Supplementary Information

Supplementary Table 1. List of integrases used for the development of PASTE.

Database	SRA accession	bioproject_acc	nucleotide accession	protein accession or ORF ID	internal protein ID	Proposed names	Alternative names	organism/source	description	Sequence	Length	Group
ENA	SRS12052958	PRJEB26277	NA	NA	N189929_49_54	SsuINT	NA	human gut metagenome	stool sample from male in USA	MEKNRAVLYLRLSKEDVDKVNKGDDSSSIKSQRLLLTDFALERGFKIVGVYSDDDESGLYDDRPDFERMMTDAKLDEFDIIIAKTQSRFSRNMEHIEKYLHHDLPNLGIRFIGAVDGVDTESDENKKSRQINGLVNEWYCEDLSKNIRSAFKAKMKDGQFLGSSCPYGYKKDPQNHNHLVVDDYAAKVVQKIFNLYLEGYGKAKIGSILSSEGILIPTLYKKDILKQNYHNSKALDTTQNWSYQTIHTILNNEVYLGHLIQNKVNTMSYKDKNKRILPKEKWIIVRNTHEPIITEEMFQDVQKLQKNRTRSVENIEPNGLFSGLIFCADCKHAMSRKYARRGEKGFVGYVCKTYKTQGKNFCESHSIDYDELEEAVLFSIKNEARSILQQEEIDELRKVQAYDETKSYYEMQLENIKSRMEKIEKYKKKTYDNYMDDLISRDDYKKYVTEYDKEIGGLKQQQELINSKTDLEKEISTQYDEWVEAFINYVDIDKLTREIVIELIEKIEVNKDGSINIYYKFKNPYIS	527	INTc
ENA	ERS396461	PRJEB26280	NA	NA	N190156_234_12	SssINT	NA	human gut metagenome	stool sample from Spain	MNTVIYARYSAGPRQTDQSIDGQLRVCTEFCKQRGLTVVDTYCDRHISGRTDERPEFQRLIADAKAHKFEAVVVYKTDRFARNKYDSAIYKRELRRNGIQIFYAAEAIPEGPEGIILESLMEGLAEYYSAELAQKIKRGLNESALKCQSLGSGRPLGYTVDEQKHFQIDPESSQAVKTIFEMYIKGESNAAICDYLNARGLRTSQGNLFNKNSINRIIKNRKYIGEYRYNDIVVEGGMPAIISKETFCMAQAEMERRRTHRAPVSPKAEYLLAGKLFCGHCKGPMQGVSGTGKSGNKWYYYYCANTRGKERTCDKKQVSRDRLEKAVVDFTVRYILQENVLEELSKKVYAAQERQNNTASEIAFYEKKLAENKKAIANILRAIESGAMTQALPARLQELENEQTVIQGELSYLKGARLAFTEDQILFALLQHLDPRPGESERDYHRRIITDFVSEVYLYDDRMLIYFNISSADGKLKHADLSAIESGVFDAGLISSSSRASSFSTRCALI	510	INTd
ENA	ERS101583 7	PRJEB26832	NA	NA	N191352_143_72	SscINT	NA	human gut metagenome	stool sample from China	MNEKNLEIGAAYIRVSTDDQTELSPDAQLRVILEAAKKDGIIIPQEFVFMEDRGRSGRRADNRPEFQRMISTARQNPSPFRYLYLWKFSRFARNQEESAFYKGILRKKCGVTIKSVSEPIMEGMFGRLVEMIIEWSDEFYSVNLSGEVLRGMTQKALEHGYQLTPCLGYDAVGHGRPYVINEEQYQIVEFIHRSFFDGKDMTWIAREANRRGYHTRRGNPFDTRAVRIILTNSFYVGLVKWNDVTFQGTHECRESVTSVFSANQERLNRIHRPRGRRQASSCKHWLSGLLKCSICGASLGYNQTKDLTKRGHAFQCWKYTKGIHPGSCSVSSLKAEAAVLESLQMILETGEVEYTYEQREKHLDDNKLTLIQKSLERLDTKELRIREAYESGIDTLDEFKTNKARLQRERDQLMEELEELHSQEEPEDVPGKEILIERIQNVYDLLQSPDVDNDDKGNAVRSIIKKIVYIKESKTFCFYYYV	482	INTd
ENA	ERS128967 7	PRJEB26924	NA	NA	N191533_224_76	Ssc2INT	NA	human gut metagenome	stool sample from China	MERTIKVIQPGTVKIPTKKRVAAYARVSSGKDAMLHSLSAQVSYYSNMIQQKNEWSYVGIYADEAITGTKDRRVEFNRLIQDCTDGKIDMIITKSISRFARNTLTMLEVVRKLKNINVDVYFEKENIHSISGDGELMLTILASFAQEESRSVSENCKWRIRKGFEQGELINLRFLYGYRINKGKIEIYEKEAEIVRMIFDDYLNGEGCTRIGNKLRKMKVNKLRGGMWNSERVVDIIKNEKYTGNALLQKKYVKDH	406	INTc

										LSKKLVRNKGILTQYYAEGTHPAIID IKTFEIAQKIMEANRTKFQGKCGSNR YLFTSKIECGICGKNYRHKDREGKST WVCANHLKYGNSRCIAKPLNEEKLK KLINEALELKYFDEEIFIRNIKRIKVT GNQTIEFILKDGKVIEEGMI		
ENA	ERS2655827	PRJEB28245	NA	NA	N203911_45186_6	SsdINT	NA	human gut metagenome	stool sample from Denmark	MKKIKIDRAIQERPATRKQTRNEKIR QSLTEHVDVQVIPAITDREGYEKPKL RVCAYCRVSTDMDTQALSYELQVQ NYTDYIRGNDEWRFAGIYADRGISG TSLKHRDEFNRMIEDCKAGKIDLIIT KAVTRFARNVLDCISTIRMLKQLEHP VAVYFETERINTLDTTSETYLGLISLF AQGESESKSESLKWSYIRRWKRGTG IYPAWSLLGYEMGEDGKWQIVEAE AELVRIIYDMYLNGYSSPQIAEILTRS GVPTATNQTVWSSGGVLGILRNEKY CGNVLCQKTMTVDVFSHKAIKNTG QKTQYFIEGHHDPIILRSDWDRVQQ MIDEKYYRKRRGRRTKPRIVLKGCL AGFTQIDLDWDEDDIARIFYSTTPAA EVATPAMADHIEIIKVKGEN	401	INTc
ENA	SRS294942	PRJEB30046	NA	NA	N208621_9_15	SmcINT	NA	human gut metagenome	sample from 72-year-old male from China	MKTAAAYIRVSTDDQVEYSPDSQIK LIRDYAKRNDYILPDEFIFRDDGISGK SAKHRPEFTKMIALAKSPEHPFDAIL VWKFSRFARNQEESIVFKNILRKIGV EVRSVSEPISEDPFGSLVERIIEWTDE YYIINLSGEVKRGMLEKISRGQPVVP PPVGYKMENGQYIPDENAHFIKEIFE AYAAGEGARHIAQRLAAQGCLTKR GNPIDNRFVDYVLHNPVYIGKLRWS VNSHAASSRHYDSADIIVFDGTHEPL ISSELWESVQKRLHEVKTLYPKYQR REQPVSFMLKGLVRCSSCGSTLCYC RTSEPSLQCHSYARGSCRQSHSINIAT ANEAVIKGLQLAVDKLDFAIAPAKP HYSADAPGTNKLLAAEYKKMERIK AAYANGTDTLEEYAANKKKISAEIA RLEAELQQESNVKPINKKAFAKRVS EIIKYISDPHNSEAAKNQALRTVISYII FDRAATTFNIIFHF	476	INTd
MetaSUB	NA	NA	NA	NA	N675015_95_5	UhmINT	NA	urban human microbiome	NA	MKIAIYARKSKYSPTGESVENQIQLC KEYLQAKYKSETLEIDEYKDEGYSG GNTNRPDFKKLIAQIEDYDMLICYRL DRISRNVADFSSTLTLLQNNKCDFVS IKEQFDTTSPMGRAMIYISSVFAQLE RETIAERIRDNMMELAKMGRWLGG TIPMGFDSEPITFIDENMKERSMTKLI PNVEELKVIELIYEKYLQLGSMGKV VTYLLQNNIKTKKGKDFTLGSIKVIL TNPIYVKANQEVVNHLKTQGITICGD VDGKKALLTYNKTTGISNDVGTKTI VKDKSEWIAAVANHKGIIPADKWLQ AQNIKDKNKDSFPALGRSNTTIASRV LRCDKCESTMGVTHGHINPVTGKKH YYYNCTLKKRSKGVRCDNKPAKAA EVDEAILITLENMFKAKSSIIDNLKAK NKARRIEMISSNRVDVINKIIEDKTK QIDNLVNKLSLDDDLTDILFKKIKGL KAEIKELEDELLTLTSDNIKLNEDEV VLDFTEKLLEKCSIIRTLDILEQQQIV DALIPLVTWNGDTEVLNIYPLGSPEL ELKEAESKKK	550	INTd
Segata-Pasolli	NA	PRJNA422434	NA	NA	N684346_90_69	SacINT	NA	human gut metagenome	stool sample from adult in China	MKEKVSERKTGAIYIRVSTDKQEELS PDAQLRLLLDYAKKDSIDVPKEYIFQ DNGISGRKANKRPAFQNMIALAKSK EHPIDTIIVWKFSRFARNQEESIVYKS LLKKNNVDVVSVSEPLIDGPFGSLIE RIIEWMDEYYSIRLSGEVMRGMTQN AMRGHYQSDAPIGYTSPGDKKPPVI NPDTVQIPLMIKDMFLSGSTQLQIAR KLNDSGYRTKRGNLWDARGVRYVL ENPFYIGKSRWNYTERGRRLKPADE VIYADGNWEALWDEDTFKEIQKRLA LNMRKSKSRDISAAKHWLSGLLICSS CGGTLAFGGAHNMRGFQCWKYSKG FCSESHYISTGPIEKMVLEYLEAVMH SPALSYTVISSSSVDASSKLSDLERQL QKIDAKEKRIKAAYLNEIDTLEEYKA NKTALEEERRTVEKEIEELTLSDVKY SKEDLDKKMKQNISDLLRVLRDESA DYIQKGNMMRNVVDHIVFNRKNTS LDVFLKLVV	493	INTd
Segata-	ERR113	PRJEB1	NA	NA	N687611_90_6	RsaINT	NA	human gut metagenom	rectal swab from adult in	MKITKKQPLRPRGRSEDKRQSTKNVI RDAYINGPQKEVQIIPAKRDMEAETE KKKLRVCAYCRVSTDEDTQASSYEL QVQNYTRMIRENPEWEFAGIFADEGI	404	INTc

