**Supplemental File 1: DNA sequences**

**Supplemental file 1A : *Lp::Sc2A10* knock-in plasmid**

LOCUS pENTR3xgRNALp-Sc2A10 8489 bp DNA circular FEATURES Location/Qualifiers

 misc\_feature 537..552

 /note="M13F"

 misc\_feature complement(6750..6768)

 /note="M13R"

 misc\_feature 3637..3645

 /note=""

 misc\_feature 3659..3736

 /note="re-coded signal peptide"

 /note=""

 misc\_feature 3737..4090

 /note="heavy chain\_2A10%E2%80%9D misc\_feature

 3737..4465 /note=%222A10"

 misc\_feature 4502..4507

 /note="perfect intron splice acceptor site"

 misc\_feature 4475..4486

 /note="cleavage site"

 misc\_feature 4466..4498

 /note="encompasses cleavage site"

 misc\_feature complement(4520..5668)

 /note="3xP3-GFP-pAtub56D"

 misc\_feature 4499..4519

 /note="PRESERVE"

 misc\_feature 4097..4141

 /note="(G4S)3-linker"

 misc\_feature 4142..4465

 /note="light chain\_2A10%E2%80%9D misc\_feature

 4487..4507 /note=%22peptide added to ApoII"

 misc\_feature complement(4520..4688)

 /note="Dm beta-Tub56D terminator"

 misc\_feature 4469..4687

 /note="gBlock"

 misc\_feature 4689..5407

 /note="GFP"

 misc\_feature complement(4575..4580)

 /note="polyA site"

 misc\_feature 5619..5668

 /note="3xPax6 binding sites"

 misc\_feature 5572..5579

 /note="TATA box"

 misc\_feature 6688..6688

 /note="mutated to T"

 misc\_feature 2133..3652

 /note="Lp promoter 5%82%C4%F4flk HA"

 misc\_feature complement(906..1226)

 /note="AGAP013557 U6 prom"

 misc\_feature complement(810..881)

 /note="pX330 chimeric guide RNA scaffold"

 misc\_feature complement(875..881)

 /note="CRISPR end"

 misc\_feature complement(807..870)

 /note="tracer"

 misc\_feature 774..809

 /note="from Ag U6"

 misc\_feature complement(1359..1679)

 /note="AGAP013557 U6 prom"

 misc\_feature complement(1263..1334)

 /note="pX330 chimeric guide RNA scaffold"

 misc\_feature complement(1328..1334)

 /note="CRISPR end"

 misc\_feature complement(1260..1323)

 /note="tracer"

 misc\_feature 1231..1262

 /note="from Ag U6"

 misc\_feature complement(1812..2132)

 /note="AGAP013557 U6 prom"

 misc\_feature complement(1716..1787)

 /note="pX330 chimeric guide RNA scaffold"

 misc\_feature complement(1781..1787)

 /note="CRISPR end"

 misc\_feature complement(1713..1776)

 /note="tracer"

 misc\_feature 1684..1715

 /note="from Ag U6"

 misc\_feature complement(882..905)

 /note="sgRNA1 EM1096"

 misc\_feature 1335..1358

 /note="sgRNA2 EM1098"

 misc\_feature 1788..1811

 /note="sgRNA3 EM1100"

 misc\_feature complement(6701..6726)

 /note="EM1103 gRNA2 target"

 misc\_feature 5671..6697

 /note="Lp 3%82%C4%F4flk HA"

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 121 GCGCCCAATA CGCAAACCGC CTCTCCCCGC GCGTTGGCCG ATTCATTAAT GCAGCTGGCA

