

Supplementary Sequence File

This file contains the full-length amino acid sequences of engineered viral glycoprotein constructs fused to fluorescent reporters, luciferase, selection markers, or exosomal proteins, as used in this study. Each construct is annotated by its total amino acid (aa) length.

Construct List and Sequence Descriptions

1. VSVG-copGFP (800 aa)
Previously published in Int J Nanomedicine (2017;12:3153–3170. doi:10.2147/IJN.S133430)
2. VSVG-rubyRFP (783 aa)
Previously published in Int J Nanomedicine (2017;12:3153–3170. doi:10.2147/IJN.S133430)
3. VSVG-copGFP-Puro (961 aa)
VSVG-copGFP fusion with a puromycin resistance cassette.
4. VSVG-rubyRFP-Puro (946 aa)
VSVG-rubyRFP fusion with a puromycin resistance cassette.
5. RD114A-gLuc-copGFP (1001 aa)
RD114A envelope glycoprotein fused to Gaussia luciferase and copGFP.
6. RD114A-gLuc-rubyRFP (994 aa)
RD114A envelope glycoprotein fused to Gaussia luciferase and rubyRFP.
7. SARS-CoV-1-spike-eGFP (1525 aa)
Full-length SARS-CoV-1 spike glycoprotein fused to enhanced GFP.
8. SARS-CoV-2-spike-eGFP (1507 aa)
Full-length SARS-CoV-2 spike glycoprotein fused to enhanced GFP.
9. HSV-gpB-eGFP (1150 aa)
Herpes Simplex Virus glycoprotein B fused to enhanced GFP.
10. VSVG-rubyRFP-P2A-CD63-eGFP (1261 aa)
Bicistronic construct with VSVG-rubyRFP, a P2A linker, and CD63-eGFP.

Full-length Amino Acid Sequences and Annotations (1-10)

1. VSVG-copGFP (800 aa)
This sequence was previously published in Int J Nanomedicine (2017 Apr 18;12:3153–3170. doi: 10.2147/IJN.S133430)
2. VSVG-rubyRFP (783 aa)
This sequence was previously published in Int J Nanomedicine (2017 Apr 18;12:3153–3170. doi: 10.2147/IJN.S133430).
3. VSVG-copGFP-Puro (961aa)

MKCLLYLAFLFIGVNCKFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCH
ASKWVTTCDFRWYGPKYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAAEVIVQVTPHHVLVDEY
TGEWVDSQFINGKCSNYICPTVHNSTTWHSYKVKGLCDSNLISMDITFFSEDGELSSLGKEGTGFRSNFYAYETGGKA
CKMQYCKHWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPI
SPVDLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMIISGTTTERELWDDWAPYEDVEIGPNGVLRSS
GYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESFFGDTGLSKNPIELVEGWFSWSSIASFFFIIGLII
GLFLVLRVGIHLCKIKHTKKRQIYTDIEMNRLGKESDESGLPAMEIECRITGTLNGVEFELVGGGEGTPKQGRMTNKMK
STKGALTSPYLLSHVMGYGFYHFGTYPSTGYENPFLHAINNGGYTNTRIEKYEDGGVLHVFSFSYRYEAGRIGDFKVVGT
GFPEDSVIFTDKIIRSNATVEHLHPMGDNVLVGSFARTFSLRDGGYYSFVVDSHMHFKSAIHPSILQNGGPMFAFRVE
ELHSNTELGIVEYQHAFKTPIAFARSRAQSSNSAVDGTAGPGSTGSRMTEYKPTVRLATRDDVPRAVRTLAAAFADYPA
TRHTVDPDRHIERVTELQELFLTRVGLDIGKVVVADDGAAVAVWTTPESEAGAVFAEIGPRMAELSGSRLAAQQQM
EGLLAPHRPKPAWFLATVGVSPDHQKGLGSAVVLPGVEAAERAGVPAFLETSAPRNLPFYERLGTFTADVEVPEG
PRTWCMTRKPGA*