Pasolli	6864	1532			8			e	Isreal	SGTSVLHREHFLEMIEKCKAGEIDLII TKQVSRFARNVLDSLNYIFMLRKLD PPVGVYFETEKLNTLDKSSDMVITVL SLVAQSESEQKSNSLKWSFKRRRAQ GLGIYPSWALLGYRLDDEKNWEIVE DEADIVRTIYSLYLDGYSSTQIAELLT KSGIPTVKGLSVWSSGSVLGILKNEK FCGDALCQKTVTIDFFTHKSVKNNGI EPQYFVEGHHIPIIEKNDWLLAQQIR KERRYRKRRSTHRKPRIVVKGALSG FMIVDTSWDEEYVDSLLISATQKPEP APVIAEEDENFIVIEKE		
Segata-Pasolli	ERR1136737	PRJEB11532	NA	NA	N687663_53_29	Rsa2INT	NA	human gut metagenome	rectal swab from adult in Isreal	MADIQPVKNGALYIRVSTHLQEELSP DAQKRLLMEYAEAHNIIVLKEHIYID SGISGRSARQRPQFNNMIAEAKSKEH PFDVILVWKYSRFARNQEESIVYKS MLKRENVDVISVSEPISDDPFGSLIER IIEWMDEYYSIRLSGEVSRGMAENA MRGNYQARPPLGYRIPGYRQTPVIV PEEAELIQLIFDLYTEKKMGIFEIVRY LNEHGYQTGHKKPFQRRSVTYILKN PTYIGKTIWNQHDQDHKLRDKSEWII ADGKHEPIISKEQFDKAQKRIESTYK PAYRKPTSVCHHWLSSLLKCSSCGR TLVVKRTASKKKDRMYVNFQCYGY QKGICNTNQSISAIKLEPVIMHALED AMTSGKIHFDVLNPTTLDSSQKQQF LTRLNEIEKKEERIKRAYRDGIDTLE EYKENKSIIQTEKEMLLKKIEHIEEPA LSPEEAKPIMMDRIKNVYEIITNPDIG MEEKNKAARSIIEKIVFDRATGSVNI FFYLAHCP	498	INTd
NCBI	NA	NA	NC_002656.1	NP_075302.1	NA	BxbINT	Bxb1 integrase	Mycobacterium phage Bxb1	NA	MRALVVIRLSRVTDATTSPERQLESC QQLCAQRGWDVVGVAEDLDVSGA VDPFDRKRRPNLARWLAFEEQPFDV IVAYRVDRLTRSIRHLQQLVHWAED HKKLVVSATEAHFDTTTPFAAVVIA LMGTVAQMELEAIKERNRSAAHFNI RAGKYRGSLPPWGYLPTRVDGEWR LVPDPVQRERILEVYHRVVDNHEPL HLVAHDLNRRGVLSPKDYFAQLQG REPQGREWSATALKRSMISEAMLGY ATLNGKTVRDDDGAPLVRAEPILTR EQLEALRAELVKTSRAKPAVSTPSLL LRVLFCAVCGEPAYKFAGGGRKHPR YRCRSMGFPKHCGNGTVAMAEWD AFCEEQVLDLLGDAERLEKVWVAG SDSAVELAEVNAELVDLTSLIGSPAY RAGSPQREALDARIAALAARQEELE GLEARPSGWEWRETGQRFGDWWRE QDTAAKNTWLRSMNVRLTFDVRGG LTRTIDFGDLQEYEQHLRLGSVVERL HTGMS*	501	INTa
NCBI	NA	NA	NC_002747.1	NP_112664.1	NA	Tp9INT	TP901-1 integrase	Lactococcus phage TP901-1	NA	MTKKVAIYTRVSTTNQAEEGFSIDEQ IDRLTKYAEAMGWQVSDTYTDAGF SGAKLERPAMQRLINDIENKAFDTV LVYKLDRLSRSVRDTLYLVKDVFTK NKIDFISLNESIDTSSAMGSLFLTILSA INEFERENIKERMTMGKLGRAKSGK SMMWTKTAFGYYHNRKTGILEIVPL QATIVEQIFTDYLSGISLTKLRDKLNE SGHIGKDIPWSYRTLRQTLDNPVYC GYIKFKDSLFEGMHKPIIPYETYLKV QKELEERQQQTYERNNNPRPFQAKY MLSGMARCGYCGAPLKIVLGHKRK DGSRTMKYHCANRFPRKTKGITVYN DNKKCDSGTYDLSNLENTVIDNLIGF QENNDSLLKIINGNNQPILDTSSFKK QISQIDKKIQKNSDLYLNDFITMDEL KDRTDSLQAEKKLLKAKISENKFND STDVFELVKTQLGSIPINELSYDNKK KIVNNLVSKVDVTADNVDIIFKFQLA *	486	INTd
NCBI	NA	NA	NC_004664.2	NP_813744.2	NA	Bt1INT	PhiBT integrase	Streptomyces virus phiBT1	NA	MSPFIAPDVPEHLLDTVRVFLYARQS KGRSDGSDVSTEAQLAAGRALVASR NAQGGARWVVAGEFVDVGRSGWD PNVTRADFERMMGEVRAGEGDVVV VNELSRLTRKGAHDALEIDNELKKH GVRFMSVLEPFLDTSTPIGVAIFALIA ALAKQDSDLKAERLKGAKDEIAALG GVHSSSAPFGMRAVRKKVDNLVISV LEPDEDNPDHVELVERMAKMSFEG VSDNAIATTFEKEKIPSPGMAERRAT EKRLASIKARRLNGAEKPIMWRAQT VRWILNHPAIGGFAFERVKHGKAHI NVIRRDPGGKPLTPHTGILSGSKWLE LQEKRSGKNLSDRKPGAEVEPTLLS GWRFLGCRICGGSMGQSQGGRKRN GDLAEGNYMCANPKGHGGLSVKRS	595	INTa

										ELDEFVASKVWARLRTADMEDEHD QAWIAAAAERFALQHDLAGVADER REQQAHLDNVRRSIKDLQADRKAGL YVGREELETWRSTVLQYRSYEAECT TRLAELDEKMNGSTRVPSEWFSGED PTAEGGIWASWDVYERREFLSFFLD SVMVDRGRHPETKKYIPLKDRVTLK WAELLKEEDEASEATERELAAL*		
NCBI	NA	NA	NC_011658.1	WP_000286206.1	NA	BceINT	NA	Bacillus cereus AH187	NA	MYPYDVPDYAGSYRPESLDVCIYLR KSRKDVEEERRAIEEGSSYNALERHR KRLFAIAKAENHNIIDIFEEVASGESI QERPQMQQLLRKLEGNEIDGVLVID LDRLGRGDMLDAGMIDRAFRYSSTK IITPTDVYDPDDESWELVFGIKSLISR QELKSITKRLQNGRIDSVKEGKHIGK KPPYGYLKDENLRLYPDPEKAWIVK KIFELMCDGKGRQMIAAELDRLGID PPVTKRGAWDSSTITSIIKNEVYTGVI VWGKFKHKKRNGKYTRHKNPQEK WIMYENAHEPIISKELFDAANEAHSS RHKPAVITSKKLTNPLAGILKCKLCG YTMLIQTRKDRPHNYLRCNNPACKG KQKQSVFNLVEEKLLYSLQQIVDEY QAAQKVEEVEIDDSKLISFKEKAIISKE KELKELQAAQKGNLHDLLEQGIYTVE IFLERQKNLVERITSIENDIEVLQKEIE TEQIKEHNKTEFIPALKTVIESYHKTT NIELKNQLLKTILSTVTYYRHPDWKT NEFEIQVYFKIS*	529	INTc
NCBI	NA	NA	NC_009674.1	WP_012095429.1	NA	BcyINT	NA	Bacillus cytotoxicus NVH 391-98	NA	MYPYDVPDYAGSAVGIYIRVSTQEQ ASEGHSIESQKKKLASYCEIQGWDD YRFYIEEGISGKNTNRPKLKLLMEHI EKGKINILLVYRLDRLTRSVIDLHKL LNFLQEHGCAFKSATETYDTTTANG RMSMGIVSLLAQWETENMSERIKLN LEHKVLVEGERVGAIPYGFDLSDDE KLVKNEKSAILLDMVERVENGWSV NRIVNYLNLTNNDRNWSPNGVLRLL RNPALYGATRWNDKIAENTHEGIISK ERFNRLQQILADRSIHHRRDVKGTYI FQGVLRCPVCDQTLSVNRFIKKRKD GTEYCGVLYRCQPCIKQNKYNLAIG EARFLKALNEYMSTVEFQTVEDEVIP KKSEREMLESQLQQIARKREKYQKA WASDLMSDDEFEKLMVETRETYDE CKQKLESCEDPIKIDETYLKEIVYMF HQTFNDLESEKQKEFISKFIRTIRYTV KEQQPIRPDKSKTGKGKQKVIITEVE FYQS*	487	INTd
NCBI	NA	NA	NC_017353.1	WP_014533238.1	NA	SluINT	NA	Staphylococcus lugdunensis N920143	NA	MYPYDVPDYAGSKVAIYTRVSSAEQ ANEGYSIHEQKKKLISYCEIHDWNE YKVFTDAGISGGSMKRPALQKLMK HLSSFDLVLVYKLDRLTRNVRDLLD MLEEFEQYNVSFKSATEVFDTTSAIG KLFITMVGAMAEWERETIRERSLFGS RAAVREGNYIREAPFCYDNIEGKLHP NEYAKVIDLIVSMFKKGISANEIARR LNSSKVHVPNKKSWNRNSLIRLMRS PVLRGHTKYGDMLIENTHEPVLSEH DYNAINNAISSKTHKSKVKHHAIFRG ALVCPQCNRRLHLYAGTVKDRKGY KYDVRRYKCETCSKNKDVKNVSFN ESEVENKFVNLLKSYELNKFHIRKVE PVKKIEYDIDKINKQKINYTRSWSLG YIEDDEYFELMEEINATKKMIEEQTT ENKQSVSKEQIQSINNFILKGWEELTI KDKEELILSTVDKIEFNFIPKDKKHK TNTLDINNIHFKFS*	473	INTd

Supplementary Table 2. Linker sequences

Description	Sequence (5'-3')	Amino acid sequence
A - P2A	GGAAGCGGAGCTACTAACTTCAGCCT GCTGAAGCAGGCTGGCGACGTGGAGG AGAACCCTGGACCT	GSGATNFSLLKQAGDVEENPGP
B - (GGGS)3	GGGGGAGGAGGTTCTGGAGGCGGAGG CTCCGGAGGCGGAGGGTCA	GGGGSGGGGSGGGGS
C - GGGGS	GGAGGTGGCGGGAGC	GGGGS
D - PAPAP	CCCGCACCAGCGCCT	PAPAP
E - (EAAAK)3	GAGGCAGCTGCCAAGGAAGCCGCT GCCAAGGAGGCGGCCGCAAAG	EAAAKEAAAKEAAAK
F - XTEN	AGTGGGAGCGAGACCCCTGGGACT AGCGAGTCAGCTACACCCGAAAGC	SGSETPGTSESATPES
G - (GGS)6	GGGGGGTCAGGTGGATCCGGCGG AAGTGGCGGATCCGGTGGATCTGG CGGCAGT	GGSGGSGGSGGSGGSGGS
H - EAAAK	GAAGCTGCTGCTAAG	EAAAK

Supplementary Table 3. Sequences of RT mutants

Description	Forward Sequence (5'-3')
RT_mut_L139P	ttgagcgggCCCccaccgt
RT_mut_E562Q	cagcgggctCAGctgatagca
RT_mut_D653N	cggatggctAACcaagcggcc
RT(1-478)_Sto7d fusion [MMulv sequence, Sto7d sequence]	atgactcactatcaggccttgcttttggacacggaccgggtccagttcggaccggtggtagccctgaacccggctacgctgctccc actgcctgaggaagggctgcaacacaactgccttgatGGGACAGGTGGCGGTGGTGTCACCGTCAA GTTCAAGTACAAGGGTGAGGAACTTGAAGTTGATATTAGCAAAATCAAGAAG GTTTGGCGCGTTGGTAAAATGATATCTTTTACTTATGACGACAACGGCAAGAC AGGTAGAGGGGCAGTGTCTGAGAAAGACGCCCCCAAGGAGCTGTTGCAAATG TTGGAAAAGTCTGGGAAAAAGtctggcggctcaaaaagaaccgccgacggcagcgaattcgagcccaaga agaagaggaaagtc

Supplementary Table 4. Sequences of atgRNAs, sgRNAs and nicking guides. Spacers are labeled in blue, RT regions in green, AttB sites in red, and PBS in orange. Unless otherwise denoted, the AttB is for Bxb1.