 181 CGACAGGTTT CCCGACTGGA AAGCGGGCAG TGAGCGCAAC GCAATTAATA CGCGTACCGC

 241 TAGCCAGGAA GAGTTTGTAG AAACGCAAAA AGGCCATCCG TCAGGATGGC CTTCTGCTTA

 301 GTTTGATGCC TGGCAGTTTA TGGCGGGCGT CCTGCCCGCC ACCCTCCGGG CCGTTGCTTC

 361 ACAACGTTCA AATCCGCTCC CGGCGGATTT GTCCTACTCA GGAGAGCGTT CACCGACAAA

 421 CAACAGATAA AACGAAAGGC CCAGTCTTCC GACTGAGCCT TTCGTTTTAT TTGATGCCTG

 481 GCAGTTCCCT ACTCTCGCGT TAACGCTAGC ATGGATGTTT TCCCAGTCAC GACGTTGTAA

 541 AACGACGGCC AGTCTTAAGC TCGGGCCCCT ACAGGTCACT AATACCATCT AAGTAGTTGA

 601 TTCATAGTGA CTGGATATGT TGTGTTTTAC AGTATTATGT AGTCTGTTTT TTATGCAAAA

 661 TCTAATTTAA TATATTGATA TTTATATCAT TTTACGTTTC TCGTTCAACT TTTCTATACA

 721 AAGTTGGTAC CGGGCCCCCC GCTAGCGTCG ACGGTATCGA TAAGCTTGAT cggatccGAT

 781 GAAAATAAGA AAAACATTTG ACAAAAAAAg caccgactcg gtgccacttt ttcaagttga

 841 taacggacta gccttatttt aacttgctaT TTCtagctct aaaacGGTGT CGCTAGTGCT

 901 GATTCAAGGA CGAGGGGAAA AAAGGTTGTA TATATACTTT GCGCTTTCAA TCCTTGCTCT

 961 AGCGATGCAT AAAGGATATT CAAGAAGGAT TTTTTGCCTG AGTGTGACTG TTATAAGGTT

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 1201 GCCAAACCGC TTCAGTGTAT ATGTGGggaa GATGAAAATA AGAAAAACAT TTGACAAAAA

 1261 AAgcaccgac tcggtgccac tttttcaagt tgataacgga ctagccttat tttaacttgc

 1321 taTTTCtagc tctaaaacTC CCTGACGATA TTTCACGCAA GGACGAGGGG AAAAAAGGTT

 1381 GTATATATAC TTTGCGCTTT CAATCCTTGC TCTAGCGATG CATAAAGGAT ATTCAAGAAG

 1441 GATTTTTTGC CTGAGTGTGA CTGTTATAAG GTTTTGATCC TGCCGTAACT CACGCTAATG

 1501 TGATGTTTCA TAAACTTTTC AACATTTCTT GTATTGCTTC ATCTCTTTTT TAATCAAAAG

 1561 TTACTATTCA TTGTAATACG TTGAAATATC AAAAAAGAAT AAACAGTTTT CCTATGATTA

 1621 ATTCAAAAAC AGAGTTTTCT AGAATAACCA AGAGCCAAAC CGCTTCAGTG TATATGTGGa

 1681 gagGATGAAA ATAAGAAAAA CATTTGACAA AAAAAgcacc gactcggtgc cactttttca

 1741 agttgataac ggactagcct tattttaact tgctaTTTCt agctctaaaa cCCGAGGACC

 1801 CACATCGTTC CAAGGACGAG GGGAAAAAAG GTTGTATATA TACTTTGCGC TTTCAATCCT

 1861 TGCTCTAGCG ATGCATAAAG GATATTCAAG AAGGATTTTT TGCCTGAGTG TGACTGTTAT

 1921 AAGGTTTTGA TCCTGCCGTA ACTCACGCTA ATGTGATGTT TCATAAACTT TTCAACATTT

 1981 CTTGTATTGC TTCATCTCTT TTTTAATCAA AAGTTACTAT TCATTGTAAT ACGTTGAAAT

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 2101 CCAAGAGCCA AACCGCTTCA GTGTATATGT GGAACAGTTC ATTCCCGATT GAGGGATTTT

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 2221 GGTTAGTTTA CTGTAATGGT GTAATTGTCA TCTTACACCT CCGTCTGATA AGAGATTACG

