

Vector Name	AR	Tag/Flag	Protease cleavage	Tag and linker	Sequence primers
pLEICS-01	Amp	N-His ₆	TEV Extra SM	His6-SSGVDLGT-TEV site-1	T7 Promoter pLEICS-01-Seq-R
pLEICS-02	Amp	N-GST	TEV Extra SM	GST-SS-TEV Site-1	pGEX5 pGEX3
pLEICS-03	Kan	N-His ₆	TEV Extra SM	His6-SSGVDLGT-TEV site-1	T7 Promoter T7 terminator
pLEICS-04	Kan	N-GST	TEV Extra SM	GST-SS-TEV Site-1	pGEX5 T7 terminator
pLEICS-05	Amp	C-His ₆	TEV Extra ENLYFQ	TEV site-1-LE-His6	T7 Promoter T7 terminator
pLEICS-06	Amp	N-His ₆ for first gene C- His ₆ /S for second gene	TEV Extra SM Extra ENLYFQ	His6-SSGVDLGT-TEV site-1 TEV site-1-LE-His6-LESG-S-STSAA	pLEICS-06-F1-Seq pLEICS-06-R1-Seq pLEICS-06-F2-Seq T7 terminator
pLEICS-07	Kan	N-His ₆ /S	TEV Extra GA	His6-SSGLVPRGSGM-S-PDLGTGS-TEV site-2	T7 Promoter T7 terminator
pLEICS-08	Kan	N-GST/ N-His ₆ /S	TEV Extra GA	GST-DGSTSGSG-His6-SAGLVPRGSTAIGM-S-PDLGTGS-TEV site-2	pGEX5 T7 terminator
pLEICS-09	Amp	N-Trx N-His ₆ /S	TEV Extra GA	Trx-GSGSGHM-His6-SSGLVPRGSGM-S-PDLGTGS-TEV site-2	pLEICS-09-Seq-F T7 terminator
pLEICS-10	Amp	N-MBP	TEV Extra GA	MBP-SNNNNNNNNNNNLG-TEV site-2	pLEICS-10-Seq-F pLEICS-10-Seq-R
pLEICS-11	Amp	N-His ₆	TEV Extra GA	His6-DYDIPTT-TEV site-2	pLEICS-11-Seq-F pLEICS-11-Seq-R
pLEICS-12	Amp/Neo	N-His ₁₀ /3 x Flag	TEV Extra GA	His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2	pLEICS-12-Seq-F pLEICS-12-Seq-R
pLEICS-13	Amp/Zeo	N-His ₁₀ /3 x Flag	TEV Extra GA	His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2	pLEICS-12-Seq-F pLEICS-12-Seq-R
pLEICS-14	Amp	N-GST	TEV Extra GA	GST-GS-TEV site-2	pGEX5 pGEX3
pLEICS-15	Kan/Neo	N-TAP	TEV Extra GA	TAP-CPGGS-TEV site-2	pLEICS-15-Seq-F T7 Promoter
pLEICS-16	Amp	N-GST	TEV Extra GA	GST-DLVPRGS-TEV site-2	pGEX5 pLEICS-11-Seq-R
pLEICS-17	Kan	N-GST/His ₆	TEV Extra GA	GST-GSTSGGGGSSNNNPPTPTPSSGSG-His6-SAALEVLFGQPGYQDP-TEV site-2	pLEICS-17-Seq-F T7 terminator
pLEICS-18	Kan	N-MBP	TEV Extra GA	MBP-SNNNNNNNNNNPMS-TEV site-2	pLEICS-10-Seq-F T7 terminator
pLEICS-19	Amp	N-HA	TEV Extra GA	HA(MYPYDVPDYA)-LMAMEAR-TEV site-2	pLEICS-19-Seq-F pLEICS-19-Seq-R
pLEICS-20	Amp	N-myc	TEV Extra GA	Myc(ASMQUALISEEDL)- LMAMEAR-TEV site-2	pLEICS-19-Seq-F pLEICS-19-Seq-R