Description	Sequence (5'-3')
ACTB N-term PBS 13 RT 29 AttB 46 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 atgRNA with v2 scaffold	GCTATTCTCGCAGCTCACCAgtttgagagctatgctggaaacagcatagcaagttcaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAA
ACTB N-term PBS_13_RT_29_with TP901-1 minimal AttB f atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGAGTCGGTGCGACGAGCGCGGCGATATCATCATCCATGGcacaattaacatctcaatcaaggtaaaTGCTTGAGCTGCGAGAA
ACTB N-term PBS_13_RT_29_with TP901-1 minimal AttB rc atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGAGTCGGTGCGACGAGCGCGGCGATATCATCATCCATGGagcatttaccttgattgagatgttaattgtgTGAGCTGCGAGAA
ACTB N-term PBS_13_RT_29_with PhiBT1 minimal AttB f atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGAGTCGGTGCGACGAGCGCGGCGATATCATCATCCATGGcaggtttttgacgaaagtgatccagatgatccagTGAGCTGCGAGAA
ACTB N-term PBS_13_RT_29_with PhiBT1 minimal AttB rc atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGAGTCGGTGCGACGAGCGCGGCGATATCATCATCCATGGctggatcatctggatcactttcgtcaaaaacctgTGAGCTGCGAGAA
ACTB N-term Nicking guide 1 +48 guide	GAAGCCGGCCTTGCACATGCgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
ACTB N-term PBS_18_RT_16_with_Lox71_Cre atgRNA	GAAGCCGGCCTTGCACATGCgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcATATCATCATCCATGGtaccgttcgtatagcatacattatacgaagttatTGAGCTGCGAGAATAGCC
ACTB N-term PBS_13_RT_29_with_Lox71_Cre atgRNA	GAAGCCGGCCTTGCACATGCgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtaccgttcgtatagcatacattatacgaagttatTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 34 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcTCGACGACGAGCGCGGCGATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 26 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGAGCGCGGCGATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAA

ACTB N-term PBS 13 RT 23 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcCGCGGCGATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 20 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGGCGATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 16 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAA
ACTB N-term PBS 18 RT 34 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcTCGACGACGAGCGCGGCGATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAATAGCC
ACTB N-term PBS 18 RT 29 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAATAGCC
ACTB N-term PBS 18 RT 16 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcATATCATCATCCATGGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGAGCTGCGAGAATAGCC
LMNB1 N-term PBS 13 RT 39 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcCTGCCCATCCGCGGCGGCACGGGGGTCGCAGTCGCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGA
LMNB1 N-term PBS 13 RT 34 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcCATCCGCGGCGGCACGGGGGTCGCAGTCGCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGA
LMNB1 N-term PBS 13 RT 29 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGCGGCGGCACGGGGGTCGCAGTCGCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGA
LMNB1 N-term PBS 13 RT 24 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGGCACGGGGGTCGCAGTCGCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGA
LMNB1 N-term PBS 13 RT 19 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGGGGGTCGCAGTCGCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGA
LMNB1 N-term PBS 18 RT 39 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcCTGCCCATCCGCGGCGGCACGGGGGTCGCAGTCGCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGACAGCG
LMNB1 N-term PBS 18 RT 34 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcCATCCGCGGCGGCACGGGGGTCGCAGTC

	GCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGACAGCG
LMNB1 N-term PBS 18 RT 29 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGCGGCGGCACGGGGGGTCGCAGTCGCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGACAGCG
LMNB1 N-term PBS 18 RT 24 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGGCACGGGGGGTCGCAGTCGCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGACAGCG
LMNB1 N-term PBS 18 RT 19 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGGGGGTCGCAGTCGCCATGccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCGGGCGGCGGAGACAGCG
LMNB1 N-term Nicking guide 1 +46	GCGTGGTGGGGCCGCCAGCGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
ACTB N-term PBS 13 RT 29 AttB 42 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGggatgatcctgacgacggagaccgccgtcgtcgacaagccggTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 40 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGgatgatcctgacgacggagaccgccgtcgtcgacaagccgTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 38 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGatgatcctgacgacggagaccgccgtcgtcgacaagccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 36 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtgatcctgacgacggagaccgccgtcgtcgacaagcTGAGCTGCGAGAA
LMNB1 N-term PBS 13 RT 29 AttB 44 atgRNA v2	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGCGGCGGCACGGGGGGTCGCAGTCGCCATGcggatgatcctgacgacggagaccgccgtcgtcgacaagccggcCGGGCGGCGGAGA
LMNB1 N-term PBS 13 RT 29 AttB 42 atgRNA v2	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGCGGCGGCACGGGGGGTCGCAGTCGCCATGgatgatcctgacgacggagaccgccgtcgtcgacaagccggCGGGCGGCGGAGA
LMNB1 N-term PBS 13 RT 29 AttB 40 atgRNA v2	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGCGGCGGCACGGGGGGTCGCAGTCGCCATGgatgatcctgacgacggagaccgccgtcgtcgacaagccgCGGGCGGCGGAGA
LMNB1 N-term PBS 13 RT 29 AttB 38 atgRNA v2	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGCGGCGGCACGGGGGGTCGCAGTCGCCATGatgatcctgacgacggagaccgccgtcgtcgacaagccCGGGCGGCGGAGA
NOLC1 N-term PBS 18 RT 29 AttB 46 atgRNA	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGAACCACGCGGCGAATGCCGGCGTCCGCCccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTCCTCCAGGCAATACGCG
NOLC1 N-term PBS 13	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttat

RT 29 AttB 46 atgRNA	caacttgaaaaagtggcaccgagtcggtgcGAACCACGCGGCGAATGCCGGCGTCCGC CcggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTCCTCCAGGCAAT
NOLC1 N-term PBS 13 RT 29 AttB 44 atgRNA	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcGAACCACGCGGCGAATGCCGGCGTCCGC CcggatgatcctgacgacggagaccgccgtcgtcgacaagccggcTCCTCCAGGCAAT
NOLC1 N-term PBS 13 RT 29 AttB 42 atgRNA	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcGAACCACGCGGCGAATGCCGGCGTCCGC CggatgatcctgacgacggagaccgccgtcgtcgacaagccggTCCTCCAGGCAAT
NOLC1 N-term PBS 13 RT 29 AttB 40 atgRNA	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcGAACCACGCGGCGAATGCCGGCGTCCGC CgatgatcctgacgacggagaccgccgtcgtcgacaagccgTCCTCCAGGCAAT
NOLC1 N-term PBS 13 RT 29 AttB 38 atgRNA	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcGAACCACGCGGCGAATGCCGGCGTCCGC CatgatcctgacgacggagaccgccgtcgtcgacaagccTCCTCCAGGCAAT
NOLC1 nicking guide -43	GAGCCGAGCACGAGGGGATACgttttagagctagaaatagcaagttaaaataaggctagtccgt tatcaacttgaaaaagtggcaccgagtcggtgc
ACTB N-term PBS 13 RT 20 AttB 38 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcGGCGATATCATCATCCATGGatgatcctgacgacg gagaccgccgtcgtcgacaagccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 15 AttB 38 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcTATCATCATCCATGGatgatcctgacgacggagaccg ccgtcgtcgacaagccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 10 AttB 38 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcTCATCCATGGatgatcctgacgacggagaccgccgtcgtc gacaagccTGAGCTGCGAGAA
ACTB N-term PBS 9 RT 20 AttB 38 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcGGCGATATCATCATCCATGGatgatcctgacgacg gagaccgccgtcgtcgacaagccTGAGCTGCG
ACTB N-term PBS 9 RT 15 AttB 38 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcTATCATCATCCATGGatgatcctgacgacggagaccg ccgtcgtcgacaagccTGAGCTGCG
ACTB N-term PBS 9 RT 10 AttB 38 atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcTCATCCATGGatgatcctgacgacggagaccgccgtcgtc gacaagccTGAGCTGCG
LMNB1 N-term PBS 13 RT 20 AttB 38 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcCGGGGGTCGCAGTCGCCATGatgatcctgacga cggagaccgccgtcgtcgacaagccCGGGCGGCGGAGA
LMNB1 N-term PBS 13 RT 15 AttB 38 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcGTCGCAGTCGCCATGatgatcctgacgacggagacc gccgtcgtcgacaagccCGGGCGGCGGAGA
LMNB1 N-term PBS 13 RT 10 AttB 38 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcAGTCGCCATGatgatcctgacgacggagaccgccgtcgt cgacaagccCGGGCGGCGGAGA
LMNB1 N-term PBS 9	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttat

RT 20 AttB 38 atgRNA	caacttgaaaaagtggcaccgagtcggtgcCGGGGGTCGCAGTCGCCATGatgatcctgacga cggagaccgccgtcgtcgacaagccCGGGCGGCG
LMNB1 N-term PBS 9 RT 15 AttB 38 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcGTCGCAGTCGCCATGatgatcctgacgacggagacc gccgtcgtcgacaagccCGGGCGGCG
LMNB1 N-term PBS 9 RT 10 AttB 38 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcAGTCGCCATGatgatcctgacgacggagaccgccgtcgt cgacaagccCGGGCGGCG
SUPT16H N-term PBS 13 RT 24 Bxb1-GT_Initial length	GAGAAGCGGCGTCCGGGGCTAgttttagagctagaaatagcaagttaaaataaggctagtccgtt atcaacttgaaaaagtggcaccgagtcggtgcTCTTTGTCCAGAGTCACAGCCATAccggat gatcctgacgacggagaccgccgtcgtcgacaagccggccCCCCGGACGCCGC
SRRM2 N-term PBS 13 RT 24 Bxb1 Initial length	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcGGCGTCGGCAGCCCGATCCCGTTGccggatg atcctgacgacggagaccgccgtcgtcgacaagccggccTACATGGCCCCGT
DEPDC4 N-term PBS 18 RT 24 Bxb1 Initial length	GTGTCAGGTGGGGCGGGGCTAgttttagagctagaaatagcaagttaaaataaggctagtccgtt atcaacttgaaaaagtggcaccgagtcggtgcGCTGGCTCCTCCCCTGGCACCATA ccggatgatcctgacgacggagaccgccgtcgtcgacaagccggccCCCCGCCCCACCTGACA C
NES N-term PBS 13 RT 29 Bxb1 Initial length	GAGTGGGTCAGACGAGCAGGAgttttagagctagaaatagcaagttaaaataaggctagtccgt tatcaacttgaaaaagtggcaccgagtcggtgcCGACTCCTCCCCCATGCAGCCCTCCAT CcggatgatcctgacgacggagaccgccgtcgtcgacaagccggccTGCTCGTCTGACC
SUPT16H nicking guide -53	GCAGCCACCCGCTCTCGGCCCgttttagagctagaaatagcaagttaaaataaggctagtccgtt atcaacttgaaaaagtggcaccgagtcggtgc
SRRM2 N-term nicking guide 1 +87	GTGTAGTCAGGCCGCTCACCCgttttagagctagaaatagcaagttaaaataaggctagtccgtt atcaacttgaaaaagtggcaccgagtcggtgc
DEPDC4 N-term Nicking guide 1 +59	GCTGACAAGTCTACGGAACCTgttttagagctagaaatagcaagttaaaataaggctagtccgtt atcaacttgaaaaagtggcaccgagtcggtgc
NES N-term Nicking guide 2 +79	GCTCCTCCAGCGCCTTGACCgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgc
HITI_ACTB_guide	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgc
HITI_SUPTH16_guide	AGAAGCGGCGTCCGGGGCTAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgc
HITI_SRRM2_guide	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgc
HITI_NOLC1_guide	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgc
HITI_DEPDC4_guide	TGTCAGGTGGGGCGGGGCTAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgc
HITI_NES_guide	AGTGGGTCAGACGAGCAGGAgttttagagctagaaatagcaagttaaaataaggctagtccgtta

	tcaacttgaaaaagtggcaccgagtcggtgc
HITI_LMNB1_guide	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgc
HDR Cas9 ACTB guide	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgc
HDR Cas9 LMNB1 guide	GGGGTCGCAGTCGCCATGGCgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgc
ACTB N-term PBS 13 RT 29 AttB original length atgRNAs for dinucleotides	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGG ccggatgatcctgacgacggagXXcgccgtcgtcgacaagccggccTGAGCTGCGAGAA XX: CG, GC, AT, TA, GG, TT, GA, AG, CC, TC, CT, AA, TG, GT, CA, AC
ACTB N-term PBS 13 RT 29 atgRNA with AttB 46 GT for fusion	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGc cggatgatcctgacgacggagACcgccgtcgtcgacaagccggccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 atgRNA with AttB 46 CT for multiplexing	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGc cggatgatcctgacgacggagAGcgccgtcgtcgacaagccggccTGAGCTGCGAGAA
NOLC1 N-term PBS 18 RT 29 atgRNA with AttB 46 GA for multiplexing	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcGAACCACGCGGCGAATGCCGGCGTCCGC CccggatgatcctgacgacggagTCcgccgtcgtcgacaagccggccTCCTCCAGGCAATACG CG
LMNB1 N-term PBS 18 RT 29 atgRNA with AttB 46 AG for multiplexing	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgcGCGGCGGCACGGGGGTCGCAGTCGCCAT GccggatgatcctgacgacggagCTcgccgtcgtcgacaagccggccCGGGCGGCGGAGACA GCG
EMX1 Cas9 guide 1	GTCACCTCCAATGACTAGGGgttttagagctagaaatagcaagttaaaataaggctagtccgttat caacttgaaaaagtggcaccgagtcggtgc
EMX1 Cas9 guide 2	GGGCAACCACAAACCCACGAgttttagagctagaaatagcaagttaaaataaggctagtccgtta tcaacttgaaaaagtggcaccgagtcggtgc
ACTB N-term PBS 13 RT 29 AttB 56 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGG ctatgccggatgatcctgacgacggagtccgccgtcgtcgacaagccggccctagcTGAGCTGCGAG AA
ACTB N-term PBS 13 RT 29 AttB 51 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGG tgccggatgatcctgacgacggagtccgccgtcgtcgacaagccggccctaTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGG ccggatgatcctgacgacggagtccgccgtcgtcgacaagccggccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 41 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatc aacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGG ggatgatcctgacgacggagtccgccgtcgtcgacaagccgTGAGCTGCGAGAA

ACTB N-term PBS 13 RT 29 AttB 36 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtgatcctgacgacggagtccgccgtcgtcgacaagcTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 31 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGatcctgacgacggagtccgccgtcgtcgacaTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 26 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGcctgacgacggagtccgccgtcgtcgTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 21 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtgacgacggagtccgccgtcgTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 16 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGacgacggagtccgccgTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 11 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGgacggagtccgTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 6 GA atgRNA	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGcggagtTGAGCTGCGAGAA
ACTB N-term PBS_18_RT_34_with_Lox71_Cre atgRNA	GAAGCCGGCCTTGCACATGCgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcTCGACGACGAGCGCGGCGATATCATCATCCATGGtaccgttcgtatagcatacattatacgaagttatTGAGCTGCGAGAATAGCC
ACTB N-term PBS_18_RT_29_with_Lox71_Cre atgRNA	GAAGCCGGCCTTGCACATGCgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtaccgttcgtatagcatacattatacgaagttatTGAGCTGCGAGAATAGCC
ACTB N-term PBS_13_RT_34_with_Lox71_Cre atgRNA	GAAGCCGGCCTTGCACATGCgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcTCGACGACGAGCGCGGCGATATCATCATCCATGGtaccgttcgtatagcatacattatacgaagttatTGAGCTGCGAGAA
ACTB N-term PBS_13_RT_16_with_Lox71_Cre atgRNA	GAAGCCGGCCTTGCACATGCgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcATATCATCATCCATGGtaccgttcgtatagcatacattatacgaagttatTGAGCTGCGAGAA
ACTB N-term Nicking guide 2 +93 guide	CCCCACGATGGAGGGGAAGAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
LMNB1 N-term Nicking guide 2 +87 guide	CCTTCTCCTGGAGCCGCGACgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
ACTB N-term PBS 13 RT 29 AttB 46 N191352_143_72 integrase	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGcatatatgttcttacagtatggcggcccggattgtaaaaacatataatgTGAGCTGCGAGAA
ACTB N-term PBS 13 RT	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca

29 AttB 46 N684346_90_69 integrase	acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGcgt tatagggtattacagtatggcggtcggtactgcaataccctataacgTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 N675015_95_5 integrase	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtgt atcattttcatatagttagcacctgcacactatatgaaaatgatacaTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 N189929_49_54 integrase	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtgt ctactatctgtatatgcgacacatgtggcataaagacatagtagacaTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 N203911_45186_6 integrase	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGcat cgaccctgacgcatgcggaggcggcgctccatgcgtctgacctcattTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 N687663_53_29 integrase	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGgtt agtacccaaatgacaaaaggtcatccttttatcatttgggtactaacTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 N687611_90_68 integrase	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGctt attaaaacccgttccgcttctgtcaaagcggcatcggttttataaacTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 N190156_234_12 integrase	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGgg cgtgatggtcgtgaacctcaacatgacgacgaacacgacctcgcggccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 N191533_224_76 integrase	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtct acatcttgaatatatcaagttataactttgaattatatcagtttataTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 N208621_9_15 integrase	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGaat tatatctaaaagcactaagctccgccatactgcttttagatataataTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cereus_AH187_38 bp_Att	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGgat atggggaagtgaatcagtacaaccgccacagtaccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cereus_AH187_38 bp_Att_rc	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGggt actgtggcggttgtactgattcacttccccatatcTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Staphylococcus_lugdunensis_N920143_38bp_Att	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtgg gtggtacaggtgccacattagttgtaccatttatgTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Staphylococcus_lugdunensis_N920143_38bp_Att_rc	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGcat aaatggtacaactaatgtggcacctgtaccacccaTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cytotoxicus_NVH_391-98_38bp_Att	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca acttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGgtt gtttttccagatccagttggtcctgtaaatataagTGAGCTGCGAGAA

ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cytotoxicus_NVH_391-98_38bp_Att_rc	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGcttatatttacaggaccaactggatctggaaaaacaacTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cereus_AH187_Att 36bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGgtactgtggcggttgtactgattcacttccccatatTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cereus_AH187_Att 34bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtactgtggcggttgtactgattcacttccccataTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cereus_AH187_Att 32bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGactgtggcggttgtactgattcacttccccatTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cereus_AH187_Att_rc 36bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGatatggggaagtgaatcagtacaaccgccacagtacTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cereus_AH187_Att_rc 34bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtatggggaagtgaatcagtacaaccgccacagtaTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cereus_AH187_Att_rc 32bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGatggggaagtgaatcagtacaaccgccacagtTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Staphylococcus_lugdunensis_N920143_Att 36bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGataaatggtacaactaatgtggcacctgtaccacccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Staphylococcus_lugdunensis_N920143_Att 34bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtaaatggtacaactaatgtggcacctgtaccaccTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Staphylococcus_lugdunensis_N920143_Att 32bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGaaatggtacaactaatgtggcacctgtaccacTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Staphylococcus_lugdunensis_N920143_Att_rc 36bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGggtggtacaggtgccacattagttgtaccatttatTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Staphylococcus_lugdunensis_N920143_Att_rc 34bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGggtggtacaggtgccacattagttgtaccatttaTGAGCTGCGAGAA

