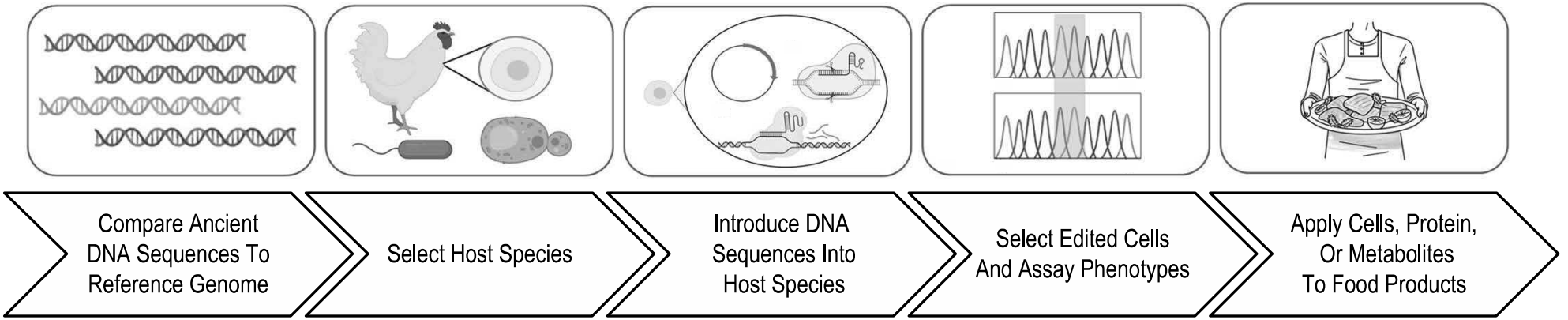

Compare Ancient DNA Sequences To Reference Genome
Select Host Species
Introduce DNA Sequences Into Host Species
Select Edited Cells And Assay Phenotypes
Apply Cells, Protein, Or Metabolites To Food Products

Fig. 1

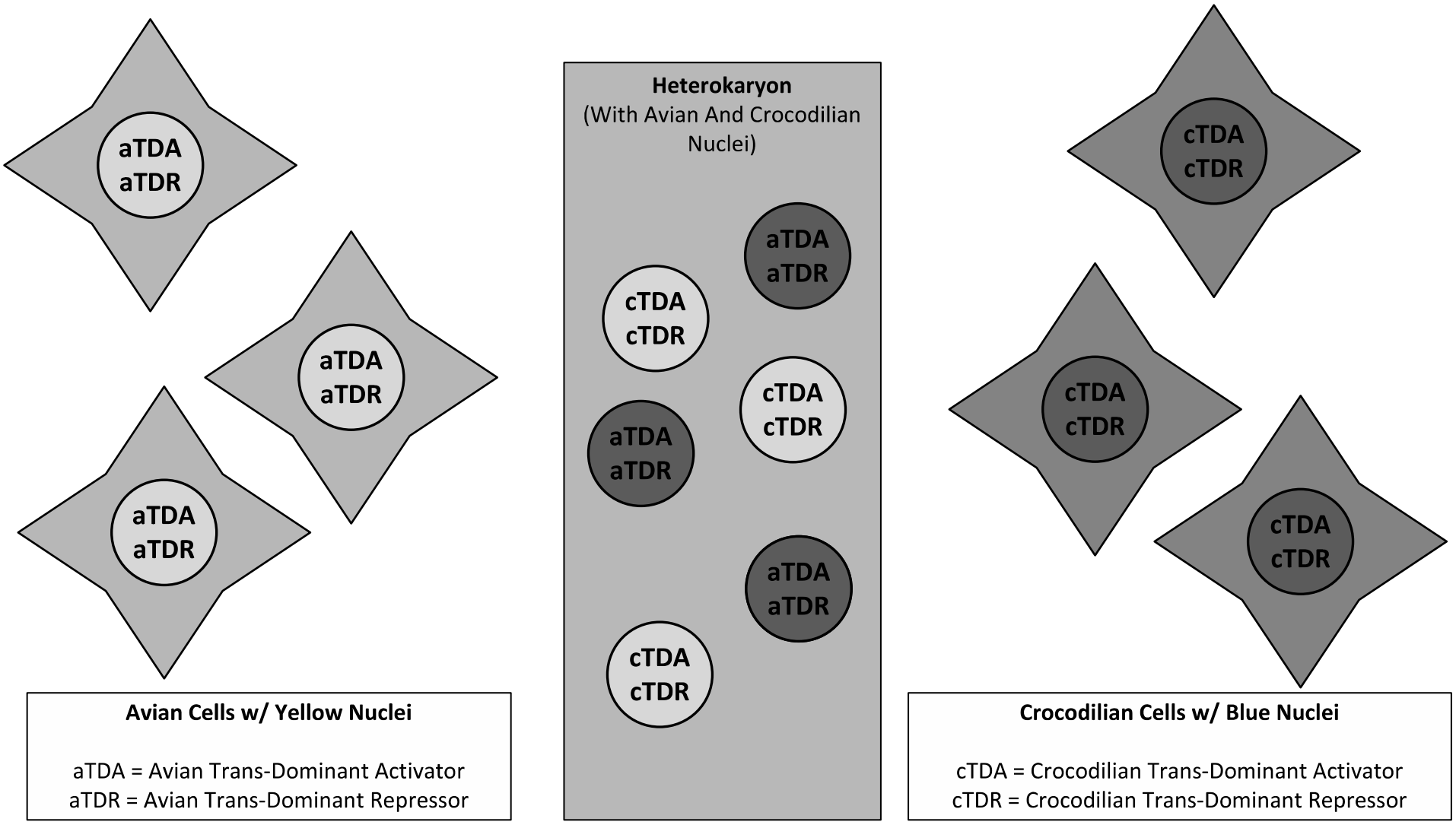

aTDA
aTDR
aTDA
aTDR
aTDA
aTDR
Avian Cells w/ Yellow Nuclei
aTDA = Avian Trans-Dominant Activator
aTDR = Avian Trans-Dominant Repressor
Heterokaryon
(With Avian And Crocodilian Nuclei)
aTDA
aTDR
cTDA
cTDR
cTDA
cTDR
aTDA
aTDR
aTDA
aTDR
cTDA
cTDR
cTDA
cTDR
cTDA
cTDR
cTDA
cTDR
Crocodilian Cells w/ Blue Nuclei
cTDA = Crocodilian Trans-Dominant Activator
cTDR = Crocodilian Trans-Dominant Repressor

Fig. 2

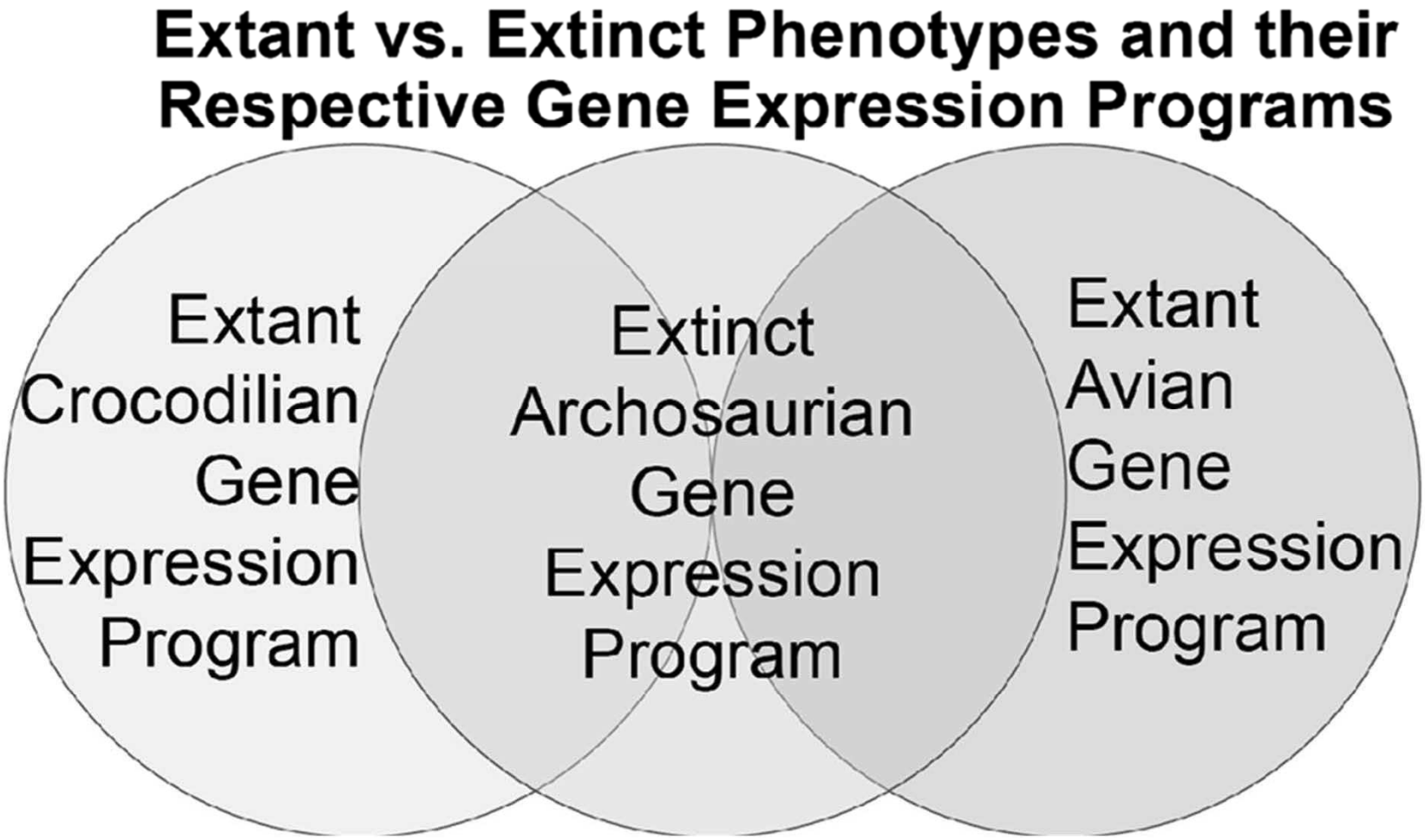
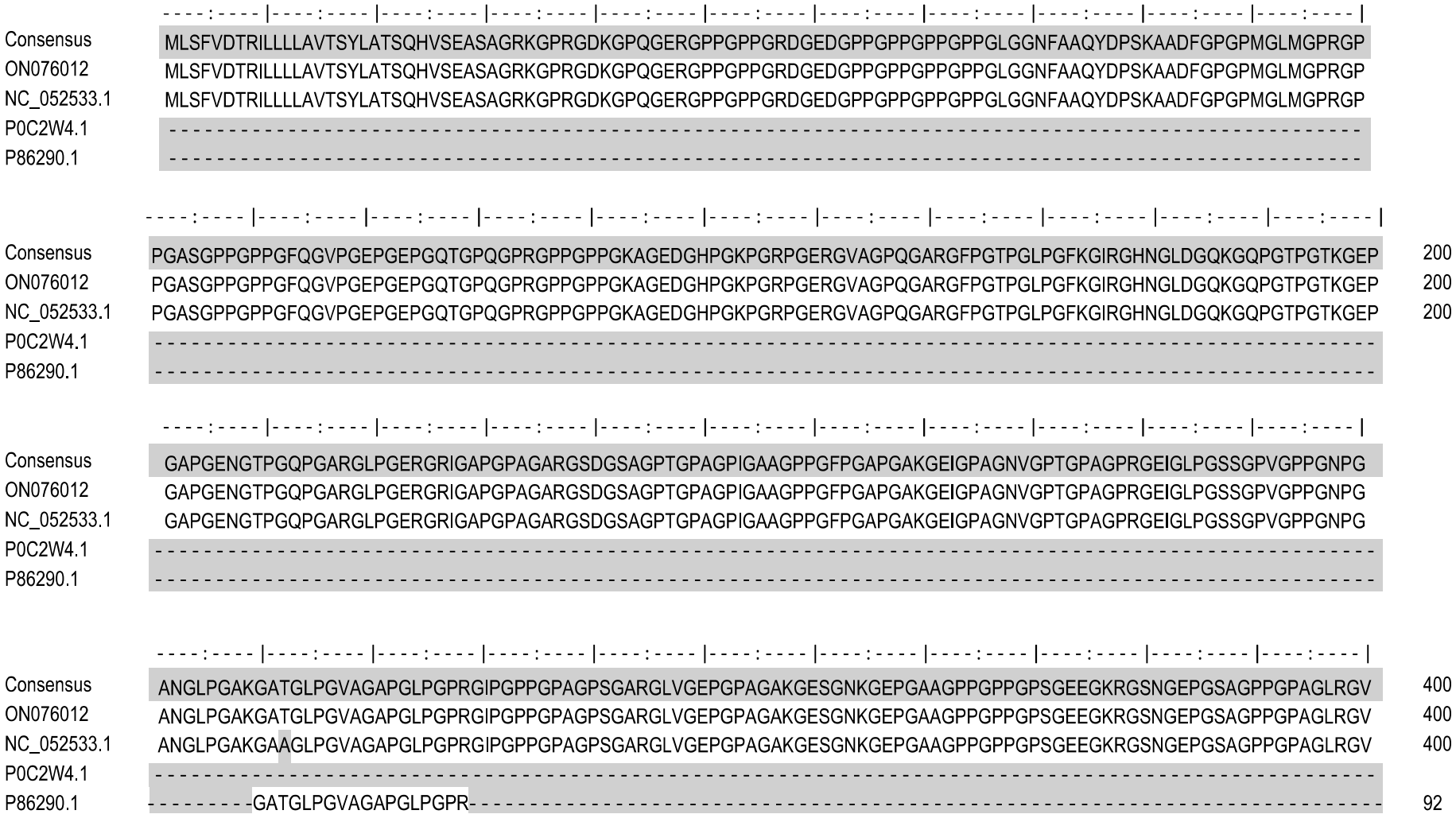