Vector Name	AR	Tag/Flag	Protease cleavage	Tag and linker	Sequence primers
pLEICS-21	Kan/Neo	N-EGFP	TEV Extra GA	EGFP-SGLRSR-TEV site-2 EGFP-SGLRS	pLEICS-21-Seq-F pLEICS-21-Seq-R
pLEICS-22	Kan/Neo	N-EGYP	TEV Extra GA	EYFP-SGLRSR-TEV site-2 EYFP-SGLRS	pLEICS-21-Seq-F pLEICS-21-Seq-R
pLEICS-23	Kan/Neo	N-mCherry	TEV Extra GA	mCherry-SGLRSR-TEV site-2 mCherry-SGLRS	pLEICS-23-Seq-F pLEICS-21-Seq-R
pLEICS-24	Kan/Neo	N-ECFP	TEV Extra GA	ECFP-SGLRSR-TEV site-2 ECFP-SGLRS	pLEICS-21-Seq-F pLEICS-21-Seq-R
pLEICS-25	Kan/Neo	N-mEGFP (A206K)	TEV Extra GA	mEGFP-SGLRSR-TEV site-2 mEGFP-SGLRS	pLEICS-21-Seq-F pLEICS-21-Seq-R
pLEICS-26	Kan/Neo	N-mEYFP (A206K)	TEV Extra GA	mEYFP-SGLRSR-TEV site-2 mEYFP-SGLRS	pLEICS-21-Seq-F pLEICS-21-Seq-R
pLEICS-27	Kan/Neo	N-mECFP (A206K)	TEV Extra GA	mECFP-SGLRSR-TEV site-2 mECFP-SGLRS	pLEICS-21-Seq-F pLEICS-21-Seq-R
pLEICS-29	Kan/Neo	C-EGFP	TEV, Extra ENLYFQ	L-TEV site-2- EFMQSTVPRARDPPVAT -EGFP EFMQSTVPRARDPPVAT -EGFP	pLEICS-29-Seq-F pLEICS-29-Seq-R
pLEICS-30	Kan/Neo	C-mCherry	TEV, Extra ENLYFQ	L-TEV site-2- EFMQSTVPRARDPPVAT -mCherry EFMQSTVPRARDPPVAT -mCherry	pLEICS-29-Seq-F pLEICS-30-Seq-R

Vector Name	AR	Tag/Flag	Secretion Signal	Protease cleavage	Tag and linker	Sequence primers	
pLEICS-31	Amp	C-His ₆	No	TEV Extra ENLYFQ	TEV site-1-LE-His6	5' AOX1-F	3' AOX1-R
pLEICS-32	Amp	C-His ₆	PHO1	TEV Extra ENLYFQ	TEV site-1-LE-His6	5' AOX1-F	3' AOX1-R
pLEICS-33	Amp	C-His ₆	No	TEV Extra ENLYFQ	TEV site-1-LE-His6	5' AOX1-F	3' AOX1-R
pLEICS-34	Amp	C-His ₆	α -factor	TEV Extra ENLYFQ	TEV site-1-LE-His6	5' AOX1-F	3' AOX1-R

Vector Name	AR	Tag/Flag	Protease cleavage	Tag and linker	Sequence primers	
pLEICS-35	Kan	GAL4-BD			T7 Promoter	pLEICS-35-Seq-R
pLEICS-36	Amp	GAL4-AD			T7 Promoter	pLEICS-36-Seq-R
pLEICS-37	Amp	RFP			pLEICS-37-Seq-F	pLEICS-72-Seq-R
pLEICS-38	Amp				pLEICS-37-Seq-F	pLEICS-72-Seq-R
pLEICS-39	Amp	N-His ₁₀ -3 x Flag C-Halo	TEV Extra GA at N-terminal	N terminal: His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C terminal: EFELRLE-Halo	T7 Promoter	pLEICS-39-Seq-R
pLEICS-40	Amp	N-His ₁₀ -3 x Flag C-hBirA	TEV Extra GA at N-terminal	N terminal: His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C terminal: LE-hBirA	T7 Promoter	pLEICS-40-Seq-R
pLEICS-41	Amp	N-His ₆	TEV Extra SM	His6-SSGVDLGT-TEV site-1	pLEICS-41-Seq-F	pLEICS-41-Seq-R
pLEICS-42	Amp	C-His ₆	TEV Extra ENLYFQ	TEV site-1-LE-His6	pLEICS-41-Seq-F	pLEICS-41-Seq-R
pLEICS-43	Amp	N-His ₆ /Mistic	TEV Extra SM	His6-PG-Mistic-PWSSGVDLGT-TEV site-1	pLEICS-43-Seq-F	pLEICS-01-Seq-R
pLEICS-44	Kan	N-His ₆ /Mistic	TEV Extra SM	His6-PG-Mistic-PWSSGVDLGT-TEV site-1	pLEICS-43-Seq-F	T7 terminator
pLEICS-45	Amp	N-His ₆ /mEGFP (A206K)	TEV Extra GA	His6-PG- mEGFP-SGLRSR-TEV site-2 His6-mEGFP-SGLRS	pLEICS-45-Seq-F	pLEICS-45-Seq-R
pLEICS-46	Kan	N-GB1/His6	TEV Extra GA	GB1-His6-GS-TEV site-2	T7 Promoter	T7 terminator
pLEICS-47	Amp	N-His ₁₀ / 3 x Flag	TEV Extra GA	His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2	pLEICS-12-Seq-F	pLEICS-11-Seq-R
pLEICS-48	Amp				pLEICS-48-Seq-F	pLEICS-11-Seq-R