ACTB N-term PBS 13 RT 29 AttB 46 Staphylococcus_lugdunensis_N920143_Att_rc 32bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGgtggtacaggtgccacattagttgtaccatttTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cytotoxicus_NVH_391-98_Att 36bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGttatatttacaggaccaactggatctggaaaaacaaTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cytotoxicus_NVH_391-98_Att 34bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtatatttacaggaccaactggatctggaaaaacaTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cytotoxicus_NVH_391-98_Att 32bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGatattttacaggaccaactggatctggaaaaacTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cytotoxicus_NVH_391-98_Att_rc 36bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGttgttttttccagatccagttggtcctgtaaatataaTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cytotoxicus_NVH_391-98_Att_rc 34bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGtgtttttccagatccagttggtcctgtaaatataTGAGCTGCGAGAA
ACTB N-term PBS 13 RT 29 AttB 46 Bacillus_cytotoxicus_NVH_391-98_Att_rc 32bp	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGACGAGCGCGGCGATATCATCATCCATGGgtttttccagatccagttggtcctgtaaatatTGAGCTGCGAGAA
Bacillus_cereus_AH187_Att_rc_36 LMNB1_PBS 9 RT 10 AttB 36 atgRNA	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcAGTCGCCATGatatggggaagtgaatcagtacaaccgccacagtacCGGGCGGCG
Bacillus_cereus_AH187_Att_rc_36 NOLC1_PBS 18 RT 29 AttB 36 atgRNA	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGAACCACGCGGCGAATGCCGGCGTCCGCCatatggggaagtgaatcagtacaaccgccacagtacTCCTCCAGGCAATACGCG
Bacillus_cereus_AH187_Att_rc_36 SUPT16H_PBS 13 RT 24 AttB 36 atgRNA	GAGAAGCGGCGTCCGGGGCTAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcTCTTTGTCCAGAGTCACAGCCATAatatggggaagtgaatcagtacaaccgccacagtacCCCCGGACGCCGC
Bacillus_cereus_AH187_Att_rc_36 SRRM2_PBS 13 RT 24 AttB 36 atgRNA	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGGCGTCGGCAGCCCGATCCCGTTGatatggggaagtgaatcagtacaaccgccacagtacTACATGGCCCCGT
Bacillus_cereus_AH187_Att_rc_36 DEPDC4_PBS 18 RT 24 AttB 36 atgRNA	GTGTCAGGTGGGGCGGGGCTAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGCTGGCTCCTCCCCTGGCACCATAatatggggaagtgaatcagtacaaccgccacagtacCCCCGCCCCACCTGACAC
Bacillus_cereus_AH187_Att_rc_36 NES_PBS 13 RT 28 AttB 36 atgRNA	GAGTGGGTCAGACGAGCAGGAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcCGACTCCTCCCCCATGCAGCCCTCCATCatatggggaagtgaatcagtacaaccgccacagtacTGCTCGTCTGACC
B. cereus LMNB1_PBS 9	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatca

RT 20 AttB 36 atgRNA	acttgaaaaagtggcaccgagtcggtgcCGGGGGTCGCAGTCGCCATGatatggggaagtgaatcagtacaaccgccacagtacCGGGCGGCG
B. cereus LMNB1_PBS 13 RT 20 AttB 36 atgRNA	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcCGGGGGTCGCAGTCGCCATGatatggggaagtgaatcagtacaaccgccacagtacCGGGCGGCGGAGA
B. cereus LMNB1_PBS 13 RT 29 AttB 36 atgRNA	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGCGGCGGCACGGGGGTCGCAGTCGCCATGatatggggaagtgaatcagtacaaccgccacagtacCGGGCGGCGGAGA
B. cereus NOLC1_PBS 13 RT 29 AttB 36 atgRNA	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGAACCACGCGGCGAATGCCGGCGTCCGCCatatggggaagtgaatcagtacaaccgccacagtacTCCTCCAGGCAAT
B. cereus NOLC1_PBS 13 RT 20 AttB 36 atgRNA	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGGCGAATGCCGGCGTCCGCCatatggggaagtgaatcagtacaaccgccacagtacTCCTCCAGGCAAT
B. cereus NOLC1_PBS 18 RT 20 AttB 36 atgRNA	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGGCGAATGCCGGCGTCCGCCatatggggaagtgaatcagtacaaccgccacagtacTCCTCCAGGCAATACGCG
B. cereus SRRM2_PBS 9 RT 24 AttB 36 atgRNA	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGGCGTCGGCAGCCCGATCCCGTTGatatggggaagtgaatcagtacaaccgccacagtacTACATGGCC
B. cereus SRRM2_PBS 9 RT 10 AttB 36 atgRNA	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGATCCCGTTGatatggggaagtgaatcagtacaaccgccacagtacTACATGGCC
B. cereus SRRM2_PBS 13 RT 10 AttB 36 atgRNA	GGGCACGGGGCCATGTACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcGATCCCGTTGatatggggaagtgaatcagtacaaccgccacagtacTACATGGCCCCGT
Screen validation guides ACTB_1_11_24_38	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcgcgcggcgatatcatcatccatggatgatcctgacgacggagaccgccgtcgtcgacaagcctgagctgcgag
Screen validation guides ACTB_1_16_18_43	GCTATTCTCGCAGCTCACCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgccgatatcatcatccatggcggatgatcctgacgacggagaccgccgtcgtcgacaagccggctgagctgcgagaatag
Screen validation guides LMNB1_1_8_26_38	GCTGTCTCCGCCGCCCGCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcgcggcacgggggtcgcagtcgccatgatgatcctgacgacggagaccgccgtcgtcgacaagcccgggcggc
Screen validation guides NOLC1_1_15_16_43	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcaatgccggcgtccgcccggatgatcctgacgacggagaccgccgtcgtcgacaagccggctcctccaggcaatac
Screen validation guides NOLC1_1_14_10_38	GCGTATTGCCTGGAGGATGGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcggcgtccgccatgatcctgacgacggagaccgccgtcgtcgacaagcctcctccaggcaata
Screen validation guides SERPIN_13_32_38	GGGAAATGCATCTTGCACAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcagcccctccatgctctctagctgttgccattgggcttgtcgacgacggcggtctccgtcgtcaggatcattgcaagatgcatt
Screen validation guides DEPDC4_8_10_38	GTGTCAGGTGGGGCGGGGCTAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgctggcaccataatgatcctgacgacggagaccgccgtcgtcgacaag

	ccccccgccc
SERPIN Nicking guide -107 guide	GTGGGGACAGCCCCGTCTCTgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide -91 guide	GCTCTTGGGAAAAAAACCCTAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide -90 guide	GTCTTGGGAAAAAAACCCTAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide -84 guide	GAAAAAAACCCTAAGGGCTGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide -67 guide	GCTGAGGATCCTTGTGAGTGTgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide -66 guide	GTGAGGATCCTTGTGAGTGTTgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide -63 guide	GGATCCTTGTGAGTGTTGGGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide -62 guide	GATCCTTGTGAGTGTTGGGTgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide -49 guide	GTTGGGTGGGAACAGCTCCCgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide -46 guide	GGGTGGGAACAGCTCCCAGGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide +34 guide	GCTTCTGTGCAGCAGTTTCCCgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide +48 guide	GTTTCCCTGGCCACTAAATAGgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide +49 guide	GTTCCCTGGCCACTAAATAGTgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide +71 guide	GATTAGATAGAAGCCCTCCAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc
SERPIN Nicking guide +72 guide	GATTAGATAGAAGCCCTCCAAgttttagagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgc

Supplementary Table 5. Sequences of insertion sites

Description	Forward Sequence (5'-3')	Reverse Sequence (5'-3')
Bxb1_AttP_GT_original_site	GTGGTTTGTCTGGTCAACCACCGCGGTCTCA GTGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGACCGCGGT GGTTGACCAGACAAACCAC
Bxb1_AttP_CG_site	GTGGTTTGTCTGGTCAACCACCGCGcgCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGCGCGCGGT GGTTGACCAGACAAACCAC
Bxb1_AttP_GC_site	GTGGTTTGTCTGGTCAACCACCGCGgcCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGGCCGCGGT GGTTGACCAGACAAACCAC
Bxb1_AttP_AT_site	GTGGTTTGTCTGGTCAACCACCGCGatCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGATCGCGGTG GTTGACCAGACAAACCAC
Bxb1_AttP_TA_site	GTGGTTTGTCTGGTCAACCACCGCGtaCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGTACGCGGTG GTTGACCAGACAAACCAC
Bxb1_AttP_GG_site	GTGGTTTGTCTGGTCAACCACCGCGggCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGCCCGCGGTG GTTGACCAGACAAACCAC
Bxb1_AttP_TT_site	GTGGTTTGTCTGGTCAACCACCGCGttCTCAGT GGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGAACGCGGT GGTTGACCAGACAAACCAC
Bxb1_AttP_GA_site	GTGGTTTGTCTGGTCAACCACCGCGgaCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGTCCGCGGTG GTTGACCAGACAAACCAC
Bxb1_AttP_AG_site	GTGGTTTGTCTGGTCAACCACCGCGagCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGCTCGCGGTG GTTGACCAGACAAACCAC
Bxb1_AttP_CC_site	GTGGTTTGTCTGGTCAACCACCGCGccCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGGGCGCGGT GGTTGACCAGACAAACCAC
Bxb1_AttP_TC_site	GTGGTTTGTCTGGTCAACCACCGCGtcCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGGACGCGGT GGTTGACCAGACAAACCAC
Bxb1_AttP_CT_site	GTGGTTTGTCTGGTCAACCACCGCGctCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGAGCGCGGT GGTTGACCAGACAAACCAC
Bxb1_AttP_AA_site	GTGGTTTGTCTGGTCAACCACCGCGaaCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGTTCGCGGTG GTTGACCAGACAAACCAC
Bxb1_AttP_CA_site	GTGGTTTGTCTGGTCAACCACCGCGcaCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGTGCGCGGTG GTTGACCAGACAAACCAC
Bxb1_AttP_AC_site	GTGGTTTGTCTGGTCAACCACCGCGacCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGGTCGCGGTG GTTGACCAGACAAACCAC
Bxb1_AttP_TG_site	GTGGTTTGTCTGGTCAACCACCGCGtgCTCAG TGGTGTACGGTACAAACCCA	TGGGTTTGTACCGTACACCACTGAGCACGCGGT GGTTGACCAGACAAACCAC
Bxb1_AttB_46_GT_original_site	GGCCGGCTTGTCGACGACGGCGGTCTCCGTC GTCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGACCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_AA_site	GGCCGGCTTGTCGACGACGGCGaaCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGTTCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_GA_site	GGCCGGCTTGTCGACGACGGCGgaCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGTCCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_CA_site	GGCCGGCTTGTCGACGACGGCGcaCTCCGTCG	CCGGATGATCCTGACGACGGAGTGCGCCGTCGT

	TCAGGATCATCCGG	CGACAAGCCGGCC
Bxb1_AttB_46_TA_site	GGCCGGCTTGTCGACGACGGCGtaCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGTACGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_AG_site	GGCCGGCTTGTCGACGACGGCGagCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGCTCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_GG_site	GGCCGGCTTGTCGACGACGGCGggCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGCCCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_CG_site	GGCCGGCTTGTCGACGACGGCGcgCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGCGCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_TG_site	GGCCGGCTTGTCGACGACGGCGtgCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGCACGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_AC_site	GGCCGGCTTGTCGACGACGGCGacCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGGTCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_GC_site	GGCCGGCTTGTCGACGACGGCGgcCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGGCCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_CC_site	GGCCGGCTTGTCGACGACGGCGccCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGGGCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_TC_site	GGCCGGCTTGTCGACGACGGCGtcCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGGACGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_AT_site	GGCCGGCTTGTCGACGACGGCGatCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGATCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_CT_site	GGCCGGCTTGTCGACGACGGCGctCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGAGCGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_46_TT_site	GGCCGGCTTGTCGACGACGGCGttCTCCGTCG TCAGGATCATCCGG	CCGGATGATCCTGACGACGGAGAACGCCGTCGT CGACAAGCCGGCC
Bxb1_AttB_38_GT_site	GGCTTGTCGACGACGGCGGTCTCCGTCGTCA GGATCAT	ATGATCCTGACGACGGAGACCGCCGTCGTCGAC AAGCC
Bxb1_AttB_38_AA_site	GGCTTGTCGACGACGGCGaaCTCCGTCGTCAG GATCAT	ATGATCCTGACGACGGAGTTCGCCGTCGTCGAC AAGCC
Bxb1_AttB_38_GA_site	GGCTTGTCGACGACGGCGgaCTCCGTCGTCAG GATCAT	ATGATCCTGACGACGGAGTCCGCCGTCGTCGAC AAGCC
Bxb1_AttB_38_CA_site	GGCTTGTCGACGACGGCGcaCTCCGTCGTCAG GATCAT	ATGATCCTGACGACGGAGTGCGCCGTCGTCGAC AAGCC
Bxb1_AttB_38_TA_site	GGCTTGTCGACGACGGCGtaCTCCGTCGTCAG GATCAT	ATGATCCTGACGACGGAGTACGCCGTCGTCGAC AAGCC
Bxb1_AttB_38_AG_site	GGCTTGTCGACGACGGCGagCTCCGTCGTCAG GATCAT	ATGATCCTGACGACGGAGCTCGCCGTCGTCGAC AAGCC
Bxb1_AttB_38_GG_site	GGCTTGTCGACGACGGCGggCTCCGTCGTCAG GATCAT	ATGATCCTGACGACGGAGCCCGCCGTCGTCGAC AAGCC
Bxb1_AttB_38_CG_site	GGCTTGTCGACGACGGCGcgCTCCGTCGTCAG GATCAT	ATGATCCTGACGACGGAGCGCGCCGTCGTCGAC AAGCC
Bxb1_AttB_38_TG_site	GGCTTGTCGACGACGGCGtgCTCCGTCGTCAG GATCAT	ATGATCCTGACGACGGAGCACGCCGTCGTCGAC AAGCC