 2281 AAGCTCAGTA TGATGAAATA AATAAGATAA ATTTATTTAA AAAAGAACAA TTGCTATGAG

 2341 AGTGAAATAC AACAGTGGCG TTCACAATAT TCGAAAAACA ATAAAATTAA AAAAAAAACA

 2401 AGAAAACATT CACAAACATA TCAATCTGCT TTCATCGACA CCGAACTGCT AGCCTCCCCA

 2461 GTCTAACCGC GGTGGGGACG TTTAATTGCC TTTGTTCTCG CACCCGGTCA AACATACACT

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 2581 TGCTAAGCGT GCATTATTTT CACAACTTAG CGTAATGCTA GCGTGCGCTA GCAACAAACT

 2641 CGCCCGCAGA CTCGTCACAG CACCGGTACG ATCGATCGTT TACCGTTCCC TTTCCCGATC

 2701 GGGTTGGCTG CGATATCCGT GTCCGGGTAG AAAACTTCCC CTTTTACACA CACACACTCA

 2761 CATACACACA GAGCTGAATA GCAACTTACC TTATCTGTTC GTCATCGCTC GGCCGGATCT

 2821 GGACGAATCT TCGCACCGAT AACCATGTGG ATCTACGACC TCCGCTTGGC TGTCTCTCTG

 2881 CTCATGTGTA TGTCTGTGTG TGTGTGTATG TGAGCTTCTT CCCTCAAATC CCTCGATCTC

 2941 GCTGTGCCAA CAATCAAACG TGCAAGTGCA AACATTGCAC CCCATTGATT ATACACCAAC

 3001 ACCAACCAAT TCCCCTTGCG GAGGCATCTC TGTGCTCGGC AGCATGTTTA CCGCAGATCT

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 3301 CTGATGTGAA CCCCCGTTCA AACCCCAAAT GCAGTGTTTG TATTGCTGTG TGTATGTGTA

 3361 CGTGCGTGTG TGTGGAAATT CTATAAAAGT AGGCACCCGT GGCCGGGATC CGTTATTCCC

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 3481 GTGCCCGATC GGTAAAGAGT GAACCGTCTT CTCTGCAGTG TAGGAGAGAA CGGTTTCATC

 3541 TTTTTCGCCC ACACCCCCCC GGTTACATTC CATGTTGAAC TGTAAGGTCT AGTGAACATT

 3601 TCCTGAGTGT GGAAAGTGTG GTTTAGTGCG TGAGAGTGCA CGGACACGAC ACGGAACGAT

 3661 GTGGGTgCTg GGaGGcAGaA GaCTcCTgTG GtcgTTtCTc GTcagctTgG TcCTcATcCA

 3721 gtccGTcagC gcagccCAGA TCCAGCTGGT GCAGTCGGGC CCCGAGCTGA AGAAGCCCGG

 3781 CGAAACGGTG AAGATCAGCT GTAAGGCGAG CGGTTACACC TTCACCAACT ACGGCATCAA

 3841 CTGGGTGAAG CAGGCGCCGG GCAAGGGTCT GAAGTGGATG GGATGGATCA ACACGATCAC

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 4261 GGACGGTACC GTCAAGCTGC TGATCTTCTA CACCTCGACC CTGTACTCGG GTGTGCCGTC

 4321 GCGTTTCTCG GGTTCGGGCT CGGGCACCGA TTACTCGCTG ACCATCTCGA ACCTGGAGCC

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 4501 CGCAGGTATG TTCCTATACg aaaccccaac aaaaaccata attgtttAGA CTTGTGAACA

 4561 AAATTGGATC CGACTTTATT GATTACGTTG TTAAGAGAAC AAATCTTTTA CAACTGAATT

 4621 CATTTGTTCT CGTTTCATTT TTTTTCGCAA AACATTGATC GAGAATTCGA TTGATTTCCG

 4681 ATTCGAATTT ACTTGTACAG CTCGTCCATG CCGAGAGTGA TCCCGGCGGC GGTCACGAAC

 4741 TCCAGCAGGA CCATGTGATC GCGCTTCTCG TTGGGGTCTT TGCTCAGGGC GGACTGGGTG

 4801 CTCAGGTAGT GGTTGTCGGG CAGCAGCACG GGGCCGTCGC CGATGGGGGT GTTCTGCTGG

 4861 TAGTGGTCGG CGAGCTGCAC GCTGCCGTCC TCGATGTTGT GGCGGATCTT GAAGTTCACC

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 4981 TCCAGCTTGT GCCCCAGGAT GTTGCCGTCC TCCTTGAAGT CGATGCCCTT CAGCTCGATG