pLEICS-49	Amp	C-His ₄ /3 x Flag	TEV, Extra ENLYFQ	TEV-2-His4-DYKDDDDKDYKDDDDKDYKDDDDK-GSEN	T7 Promoter pLEICS-12-Seq-R
pLEICS-50	Amp	C-GST	TEV, Extra ENLYFQ	TEV site-1-LE-GST	T7 Promoter pLEICS-50-Seq-R

Vector Name	AR	Tag/Flag	Protease cleavage	Tag and linker	Sequence primers
pLEICS-51	Kan	N-FlAsH	TEV Extra SM	His6-PG-CCPGCC-PWSSGVDLGT-TEV site-1	T7 Promoter T7 terminator
pLEICS-52	Kan	N-FlAsH/ mEGFP1-128	TEV Extra SM	His6-PG-CCPGCC-PW-mEGFP1-128-PWSSGVDLGT-TEV site-1	pLEICS-52-Seq-F T7 terminator
pLEICS-53	Kan	N-FlAsH/ mEGFP129-238	TEV Extra SM	His6-PG-CCPGCC-PW-mEGFP129-238-PWSSGVDLGT-TEV site-1	pLEICS-53-Seq-F T7 terminator
pLEICS-54	Kan	N-mEGFP1-128	TEV Extra SM	His6-PG-mEGFP1-128-PWSSGVDLGT-TEVsite-1	pLEICS-52-Seq-F T7 terminator
pLEICS-55	Kan	N-mEGFP129-138	TEV Extra SM	His6-PG-mEGFP129-238-PWSSGVDLGT-TEVsite-1	pLEICS-53-Seq-F T7 terminator
pLEICS-56	Amp	Super-folded EGFP (1-10)	TEV Extra SM		
pLEICS-57	Kan	N-mEGFP11	TEV Extra SM	His6-PG-mEGFP11-PWSSGVDLGT-TEV site-1	T7 Promoter T7 terminator
pLEICS-58	Amp	mEGFP1-128	TEV Extra SM		
pLEICS-59	Amp	mEGFP129-138	TEV Extra SM		
pLEICS-60	Kan	N-FlAsH /Super-folded EGFP (1-10)	TEV Extra SM	His6-PG-CCPGCC-PW-super-folded EGFP1-10-PWSSGVDLGT-TEV site-1	pLEICS-60-Seq-F T7 terminator
pLEICS-61	Amp	N-FlAsH	TEV Extra SM	His6-PG-CCPGCC-PWSSGVDLGT-TEV site-1	T7 Promoter pLEICS-01-Seq-R
pLEICS-63	Amp	C- Super-folded mEGFP /His6	TEV Extra ENLYFQ	TEV site-1-LE-super-folded mEGFP-LE-His6	T7 Promoter pLEICS-63-Seq-R
pLEICS-64	Amp	C- mEGFP /His6	TEV Extra ENLYFQ	TEV site-1-LE-mEGFP-LE-His6	T7 Promoter pLEICS-63-Seq-R
pLEICS-65	Amp	C- Super-folded mEGFP1-10 /His6	TEV Extra ENLYFQ	TEV site-1-LE-super-folded mEGFP(1-10)-LE-His6	T7 Promoter pLEICS-63-Seq-R
pLEICS-66	Amp	C- Super-folded mEGFP11 /His6	TEV Extra ENLYFQ	TEV site-1-LE-super-folded mEGFP(11)-LE-His6	T7 Promoter T7 terminator
pLEICS-67	Amp	N-His ₆ /mCherry	TEV Extra GA	His6-PG- mCherry-SGLRSR-TEV site-2 His6-mEGFP-SGLRS	pLEICS-67-Seq-F pLEICS-45-Seq-R
pLEICS-68	Amp		TEV Extra GA	His6-PG- mEYFP-SGLRSR-TEV site-2	pLEICS-68-Seq-F pLEICS-45-Seq-R

