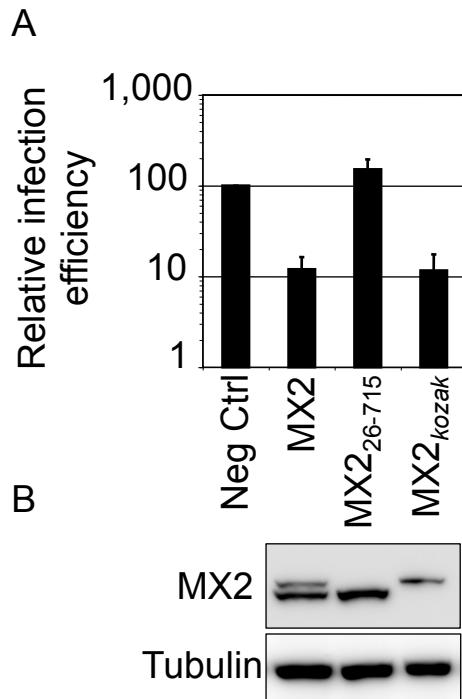
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mmMx2-Flag

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mmMx2(N_{Mx2})-Flag

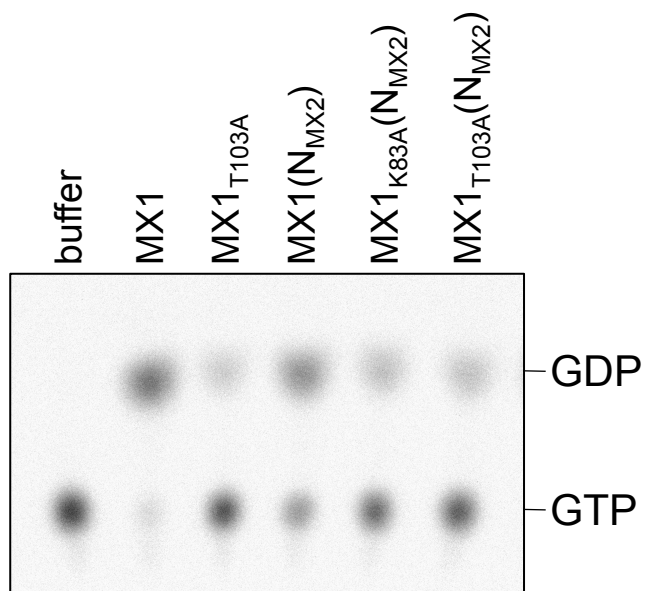
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Supplementary Figure 2. The full-length isoform of MX2 is uniquely responsible for the anti-HIV-1 activity.