Bxb1_AttB_38_AC_site	GGCTTGTCGACGACGGCGacCTCCGTCGTCAGGATCAT	ATGATCCTGACGACGGAGGTCGCCGTCGTCGACAAGCC
Bxb1_AttB_38_GC_site	GGCTTGTCGACGACGGCGgcCTCCGTCGTCAGGATCAT	ATGATCCTGACGACGGAGGCCGCCGTCGTCGACAAGCC
Bxb1_AttB_38_CC_site	GGCTTGTCGACGACGGCGccCTCCGTCGTCAGGATCAT	ATGATCCTGACGACGGAGGGCGCCGTCGTCGACAAGCC
Bxb1_AttB_38_TC_site	GGCTTGTCGACGACGGCGtcCTCCGTCGTCAGGATCAT	ATGATCCTGACGACGGAGGACGCCGTCGTCGACAAGCC
Bxb1_AttB_38_AT_site	GGCTTGTCGACGACGGCGatCTCCGTCGTCAGGATCAT	ATGATCCTGACGACGGAGATCGCCGTCGTCGACAAGCC
Bxb1_AttB_38_CT_site	GGCTTGTCGACGACGGCGctCTCCGTCGTCAGGATCAT	ATGATCCTGACGACGGAGAGCGCCGTCGTCGACAAGCC
Bxb1_AttB_38_TT_site	GGCTTGTCGACGACGGCGttCTCCGTCGTCAGGATCAT	ATGATCCTGACGACGGAGAACGCCGTCGTCGACAAGCC
Cre Lox 66 site	TACCGTTCGTATAATGTATGCTATACGAAGTTAT	ATAACTTCGTATAGCATACATTATACGAACGGTA
Cre Lox 71 site	ATAACTTCGTATAATGTATGCTATACGAACGGTA	TACCGTTCGTATAGCATACATTATACGAAGTTAT
TP901-1 minimal AttB site	TTTACCTTGATTGAGATGTTAATTGTG	CACAATTAACATCTCAATCAAGGTAAA
TP901-1 minimal AttP site	GCGAGTTTTTATTTCGTTTATTTCAATTAAGGTAACTAAAAAACTCCTTT	AAAGGAGTTTTTTAGTTACCTTAATTGAAATAAACGAAATAAAAACTCGC
PhiBT1 minimal AttB site	CTGGATCATCTGGATCACTTTCGTCAAAAACCTG	CAGGTTTTTGACGAAAGTGATCCAGATGATCCAG
PhiBT1 minimal AttP site	TTCGGGTGCTGGGTTGTTGTCTCTGGACAGTGATCCATGGGAAACTACTCAGCACCA	TGGTGCTGAGTAGTTTCCCATGGATCACTGTCCAGAGACAACAACCCAGCACCCGAA
Bacillus_cereus_AH187_Int30_38bp_Att	gatatggggaagtgaatcagtacaaccgccacagtacc	ggtactgtggcggttgtactgattcacttccccatatc
Staphylococcus_lugdunensis_N920143_Int12_38bp_Att	tgggtggtacaggtgccacattagttgtaccatttatg	cataaatggtacaactaatgtggcacctgtaccaccca
Bacillus_cytotoxicus_NVH_391-98_Int13_38bp_Att	gttgtttttccagatccagttggtcctgtaaatataag	cttatatttacaggaccaactggatctggaaaaacaac
Bacillus_cereus_AH187_Int30_Att_30	tggggaagtgaatcagtacaaccgccacag	ctgtggcggttgtactgattcacttcccca
Bacillus_cereus_AH187_Int30_Att_28	ggggaagtgaatcagtacaaccgccaca	tgtggcggttgtactgattcacttcccc
Bacillus_cereus_AH187_Int30_Att_26	gggaagtgaatcagtacaaccgccac	gtggcggttgtactgattcacttccc
Bacillus_cereus_AH187_Int30_Att_rc_30	ctgtggcggttgtactgattcacttcccca	tggggaagtgaatcagtacaaccgccacag
Bacillus_cereus_AH1	tgtggcggttgtactgattcacttcccc	ggggaagtgaatcagtacaaccgccaca

87_Int30_Att_rc_28		
Bacillus_cereus_AH187_Int30_Att_rc_26	gtggcggttgtactgattcacttccc	gggaagtgaatcagtacaaccgccac
Bacillus_cytotoxicus_NVH_391-98_Int13_Att_30	tttttccagatccagttggtcctgtaaata	tatttacaggaccaactggatctggaaaaa
Bacillus_cytotoxicus_NVH_391-98_Int13_Att_28	ttttccagatccagttggtcctgtaaat	atttacaggaccaactggatctggaaaa
Bacillus_cytotoxicus_NVH_391-98_Int13_Att_26	tttccagatccagttggtcctgtaaa	tttacaggaccaactggatctggaaa
Bacillus_cytotoxicus_NVH_391-98_Int13_Att_rc_30	tatttacaggaccaactggatctggaaaaa	tttttccagatccagttggtcctgtaaata
Bacillus_cytotoxicus_NVH_391-98_Int13_Att_rc_28	atttacaggaccaactggatctggaaaa	ttttccagatccagttggtcctgtaaat
Bacillus_cytotoxicus_NVH_391-98_Int13_Att_rc_26	tttacaggaccaactggatctggaaa	tttccagatccagttggtcctgtaaa
N680429_560_31_50bp	CATTATATGTTTTTACAATCCGGGCCGCCATACTGTAAGAACATATAATG	cattatatgttcttacagtatggcggcccggattgtaaaaacatataatg
N191607_8_101_50bp	CGTTATAGGGTATTGCAGTACCGACCGCCATACTGTAATACCCTATAACG	cgttatagggtattacagtatggcggtcggtactgcaataccctataacg
N674992_1_1308_50bp	TGTATCATTTTCATATAGTGTGCAGGTGCTAACTATATGAAAATGATACA	tgtatcattttcatatagttagcacctgcacactatatgaaaatgatacaa
N684613_54_96_50bp	TGTCTACTATGTCTTTATGCCACATGTGTCGCATATACAGATAGTAGACA	tgtctactatctgtatatgcgacacatgtggcataaagacatagtagaca
N252616_121_74_50bp	AATGAGGTCAGACGCATGGAGCGCCGCCTCCGCATGCGTCAGGGTCGATG	catcgaccctgacgcatgcggaggcggcgctccatgcgtctgactcatt
N683040_222_19_50bp	GTTAGTACCCAAATGATAAAAGGATGACCTTTTGTCATTTGGGTACTAAC	gttagtacccaaatgacaaaaggtcatccttttatcatttgggtactaac
N687537_173_59_50bp	GTTTATAAAACCGATGCCGCTTTGACAGAAGCGGAACGGGTTTTAATAAG	cttattaaaacccgttccgcttctgtcaaagcggcatcggttttataaac
N183629_47_40_50bp	GGCCGCGAGGTCGTGTTCGTCGTCATGTTGAGGTTCACGACCATCACGCC	ggcgtgatggtcgtgaacctcaacatgacgacgaacacgacctcgcggcc
N191533_224_76_50bp	TATAAACTGATATAATTCAAAGTTATAACTTGATATATTCAAGATGTAGA	tctacatcttgaatatatcaagttataactttgaattatatcagtttata
N682356_188_20_50bp	TATTATATCTAAAAGCAGTATGGCGGAGCTTAGTGCTTTTAGATATAATT	aattatatctaaaagcactaagctccgccatactgcttttagatataata

Supplementary Table 6. Mammalian expression plasmids

Name	Full Description	Benchling link
PE2-Bxb1 Single Vector	pCMV-PE2-P2A-Bxb1	https://benchling.com/s/seq-NIW2rI9OUqYpAmedqicN
PE2 prime editor	pCMV-PE2 / Addgene #132775	https://benchling.com/s/seq-C6YkN30h9vvBPv8XKj47
PASTEv3	pCMV-SpCas9-XTEN3-RT(L139P)-(GGS)6-BxbINT	https://benchling.com/s/seq-6PrptF4jyyE6fkDLKc88
PASTEv4	pCMV-SpCas9-XTEN-RT(L139P)-(GGGS)3-BceINT	https://benchling.com/s/seq-mGirm9x1J7IS0fKRHhXE
ACTB atgRNA with v1 scaffold	ACTB N-term PBS 13 RT 29 AttB 46 atgRNA	https://benchling.com/s/seq-h2yh6lfsvGpgG7XRRLbT
ACTB atgRNA with v2 scaffold	ACTB N-term PBS 13 RT 29 AttB 46 atgRNA with v2 scaffold	https://benchling.com/s/seq-qsyXbHzeyxBMzPJEciMg
ACTB Nicking +48	ACTB N-term Nicking guide 1 +48 guide	https://benchling.com/s/seq-VWT8CHMkrIRRnsqoIRUS
Bxb1 integrase	pCAG-NLS-HA-Bxb1integrase / Addgene #51271	https://benchling.com/s/seq-bLuI9aGZCKRbquNPXpjy
TP901-1 Integrase	TP901-1 Integrase	https://benchling.com/s/seq-TV8nlYedd6KaXcyMYQ3O
PhiBT Integrase	PhiBT Integrase	https://benchling.com/s/seq-aUFmVRg2Cg7kteXnIai2
Cre recombinase	pCAG-Cre recombinase	https://benchling.com/s/seq-DOwArJA1JjD51YCsVUyd
BceINT expression vector	pCAG-NLS-BceINT	https://benchling.com/s/seq-hoKLjTbug98wVgg9cpCM
SscINT expression vector	pCAG-NLS-SscINT	https://benchling.com/s/seq-D37aMwZ0Gg5PlwLDtdCK