		N-His ₆ /mEYFP (A206K)		His6-mEGFP-SGLRS	
pLEICS-69	Amp	N-GST	PreScission Protease Extra GP	GST-SD-PreScission Site-LGS	pGEX5 pGEX3
pLEICS-72	Amp	EGFP			pLEICS-72-Seq-F pLEICS-72-Seq-R
pLEICS-73	Amp	EGFP			pLEICS-73-Seq-F pLEICS-73-Seq-R
pLEICS-74	Amp	5xGAL4/mCD8			pLEICS-74-Seq-F pLEICS-74-Seq-R
pLEICS-75	Amp	5xGAL4/mCD8			pLEICS-74-Seq-F pLEICS-74-Seq-R
pLEICS-76	Amp	5xGAL4/myr			pLEICS-76-Seq-F pLEICS-74-Seq-R
pLEICS-77	Amp				pLEICS-72-Seq-F pLEICS-12-Seq-R
pLEICS-78	Amp				pLEICS-72-Seq-F pLEICS-12-Seq-R
pLEICS-79	Amp	5xGAL4			pLEICS-74-Seq-F pLEICS-79-Seq-R
pLEICS-80	Amp	copGFP/HA			pLEICS-80-Seq-F pLEICS-80-Seq-R
pLEICS-81	Amp	LexA			pLEICS-81-Seq-F pLEICS-81-Seq-R
pLEICS-82	Amp	VP16			pLEICS-82-Seq-F pLEICS-82-Seq-R
pLEICS-83	Amp	VP16			pLEICS-83-Seq-F pLEICS-83-Seq-R
pLEICS-84	Amp	GAL4			pLEICS-83-Seq-F pLEICS-83-Seq-R
pLEICS-85	Amp	Luciferase			pLEICS-85-Seq-F pLEICS-85-Seq-R
pLEICS-86	Amp	Luciferase			pLEICS-85-Seq-F pLEICS-85-Seq-R
pLEICS-87	Amp	Luciferase			pLEICS-85-Seq-F pLEICS-85-Seq-R
pLEICS-88	Amp	EGFP and mCherry			pLEICS-73-Seq-F pLEICS-72-Seq-R
pLEICS-89	Amp	N-His ₆ /S/TEV-Halo	TEV Extra GA	His6-SSGLVPRGSGM-S-PDLGTGS-TEVsite-2- Halo-HG	pLEICS-89-Seq-F pLEICS-91-Seq-R
pLEICS-90	Amp	C-Halo-TEV- His ₆	TEV, Extra ENLYFQ	GS-Halo-TEV site-1-LE-His6	T7 Promoter pLEICS-90-Seq-R
pLEICS-91	Amp	N-GB1/His6	TEV Extra GA	GB1-His6-GS-TEV site-2	T7 Promoter pLEICS-91-Seq-R
pLEICS-92	Amp	N-GST/His ₆	TEV Extra GA	GST-GSTSGGGGSSNNPPTPTPSSGSG-His6- SAALEVLFGQPGYQDP-TEV site-2	pLEICS-17-Seq-F pLEICS-91-Seq-R
pLEICS-93	Amp	N-His ₆ /S	TEV Extra GA	His6-SSGLVPRGSGM-S-PDLGTGS-TEV site-2	T7 Promoter pLEICS-91-Seq-R
pLEICS-94	Amp	C-GFP			pLEICS-94-Seq-F pLEICS-94-Seq-R