Extant vs. Extinct Phenotypes and their Respective Gene Expression Programs
Extant Crocodilian Gene Expression Program
Extinct Archosaurian Gene Expression Program
Extant Avian Gene Expression Program

Fig. 3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P0C2W4.1
P86290.1
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GAPGENGTPGQPGARGLPGERGRIGAPGPAGARGSDGSAGPTGPAGPIGAAGPPGFPGAPGAKGEIGPAGNVGPTGPAGPRGEIGLPGSSGPVGPPGNPG
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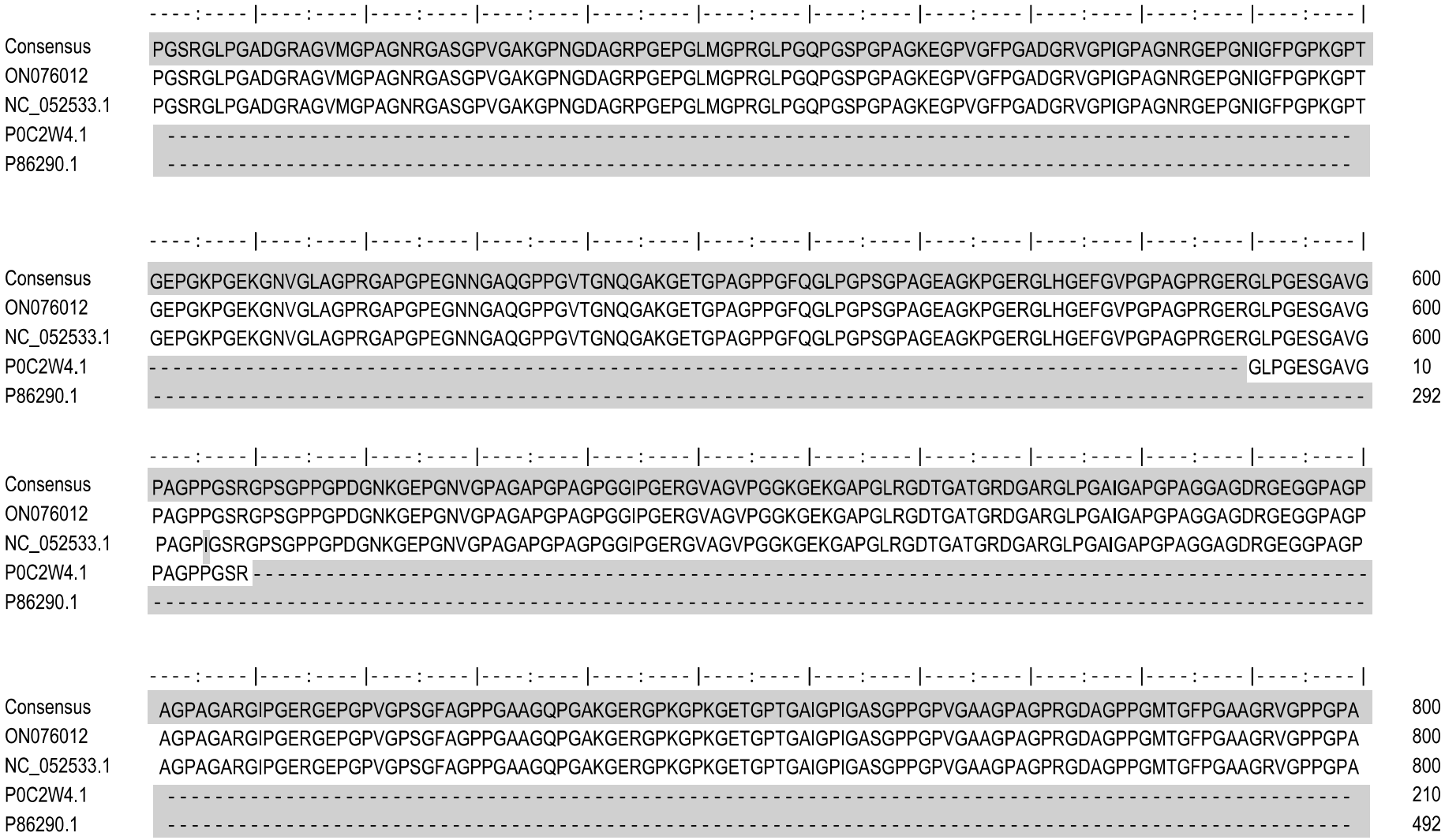
200
200
400
400
400
92

Fig. 4A-1

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ON076012         PGSRGLPGADGRAGVMGPAGNRGASGPVGAKGPNGDAGRPGEPGLMGPRGLPGQPGSPGPAGKEGPVGFPGADGRVGPIGPAGNRGEPGNIGFPGPKGPT
NC_052533.1      PGSRGLPGADGRAGVMGPAGNRGASGPVGAKGPNGDAGRPGEPGLMGPRGLPGQPGSPGPAGKEGPVGFPGADGRVGPIGPAGNRGEPGNIGFPGPKGPT
P0C2W4.1         ------------------------------------------------------------------------------------------------------
P86290.1         ------------------------------------------------------------------------------------------------------

                 ----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|
Consensus        GEPGKPGEKGNVGLAGPRGAPGPEGNNGAQGPPGVTGNQGAKGETGPAGPPGFQGLPGPSGPAGEAGKPGERGLHGEFGVPGPAGPRGERGLPGESGAVG   600
ON076012         GEPGKPGEKGNVGLAGPRGAPGPEGNNGAQGPPGVTGNQGAKGETGPAGPPGFQGLPGPSGPAGEAGKPGERGLHGEFGVPGPAGPRGERGLPGESGAVG   600
NC_052533.1      GEPGKPGEKGNVGLAGPRGAPGPEGNNGAQGPPGVTGNQGAKGETGPAGPPGFQGLPGPSGPAGEAGKPGERGLHGEFGVPGPAGPRGERGLPGESGAVG   600
P0C2W4.1         ------------------------------------------------------------------------------------------GLPGESGAVG   10
P86290.1         ------------------------------------------------------------------------------------------------------   292

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ON076012         PAGPPGSRGPSGPPGPDGNKGEPGNVGPAGAPGPAGPGGIPGERGVAGVPGGKGEKGAPGLRGDTGATGRDGARGLPGAIGAPGPAGGAGDRGEGGPAGP
NC_052533.1      PAGPIGSRGPSGPPGPDGNKGEPGNVGPAGAPGPAGPGGIPGERGVAGVPGGKGEKGAPGLRGDTGATGRDGARGLPGAIGAPGPAGGAGDRGEGGPAGP
P0C2W4.1         PAGPPGSR------------------------------------------------------------------------------------------
P86290.1         ------------------------------------------------------------------------------------------------------

