**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

1021 TTGATCCTGC CGTAACTCAC GCTAATGTGA TGTTTCATAA ACTTTTCAAC ATTTCTTGTA

1081 TTGCTTCATC TCTTTTTTAA TCAAAAGTTA CTATTCATTG TAATACGTTG AAATATCAAA

1141 AAAGAATAAA CAGTTTTCCT ATGATTAATT CAAAAACAGA GTTTTCTAGA ATAACCAAGA

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

2041 ATCAAAAAAG AATAAACAGT TTTCCTATGA TTAATTCAAA AACAGAGTTT TCTAGAATAA

2101 CCAAGAGCCA AACCGCTTCA GTGTATATGT GGAACAGTTC ATTCCCGATT GAGGGATTTT

2161 ATTCCCCGGG GGCCTTTTCA AACGGCTTAA TATAAGCAAT TAATAGTATT TTTTCTTTCA

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

2521 TCGGACCTTG CTCCGAACCC CACTGTAATC CCTAGCTCGT CATCATCATT GCCGGCATCA

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

3061 ACAGAGAACT TCAATTGAGG TCCTTTCCAC CCCCAGCCCT CAACCGGCAA TCCGGCAGCC

3121 ACTGGATCAT CAGCGAAAGA GAGAGAGAGC AGAGCAGAAC AGAGGTGACC AACTGTGGTA

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3241 CAGCACCGTC CACCGATCAG TCACAAAAAC GCTCTCCAAA CCCCTTATCA GCACCGTTCG

3301 CTGATGTGAA CCCCCGTTCA AACCCCAAAT GCAGTGTTTG TATTGCTGTG TGTATGTGTA

3361 CGTGCGTGTG TGTGGAAATT CTATAAAAGT AGGCACCCGT GGCCGGGATC CGTTATTCCC

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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

3901 CGAGGAGCCC ACCTTCGCCG AAGAGTTCAC GGGACGCTTC GCCTTCAGCC TGGAAACCTC

3961 GGCGAGCACC GCCTACCTCC AGATCAACAA CCTGAAGAAC GAGGACACGG CCACGTACTT

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4141 CGACATCCAG ATGACGCAGA CGACGAGCTC GCTGTCGGCC TCGCTGGGCG ATCGTGTGAC

4201 GATCTCGTGC AGCGCCTCGC AGGGCATCAG CAACTACCTG AACTGGTACC AGCAGAAGCC

4261 GGACGGTACC GTCAAGCTGC TGATCTTCTA CACCTCGACC CTGTACTCGG GTGTGCCGTC

4321 GCGTTTCTCG GGTTCGGGCT CGGGCACCGA TTACTCGCTG ACCATCTCGA ACCTGGAGCC

4381 CGAGGACATC GCGACGTACT ACTGCCAGCA GTACTCGCGT TTCCCGTACG TGTTCGGCGG

4441 CGGCACGAAG CTGGAGATCA AGCGCGCcAA GGAaCGtTTC CGtCGCGGaA TtCGtGAaTC

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

4921 TTGATGCCGT TCTTCTGCTT GTCGGCCATG ATATAGACGT TGTGGCTGTT GTAGTTGTAC

4981 TCCAGCTTGT GCCCCAGGAT GTTGCCGTCC TCCTTGAAGT CGATGCCCTT CAGCTCGATG

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5101 TCCTTGAAGA AGATGGTGCG CTCCTGGACG TAGCCTTCGG GCATGGCGGA CTTGAAGAAG

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5281 AGCTTGCCGT AGGTGGCATC GCCCTCGCCC TCGCCGGACA CGCTGAACTT GTGGCCGTTT

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5401 CTCACCATGG TGGCGACCGG TGGATCCCGG GCCCGCGGTA CCGTCGACTC TAGCGGTACC

5461 CCGATTGTTT AGCTTGTTCA GCTGCGCTTG TTTATTTGCT TAGCTTTCGC TTAGCGACGT

5521 GTTCACTTTG CTTGTTTGAA TTGAATTGTC GCTCCGTAGA CGAAGCGCCT CTATTTATAC

5581 TCCGGCGGTC GAGGGTTCGA AATCGATAAG CTTGGATCCT AATTGAATTA GCTCTAATTG

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

5941 TGGTGATCGT GTTGTTTTGG TATCACGAAA ACAAGATAGA ATCTGAGAAA AAAGAACCTT

6001 TTTATCACTT TACCCGCACC GATACTGGTC TTTCTTAGAT CATTTCGGGG CGAAGCAAAC

6061 AAGTCAGCAC GGCATACAAA TTTTGGGATA ATCCCTTAGT CAGTGCCTGT GTCTTTCTAA

6121 TGAAGATTGA CAATGGCGGC GGCGGCGGCG GTGGTAGCAA CCAACGCACT GGCCTTTGTT

6181 TTCATACTTT TCAATGAATT CAATTAGCTT AACCAACGAG GTTGTTGTTG ATGTTCTCAC

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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6481 CTGCAGCTAA CTACAAACTG AGAGAGCTTT CAGCTGGCAG GTGTCCCTAC TTGGTGGTCT