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 5401 CTCACCATGG TGGCGACCGG TGGATCCCGG GCCCGCGGTA CCGTCGACTC TAGCGGTACC

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 5641 AATTAGTCTC TAATTGAATT AGATCCCCGA TGGAAGAGAT GGCGAAGGTT CTCATCCACA

 5701 AGTTGTTGGT GATGCTAACA TTGCTTCCGA GCAATGTATT GCTGCCGAGG GTGTCGATTA

 5761 GTACAGCAAA GCGCGAGAAA CAAGTGGCTG CTGTGGCCGG CGGTACCCAT AAACCAGTTG

 5821 AGATAATTTA GACAATAAAT TGTAATAGGC AATTTGATGA CGTCCCGCAT GTACGGATCG

 5881 TCAACGCTGC ACGCTCGGGA ATAGGGTGAG AAGTGCTGCC CGTTTGTTGG ACAGCGCAGG

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 6241 GGAAGTCAGG AGAAGCTCCG ACGGGCGTGT AGGGTAAGTC GCAGTTCGGC AGCATTCTGG

 6301 CAGTGTACAC CCAGCACACC GAGCGTTCTA GAACGCTGAA TCGTTGAAAC AGAGCAAATG

 6361 ACTGAAGGGC TGTGTCTATT GCTGGGCTGT ACAGAATGAC GCATTTCGTG TGGCAATGTG

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 7381 GAGCGTAATG GCTGGCCTGT TGAACAAGTC TGGAAAGAAA TGCATAAACT TTTGCCATTC

 7441 TCACCGGATT CAGTCGTCAC TCATGGTGAT TTCTCACTTG ATAACCTTAT TTTTGACGAG

 7501 GGGAAATTAA TAGGTTGTAT TGATGTTGGA CGAGTCGGAA TCGCAGACCG ATACCAGGAT

 7561 CTTGCCATCC TATGGAACTG CCTCGGTGAG TTTTCTCCTT CATTACAGAA ACGGCTTTTT

 7621 CAAAAATATG GTATTGATAA TCCTGATATG AATAAATTGC AGTTTCATTT GATGCTCGAT

 7681 GAGTTTTTCT AATCAGAATT GGTTAATTGG TTGTAACACT GGCAGAGCAT TACGCTGACT

 7741 TGACGGGACG GCGCAAGCTC ATGACCAAAA TCCCTTAACG TGAGTTACGC GTCGTTCCAC

 7801 TGAGCGTCAG ACCCCGTAGA AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTTCTGCGC

 7861 GTAATCTGCT GCTTGCAAAC AAAAAAACCA CCGCTACCAG CGGTGGTTTG TTTGCCGGAT

 7921 CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA GATACCAAAT

 7981 ACTGTTCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT

 8041 ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT

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 8161 GGGGGTTCGT GCACACAGCC CAGCTTGGAG CGAACGACCT ACACCGAACT GAGATACCTA

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 8281 GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCTGG

 8341 TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG AGCGTCGATT TTTGTGATGC

 8401 TCGTCAGGGG GGCGGAGCCT ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCCTG

 8461 GCCTTTTGCT GGCCTTTTGC TCACATGTT

//

**Supplemental File 1B: *Lp::2A10* knockin in genomic context**

LOCUS Lp-2A10 14919 bp DNA linear

FEATURES Location/Qualifiers

 misc\_feature 1..1622

 /note="Lp promoter"

 exon 5369..9341

 /note="exon\_id=AGAP001826-RA-E2.1"

 misc\_feature 7396..7407

 /note="cleavage site"

 exon 9406..9535

 /note="exon\_id=AGAP001826-RA-E3.1"

 exon 9610..14919

 /note="exon\_id=AGAP001826-RA-E4.1"

 misc\_feature 2472..2477

 /note="perfect intron splice acceptor site"

 misc\_feature 2445..2456

 /note="cleavage site"

 misc\_feature 2436..2468

 /note="encompasses cleavage site"

 misc\_feature complement(2490..3638)