                 ----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|
Consensus        AGPAGARGIPGERGEPGPVGPSGFAGPPGAAGQPGAKGERGPKGPKGETGPTGAIGPIGASGPPGPVGAAGPAGPRGDAGPPGMTGFPGAAGRVGPPGPA   800
ON076012         AGPAGARGIPGERGEPGPVGPSGFAGPPGAAGQPGAKGERGPKGPKGETGPTGAIGPIGASGPPGPVGAAGPAGPRGDAGPPGMTGFPGAAGRVGPPGPA   800
NC_052533.1      AGPAGARGIPGERGEPGPVGPSGFAGPPGAAGQPGAKGERGPKGPKGETGPTGAIGPIGASGPPGPVGAAGPAGPRGDAGPPGMTGFPGAAGRVGPPGPA   800
P0C2W4.1         ------------------------------------------------------------------------------------------------------   210
P86290.1         ------------------------------------------------------------------------------------------------------   492
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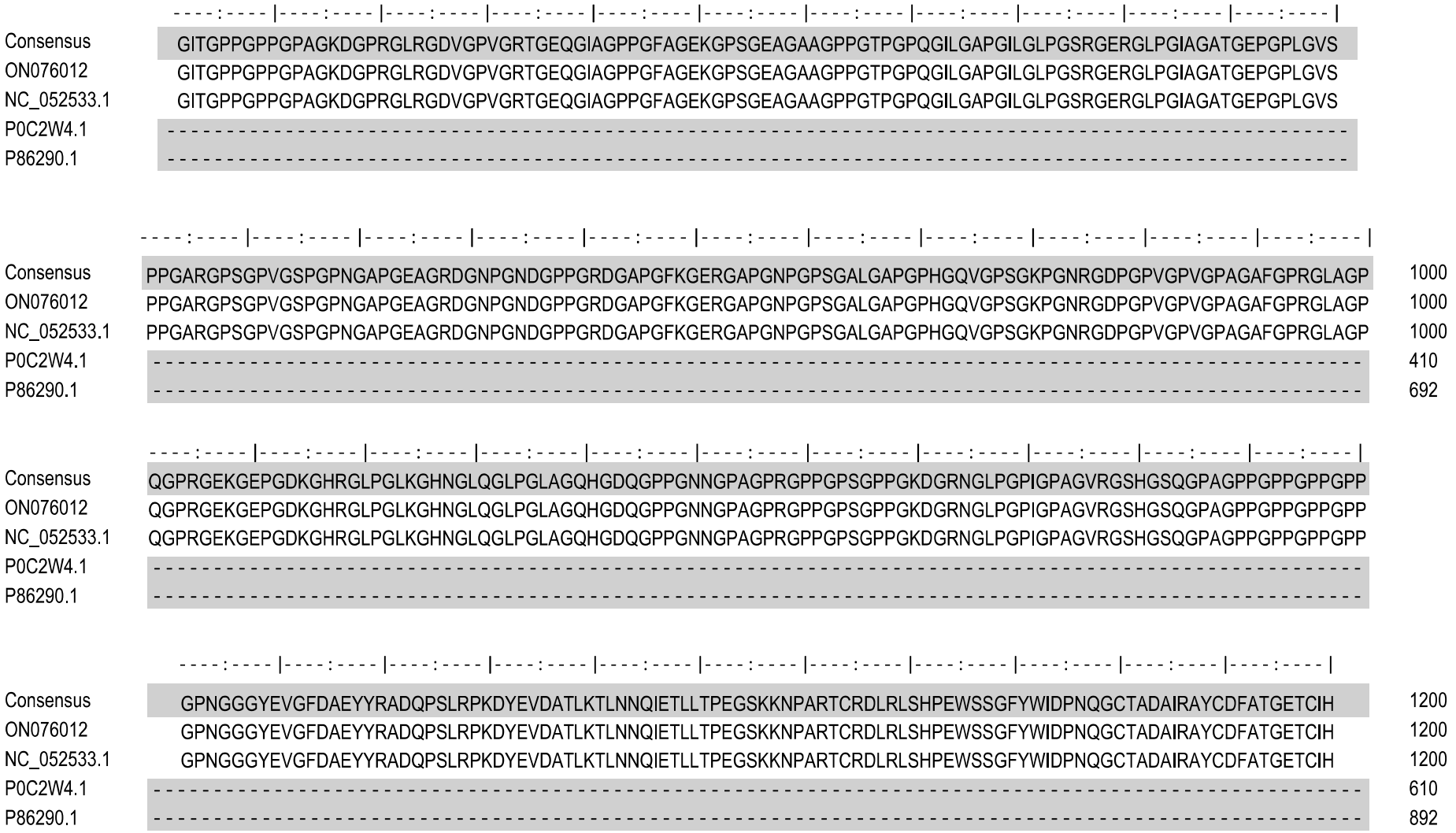
Fig. 4A-2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NC_052533.1 GITGPPGPPGPAGKDGPRGLRGDVGPVGRTGEQGIAGPPGFAGEKGPSGEAGAAGPPGTPGPQGILGAPGILGLPGSRGERGLPGIAGATGEPGPLGVS
P0C2W4.1
P86290.1
Consensus PPGARGPSGPVGSPGPNGAPGEAGRDGNPGNDGPPGRDGAPGFKGERGAPGNPGPSGALGAPGPHGQVGPSGKPGNRGDPGPVGPVGPAGAFGPRGLAGP 1000
ON076012 PPGARGPSGPVGSPGPNGAPGEAGRDGNPGNDGPPGRDGAPGFKGERGAPGNPGPSGALGAPGPHGQVGPSGKPGNRGDPGPVGPVGPAGAFGPRGLAGP 1000
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P0C2W4.1 410
P86290.1 692
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NC_052533.1 QGPRGEKGEPGDKGHRGLPGLKGHNGLQGLPGLAGQHGDQGPPGNNGPAGPRGPPGPSGPPGKDGRNGLPGPIGPAGVRGSHGSQGPAGPPGPPGPPGPP
P0C2W4.1
P86290.1
Consensus GPNGGGYEVGFDAEYYRADQPSLRPKDYEVDATLKTLNNQIETLLTPEGSKKNPARTCRDLRLSHPEWSSGFYWIDPNQGCTADAIRAYCDFATGETCIH 1200
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NC_052533.1 GPNGGGYEVGFDAEYYRADQPSLRPKDYEVDATLKTLNNQIETLLTPEGSKKNPARTCRDLRLSHPEWSSGFYWIDPNQGCTADAIRAYCDFATGETCIH 1200
P0C2W4.1 610
P86290.1 892

Fig. 4A-3


Consensus
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NC_052533.1
P0C2W4.1
P86290.1
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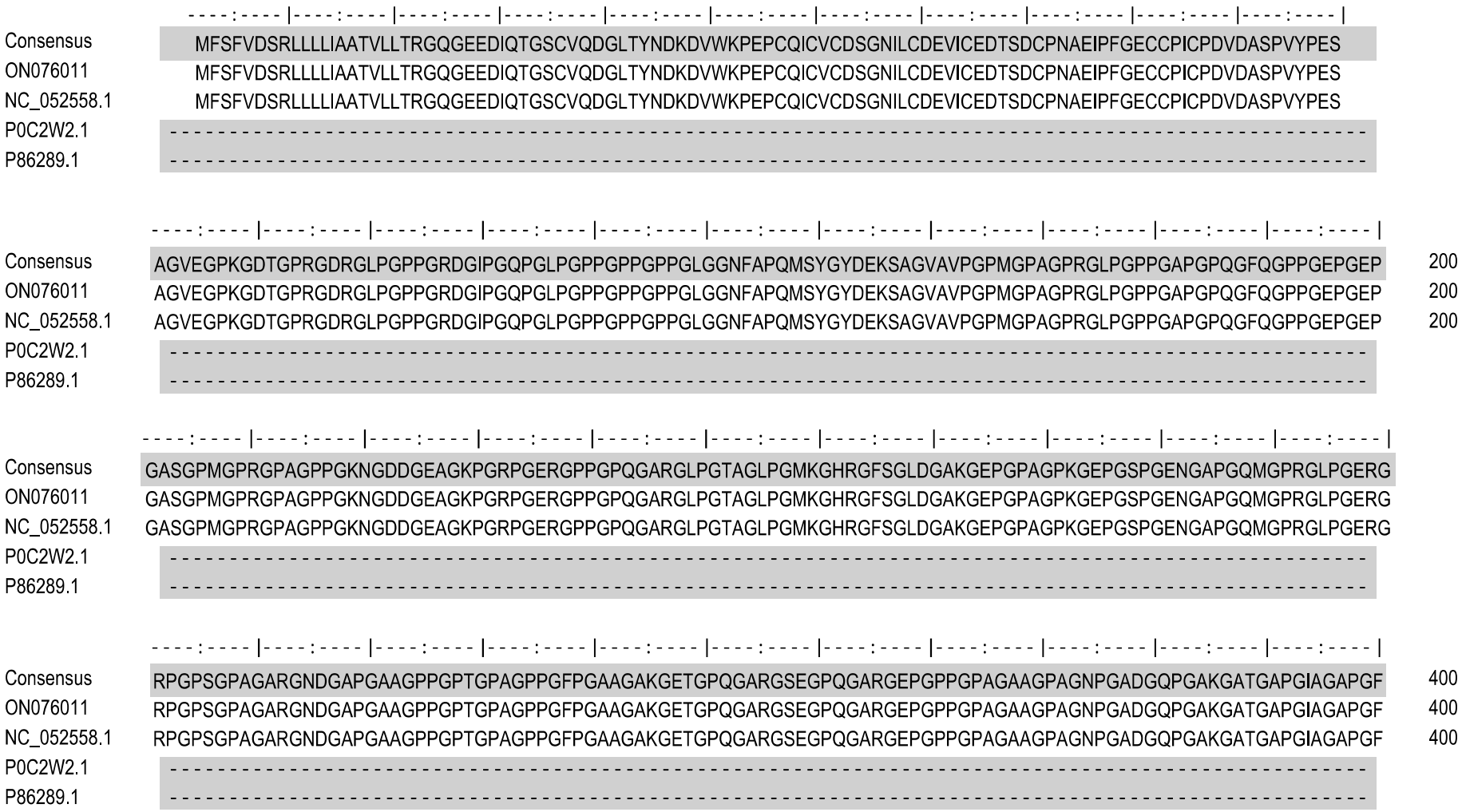
1363
18