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6781 CCCGTGTCTC AAAATCTCTG ATGTTACATT GCACAAGATA AAAATATATC ATCATGAACA

6841 ATAAAACTGT CTGCTTACAT AAACAGTAAT ACAAGGGGTG TTATGAGCCA TATTCAACGG

6901 GAAACGTCGA GGCCGCGATT AAATTCCAAC ATGGATGCTG ATTTATATGG GTATAAATGG

6961 GCTCGCGATA ATGTCGGGCA ATCAGGTGCG ACAATCTATC GCTTGTATGG GAAGCCCGAT

7021 GCGCCAGAGT TGTTTCTGAA ACATGGCAAA GGTAGCGTTG CCAATGATGT TACAGATGAG

7081 ATGGTCAGAC TAAACTGGCT GACGGAATTT ATGCCTCTTC CGACCATCAA GCATTTTATC

7141 CGTACTCCTG ATGATGCATG GTTACTCACC ACTGCGATCC CCGGAAAAAC AGCATTCCAG

7201 GTATTAGAAG AATATCCTGA TTCAGGTGAA AATATTGTTG ATGCGCTGGC AGTGTTCCTG

7261 CGCCGGTTGC ATTCGATTCC TGTTTGTAAT TGTCCTTTTA ACAGCGATCG CGTATTTCGT

7321 CTCGCTCAGG CGCAATCACG AATGAATAAC GGTTTGGTTG ATGCGAGTGA TTTTGATGAC

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

8101 CTTACCGGGT TGGACTCAAG ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG

8161 GGGGGTTCGT GCACACAGCC CAGCTTGGAG CGAACGACCT ACACCGAACT GAGATACCTA

8221 CAGCGTGAGC TATGAGAAAG CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG

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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61 ATACGTTCAG CTGTGAGAAT AATCATCCAT CTTTCTGCAA TGAACAGTTC ATTCCCGATT

121 GAGGGATTTT ATTCCCCGGG GGCCTTTTCA AACGGCTTAA TATAAGCAAT TAATAGTATT

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

661 TTTCCCGATC GGGTTGGCTG CGATATCCGT GTCCGGGTAG AAAACTTCCC CTTTTACACA

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

961 ATACACCAAC ACCAACCAAT TCCCCTTGCG GAGGCATCTC TGTGCTCGGC AGCATGTTTA

1021 CCGCAGATCT ACAGAGAACT TCAATTGAGG TCCTTTCCAC CCCCAGCCCT CAACCGGCAA

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

1501 CGGTTTCATC TTTTTCGCCC ACACCCCCCC GGTTACATTC CATGTTGAAC TGTAAGGTCT

1561 AGTGAACATT TCCTGAGTGT GGAAAGTGTG GTTTAGTGCG TGAGAGTGCA CGGACACGAC

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

2581 CAACTGAATT CATTTGTTCT CGTTTCATTT TTTTTCGCAA AACATTGATC GAGAATTCGA

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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/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"

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/note="p610"

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/note="linker EM663/664"

misc\_feature complement(3527..3634)

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misc\_feature 3527..3979

/note="p611"

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misc\_feature 3635..3658

/note="Linker EM665/666"

misc\_feature 3980..3995

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regulatory 6418..7491

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regulatory 11778..12815

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421 CAACAGATAA AACGAAAGGC CCAGTCTTCC GACTGAGCCT TTCGTTTTAT TTGATGCCTG

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601 TTCATAGTGA CTGGATATGT TGTGTTTTAC AGTATTATGT AGTCTGTTTT TTATGCAAAA

661 TCTAATTTAA TATATTGATA TTTATATCAT TTTACGTTTC TCGTTCAACT TTTCTATACA

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781 GGGTGCCAGG GCGTGCCCTT GGGCTCCCCG GGCGCGTACT CCACCTCACC CATaggcctg

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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

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FEATURES Location/Qualifiers

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