 /note="3xP3-GFP-pAtub deletes 3 cas9 target sites in

 intron"

 misc\_feature 1623..1642

 /note="disabled gRNA target site”

 misc\_feature 1630..1649

 /note="disabled gRNA target site"

 misc\_feature 1639..1658

 /note="disabled gRNA target site"

 misc\_feature 1650..1668

 /note="disabled gRNA target site"

 misc\_feature 1641..1659

 /note="disabled gRNA target site"

 misc\_feature 1670..1689

 /note="disabled gRNA target site"

 misc\_feature 1629..1703

 /note="re-coded signal peptide"

 misc\_feature 1683..1703

 /note="disabled gRNA target site"

 misc\_feature 2469..2489

 /note="PRESERVED around splice junction”

 misc\_feature 1707..2060

 /note=“Sc2A10 heavy chain"

 misc\_feature 2067..2111

 /note="(G4S)3-linker"

 misc\_feature 2112..2435

 /note=“Sc2A10 light chain"

 misc\_feature 1707..2435

 /note=“Sc2A10"

 misc\_feature 2457..2477

 /note="peptide added to ApoII"

 misc\_feature 3589..3638

 /note="3xPax6 binding sites"

 misc\_feature 3542..3549

 /note="TATA box"

 misc\_feature 2659..3377

 /note="GFP"

 misc\_feature complement(2490..2658)

 /note="Dm beta-Tub56D terminator"

 misc\_feature complement(2545..2550)

 /note="polyA site"

 misc\_feature complement(4639..4667)

 /note="EM894 GGTCTC-> GGTCTT"

 misc\_feature 4658..4658

 /note="mutated to T"

 source 1..14919

 /dnas\_title=“Sc2A10 inserted in Lp genomic fg"

ORIGIN

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 181 TTTTCTTTCA GGTTAGTTTA CTGTAATGGT GTAATTGTCA TCTTACACCT CCGTCTGATA

 241 AGAGATTACG AAGCTCAGTA TGATGAAATA AATAAGATAA ATTTATTTAA AAAAGAACAA

 301 TTGCTATGAG AGTGAAATAC AACAGTGGCG TTCACAATAT TCGAAAAACA ATAAAATTAA

 361 AAAAAAAACA AGAAAACATT CACAAACATA TCAATCTGCT TTCATCGACA CCGAACTGCT

 421 AGCCTCCCCA GTCTAACCGC GGTGGGGACG TTTAATTGCC TTTGTTCTCG CACCCGGTCA

 481 AACATACACT TCGGACCTTG CTCCGAACCC CACTGTAATC CCTAGCTCGT CATCATCATT

 541 GCCGGCATCA TGCTAAGCGT GCATTATTTT CACAACTTAG CGTAATGCTA GCGTGCGCTA

 601 GCAACAAACT CGCCCGCAGA CTCGTCACAG CACCGGTACG ATCGATCGTT TACCGTTCCC

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 721 CACACACTCA CATACACACA GAGCTGAATA GCAACTTACC TTATCTGTTC GTCATCGCTC

 781 GGCCGGATCT GGACGAATCT TCGCACCGAT AACCATGTGG ATCTACGACC TCCGCTTGGC

 841 TGTCTCTCTG CTCATGTGTA TGTCTGTGTG TGTGTGTATG TGAGCTTCTT CCCTCAAATC

 901 CCTCGATCTC GCTGTGCCAA CAATCAAACG TGCAAGTGCA AACATTGCAC CCCATTGATT

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 1081 TCCGGCAGCC ACTGGATCAT CAGCGAAAGA GAGAGAGAGC AGAGCAGAAC AGAGGTGACC