Fig. 4A-4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P86289.1
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200
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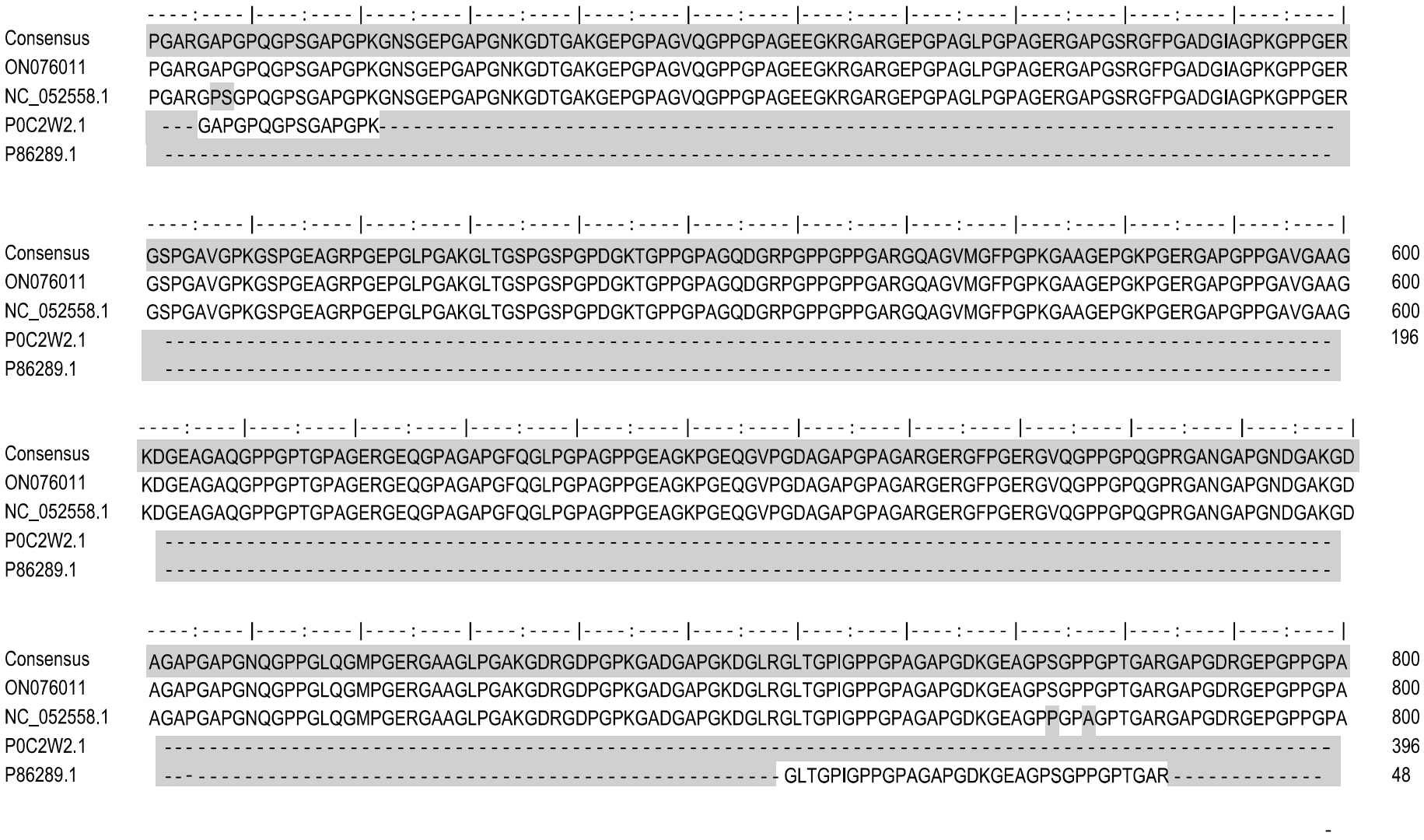
Fig. 4B-1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P0C2W2.1 GAPGPQGPSGAPGPK
P86289.1
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ON076011 GSPGAVGPKGSPGEAGRPGEPGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKPGERGAPGPPGAVGAAG 600
NC_052558.1 GSPGAVGPKGSPGEAGRPGEPGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKPGERGAPGPPGAVGAAG 600
P0C2W2.1 196
P86289.1
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P0C2W2.1
P86289.1
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NC_052558.1 AGAPGAPGNQGPPGLQGMPGERGAAGLPGAKGDRGDPGPKGADGAPGKDGLRGLTGPIGPPGPAGAPGDKGEAGPPGPAGPTGARGAPGDRGEPGPPGPA 800
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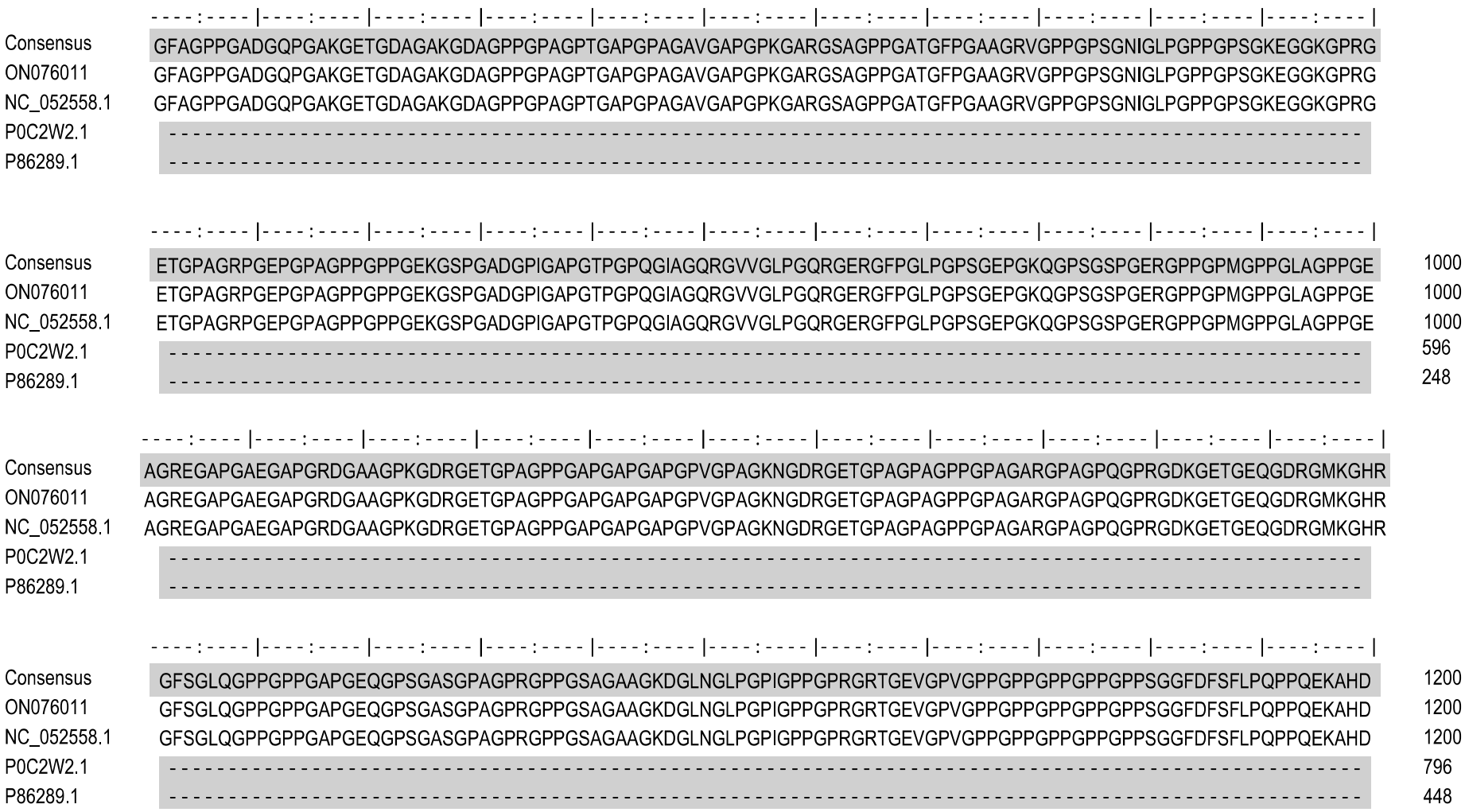
P86289.1 GLTGPIGPPGPAGAPGDKGEAGPSGPPGPTGAR 48

Fig. 4B-2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P86289.1
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1200
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1200
796
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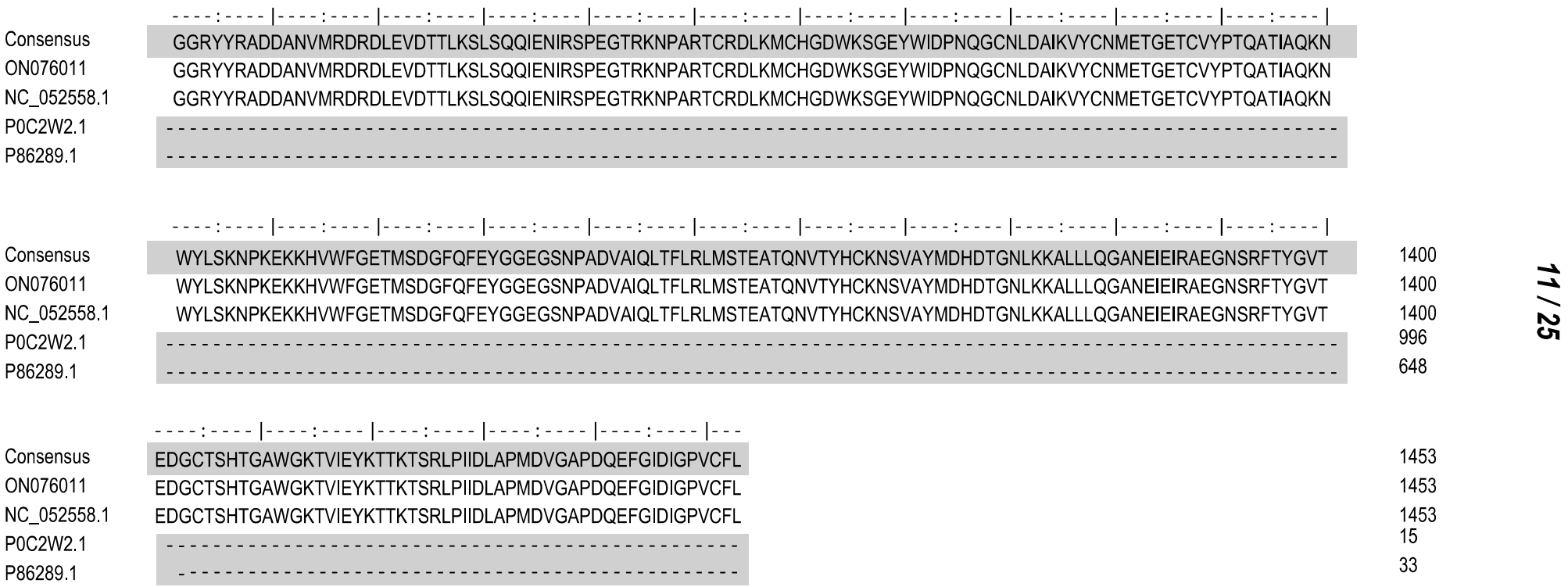
Fig. 4B-3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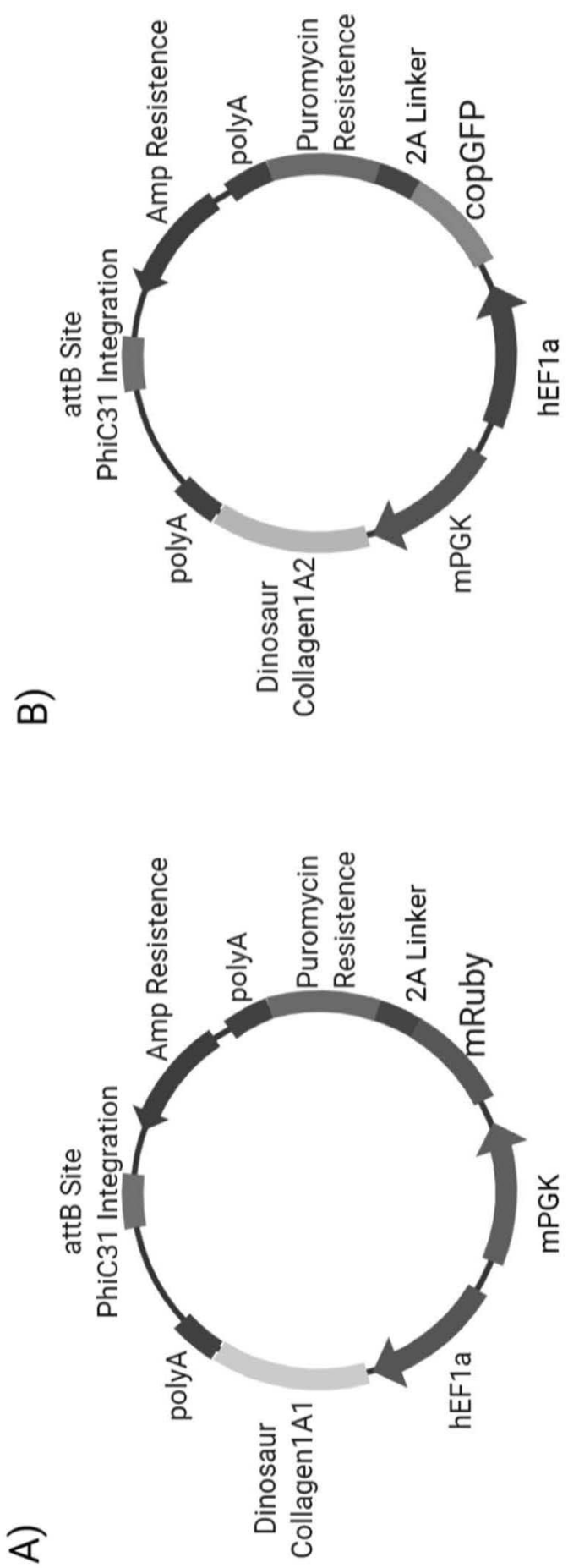
648
15
33