Vector Name	AR	Selection	CRISPR Effector	Cleavage	PAM Sequence	gRNA	Sequence primers
pLEICS-95	Amp	EGFP	Cas9	Nick (D10A)	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-96	Amp	Puromycin	Cas9	Nick (D10A)	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-97	Amp	Puromycin	Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-98	Kan		Cas9			gRNA	pLEICS-98-Seq-F pLEICS-98-Seq-R
pLEICS-99	Amp	mCherry	Cas9	Nick (D10A)	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-100	Amp	mCherry	Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-101	Amp	mEGFP	Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-102	Amp	Neomycin	Cas9	Nick (D10A)	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-103	Amp	Neomycin	Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-104	Amp	Zeocin	Cas9	Nick (D10A)	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-105	Amp	Zeocin	Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-106	Amp	Puromycin	Cas9	All-in-one, Cut	3'-NGG	Lentivirus	pLEICS-106-Seq-F pLEICS-106-Seq-R
pLEICS-107	Amp	Puromycin	Cas9	gRNA		Lentivirus	pLEICS-107-Seq-F pLEICS-107-Seq-R
pLEICS-108	Amp	blasticidin	Cas9	Cas9	3'-NGG	Lentivirus	
pLEICS-109	Amp	Puromycin	Cas9	All-in-one, Inducible Cas9	3'-NGG	Lentivirus	pLEICS-106-Seq-F pLEICS-106-Seq-R
pLEICS-110	Amp	Puromycin	Cas9	All-in-one, Inducible Cas9	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-111	Amp	Neomycin	Cas9	All-in-one, Inducible Cas9	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-112	Amp	Puromycin	Cas9	Nick (D10A)	3'-NGAG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-113	Amp	Puromycin	Cas9	Cut	3'-NGAG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-114	Amp	mCherry	Cas9	Nick (D10A)	3'-NGAG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-115	Amp	mCherry	Cas9	Cut	3'-NGAG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-116	Amp	Neomycin	Cas9	Nick (D10A)	3'-NGAG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-117	Amp	Neomycin	Cas9	Cut	3'-NGAG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-118	Amp	Puromycin	Cpf1	Staggered Cut	5'-TTN	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-119	Amp	Neomycin	Cpf1	Staggered Cut	5'-TTN	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-120	Amp	mEGFP	Cpf1	Staggered Cut	5'-TTN	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-121	Amp	mCherry	Cpf1	Staggered Cut	5'-TTN	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-122	Amp	Puromycin	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-123	Amp	Neomycin	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-124	Amp	mEGFP	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-125	Amp	mCherry	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-126	Amp	Puromycin	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R

pLEICS-127	Amp	Neomycin	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-128	Amp	mEGFP	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-129	Amp	mCherry	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-140	Amp	mEGFP	Cas9	Nick (D10A), direct mutations of C to T or G to A	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-141	Amp	mCherry	Cas9	Nick (D10A), direct mutations of C to T or G to A	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-142	Amp	Puromycin	Cas9	Nick (D10A), direct mutations of C to T or G to A	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-143	Amp	Neomycin	Cas9	Nick (D10A), direct mutations of C to T or G to A	3'-NGG	All-in-one	pLEICS-95-Seq-F pLEICS-95-Seq-R
pLEICS-144	Kan	mEGFP Hygromycin	Cas9	Cut	3'-NGG	All-in-one	pLEICS-144-Seq-F
pLEICS-145	Kan	mCherry Hygromycin	Cas9	Cut	3'-NGG	All-in-one	pLEICS-144-Seq-F
pLEICS-146	Kan	mEGFP Hygromycin	Cas9	Nick (D10A)	3'-NGG	All-in-one	pLEICS-144-Seq-F
pLEICS-147	Kan	mCherry Hygromycin	Cas9	Nick (D10A)	3'-NGG	All-in-one	pLEICS-144-Seq-F
pLEICS-148	Kan	mEGFP Hygromycin	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-144-Seq-F
pLEICS-149	Kan	mCherry Hygromycin	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-144-Seq-F
pLEICS-150	Kan	Hygromycin	High-fidelity Cas9	Cut	3'-NGG	All-in-one	pLEICS-144-Seq-F
pLEICS-151	Tet						pLEICS-151-Seq-F pLEICS-151-Seq-R