SacINT expression vector	pCAG-NLS-SacINT	https://benchling.com/s/seq-dVDhPf8bez3pHz1WxLkI
HDR sgRNA guide backbone	Minicircle U6-sgRNA EFS-SpCas9	https://benchling.com/s/seq-2k8wqDuZZC8JY5wD1qGo
HDR EGFP cargo	Cas9 HDR template site with EGFP	https://benchling.com/s/seq-K79T50GVDRzDWmZLzxry
AAV helper plasmid	PDF6 AAV helper plasmid	https://benchling.com/s/seq-wGjfkT7PBA2YmmgrWuyn
AAV EGFP donor	GFP AAV donor plasmid	https://benchling.com/s/seq-BNsdctCG40dNVgOEs4pA
AAV2/8	AAV2/8 capsid protein	https://benchling.com/s/seq-Pk1fGlxnNCAsriHCCBfo
Adenovirus EGFP donor	Adenovirus AdEasy-1 backbone with EGFP gene	https://benchling.com/s/seq-HOCw7Wq0ifHTMak47oIA
Adenovirus for SpCas9-RT expression	Adenovirus AdEasy-1 backbone pCMV-SpCas9-RT-P2A-Blast	https://benchling.com/s/seq-G9fBVk4IB310dSQ3yF2P
Adenovirus for Bxb1 and guide expression	Adenovirus AdEasy-1 backbone pCMV-NLS-Bxb1Blast; pCAG-EGFP; ACTB atgRNA and nicking guide	https://benchling.com/s/seq-1rvrcTnyksAjHncDKCp2

Supplementary Table 7. Minicircle cargo gene maps

Name	Full Description	Benchling link
Cargo EGFP	Parent minicircle plasmid - Cargo EGFP with AttP Bxb1 site	https://benchling.com/s/seq-RksgOMHffn5auc9ZbcHA
Cargo EGFP post cleavage	Cargo EGFP with AttP Bxb1 site - post minicircle cleavage	https://benchling.com/s/seq-Na8dODu7S991LQkifkPB
Cargo EGFP for fusion	Parent minicircle plasmid - Cargo EGFP with AttP Bxb1 site for fusion	https://benchling.com/s/seq-xdAIg3Ows9xH4RmIv6wP
mCherry Cargo post cleavage	Cargo mCherry with AttP Bxb1 site - post minicircle cleavage	https://benchling.com/s/seq-j7JDfHwufSdGxkskf9q8
YFP Cargo post cleavage	Cargo YFP with AttP Bxb1 site - post minicircle cleavage	https://benchling.com/s/seq-161oVqnrJvKvT5Gckzc1
SERPINA1 Cargo post cleavage	Cargo SERPINA1 with AttP Bxb1 site - post minicircle cleavage	https://benchling.com/s/seq-mJmyrX4bGCemUysu4obP
CPS1 Cargo post cleavage	Cargo CPS1 with AttP Bxb1 site - post minicircle cleavage	https://benchling.com/s/seq-5VlYu3w2FQUWIfAETQvJ
NYESO TCR Cargo post cleavage	Cargo NYESO TCR with AttP Bxb1 site - post minicircle cleavage	https://benchling.com/s/seq-ZgCsKas7TIkxis23XEDq
HBB Cargo	Parent minicircle plasmid - Cargo HBB with AttP Bxb1 site	https://benchling.com/s/seq-SjQrU2dc7rCjZ5ktbTVE

Hexa Cargo	Parent minicircle plasmid - Cargo Hexa with AttP Bxb1 site	https://benchling.com/s/seq-JlrqcAgvuRBTvoBrocEM
PAH Cargo	Parent minicircle plasmid - Cargo PAH with AttP Bxb1 site	https://benchling.com/s/seq-tmrugQOvFp1TyMDy95tE
GBA Cargo	Parent minicircle plasmid - Cargo GBA with AttP Bxb1 site	https://benchling.com/s/seq-sRE7PLmHEA269xToMHyI
ADA Cargo	Parent minicircle plasmid - Cargo ADA with AttP Bxb1 site	https://benchling.com/s/seq-1cxKDHbDJisWtqLzWOJW
CEP290 Cargo	Parent minicircle plasmid - Cargo CEP290 with AttP Bxb1 site	https://benchling.com/s/seq-nkJagJzDXsN4kNJGYXYq
SERPINA1-HIBIT Cargo	Parent minicircle plasmid - Cargo SERPINA1-HIBIT with AttP Bxb1 site	https://benchling.com/s/seq-Gfx0YkqhDaJCr8RjYL1G
CPS1-HIBIT Cargo	Parent minicircle plasmid - Cargo CPS1- HIBIT with AttP Bxb1 site	https://benchling.com/s/seq-CnPeB8MAX1V943N47B3q
ACTB HITI post cleavage	HITI template for ACTB locus - post minicircle cleavage	https://benchling.com/s/seq-q3ExdFaCoiExkr9cZAvx
SUPTH16 HITI post cleavage	HITI template for SUPTH16 locus - post minicircle cleavage	https://benchling.com/s/seq-N3JNZ3DSi7h2YlOo2ELQ
SRRM2 HITI post cleavage	HITI template for SRRM2 locus - post minicircle cleavage	https://benchling.com/s/seq-xORs0oLiIQI56GrZc0aJ
NOLC1 HITI post cleavage	HITI template for NOLC1 locus - post minicircle	https://benchling.com/s/seq-uSGfnt2OkPS5UCtPJFMj

	cleavage	
LMNB1 HITI post cleavage	HITI template for LMNB1 locus - post minicircle cleavage	https://benchling.com/s/seq-jYHbVXXsBKxxcEytXC01
DEPDC4 HITI post cleavage	HITI template for DEPDC4 locus - post minicircle cleavage	https://benchling.com/s/seq-fS7vKseJCDTjJJITfzzd
NES HITI post cleavage	HITI template for NES locus - post minicircle cleavage	https://benchling.com/s/seq-Tx6nu4NiQkN7cYzjRujo

Supplementary Table 8. Primers, probes and restriction enzymes used in ddPCR readout

Locus	Cargo	Forward Primer	Reverse Primer	Probe	Restriction Enzymes
ACTB	GFP (pDY0186)	CCCGGCTTCCTTTGTCC	GAACTCCACGCCGTTCA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco91I, HindIII
ACTB	TP90-1 GFP (pDY0333)	CCCGGCTTCCTTTGTCC	AACCACAACTAGAATGCAGTGA	/56-FAM/TG CTA TTG C/ZEN/T TTA TTT GTG GGC CCG /3IABkFQ/	None
ACTB	TP90-1 rc GFP (pDY0334)	CCCGGCTTCCTTTGTCC	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	None
ACTB	Bt1INT GFP (pDY0367)	CCCGGCTTCCTTTGTCC	AACCACAACTAGAATGCAGTGA	/56-FAM/TG CTA TTG C/ZEN/T TTA TTT GTG GGC CCG /3IABkFQ/	None
ACTB	Bt1INT rc GFP (pDY0368)	CCCGGCTTCCTTTGTCC	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	None
LMNB1	GFP (pDY0186)	TCCTTATCACGGTCCCGCTCG	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I, HindIII
NOLC1	GFP (pDY0186)	CGTCGACAACGGTAGTG	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I, HindIII
SERPIN1	GFP (pDY0186)	GGATCCTTGTGAGTGTTGGG	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I, HindIII
SUPT16H	GFP (pDY0186)	TCGCGTGATTCTCGGAAC	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I, HindIII
SRRM2	GFP (pDY0186)	GGGCGGTAAGTGGTTAGTTT	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I, HindIII
DEPDC4	GFP (pDY0186)	AAGAGGCGGAGCCAGTA	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I, HindIII
NES	GFP (pDY0186)	CTCCCTTCTCCCGGTGCCC	GAACTCCACGCCGTTCA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco91I, HindIII
ACTB	ACTB HITI template GFP (pDY0219)	CCCGGCTTCCTTTGTCC	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I
SRRM2	SRRM2 HITI template GFP (aRY0182_A2)	GGGCGGTAAGTGGTTAGTTT	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I

NOLC1	NOLC1 HITI template GFP (aRY0182_A3)	CGTCGACAACGGTAGTG	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I
DEPDC4	DEPDC4 HITI template GFP (aRY0182_A5)	AAGAGGCGGAGCCAGTA	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I
NES	NES HITI template GFP (aRY0182_A7)	CTCCCTTCTCCCGGTGCCC	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I
LMNB1	LMNB1 HITI template GFP (aRY0182_A4)	TCCTTATCACGGTCCCGCTCG	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I
SUPT16H	SUPT16H HITI template GFP (aRY0182_A1)	TCGCGTGATTCTCGGAAC	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I
ACTB	SERPINA (pDY0298)	CCCGGCTTCCTTTGTCC	GGCCTGCCAGCAGGAGGA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	EcoRI, XhoI, HindIII
ACTB	CPS1 (pDY299)	CCCGGCTTCCTTTGTCC	GGTGTGCAGTCACATTGGTAAAGCC	/56-FAM/AC AGC TTT C/ZEN/A AAG TGG TGA GGA CAC T/3IABkFQ/	XhoI, HindIII
ACTB	CFTR (pDY0373)	CCCGGCTTCCTTTGTCC	GATGGGTCTAGTCCAGCTAAAG	/56-FAM/TACGGTACA/ZEN/AACCCACCCGAGAGA/3IABkFQ/	Eco91I, HindIII
ACTB	NYESO TRAC (pDY0318)	CCCGGCTTCCTTTGTCC	GAGAGACAAGGCTGCACA	/56-FAM/TACGGTACA/ZEN/AACCCACCCGAGAGA/3IABkFQ/	Eco47III, HindIII
LMNB1	NYESO TRAC (pDY0318)	TCCTTATCACGGTCCCGCTCG	GAGAGACAAGGCTGCACA	/56-FAM/TACGGTACA/ZEN/AACCCACCCGAGAGA/3IABkFQ/	Eco47III, HindIII
LMNB1	SERPINA (pDY0298)	TCCTTATCACGGTCCCGCTCG	GGCCTGCCAGCAGGAGGA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	EcoRI, XhoI, HindIII
NC_000003	GFP (pDY0186)	CCAGGTGAGAGTCAGGGTAGTGTTCA	GAACTCCACGCCGTTCA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco91I, HindIII
NC_000002	GFP (pDY0186)	AGGGACCTTTGCCTGTGTGAGTC	GAACTCCACGCCGTTCA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco91I, HindIII
NC_000009	GFP (pDY0186)	TCAGCTCTGTGCTGAGGCGAA	GAACTCCACGCCGTTCA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco91I, HindIII
chr6:149045959	GFP (pDY0186)	AAGCCATCTCCCAGAATATCTGCTTAGAAATG	GAACTCCACGCCGTTCA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco91I, HindIII
chr16:18607730	GFP (pDY0186)	GAGAGGAGCAACAGTGAGCATGATG	GAACTCCACGCCGTTCA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco91I, HindIII
chr6:1490459	ACTB HITI template	AAGCCATCTCCCA	GAACTCCACGCCG	/56-FAM/CC GGC TTG T/ZEN/C	Eco91I