4. VSVG-rubyRFP-Puro (946aa)

MKCLLYLAFLFIGVNCKFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCH
ASKWVTTCDFRWYGPKYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAAEVIVQVTPHHVLVDEY
TGEWVDSQFINGKCSNYICPTVHNSTTWHSYKVKGLCDSNLISMDITFFSEDGELSSLGKEGTGFRSNFYAYETGGKA
CKMQYCKHWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPI
SPVDLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMIISGTTTERELWDDWAPYEDVEIGPNGVLRSS
GYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESFFGDTGLSKNPIELVEGWFSWSSIASFFFIIGLII
GLFLVLRVGIHLCKIKHTKKRQIYTDIEMNRLGKGKLTMASSSEDVIKEFMRFKVKMEGVSNGHEFEIEGEGEGRPYEGT
QTAKLKVTKGGLPFSWDILSPQFQYGSKAYVKHPADIPDYLKLSFPEGFKWERFMNFEDGGVVTVTQDSTLQDGEFIY
KVKLRGTNFPSDGPVMQKKTMGWEASTERMYPEDGALKGEIKMRLKLDGGHYDAEVKTTYKAKKQVQLPGAYMT
DIKLDIISHNGDYTIVEQYERAEGRHSTGAGSIIRSIMTEYKPTVRLATRDDVPRAVRTLAAAFADYPATRHTVDPDRHIE
RVTELQELFLTRVGLDIGKVVVADDGAAVAVWTTPESEAGAVFAEIGPRMAELSGSRLAAQQQMEGLLAPHRPKEP
AWFLATVGVSPDHQKGLGSAVVLPGVEAAERAGVPAFLETSAPRNLPFYERLGTFTADVEVPEGPRTWCMTRKPG
A*

5. RD114A-gLuc-copGFP (1001aa)

MKLPTGMVILCSLIIVRAGFDDPRKAIALVQKQHGKPECCSGGQVSEAPPNSIQQVTCPGKTAYLMTNQKWKCRVTPK
NLTPSGGELQNCPCNTFQDSMHSSCYTEYRQCRANNKTYTATLLKIRSGSLNEVQILQNPQNQLLQSPCRGSINQPV
WSATAPIHISDGGGPLDTKRVTWTVQKRLEQIHKAMHPELQYHPLALPKVRDDLSDARTFDILNTTFRLLQMSNFSLAQ
DCWLCLKLGTPTPLAIPSTYSLADSLANASCQIIPLLVQPMQFSNSSCLSPFINDTEQIDLGAVTFTNCTSVANVSS
PLCALNGSVFLCGNNMAYTYLPQNWTGLCVQASLLPDIDIIPGDEPVPIPAIDHYIHRPKRAVQFIPLLAGLGITAAFTTG
ATGLGVSVTQYTKLSHQLISDVQVLSGTIQDLQDQVDSLAEVVLQNRRLDLLTAEQGGICLALQECCFYANKSGIVRN
KIRTLQEELQKRRESLASNPLWTGLQGFLPYLLPLGPLLTLILLITIGPCVFNRVLVQFVKDRISVVQALVLTQQYHQLKPIE
YEPMKPTENNEDFNIVAVASNFATTDLDADRGKLPKGLPLEVLKEMEANARKAGCTRGCLICLSHIKCTPKMKKFIPGR
CHTYEGDKESAQGGIGEIVDIPEIPGFKDLEPMEQFIAQVDLCVDCTTGCLKGLANVQCSDLLKKWLPQRCATFASKIQ
GQVDKIKGAGGDHHHHHHNSNLNRIRGRMESDESGLPAMEIECRITGTLNGVEFELVGGGEGTPKQGRMTNKMKST
KGALTSPYLLSHVMGYGFYHFGTYPSTGYENPFLHAINNGGYTNTRIEKYEDGGVLHVFSFSYRYEAGRIGDFKVVGTGF

PEDSVIFTDKIIRS NATVEHLHPMGDNVLVGSFARTFSLRDGGYYSFVVD SHMHFKSAIHPSILQNGGPMFAFRVEELH
SNTELGIVEYQHAFKTPIAFARSRAQSSNSAVDGTAGPGSTGSR*