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pLEICS-131	Amp/Neo	N-His10-3xFlag C-EGFP-PEX2	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-EF-EGFP-GRAKGSSTSGSG-PEX2	T7 Promoter 131-EGFP-Seq-R
		N-His10-3xFlag C-APEX2	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-GRAKGSSTSGSG-PEX2	T7 Promoter 131-APEX2-Seq-R
		C-EGFP -APEX2		C-Term-EF-EGFP-GRAKGSSTSGSG-PEX2	CMV-P-F 131-EGFP-Seq-R
		C-APEX2		C-Term-GRAKGSSTSGSG-PEX2	CMV-P-F 131-APEX2-Seq-R
pLEICS-132	Amp/Neo	N-His10-3xFlag C-mCherry-APEX2	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-EF-mCherry-GRAKGSSTSGSG-PEX2	T7 Promoter 132-mCherry-Seq-R
		N-His10-3xFlag C-APEX2	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-GRAKGSSTSGSG-PEX2	T7 Promoter 131-APEX2-Seq-R
		C-mCherry-APEX2		C-Term-EF-mCherry-GRAKGSSTSGSG-PEX2	CMV-P-F 132-mCherry-Seq-R
		C-APEX2		C-Term-GRAKGSSTSGSG-PEX2	CMV-P-F 131-APEX2-Seq-R
pLEICS-133	Amp/Neo	N-His10-3xFlag C-EGFP -miniSOG	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-EF-EGFP-GRAKGSSTSGSG-miniSOG	T7 Promoter 131-EGFP-Seq-R
		N-His10-3xFlag C-miniSOG	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-GRAKGSSTSGSG-miniSOG	T7 Promoter 133-miniSOG-Seq-R
		C-EGFP-miniSOG		C-Term-EF-EGFP-GRAKGSSTSGSG-miniSOG	CMV-P-F 131-EGFP-Seq-R
		C-miniSOG		C-Term-GRAKGSSTSGSG-PEX2	CMV-P-F 133-miniSOG-Seq-R
pLEICS-134	Amp/Neo	N-His10-3xFlag C-mCherry-miniSOG	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-EF-mCherry-GRAKGSSTSGSG-miniSOG	T7 Promoter 132-mCherry-Seq-R
		N-His10-3xFlag C-miniSOG	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-GRAKGSSTSGSG-miniSOG	T7 Promoter 133-miniSOG-Seq-R
		C-mCherry-miniSOG		C-Term-EF-mCherry-GRAKGSSTSGSG-miniSOG	CMV-P-F 132-mCherry-Seq-R
		C-miniSOG		C-Term-GRAKGSSTSGSG-miniSOG	CMV-P-F 133-miniSOG-Seq-R
pLEICS-135	Amp/Puro				pLEICS-135-Seq-F pLEICS-135-Seq-R
pLEICS-136	Amp/Neo	N-His10-3xFlag C-mEGFP	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-EF-mEGFP	T7 Promoter 131-EGFP-Seq-R
pLEICS-137	Amp/Neo	N-His10-3xFlag C-mCherry	TEV Extra GA	N-Term-His10-DYKDDDDKDYKDDDDKDYKDDDDK-GS-TEV site-2 C-Term-EF-mCherry	T7 Promoter 132-mCherry-Seq-R
pLEICS-138	Amp/Neo	N-mEGFP (A206K)	TEV Extra GA	mEGFP-SGLRSR-TEV site-2 mEGFP-SGLRS	pLEICS-21-Seq-F pLEICS-12-Seq-R
pLEICS-139	Amp/Neo	N-mCherry	TEV Extra GA	mCherry-SGLRSR-TEV site-2 mCherry-SGLRS	pLEICS-23-Seq-F pLEICS-12-Seq-R

His6-Tag:
HHHHHH

GST-Tag:
MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIRYIADKHNMLGGCPKE
RAEISMLEGAVLDIRYGVSRIAYSDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPK
LVCFFKRIEAIQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKS

S-Tag:
KETAAAKFERQHMS

Trx-Tag:
MSDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKNGEVAA
TKVGALSKGQLKEFLDANLA

TAP-Tag:
KRRWKNFIAVSAANRFKKISSSGALGSGSGTMDEKTTGWRGGHVVEGLAGELEQLRARLEHHPQGQREPSGGCKLG

MBP-Tag:
MKTEEGKLVWINGDKGYNGLAEVGGKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDREFGGYAQSGLLAEITPDKAFQD
KLYPFTWDAVRYNGKLIAYPIAVEALSIIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGK
YDIKDVGVNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGV
SAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIQMSAFWYAVRTAVINA
ASGRQTVDEALKDAQTNSS

EGFP:

MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSA
MPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDGS
VQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS KDPNEKRDHMLLEFVTAAGITLGMDELYK

EYFP:

MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTTGKLPVPWPTLVTTFGYGLQCFARYPDHMKQHDFFKS
AMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDG
SVQLADHYQQNTPIGDGPVLLPDNHYLSYQSALS KDPNEKRDHMLLEFVTAAGITLGMDELYK

mCherry:

MVSKGEEDNMAIIEKFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDY
LKLSFPEGFKWERVMNFEDEGGVVTVTQDSSLQDGEFIYKVKLRGTNFPDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLK
DGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

ECFP:

MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKS
AMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYITADKQKNGIKANFKIRHNIEDGS
VQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS KDPNEKRDHMLLEFVTAAGITLGMDELYK

Mistic:

MFCTFFEKHHRKWDILLEKSTGVMEAMKVTSEEKEQLSTAIDRMNEGLDAFIQLYNESEIDEPLIQLDDDDTAELMKQARDMYGQEKL
NEKLNNTIIKQILSISVSEEKEKE

GB1:

MQYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEGS

Halo:

EIGTGFPDPHYVEVLGERMHYVDVGPRDGTPLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKSDKPDLYFFDDHVRFMDA
FIEALGLEEVVLIHDWGSALGFHWAKRNPERVKGIAFMFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVVRP
LTEVEMDHYREPFLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDIGP
GLNLLQEDNPDIGSEIARWLSTLEISG

hBirA:

MKDNTVPLKLIALLANGEFHSGEQLGETLGMSRAAINKHQTLRDWGVVDVFTVPGKGYSLPEPIQLLNAKQILGQLDGGGSVAVLPVIDS
TNQYLLDRIGELKSGDACIAEYQQAGRGRGRKWFSPFGANLYLSMFWRLEQGPAAAIGLSLVIGIVMAEVLRLKLGADKVRVKWPND
LYLQDRKLAGILVELTGKTGDAAQIVIGAGINMAMRRVEESVVNQGWTLQEAGINLDRNTLAAMLIRELRAALELFEQGLAPYLSR
WEKLDNFNRPVKLIIGDKEIFGISRGIDKQGALLLEQDGIKPWMGGEISLRSKAEK

PEX2:

GKSYPTVSADYQDAVEKAKKKLRGFIAEKRCAPLMLRLAFHSAGTFDKGKTGGPFGTIKHPAELAHSANGLDIAVRLLEPLKAEFPI
LSYADFYQLAGVVAVTGGPKVPFHGREDKPEPPPEGRLPDPTKGSDDLRLDVFVKAMGLTDQDIVALS GGHTIGAAHKERSGFEGPW
TSNPLIFDNSYFTELLSKEKEGLLQLPSDKALLSDPVFRPLVDKYAADEDAFFADYAEAHQKLSLSELGFADA

miniSOG:

MEKSFVITDPRLPDNPIIFASDGFLELTEYSREEILGRNGRFLQGPETDQATVQKIRDAIRDQREITVQLINYTKSGKKFWNLLHLQPMRD
QKGELQYFIGVQLDG

TEV site-1:

ENLYFQS

TEV site-2:

ENLYFQGA

PreScission Protease Site:

LEVLFQGP

Primer sequence:

T7 Promoter	5'-TAATACGACTCACTATAGGG-3'
T7 Terminator	5'-GCTAGTTATTGCTCAGCGG-3'
pGEX5	5'- GGGCTGGCAAGCCACGTTTGGTG-3'
pGEX3	5'- CCGGGAGCTGCATGTGTCAGAGG-3'
5' AOX1-F	5'-GACTGGTTCCAATTGACAAGC-3'
3'AOX1-R	5'-GCAAATGGCATTCTGACATCC-3'
pLEICS-01-Seq-R	5'-ATTAACATTAGTGGTGGTGGT-3'
pLEICS-06-Seq-F1	5'-CTAGAAATAATTTTGTTTAA-3'
pLEICS-06-Seq-R1	5'-GTACAATACGATTACTTTCT-3'
pLEICS-06-Seq-F2	5'-GAAAGTAATCGTATTGTACA-3'
pLEICS-09-Seq-F	5'-CCGCTGCTGCTAAATTCGAA-3'
pLEICS-10-Seq-F	5'-AGACTAATTCGAGCTCGAACA-3'
pLEICS-10-Seq-R	5'-CCCAGTCACGACGTTGTAAAACG-3'
pLEICS-11-Seq-F	5'-GAAACCATGTCGTACTACCAT-3'
pLEICS-11-Seq-R	5'-AACCTCTACAAATGTGGTAT-3'
pLEICS-12-Seq-F	5'- GGAGACCCAAGCTTGGTACC-3'
pLEICS-12-Seq-R	5'-AAGGCACAGTCGAGGCTGA-3'
pLEICS-15-Seq-R	5'-TACCATGGACGAGAA-3'