59	GFP (pDY0219)	GAATATCTGCTTAGAAATG	TTCA	GAC GAC GGC G/3IABkFQ/	
chr16:18607730	ACTB HITI template GFP (pDY0219)	GAGAGGAGCAACAGTGAGCATGATG	GAACTCCACGCCGTTCA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco91I
ACTB	CAG_Kozak_bGH_therapeutic_genes generic minicircle	CCCGGCTTCCTTTGTCC	GGCTATGAACTAATGACCCCGT	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco91I, HindIII
ACTB	Hibit-SERPINA (pDY0405)	CCCGGCTTCCTTTGTCC	GGCCTGCCAGCAGGAGGA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	EcoRI, XhoI, HindIII
ACTB	Hibit-CPS1 (pDY406)	CCCGGCTTCCTTTGTCC	GGTGTGCAGTCACATTGGTAAAGCC	/56-FAM/AC AGC TTT C/ZEN/A AAG TGG TGA GGA CAC T/3IABkFQ/	XhoI, HindIII
LMNB1	mCherry (pDY0414)	TCCTTATCACGGTCCCGCTCG	cgcatgaactccttgatgatggcc	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	EheI, HindIII
NOLC1	(YBP pDY0415)	CGTCGACAACGGTAGTG	GGCACCACTCCGGTAAA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	Eco47I, HindIII
ACTB	AAV and Adenovirus Cargo (pDY0611)	CCCGGCTTCCTTTGTCC	GAACTCCACGCCGTTCA	/56-FAM/CC GGC TTG T/ZEN/C GAC GAC GGC G/3IABkFQ/	PacI, HindIII
ACTB	GFP universal, (novel integrases)	CCCGGCTTCCTTTGTCC	GAACTCCACGCCGTTCA	/56-FAM/CC ATG AAG A/ZEN/T CGA GTG CCG CAT CA/3IABkFQ/	Eco91I, HindIII

Supplementary Table 9. Primers used for NGS readout

Description	ID	Sequence (5'-3')
N-term ACTB Tn5 readout F 1	PD0966	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCCGACCTCGGCTCACAGCG
N-term ACTB Tn5 readout F 2	PD0967	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACCGACCTCGGCTCACAGCG
N-term ACTB Tn5 readout F 3	PD0968	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACCGACCTCGGCTCACAGCG
N-term ACTB Tn5 readout F 4	PD0969	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACCGACCTCGGCTCACAGCG
N-term ACTB Tn5 readout F 5	PD0970	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGACCGACCTCGGCTCACAGCG
N-term ACTB Tn5 readout F 6	PD0971	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACTGACCGACCTCGGCTCACAGCG
N-term ACTB Tn5 readout F 7	PD0972	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTACTGACCGACCTCGGCTCACAGCG
N-term ACTB Tn5 readout F 8	PD0973	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGTACTGACCGACCTCGGCTCACAGCG
ACTB N-term NGS R for Cas14 indels	FP0952	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCACCCAGCCAGCTCCC
LMNB1 locus NGS F 1	PD3337	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCCGCTTCGCCCCCTGCC
LMNB1 locus NGS F 2	PD3338	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACCGCTTCGCCCCCTGCC
LMNB1 locus NGS F 3	PD3339	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACCGCTTCGCCCCCTGCC
LMNB1 locus NGS F 4	PD3340	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACCGCTTCGCCCCCTGCC
LMNB1 locus NGS F 5	PD3341	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGACCGCTTCGCCCCCTGCC
LMNB1 locus NGS F 6	PD3342	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACTGACCGCTTCGCCCCCTGCC
LMNB1 locus NGS F 7	PD3343	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTACTGACCGCTTCGCCCCCTGCC
LMNB1 locus NGS F 8	PD3344	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGTACTGACCGCTTCGCCCCCTGCC
LMNB1 locus NGS R	PD3336	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGTCATTGAGCTCGCGCAGC
NOLC1 NGS F 1	A9 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCGAGTCGTGCTGCGTCGACAA
NOLC1 NGS F 2	A10 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACGAGTCGTGCTGCGTCGACAA
NOLC1 NGS F 3	A11 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACGAGTCGTGCTGCGTCGACAA

NOLC1 NGS F 4	A12 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACGAGTCGTGCTGCGTCGACAA
NOLC1 NGS R	C3 aD0046	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGGCGAACTTATTGGCCACCTCT
SUPT16H NGS F 1	A1 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCCGGGACCTCGCGTGATTCTC
SUPT16H NGS F 2	A2 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACCGGGACCTCGCGTGATTCTC
SUPT16H NGS F 3	A3 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACCGGGACCTCGCGTGATTCTC
SUPT16H NGS F 4	A4 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACCGGGACCTCGCGTGATTCTC
SUPT16H NGS R	C1 aD0046	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTCACCCGCCAATTGCTGTACA
DEPDC4 NGS F 1	B1 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCAAGAGGCGGAGCCAGTACTTCTC
DEPDC4 NGS F 2	B2 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACAAGAGGCGGAGCCAGTACTTCTC
DEPDC4 NGS F 3	B3 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACAAGAGGCGGAGCCAGTACTTCTC
DEPDC4 NGS F 4	B4 aD0046	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACAAGAGGCGGAGCCAGTACTTCTC
DEPDC4 NGS R	C4 aD0046	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCCGGAAGCTCGTTCTGACTGA
NES NGS F1	PD5198	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCAAGCTCTGCGAGCCGCTC
NES NGS F2	PD5199	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACAAGCTCTGCGAGCCGCTC
NES NGS F3	PD5200	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACAAGCTCTGCGAGCCGCTC
NES NGS F4	PD5201	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACAAGCTCTGCGAGCCGCTC
NES NGS R	PD5202	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCGCGCTGAGCAGCTCAT
CFTR NGS F 1	PD3500	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCAGCGGCAGGCACCCAGA
CFTR NGS F 2	PD3501	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACAGCGGCAGGCACCCAGA
CFTR NGS F 3	PD3502	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACAGCGGCAGGCACCCAGA
CFTR NGS F 4	PD3503	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACAGCGGCAGG

		CACCCAGA
CFTR NGS R	PD3504	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTTTTCCAGAGGCGACCTCTGC
SERPINA1 locus new NGS 1 F 1	PD3487	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGTGTCTGGGACCACAGAGCATTG
SERPINA1 locus new NGS 1 F 2	PD3488	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACTGTGTCTGGGACCACAGAGCATTG
SERPINA1 locus new NGS 1 F 3	PD3489	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACTGTGTCTGGGACCACAGAGCATTG
SERPINA1 locus new NGS 1 F 4	PD3490	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACTGTGTCTGGGACCACAGAGCATTG
SERPINA1 locus new NGS 1 F 5	PD3491	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGACTGTGTCTGGGACCACAGAGCATTG
SERPINA1 locus new NGS 1 F 6	PD3492	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACTGACTGTGTCTGGGACCACAGAGCATTG
SERPINA1 locus new NGS 1 F 7	PD3493	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTACTGACTGTGTCTGGGACCACAGAGCATTG
SERPINA1 locus new NGS 1 F 8	PD3494	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGTACTGACTGTGTCTGGGACCACAGAGCATTG
SERPINA1 locus new NGS 1 R	PD3581	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTccaggaatcgggccagatcagaatc
NGS EMX1 Forward 1	PD0313	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCCGGTGGCGCATTGCCAC
NGS EMX1 Forward 2	PD0314	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACCGGTGGCGCATTGCCAC
NGS EMX1 Forward 3	PD0315	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACCGGTGGCGCATTGCCAC
NGS EMX1 Forward 4	PD0316	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACCGGTGGCGCATTGCCAC
NGS EMX1 Forward 5	PD0317	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGACCGGTGGCGCATTGCCAC
NGS EMX1 Forward 6	PD0318	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACTGACCGGTGGCGCATTGCCAC
NGS EMX1 Forward 7	PD0319	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTACTGACCGGTGGCGCATTGCCAC
NGS EMX1 Forward 8	PD0320	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGTACTGACCGGTGGCGCATTGCCAC
NGS EMX1 Reverse	PD0321	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAGAGTCCAGCTTGGGCCCA

Supplementary Table 10. UMI TN5 primers for genome-wide off target integration detection

Tn5 off-target EGFP pDY232 minicircle Upstream Round 1 Forward primer	PD3327	AGGAGCTGCACAGCAACACC
Tn5 off-target EGFP minicircle pDY232 NGS F 1	PD3328	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCCCTTCGCCAG ATCTCGAGCTC
Tn5 off-target EGFP minicircle pDY232 NGS F 2	PD3329	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACCCTTCGCCA GATCTCGAGCTC
Tn5 off-target EGFP minicircle pDY232 NGS F 3	PD3330	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACCCTTCGCC AGATCTCGAGCTC
Tn5 off-target EGFP minicircle pDY232 NGS F 4	PD3331	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACCCTTCGCC AGATCTCGAGCTC
Tn5 off-target EGFP minicircle pDY232 NGS F 5	PD3332	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGACCCTTCGC CAGATCTCGAGCTC
Tn5 off-target EGFP minicircle pDY232 NGS F 6	PD3333	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACTGACCCTTC GCCAGATCTCGAGCTC
Tn5 off-target EGFP minicircle pDY232 NGS F 7	PD3334	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTACTGACCCTTC GCCAGATCTCGAGCTC
Tn5 off-target EGFP minicircle pDY232 NGS F 8	PD3335	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGTACTGACCCTT CGCCAGATCTCGAGCTC
nested_outside_U6_F	PD4229	TGGACTATCATATGCTTACCGTAACTTGAAAGTAT
nested_inside_Sp_scaffold_NGS_F1	PD4225	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCGTCCGTTATCA ACTTGAAAAAGTGGCACC
nested_inside_Sp_scaffold_NGS_F2	PD4226	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACGTCCGTTATC AACTTGAAAAAGTGGCACC
nested_inside_Sp_scaffold_NGS_F3	PD4227	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACGTCCGTTA TCAACTTGAAAAAGTGGCACC
nested_inside_Sp_scaffold_NGS_F4	PD4228	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGACGTCCGTT ATCAACTTGAAAAAGTGGCACC
Index primer rev	FP0808	GTGACTGGAGTTCAGACGTGTGCTC

Supplementary Table 11. Off-target sites

Description	**Sequence (5'-3')**
Cas9_chr6:149045959	GATATTTTCCCAGCTCACCA

Cas9_chr16:18607730	TCTATTCTCCCAGCTCCCCA
Bxb1_NC_000002 (chr 2)	AGCGGCTTCTGTCTCTGTGAGTGAGCTGGCGGTCTCCGTC
Bxb1_NC_000003 (chr 3)	GACTAGCCCACGCTCCGGTTCTGAGCCGCGACGGCGGTCTCCG
Bxb1_NC_000009 (chr 9)	CCCAGGGTCCCATGCGCTCCCCGGCCCTGACGGCGGTCTCC