 1141 AACTGTGGTA TCGCTTCCCG CGCGCCGGTG TGTTGGTGTC CATTTCGGTG ATCGCGATCC

 1201 CGGCCGCTTC CAGCACCGTC CACCGATCAG TCACAAAAAC GCTCTCCAAA CCCCTTATCA

 1261 GCACCGTTCG CTGATGTGAA CCCCCGTTCA AACCCCAAAT GCAGTGTTTG TATTGCTGTG

 1321 TGTATGTGTA CGTGCGTGTG TGTGGAAATT CTATAAAAGT AGGCACCCGT GGCCGGGATC

 1381 CGTTATTCCC GTCCTGAGGC CCGCCCGGGA TCGCTGGTGA CGACAGACGA GCCGCTGTGT

 1441 GACGTACGTA GTGCCCGATC GGTAAAGAGT GAACCGTCTT CTCTGCAGTG TAGGAGAGAA

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 1621 ACGGAACGAT GTGGGTgCTg GGaGGcAGaA GaCTcCTgTG GtcgTTtCTc GTcagctTgG

 1681 TcCTcATcCA gtccGTcagC gcagccCAGA TCCAGCTGGT GCAGTCGGGC CCCGAGCTGA

 1741 AGAAGCCCGG CGAAACGGTG AAGATCAGCT GTAAGGCGAG CGGTTACACC TTCACCAACT

 1801 ACGGCATCAA CTGGGTGAAG CAGGCGCCGG GCAAGGGTCT GAAGTGGATG GGATGGATCA

 1861 ACACGATCAC CGAGGAGCCC ACCTTCGCCG AAGAGTTCAC GGGACGCTTC GCCTTCAGCC

 1921 TGGAAACCTC GGCGAGCACC GCCTACCTCC AGATCAACAA CCTGAAGAAC GAGGACACGG

 1981 CCACGTACTT CTGTGCGCGC GGCAGCGAGT TCGGACGCCT GGTCTACTGG GGCCAGGGAG

 2041 CGAGCGTGAC CGTCTCGAGC TCGACCGGTG GTGGTGGCAG CGGCGGAGGA GGTAGCGGAG

 2101 GTGGCGGCAG CGACATCCAG ATGACGCAGA CGACGAGCTC GCTGTCGGCC TCGCTGGGCG

 2161 ATCGTGTGAC GATCTCGTGC AGCGCCTCGC AGGGCATCAG CAACTACCTG AACTGGTACC

 2221 AGCAGAAGCC GGACGGTACC GTCAAGCTGC TGATCTTCTA CACCTCGACC CTGTACTCGG

 2281 GTGTGCCGTC GCGTTTCTCG GGTTCGGGCT CGGGCACCGA TTACTCGCTG ACCATCTCGA

 2341 ACCTGGAGCC CGAGGACATC GCGACGTACT ACTGCCAGCA GTACTCGCGT TTCCCGTACG

 2401 TGTTCGGCGG CGGCACGAAG CTGGAGATCA AGCGCGCcAA GGAaCGtTTC CGtCGCGGaA

 2461 TtCGtGAaTC CGCAGGTATG TTCCTATACg aaaccccaac aaaaaccata attgtttAGA

 2521 CTTGTGAACA AAATTGGATC CGACTTTATT GATTACGTTG TTAAGAGAAC AAATCTTTTA

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 2641 TTGATTTCCG ATTCGAATTT ACTTGTACAG CTCGTCCATG CCGAGAGTGA TCCCGGCGGC

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//

**Supplemental File 1C: *Lp* gene drive plasmid**

LOCUS Lp-GD 13956 bp ds-DNA circular

DEFINITION synthetic circular DNA

ACCESSION .

VERSION .

KEYWORDS .