Fig. 4B-4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attB Site
PhiC31 Integration
Amp Resistence
polyA
Puromycin
Resistence
2A Linker
mRuby
mPGK
hEF1a
polyA
Dinosaur
Collagen1A1
B)
attB Site
PhiC31 Integration
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Resistence
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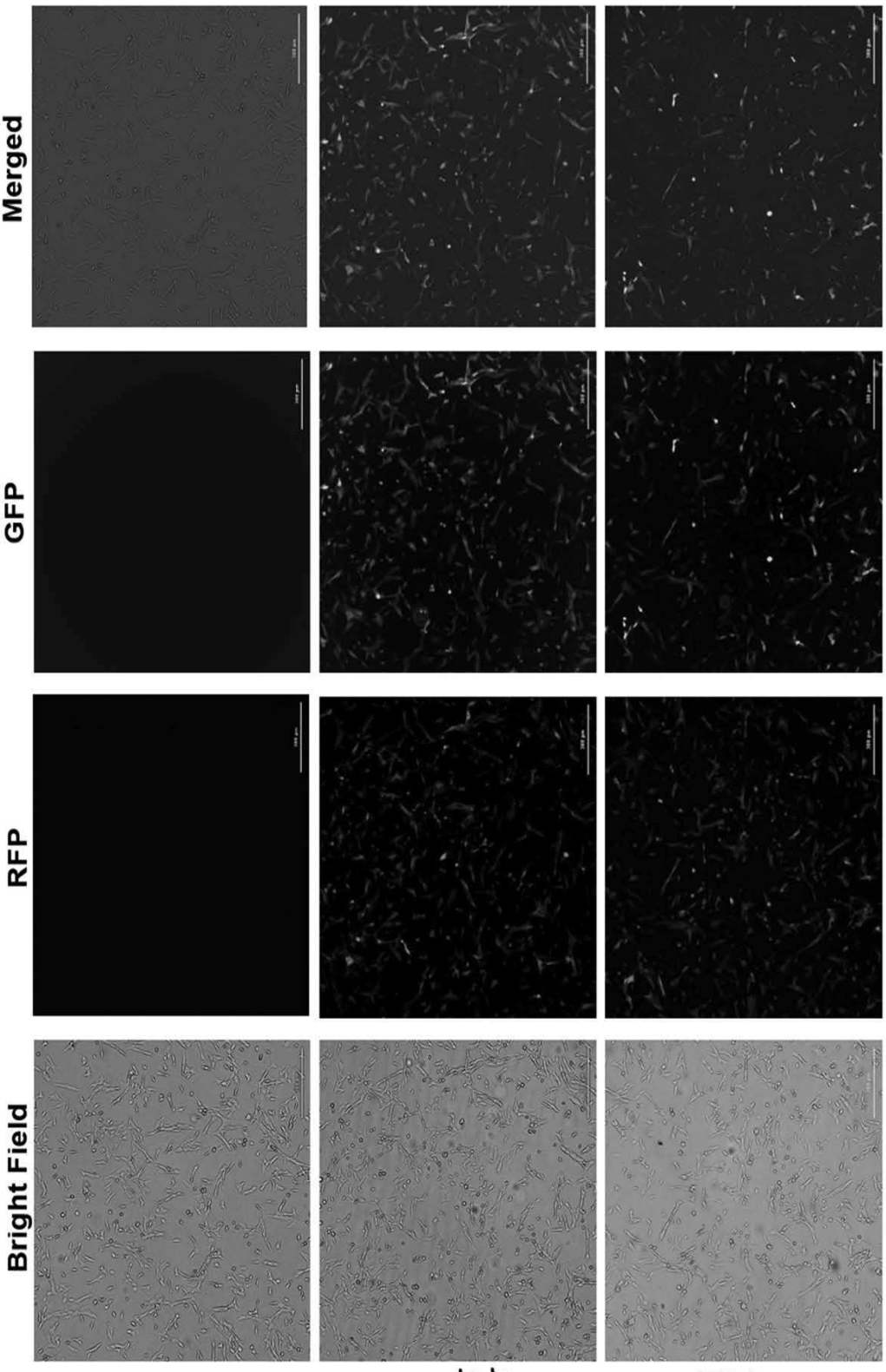
copGFP
hEF1a
mPGK
polyA
Dinosaur
Collagen1A2

Fig. 5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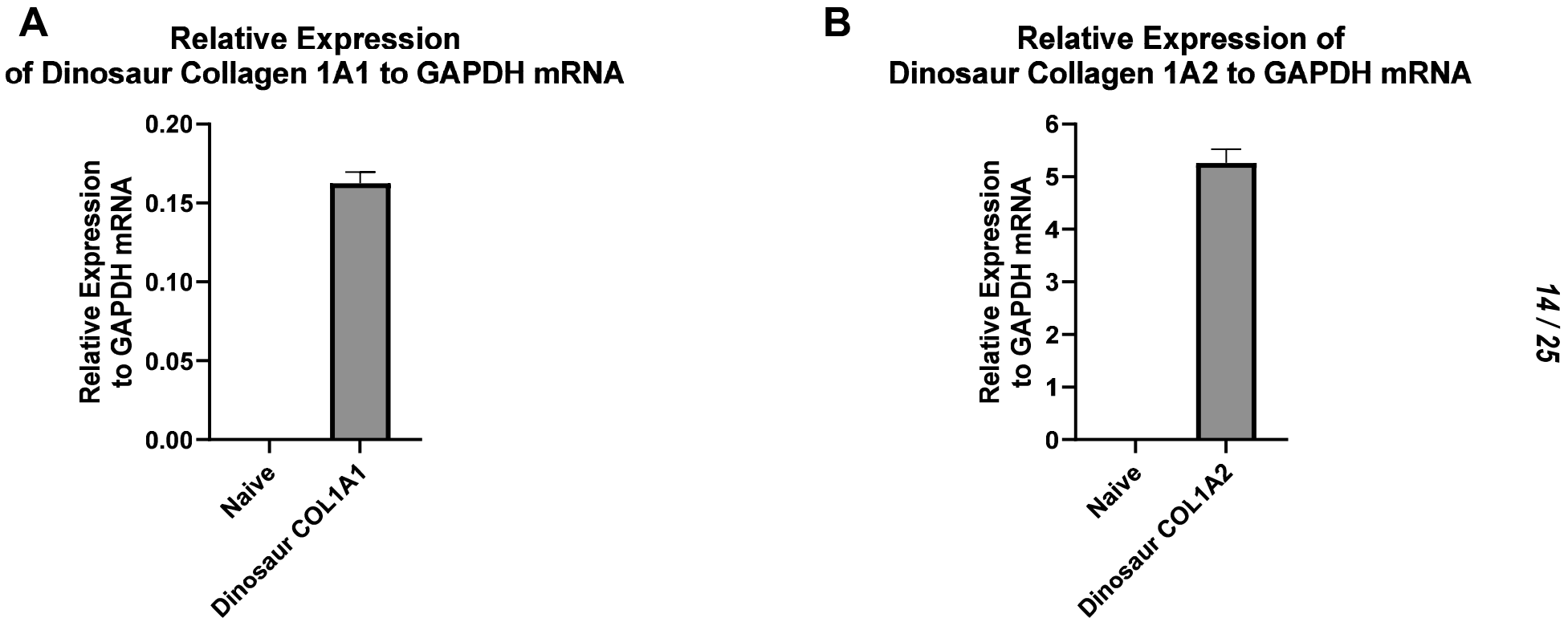
RFP
GFP
Merged
Naive
Empty Vectors
RFP-Empty Vector
GFP-Empty Vector
Dinosaur
Collagen1A1[RFP]
Collagen1A2[GFP]

Fig. 6


A
Relative Expression
of Dinosaur Collagen 1A1 to GAPDH mRNA
Relative Expression
to GAPDH mRNA
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0.15
0.10
0.05
0.00
Naive
Dinosaur COL1A1
B
Relative Expression of
Dinosaur Collagen 1A2 to GAPDH mRNA
Relative Expression
to GAPDH mRNA
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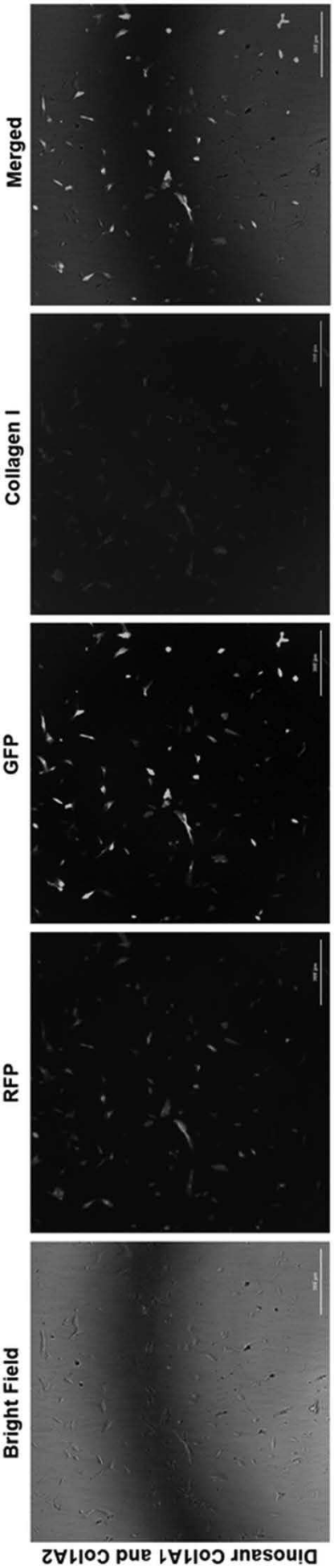
5
4
3
2
1
0
Naive
Dinosaur COL1A2

Fig. 7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Bright Field
RFP
GFP
Collagen I
Merged

Fig. 8


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ON076013 MSSDSEMAVFGEAAPYLRKPEKERTEAQNRPFDSKKACFAVDDKEVYVKGMIQNRENDKVTVKTLDDRTITLNTAQVFPMNPPKFDKIEDMAMMTHLHEP
XP_003416837.1 MSSDSEMAVFGEAAPYLRKPEKERTEAQNRPFDSKKACFAVDDKEVYVKGMIQNRENDKVTVKTLDDRTITLNTAQVFPMNPPKFDKIEDMAMMTHLHEP
Consensus AVLYNLKERYAAWMIYTYSGLFCVTVNPYKWLPVYNPEVVMAYRGKKRQEAPPHIFSISDNAYQFMLTDRDNQSILITGESGAGKTVNTKRVIQYFATIA 200
ON076013 AVLYNLKERYAAWMIYTYSGLFCVTVNPYKWLPVYNPEVVMAYRGKKRQEAPPHIFSISDNAYQFMLTDRDNQSILITGESGAGKTVNTKRVIQYFATIA 200
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ON076013 VPGDKKKEPQTGKMQGTLEDQIIQANPLLEAFGNAKTVRNDNSSRFGKFIRIHFGATGKLASADIETYLLEKSRVTFQLSSERSYHIFYQIMSNKKPELI
XP_003416837.1 VPGDKKKEPQTGKMQGTLEDQIIQANPLLEAFGNAKTVRNDNSSRFGKFIRIHFGATGKLASADIETYLLEKSRVTFQLSSERSYHIFYQIMSNKKPELI
Consensus DLLLISTNPFDFPFISQGEVTVASIDDSEELLATDNAIDILGFSSEEKVGIYKLTGAVMHYGNMKFKQKQREEQAEPDGTEVADKAGYLMGLNSAEMLKG 400
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XP_003416837.1 LCCPRVKVGNEYVTKGQNVQQVTNSVGALAKAVYEKMFLWMVARINQQLDTKQARQYFIGVLDIAGFEIFDFNSLEQLCINFTNEKLQQFFNHHMFVLEQ
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XP_003416837.1 EEYKKEGIEWEFIDFGMDLAACIELIEKPMGIFSILEEECMFPKATDTSFKNKLYDQHLGKSANFQKPKPTKGKAEAHFSLVHYAGTVDYNIVGWLDKNK 600