6. RD114A-gLuc-rubyRFP (994aa)

MKLPTGMVILCSLIIVRAGFDDPRKAIALVQKQHGKPCCESGGQVSEAPPNSIQQVTCPGKTAYLMTNQKWKCRVTPK
NLTPSGGELQNCPCNTFQDSMHSSCYTEYRQCRANNKTYTATLLKIRSGSLNEVQILQNPQNQLLQSPCRGSINQPV
WSATAPIHISDGGGGLDTRKRVWTVQKRLEQIHKAMHPELQYHPLALPKVRDDLSDARTFDILNTTFRLLQMSNFSLAQ
DCWLCLKLGTPTPLAIPTPSLTYSLADSLANASCQIIPLLVQPMQFSNSSCLSSPFINDTEQIDLGAFTFTNCTSVANVSS
PLCALNGSVFLCGNNMAYTYLPQNWTGLCVQASLLPDIDIIPGDEPVPIPAIDHYIHRPKRAVQFIPLLAGLGITAAFTTG
ATGLGVSVTQYTKLSHQLISDVQVLSGTIQDLQDQVDSLAEVVLQNRRLDLLTAEQGGICLALQEKCCFYANKSGIVRN
KIRTLQEELQKRRESLASNPLWTGLQGFLPYLLPLGPLLTLILLITIGPCVFNRLVQFVKDRISVVQALVLTQQYHQLKPIE
YEPMKPTENNEDFNIVAVASNFAATDLDADRGLPGKKLPLEVLKEMEANARKAGCTRGCLICLSHIKCTPKMKKFIGR
CHTYEGDKESAQGGIGEIVDIPEIPGFKDLEPMEQFIAQVDLCVDCTTGCLKGLANVQCSDLLKKWLPQRCATFASKIQ
GQVDKIKGAGGDHHHHHHHNSNLNRIRGRMGKLTMASSDVIKEFMRFVKMEGSVNGHEFEIEGEGEGRPYEGTQT
AKLKVTKGGLPFSWDILSPQFQYGSKAYVKHPADIPDYLKLSFPEGFKWERFMNFEDGGVVTVTQDSTLQDGEFIYKV
KLRGTNFPSDGPVMQKKTMGWEASTERMYPEDGALKGEIKMRLKLDGGHYDAEVKTTYKAKKQVQLPGAYMTDIK
LDIISHNGDYTIVEQYERAEGRHSTGAGSIIRSIIHHHHHHH*

7. SARS-CoV-1-Spike-eGFP (1525aa)

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVVYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFD
NPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVFCEFCNDPFLGVYYHKNNKSWMESEFRVY
SSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTL
ALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGIYQTSNFRVQP
TESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIR
GDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEYQAGSTPCNG
VEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLP
FQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGS
NVFQTRAGCLIGA EHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNISAIPTNFTISV
TTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFS
QILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSG
WTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAIGKIQDSLSTASALGKLQDVVNQNAQALNTL
VKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFC
GKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH DGKAHPREGVFVSNGTHWFVTQRNFYEPQIITDNTF
VSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
LGKYEYQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCCLKGCCSCGSCCKFDEDDSEPV LKGVKLHYTKLGGGGG
SGGGGSMSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT LKFICTTGKLPVPWPVLTTLTYGVQCFSRY
PDHMKQHDFFSAMPEGYVQERTIFFKDDGNYKTRA EVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYI
MADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDH MVLLEFVTAAGIT
HGMDELYK*

8. SARS-CoV-2-Spike-eGFP (1507aa)

MFIFLLFLTSTSGSDLRCTTFDDVQAPNYTQHTSSMRGVVYPDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHTFDNPVI
PFKDGIFYAATEKSNVVRGWVFGSTMNNKSQSVIIINNSTNVVIRACNFELCDNPFFAVSKPMGTQHTMIFDNAFNC
TFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQ
DTWGTSAAYFVGYLKPTTFMLKYDENGITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVRFPNITNL
CPFGEVFNATKFPSVYAWERKKISNCVADYSVLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQT
GVIADYNYKLPPDFMGCVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPPALNCYWPLND
YGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTSSKRFQPFQQFGRDVSDFD
SVRDPKTSEILDIPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQQTQAGCLIGAE
HVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNM
YICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFQVQKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDL
LFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFA
MQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVL
NDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAP
HGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVFNGTSWFITQRNFFSPQIITDNTFVSGNCDVVIGIINNTVY
DPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVUNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL
GFIAGLMAIVMVTILLCCMTSCCSCCLKGACSCGSCCKFDEDDSEPVLKGVKLHYTKLGGGGGSGGGGMSKGEELFTG
VVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKICTTGKLPVPWPTLVTTLTLYGVQCFSRYPDHMKQHDFFKSAMP
EGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRH
NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITHGMDELYK*