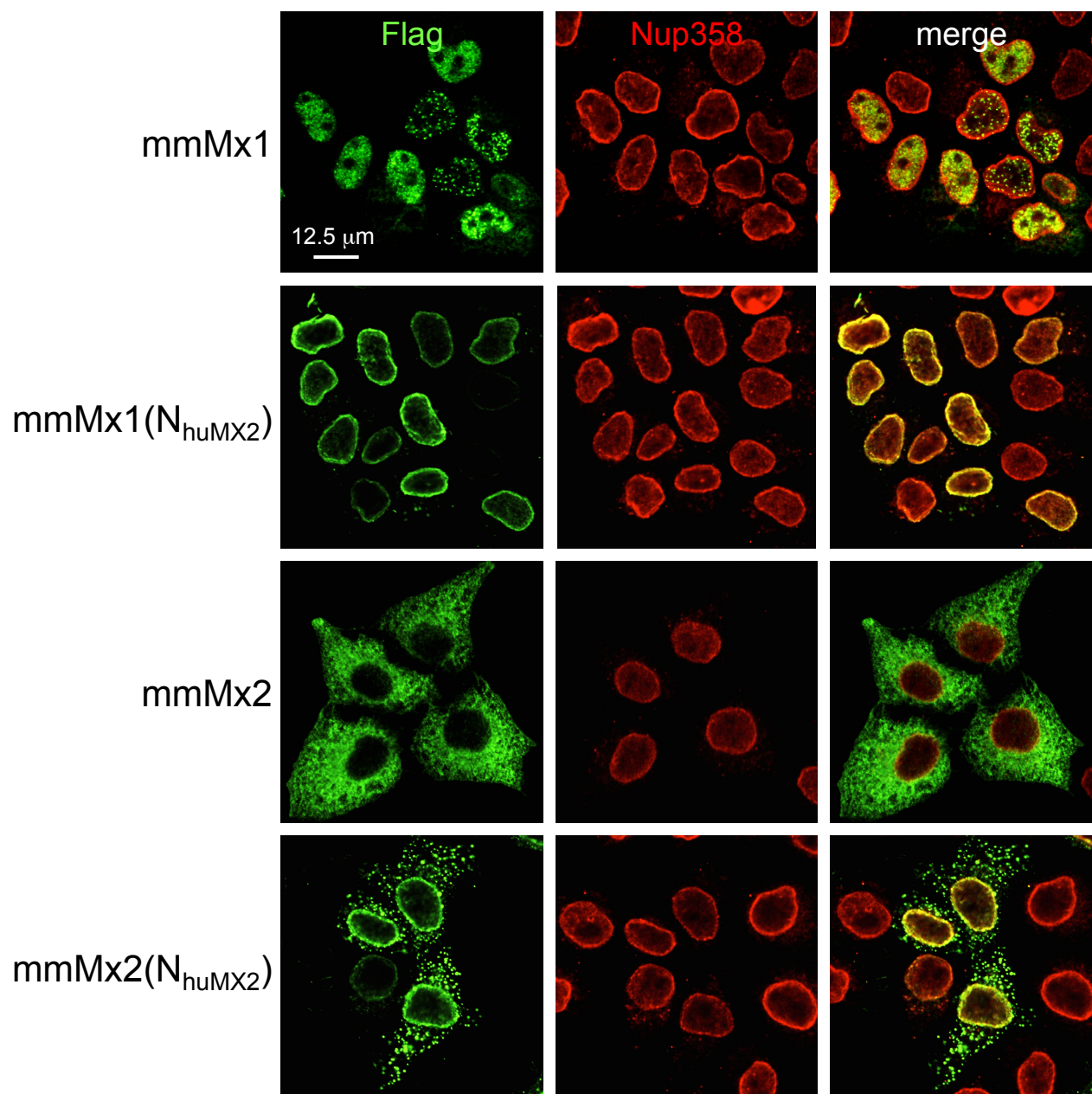
A. U87-MG/CD4/CXCR4 cells were transduced with EasiLV expressing CD8 (Neg Ctrl), MX2 wild type, MX2 short isoform (MX2₂₆₋₇₁₅) and MX2 long isoform (MX2_{kozak}) cDNAs and treated with doxycycline for 48 h prior to HIV-1 infection. The cells were infected with 25 ng p24^{Gag} of NL4-3/Nef-IRES-Renilla and infection efficiency was monitored at 48 h by measuring Renilla activity. Mean relative infection efficiencies with standard deviations from three independent experiments are shown.

B. Immunoblot analysis of parallel samples. Protein levels of MX2 wild type, MX2 short isoform (MX2₂₆₋₇₁₅) and MX2 long isoform (MX2_{kozak}) were determined using a Flag-specific antibody and tubulin served as a loading control.



Supplementary Figure 3. The MX1_{K83A}(N_{MX2}) and MX1_{T103A}(N_{MX2}) chimerae lack GTPase activity.

MX proteins were immunoprecipitated from transfected 293T cell lysates and incubated with [α -³²P] GTP using a standard GTPase assay. GDP and GTP were resolved using thin-layer chromatography and visualized by autoradiography.



Supplementary Figure 4. Mouse Mx1 and Mx2 are re-localised to the nuclear envelope when bearing the N-terminal domain of human MX2.

HeLa cells were seeded on glass coverslips, transfected with vectors expressing Flag-tagged mmMx1, mmMx1(N_{huMX2}), mmMx2 or mmMx2(N_{huMX2}) and fixed 16 h post-transfection. MX proteins and the NE were visualized by indirect immunofluorescence using Flag- or NUP358-specific antibodies, respectively, and confocal microscopy. Scale bar, 12.5 μm .