Fig. 9A


Consensus DPLNETVVGLYQKSSLKLLAFLFSNYAGAEAGDCGGSKKGGKKKGSSFQTVSAVFRENLNKLMTNLRSTHPHFVRCLIPNETKTPGVMDHYLVIHQLRCN
ON076013 DPLNETVVGLYQKSSLKLLAFLFSNYAGAEAGDCGGSKKGGKKKGSSFQTVSAVFRENLNKLMTNLRSTHPHFVRCLIPNETKTPGVMDHYLVIHQLRCN
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Consensus GVLEGIRICRKGFPSRILYGDFRQRYRILNASAIPEGQFIDSKNASEKLLNSINVDREQYRFGHTKVFFKAGLLGLLEEMRDEKLATLMTRTQAVCRGYL 800
ON076013 GVLEGIRICRKGFPSRILYGDFRQRYRILNASAIPEGQFIDSKNASEKLLNSINVDREQYRFGHTKVFFKAGLLGLLEEMRDEKLATLMTRTQAVCRGYL 800
XP_003416837.1 GVLEGIRICRKGFPSRILYGDFRQRYRILNASAIPEGQFIDSKNASEKLLNSINVDREQYRFGHTKVFFKAGLLGLLEEMRDEKLATLMTRTQAVCRGYL 800
Consensus MRVEFKKMMERRDSILCIQDNIRSFMNVKHWPWMNLFFKIQPLLKSAEAEKEMATMKENFKRAQEELARSEARRKELEEKMVSLLQEKNDLQLQVQSETE
ON076013 MRVEFKKMMERRDSILCIQDNIRSFMNVKHWPWMNLFFKIQPLLKSAEAEKEMATMKENFKRAQEELARSEARRKELEEKMVSLLQEKNDLQLQVQSETE
XP_003416837.1 MRVEFKKMMERRDSILCIQDNIRSFMNVKHWPWMNLFFKIQPLLKSAEAEKEMATMKENFKRAQEELARSEARRKELEEKMVSLLQEKNDLQLQVQSETE
Consensus NLMDAEERCEGLIKSKIQLEAKVKELNEKLEEEEEINSELVAKKRNLEDKCFSLKKDIDDLELTLTKVEKEKHATENKVKNLSEEMTALEENISKLTKEK 1000
ON076013 NLMDAEERCEGLIKSKIQLEAKVKELNEKLEEEEEINSELVAKKRNLEDKCFSLKKDIDDLELTLTKVEKEKHATENKVKNLSEEMTALEENISKLTKEK 1000
XP_003416837.1 NLMDAEERCEGLIKSKIQLEAKVKELNEKLEEEEEINSELVAKKRNLEDKCFSLKKDIDDLELTLTKVEKEKHATENKVKNLSEEMTALEENISKLTKEK 1000
Consensus KSLQEAHQQTLDGLQVEEDKVNGLIKINAKLEQQTDDLEGCLEQEKKLRADLGRLKRKLEGDLKISQESITDLENAQQQMEEKLKKKEFEISQLQTKIDG
ON076013 KSLQEAHQQTLDGLQVEEDKVNGLIKINAKLEQQTDDLEGCLEQEKKLRADLGRLKRKLEGDLKISQESITDLENAQQQMEEKLKKKEFEISQLQTKIDG
XP_003416837.1 KSLQEAHQQTLDGLQVEEDKVNGLIKINAKLEQQTDDLEGCLEQEKKLRADLGRLKRKLEGDLKISQESITDLENAQQQMEEKLKKKEFEISQLQTKIDG
Consensus EQVHSLQLQKKIKELQARTEELEEDIEAEHTLRAKLERQRSDLARELEEISERLEEASGATSAQVELNKKREAEFQKMRRDLEEATLQHEATAATLRKKH 1200
ON076013 EQVHSLQLQKKIKELQARTEELEEDIEAEHTLRAKLERQRSDLARELEEISERLEEASGATSAQVELNKKREAEFQKMRRDLEEATLQHEATAATLRKKH 1200
XP_003416837.1 EQVHSLQLQKKIKELQARTEELEEDIEAEHTLRAKLERQRSDLARELEEISERLEEASGATSAQVELNKKREAEFQKMRRDLEEATLQHEATAATLRKKH 1200

Fig. 9B


Consensus ADSVAELGEQIDNLQRVKQKLQKEKSELKMEMDDMASNIETITKSKSNMERMCRTMEDQFNELKAKDDQQTQLIHDLNMQKARLQTQNGELSHQVEEKES
ON076013 ADSVAELGEQIDNLQRVKQKLQKEKSELKMEMDDMASNIETITKSKSNMERMCRTMEDQFNELKAKDDQQTQLIHDLNMQKARLQTQNGELSHQVEEKES
XP_003416837.1 ADSVAELGEQIDNLQRVKQKLQKEKSELKMEMDDMASNIETITKSKSNMERMCRTMEDQFNELKAKDDQQTQLIHDLNMQKARLQTQNGELSHQVEEKES
Consensus LISQLXKGKQALTQQLEELKRQLEEETKAKNALAHALQSSRHDCDLLREQYEEEQEGKAEVQRALSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQR 1400
ON076013 LISQLSKGKQALTQQLEELKRQLEEETKAKNALAHALQSSRHDCDLLREQYEEEQEGKAEVQRALSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQR 1400
XP_003416837.1 LISQLTKGKQALTQQLEELKRQLEEETKAKNALAHALQSSRHDCDLLREQYEEEQEGKAEVQRALSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQR 1400
Consensus LQEAEENTEAVNSKCASLEKTKQRLQGEVDDLMLDLERANTTCATLGKKQRNFDKILADWKQKLDESHAELEAAQKESRSLSTEIFKMKNAYEEVVDQLE
ON076013 LQEAEENTEAVNSKCASLEKTKQRLQGEVDDLMLDLERANTTCATLGKKQRNFDKILADWKQKLDESHAELEAAQKESRSLSTEIFKMKNAYEEVVDQLE
XP_003416837.1 LQEAEENTEAVNSKCASLEKTKQRLQGEVDDLMLDLERANTTCATLGKKQRNFDKILADWKQKLDESHAELEAAQKESRSLSTEIFKMKNAYEEVVDQLE
Consensus TLRRENKNLQEEIHDVTEQIAETGKNLQEMEKTKKQVEQEKSDLQVALEEVEGSLEHEESKILRVQLELSQLKSELDRKVAEKDEEMEQLKRNCQRAAEA 1600
ON076013 TLRRENKNLQEEIHDVTEQIAETGKNLQEMEKTKKQVEQEKSDLQVALEEVEGSLEHEESKILRVQLELSQLKSELDRKVAEKDEEMEQLKRNCQRAAEA 1600
XP_003416837.1 TLRRENKNLQEEIHDVTEQIAETGKNLQEMEKTKKQVEQEKSDLQVALEEVEGSLEHEESKILRVQLELSQLKSELDRKVAEKDEEMEQLKRNCQRAAEA 1600
Consensus TQSLLEAESRSRKDALRLKKKMEGDLNEMEVHLGHANRQVAETQKHLRTVQGQLKGSQLHLGDALRSBEALKERLAIVGRRNGLLVEELEETKVALEQAE
ON076013 TQSLLEAESRSRKDALRLKKKMEGDLNEMEVHLGHANRQVAETQKHLRTVQGQLKGSQLHLGDALRSDEALKERLAIVGRRNGLLVEELEETKVALEQAE
XP_003416837.1 TQSLLEAESRSRKDALRLKKKMEGDLNEMEVHLGHANRQVAETQKHLRTVQGQLKGSQLHLGDALRSNEALKERLAIVGRRNGLLVEELEETKVALEQAE
Consensus RSRRLSEQELQDASDRVQLLLSRCNTSLINIKKKLETNIAQCQAEVENSVQESRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNLEQTVKDMQH 1800
ON076013 RSRRLSEQELQDASDRVQLLLSRCNTSLINIKKKLETNIAQCQAEVENSVQESRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNLEQTVKDMQH 1800
XP_003416837.1 RSRRLSEQELQDASDRVQLLLSRCNTSLINIKKKLETNIAQCQAEVENSVQESRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNLEQTVKDMQH 1800

Fig. 9C

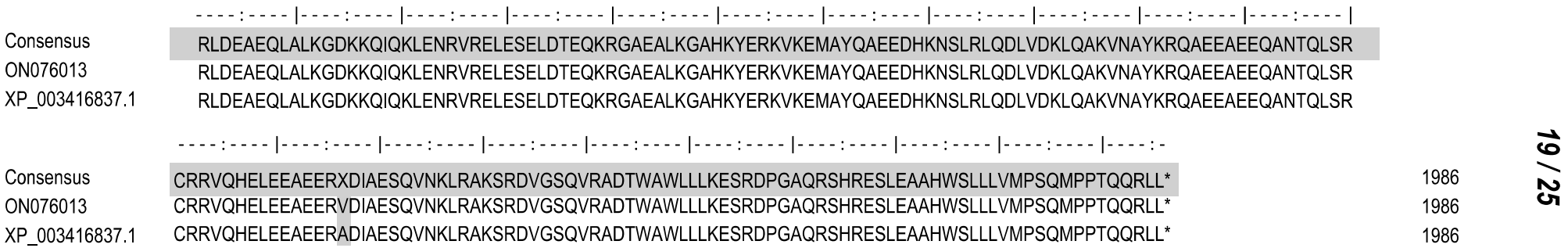
Consensus RLDEAEQLALKGDKKQIQKLENRVRELESELDTEQKRGAEALKGAHKYERKVKEMAYQAEEDHKNSLRLQDLVDKLQAKVNAYKRQAEEAEEQANTQLSR
ON076013 RLDEAEQLALKGDKKQIQKLENRVRELESELDTEQKRGAEALKGAHKYERKVKEMAYQAEEDHKNSLRLQDLVDKLQAKVNAYKRQAEEAEEQANTQLSR
XP_003416837.1 RLDEAEQLALKGDKKQIQKLENRVRELESELDTEQKRGAEALKGAHKYERKVKEMAYQAEEDHKNSLRLQDLVDKLQAKVNAYKRQAEEAEEQANTQLSR
Consensus CRRVQHELEEAEERXDIAESQVNKLRAKSRDVGSQVRADTWAWLLLKESRDPGAQRSHRESLEAAHWSLLLVMPSQMPPTQQRLL* 1986
ON076013 CRRVQHELEEAEERVDIAESQVNKLRAKSRDVGSQVRADTWAWLLLKESRDPGAQRSHRESLEAAHWSLLLVMPSQMPPTQQRLL* 1986
XP_003416837.1 CRRVQHELEEAEERADIAESQVNKLRAKSRDVGSQVRADTWAWLLLKESRDPGAQRSHRESLEAAHWSLLLVMPSQMPPTQQRLL* 1986