9. HSV-gpB-eGFP (1150aa)

MHQGAPSWGRRWFVFWALLGLTLGVLVASAAPSSPGTPGVAAATQAANGGPANPAPPALGAAPTGDPKPKKNKKP
KNPTPPRPAGDNATVAAGHATLREHLRDIKAENTDANFYVCPPTGATVVQFEQPRRCPTRPEGQNYTEGIAVVFEN
IAPYKFKATMYKDVTVSQVWFHGRYSQFMGIFEDRAPVPFEEVIDKINAKGVCRSTAKYVRNLETTAFHRDDHETD
MELKPANAATRTSRGWHTTDLKYNPSRVEAFHRYGTTVNCIVKEVDARSVYPYDEFVLATGDFVYMSPFYGYREGSHT
EHTSYAADRFKQVDGFYARDLTTKARATAPTRNLLTTPKFTVAWDWVPKRPSVCTMTKWQEVDEMLRSEYGGSFRE
SSDAISTTFTTNLTYPLSRVDLGDCIGKDARDAMDRIFARRYNATHIKVGQPQYYLANGGFLIAYQPLLSNTLAELYVRE
HLREQSRKPPNPTPPPPGASANASVERIKTTSSIEFARLQFTYNHIQRHVNDMLGRVAIAWCELQNHETLWNEARKLN
PNAIASVTVGRRVSARMLGDVMAVSTCVPAADNVIVQNSMRISRPACYSRPLVSFRYEDQGGLVEGQLGENNEL
RLTRDAIEPCTVGHRRYFTFGGGYVYFEEYAYSHQLSRADITTVSTFIDLNITMLEDFEVPLEVYTRHEIKDSGLLDYTEV
QRRNQLHDLRFADIDTVIHADANAAMFAGLGAFFEGMGDLGRAVGKVVVMGIVGGVVSASVGVSSFMSPNPFALAV
GLLVLAGLAAFFAFRYVMRLQSNPMKALYPLTTKELKNPTNPASGEEGEGGDFDEAKLAEAREMIRYMALVSAMER
TEHKAKKKGTSALLSAKVTDMMVRKRRNTNYTQVPNKDGDADDEDDLDIQHSGGRMSKGEELFTGVVPILVELDGDVN
GHKFSVSGEGEGDATYGKLTCLKICTTGKLPVPWPTLVTTLTLYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD
DGNKYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADH
YQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITHGMDELYK*

10. VSVG-rubyRFP-P2A-CD63-eGFP (1261aa)

MKCLLYLAFLFIGVNCKFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCH
 ASKWVTTCDFRWYGPKYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEY
 TGEWVDSQFINGKCSNYICPTVHNSTTWHSYKVKGLCDSNLISMDITFFSEDGELSSLGKEGTGFRSNFYAYETGGKA
 CKMQYCKHWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPI
 SPVDLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVMISGTTTERELWDDWAPYEDVEIGPNGVLRSS
 GYKFPLYMIGHGMLDSDLHLSSKAQVFEHPIHQDAASQLPDDESFFGDTGLSKNPIELVEGWFSWKSSIASFFFIIGLII
 GLFLVLRVGIHLCKLKHKKRQIYTDIEMNRLGKGGGSMGKLTMASSDVIKEFMRFKVKMEGSVNGHEFEIEGEGE
 GRPYEGTQTAKLKVTGGGPLPFSWDILSPQFQYGSKAYVKHPADIPDYLKLSFPEGFKWERFMNFEDGGVVTVTQDSTL
 QDGEFIYKVKLRGTNFPDGPVMQKKTMGWEASTERMYPEDGALKGEIKMRLKLDGGHYDAEVKTTYKAKKQVQL
 PGAYMTDIKLDIISHNGDYTIVEQYERAEGRHSTGAGSIIRSIIIGSGATNFSLLKQAGDVEENPGPMAVEGGMKCVKFL
 YVLLAFCAVGLIAGVGVAQLVLSQTIIQGATPGSLLPVVIIAVGVFLVAFVGGCGACKENYCLMITFAIFLSLIMLVE
 VAAAIAGYVFRDKVMSEFNNNFRQQMENYPKNNHTASILDRMQADFKCCGAANYTDWEKIPSMKSNRVPDSCCINV
 TVGCGINFNEKAIHKEGCVKIGGWLRKNVLVAAAAALGIAFVEVLGIVFACCLVKSIKSGYEVMDIQHSGGRMSKGEEL
 FTGVVPILVELDGDVNGHKFSVSGEGEGDATYKGLTLKFICTTGKLPVPWPTLVTTLTLYGVQCFSRYPDHMKQHDFFKS
 AMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNF
 KIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITHGMDELYK*

Note: Color Coding in Sequence Annotations

- Purple: Membrane scaffold (VSVG, RD114, SARS-CoV, HSV, CD63)
- Red: Red fluorescent protein domains (rubyRFP)
- Green: Green fluorescent protein domains (copGFP or eGFP)
- Yellow: Linkers, spacers, and P2A elements
- Blue: Gaussia luciferase (gLuc)
- Gray: Puromycin resistance gene (Puro)