SOURCE synthetic DNA construct

 ORGANISM synthetic DNA construct

REFERENCE 1 (bases 1 to 13956)

 AUTHORS Emily GREEN

 TITLE Direct Submission

 JOURNAL Exported Wednesday, Sep 18, 2019 from SnapGene 4.3.11

 https://www.snapgene.com

FEATURES Location/Qualifiers

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 /note="transcription terminator T2 from the E. coli rrnB

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**Supplemental File 1D: *SagGDzpg***

LOCUS SagGDzpg 16588 bp DNA circular 14-DEC-2021

FEATURES Location/Qualifiers

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 misc\_feature 537..552

 /note="M13F"

 misc\_feature complement(14849..14867)

 /note="M13R"

 misc\_feature 843..2587

 /note="5' homology arm saglin"

 /note="saglin ORF"

 misc\_feature complement(2568..2587)

 /note="5' flanking reverse primer"

 misc\_feature complement(2753..3073)

 /note="U6 promoter"

 misc\_feature complement(2621..2732)

 /note="gRNA template"

 misc\_feature 2621..3073

 /note="p609"

 misc\_feature 2733..2752

 /note="linker EM661/662"

 misc\_feature 2621..2649

 /note="EM556"

 misc\_feature complement(3206..3526)

 /note="U6 promoter"

 misc\_feature complement(3074..3185)

 /note="gRNA template"

 misc\_feature 3074..3526

 /note="p610"

 misc\_feature 3186..3205

 /note="linker EM663/664"

 misc\_feature complement(3527..3634)

 /note="gRNA template"

 misc\_feature 3527..3979

 /note="p611"

 misc\_feature complement(3658..3979)

 /note="U6 promoter"

 misc\_feature 3635..3658

 /note="Linker EM665/666"

 misc\_feature 3980..3995

 /note="EM723"

 regulatory 6418..7491

 /regulatory\_class="promoter"

 /note="Anopheles gambiae zero population growth"

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 CDS 7498..11769

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 /transl\_table=11

 /product="hCas9"

 /protein\_id="AXV43861.1"

 misc\_feature complement(7458..7491)

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 regulatory 11778..12815

 /regulatory\_class="terminator"

 /note="Anopheles gambiae zero population growth"

 misc\_feature 12822..14762

 /note="Saglin 3' homology arm"

 misc\_feature complement(4467..4574)

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 misc\_feature 4467..4483

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 /note="EM701"

 misc\_feature complement(4441..4466)

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 misc\_feature complement(4086..4110)

 /label=EM850

 /note="EM850"

 misc\_feature complement(4025..4095)

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 /note="tRNA-gly"

 misc\_feature 4018..4041

 /label=EM717

 /note="EM717"

 misc\_feature 4018..4019

 /note="EM1760"

 misc\_feature complement(4833..5157)

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 misc\_feature complement(4807..4832)

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 misc\_feature complement(4758..4827)

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 /note="gRNA template"

 misc\_feature 4733..4757

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 primer\_bind 4740..4757

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 misc\_feature 4650..4666

 /label=EM705

 /note="EM705"

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 misc\_feature 4550..4574

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 /label=EM895

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 primer\_bind complement(5135..5157)

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 misc\_feature 5190..6413

 /note="3xP3 DsRedNLS sv40 from 1154"

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 241 TAGCCAGGAA GAGTTTGTAG AAACGCAAAA AGGCCATCCG TCAGGATGGC CTTCTGCTTA

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 421 CAACAGATAA AACGAAAGGC CCAGTCTTCC GACTGAGCCT TTCGTTTTAT TTGATGCCTG

 481 GCAGTTCCCT ACTCTCGCGT TAACGCTAGC ATGGATGTTT TCCCAGTCAC GACGTTGTAA

 541 AACGACGGCC AGTCTTAAGC TCGGGCCCCT ACAGGTCACT AATACCATCT AAGTAGTTGA

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//

**Supplemental File 1E: *SagGDvasa***

LOCUS SagGDvasa 17175 bp ds-DNA circular

DEFINITION synthetic circular DNA

ACCESSION .

VERSION .

KEYWORDS .

SOURCE synthetic DNA construct

 ORGANISM synthetic DNA construct

REFERENCE 1 (bases 1 to 17175)

 AUTHORS .

 TITLE Direct Submission

 JOURNAL Exported Wednesday, Dec 14, 2022 from SnapGene 5.2.5

 https://www.snapgene.com

FEATURES Location/Qualifiers

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