Fig. 9D

ATGAGCAGCG ACAGCGAGAT GGCCGTGTTC GGCGAGGCCG CCCCCTACCT GAGAAAGCCC GAAAAAGAAA GAACGGAGGC TCAGAACAGA CCCTTCGACA GCAAAAAGGC CTGCTTCGCC GTGGACGACA
AAGAGGTGTA CGTGAAGGGC ATGATTCAGA ACAGAGAGAA CGACAAGGTG ACCGTGAAAA CCCTTGACGA TCGTACCATC ACCCTGAACA CCGCCCAAGT GTTCCCCATG AACCCCCCCA AGTTCGATAA
GATCGAAGAC ATGGCCATGA TGACCCACCT GCACGAGCCC GCCGTGCTGT ACAACCTGAA GGAAAGATAC GCTGCCTGGA TGATCTACAC CTACAGCGGC CTGTTCTGCG TGACCGTGAA CCCCTACAAG
TGGCTGCCCG TGTACAACCC CGAGGTGGTG ATGGCCTACA GAGGCAAGAA GAGACAAGAG GCCCCCCCCC ACATCTTTAG CATTAGCGAC AACGCCTATC AGTTCATGCT GACCGACAGA GACAATCAGA
GCATCCTGAT CACCGGCGAG AGCGGCGCCG GCAAGACCGT GAACACCAAG AGAGTGATTC AGTACTTCGC CACCATCGCC GTGCCCGGCG ACAAAAAAAA AGAACCGCAA ACGGGCAAGA TGCAAGGCAC
CCTGGAGGAT CAGATCATCC AAGCCAACCC CCTACTGGAG GCCTTCGGCA ACGCCAAGAC CGTGAGAAAC GACAACAGCA GCAGATTCGG CAAGTTCATC AGAATCCACT TCGGCGCCAC CGGCAAGCTG
GCTAGCGCCG ACATCGAGAC CTACCTGCTG GAGAAGAGCA GAGTGACCTT CCAACTAAGC TCCGAGAGAA GCTACCACAT CTTCTATCAG ATCATGAGCA ACAAGAAGCC CGAACTGATC GATTTACTGC
TGATCAGCAC CAACCCCTTC GACTTCCCCT TCATCAGCCA AGGCGAAGTA ACCGTGGCTA GCATCGACGA CAGCGAGGAG CTGCTGGCCA CCGACAACGC CATCGACATC CTGGGCTTCA GCAGCGAGGA
GAAGGTGGGC ATCTACAAGC TGACCGGCGC CGTGATGCAC TACGGCAACA TGAAGTTCAA GCAAAAACAG AGAGAGGAGC AAGCTGAGCC TGATGGCACC GAGGTGGCCG ACAAGGCCGG CTACCTGATG
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TCCATCAGCT GAGATGCAAC GGTGTTCTGG AGGGTATCAG AATCTGCAGA AAGGGCTTCC CAAGCAGAAT CCTGTACGGC GACTTCAGAC AGAGATACAG AATCCTGAAC GCTAGCGCCA TCCCCGAGGG
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GCTTCATGAA CGTGAAGCAC TGGCCCTGGA TGAACCTGTT CTTCAAGATT CAGCCCCTGC TGAAGTCAGC GGAGGCGGAA AAGGAAATGG CCACCATGAA GGAGAACTTC AAGAGAGCCC AAGAGGAGCT
GGCTAGAAGC GAGGCTAGAA GAAAGGAGCT CGAGGAGAAG ATGGTGAGCC TGCTGCAAGA GAAGAACGAC CTGCAGCTGC AAGTCCAAAG CGAGACCGAG AACCTGATGG ATGCAGAGGA GCGATGTGAG
GGTCTGATTA AGTCCAAAAT TCAGCTGGAA GCCAAAGTGA AGGAACTGAA TGAGAAGCTA GAAGAGGAGG AAGAAATAAA CAGCGAGCTG GTGGCCAAGA AGCGCAACCT GGAGGACAAG TGCTTCAGCC

Fig. 10A

TGAAGAAGGA CATCGACGAT CTTGAGCTGA CCCTGACCAA GGTGGAGAAG GAGAAGCACG CCACCGAGAA CAAGGTGAAG AACCTGAGCG AGGAGATGAC CGCCCTGGAG GAAAACATTA GCAAGCTGAC
CAAAGAGAAG AAGTCGCTGC AAGAGGCTCA CCAACAGACT CTGGATGGCC TGCAAGTGGA GGAGGATAAA GTAAACGGCT TGATCAAGAT TAACGCAAAG TTGGAACAAC AGACCGACGA TCTGGAGGGC
TGCTTAGAAC AAGAAAAGAA GCTGAGAGCC GACCTGGGCA GACTGAAGAG AAAGCTGGAG GGCGACCTGA AGATAAGCCA AGAGAGCATC ACCGACCTGG AGAACGCTCA GCAGCAGATG GAGGAGAAGC
TGAAGAAGAA AGAATTTGAG ATCAGCCAAC TGCAGACCAA GATCGACGGC GAGCAAGTGC ACAGCCTTCA GTTACAAAAG AAGATCAAGG AGCTACAAGC TAGAACCGAG GAGCTTGAGG AAGACATCGA
AGCCGAACAC ACCCTGAGAG CGAAACTGGA GAGACAGAGA AGCGACCTGG CTAGAGAGCT GGAGGAAATC AGCGAGAGAC TCGAGGAGGC TAGCGGCGCC ACTTCCGCCC AAGTGGAGCT GAACAAGAAG
AGAGAGGCCG AGTTTCAGAA GATGAGAAGA GACCTGGAAG AGGCCACTCT GCAGCACGAG GCCACCGCCG CCACCCTGAG AAAGAAGCAC GCCGACAGCG TGGCCGAGCT GGGCGAGCAG ATCGACAACC
TGCAGAGAGT GAAGCAAAAA TTACAAAAAG AAAAGAGTGA GCTGAAAATG GAGATGGACG ACATGGCTAG CAACATCGAG ACCATCACCA AGAGCAAGAG CAACATGGAG AGAATGTGCA GAACCATGGA
GGATCAGTTC AACGAGCTGA AGGCCAAGGA CGATCAGCAG ACACAGCTGA TCCACGACCT GAACATGCAG AAGGCTAGAC TGCAGACACA GAACGGCGAG CTGAGCCACC AAGTGGAGGA GAAGGAAAGC
CTGATTTCTC AGCTGAGCAA GGGCAAGCAA GCCCTGACAC AGCAATTAGA GGAACTGAAG AGGCAGCTCG AGGAGGAGAC CAAGGCCAAA AACGCCCTGG CCCACGCCCT GCAGAGCAGC AGACACGACT
GCGACCTGCT GCGGGAGCAG TACGAGGAAG AGCAAGAGGG TAAGGCTGAG GTGCAGCGAG CCCTGAGCAA GGCCAACAGC GAGGTGGCTC AGTGGAGAAC CAAGTACGAG ACCGACGCCA TTCAGAGAAC
TGAAGAATTG GAGGAAGCGA AGAAGAAGCT CGCCCAACGA TTGCAAGAAG CCGAAGAGAA CACCGAGGCC GTGAACAGCA AGTGCGCTAG CCTGGAGAAG ACGAAGCAAA GACTACAAGG TGAGGTGGAT
GATCTGATGC TGGACCTGGA GAGAGCCAAC ACCACCTGCG CCACCCTGGG CAAGAAGCAG AGAAACTTCG ACAAAATCCT GGCTGACTGG AAGCAGAAGC TGGACGAGAG CCACGCCGAG CTGGAAGCCG
CTCAGAAGGA AAGCAGATCC TTAAGCACCG AGATCTTCAA GATGAAGAAC GCCTACGAAG AGGTGGTCGA TCAGCTGGAG ACCCTGAGAA GAGAGAACAA GAACCTTCAA GAGGAGATCC ACGACGTGAC
CGAGCAGATC GCCGAGACCG GTAAAAACCT ACAAGAGATG GAGAAGACCA AGAAGCAAGT GGAACAAGAG AAGTCCGATC TGCAAGTGGC CCTGGAAGAA GTAGAGGGCA GCCTTGAACA TGAGGAGTCG
AAAATCCTGA GAGTACAGCT GGAGCTGTCT CAGCTGAAGT CTGAGTTGGA TAGAAAAGTC GCTGAAAAGG ACGAGGAGAT GGAGCAGCTG AAGAGAAACT GTCAGAGAGC CGCCGAGGCC ACACAGAGCC
TGTTAGAGGC CGAATCGAGA AGCAGAAAAG ACGCACTGAG ACTGAAGAAG AAGATGGAAG GCGATTTGAA CGAGATGGAG GTGCACCTGG GCCACGCCAA CAGACAAGTG GCCGAAACAC AGAAGCACCT
GAGAACCGTG CAAGGACAGC TGAAGGGCTC TCAGCTGCAC CTTGGCGACG CCCTAAGAAG CGATGAAGCA CTGAAGGAAC GTTTAGCTAT CGTGGGCAGA AGAAACGGCC TGCTGGTTGA GGAGCTTGAA
GAGACGAAAG TAGCCCTTGA GCAAGCCGAA AGAAGCAGAA GACTGAGCGA GCAAGAGCTA CAAGACGCTA GCGACCGTGT ACAGCTGTTG CTGAGCCGTT GTAACACAAG CCTGATCAAC ATCAAGAAGA
AACTGGAGAC AAACATCGCT CAGTGCCAAG CCGAGGTGGA GAACAGCGTG CAAGAGAGCA GAAATGCCGA GGAGAAGGCC AAGAAGGCCA TCACCGACGC CGCCATGATG GCCGAGGAGC TGAAAAAAGA
GCAAGACACG TCTGCTCATC TGGAGAGAAT GAAGAAGAAC CTGGAGCAGA CCGTGAAGGA CATGCAGCAC AGACTGGACG AGGCCGAACA GCTTGCCCTG AAGGGAGACA AAAAACAAAT TCAGAAGCTG
GAGAACCGAG TGCGCGAACT GGAGAGCGAA CTGGATACCG AGCAGAAGAG AGGCGCCGAG GCACTCAAAG GGGCCCACAA GTACGAGAGA AAAGTTAAGG AGATGGCCTA CCAAGCCGAA GAGGATCACA
AGAACAGCCT GAGGCTGCAA GACCTAGTGG ACAAGCTGCA AGCCAAAGTG AACGCCTACA AGAGACAAGC CGAGGAAGCA GAAGAACAAG CCAACACACA GCTGTCTAGG TGCAGAAGAG TGCAGCACGA
GCTGGAGGAG GCTGAAGAGA GAGTCGACAT AGCGGAGAGC CAAGTGAATA AATTAAGAGC GAAGAGCCGG GACGTGGGCA GCCAAGTGAG AGCCGACACC TGGGCCTGGC TGCTGCTGAA AGAGAGCAGA
GACCCCGGCG CTCAGAGAAG CCACAGAGAG AGCTTAGAGG CAGCGCACTG GAGCCTGCTG CTGGTGATGC CATCTCAGAT GCCCCCCACA CAGCAGCGCC TGCTTTGA

Fig. 10B

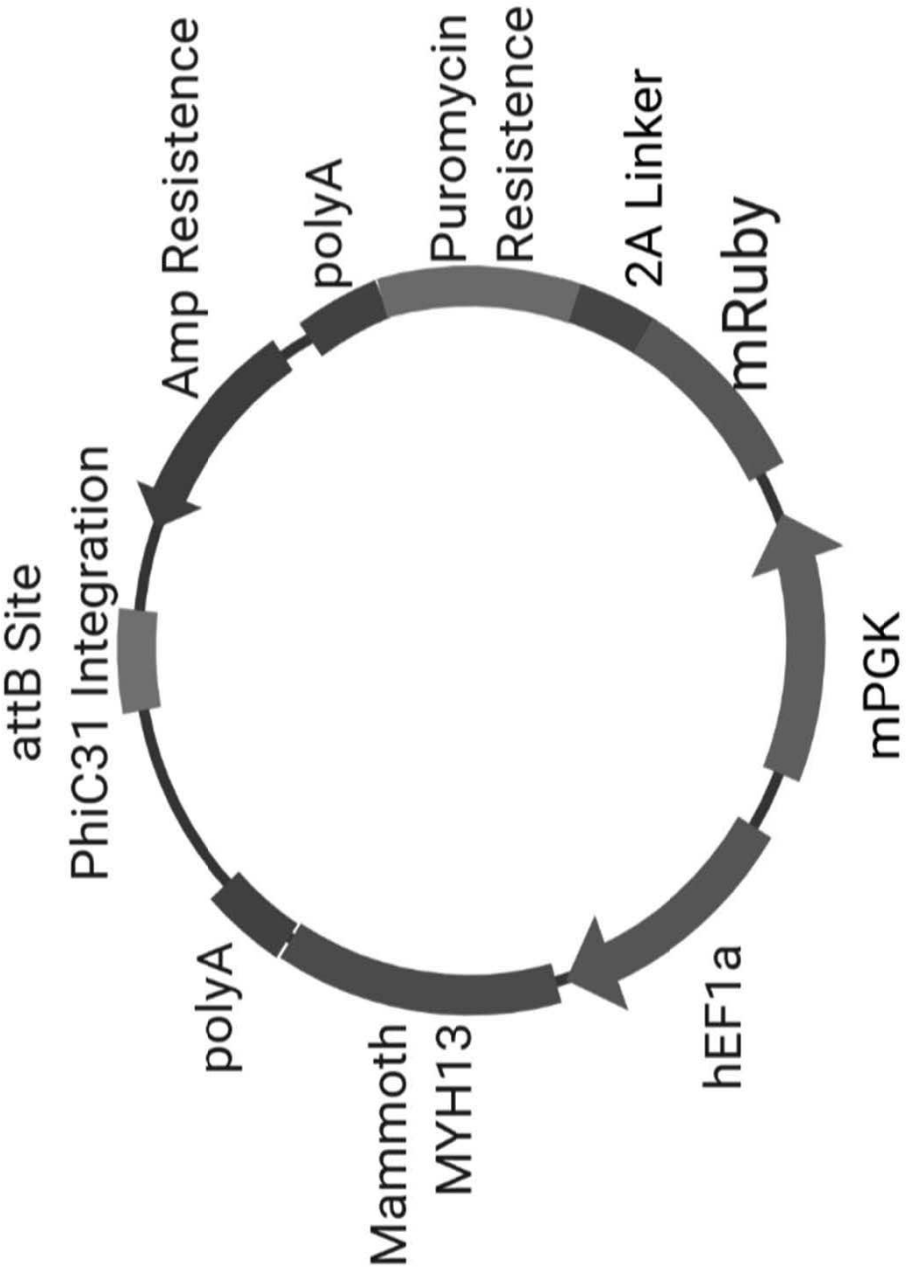
attB Site
PhiC31 Integration
Amp Resistence
polyA
Puromycin
Resistence
2A Linker
mRuby
mPGK
hEF1a
Mammoth
MYH13
polyA

Fig. 11

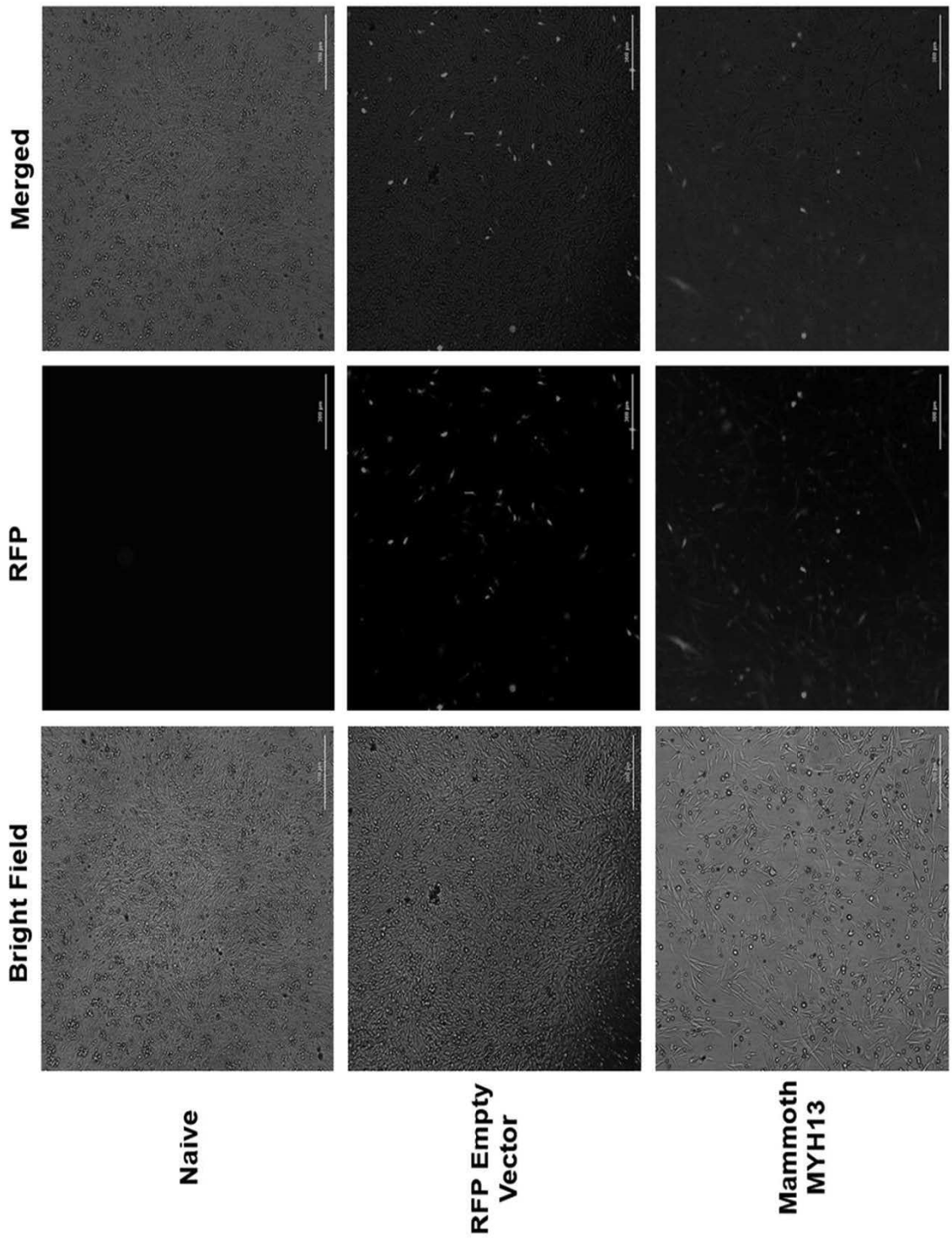
Bright Field
RFP
Merged
Naive
RFP Empty Vector
Mammoth MYH13

Fig. 12

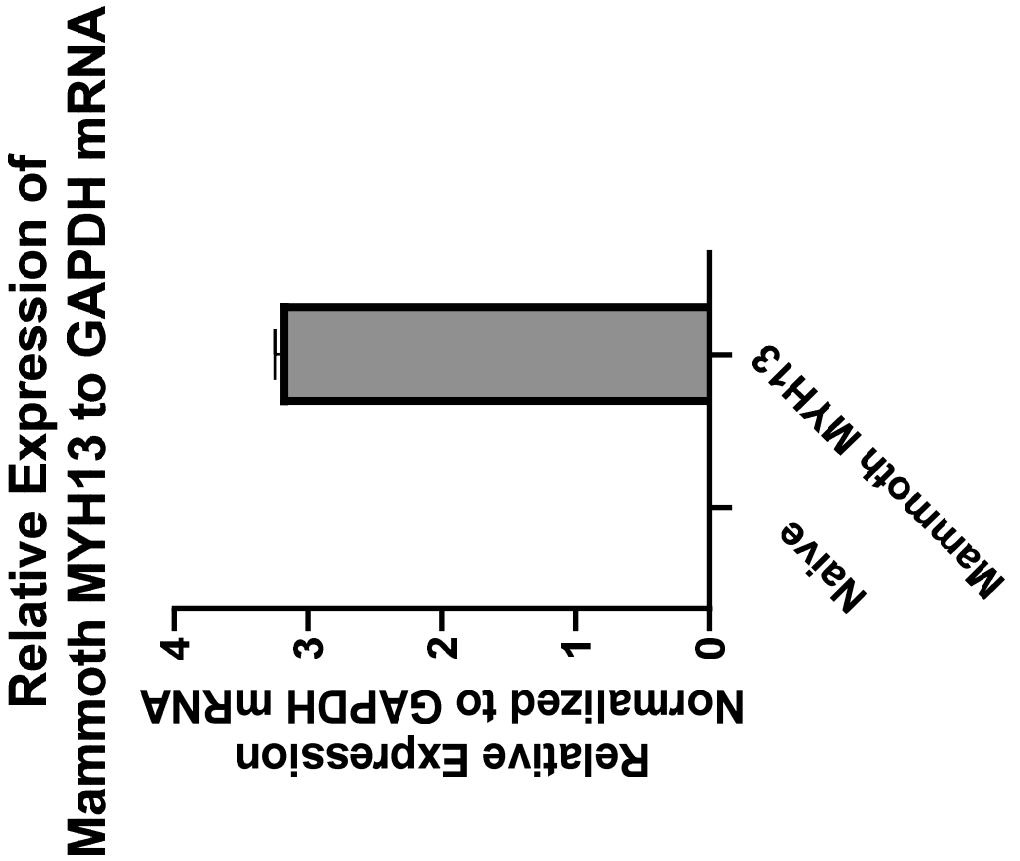
Relative Expression of
Mammoth MYH13 to GAPDH mRNA
Relative Expression
Normalized to GAPDH mRNA
0
1
2
3
4
Naive
Mammoth MYH13

Fig. 13

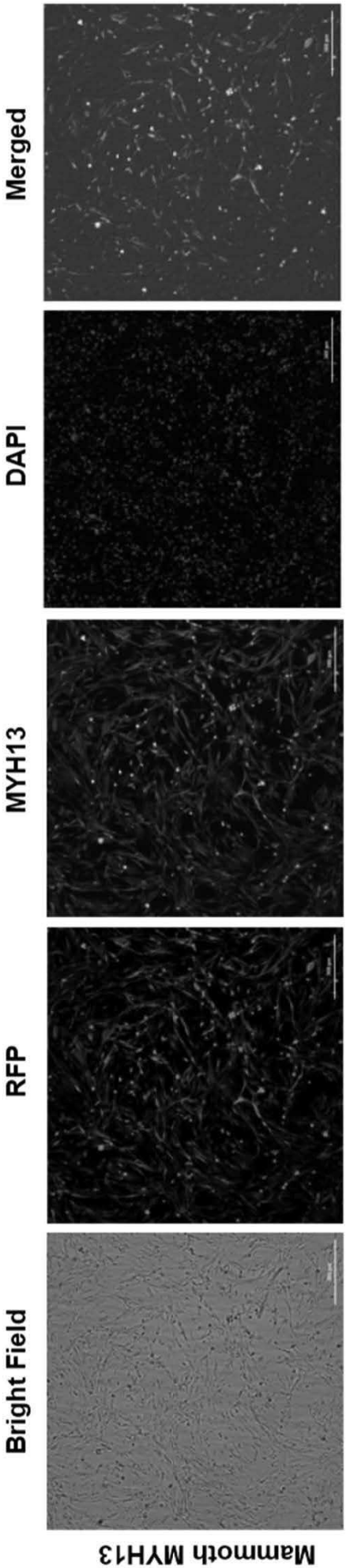

Fig. 14