pLEICS-17-Seq-F	5'-TGGTTCTGGTCATCACCAT-3'
pLEICS-19-Seq-F	5'-CTGTACGGAAGTGTTACTT-3'
pLEICS-19-Seq-R	5'-CATCACAAATTTACAAATA-3'
pLEICS-21-Seq-F	5'-CACATGGTCCTGCTGGAGTT-3'
pLEICS-21-Seq-R	5'-GCTGATTATGATCAGTTAT-3'
pLEICS-23-Seq-F	5'-CTACACCATCGTGGAACAGTA-3'
pLEICS-29-Seq-F	5'-CAAATGGGCGGTAGGCGTGTA-3'
pLEICS-29-Seq-R	5'-TCCAGCTCGACCAGGATGGGCA-3'
pLEICS-30-Seq-R	5'- TACCGTCGACTGCATGAATT-3'
pLEICS-35-Seq-R	5'- CTCAAGACCCGTTTAGAGG -3'
pLEICS-36-Seq-R	5'-ATGCACAGTTGAAGTGAAGTTG -3'
pLEICS-37-Seq-F	5'- ACGCTTTGCCTGACCCTGCTTGCTCAACTC -3'
pLEICS-39-Seq-R	5'- ATCGCGCGGACCAACATCGACGTAGT -3'
pLEICS-40-Seq-R	5'- AGCTGCTCGCCAGAGTGGAAGTCTGCCGTT -3'
pLEICS-41-Seq-F	5'-TCCCCAACACCTAATAA-3'
pLEICS-41-Seq-R	5'-CCCTATATATGGATCCAA-3'
pLEICS-43-Seq-F	5'-AAACAGATTTTATCCATCT-3'
pLEICS-45-Seq-F	5'-GCAAAGACCCCAACGAGAA-3'
pLEICS-45-Seq-R	5'-CGGCGTTTCACTTCTGAGTT-3'
pLEICS-48-Seq-F	5'-GATAACCATCTCGCAAAT -3'

pLEICS-50-Seq-R	5'- CCAAAAGAAGTCGAGTGGGT -3'
pLEICS-52-Seq-F	5'-CACCCCTGGTGAACCGCATCGA-3'
pLEICS-53-Seq-F	5'-CACTCTCGGCATGGACGAGCT-3'
pLEICS-60-Seq-F	5'-CGACAACCACTACCTGAGCA-3'
pLEICS-63-Seq-R	5'-GGCCGTTTACGTCGCCGTCCA -3'
pLEICS-67-Seq-F	5'- ATCACCTCCCACAACGAGGA-3'
pLEICS-68-Seq-F	5'- TCCAAACTGAGCAAAGACCCCAA-3'
pLEICS-71-Seq-R	5'-GTAAAGTGTAAGTTGGTATTA-3'
pLEICS-72-Seq-F	5'- GCTCTAGAGCCTCTGCTAA -3'
pLEICS-72-Seq-R	5'-GGCAATATGGTGGAAAAT -3'
pLEICS-73-Seq-F	5'-CTAGGTCGATGCAGGATAA -3'
pLEICS-74-Seq-F	5'-GATTGGACTTCGCCTGTGAT -3'
pLEICS-74-Seq-R	5'-TTCCATAGGTTGGAATCTA -3'
pLEICS-76-Seq-F	5'-AAGCATAACAACGGTGGCTC -3'
pLEICS-79-Seq-R	5'-GTTGCATCACCTTCACCCTCT -3'
pLEICS-80-Seq-F	5'- AGTTTCCAAAAACGAGGAGGATTTGATATTCAC -3'
pLEICS-80-Seq-R	5'- AATATGGTGGAAAATAACATATAGACAAAC -3'
pLEICS-81-Seq-F	5'-GTTGCCAGAAAATAGCGAGTT-3'
pLEICS-81-Seq-R	5'-CCTAAGAGTCACTTTAA-3'
pLEICS-82-Seq-F	5'- TACGGCGCTCTGGATAT-3'

pLEICS-82-Seq-R	5'-GTAACGCCAGGGTTTTCCCA-3'
pLEICS-83-Seq-F	5'- CCCACTGCTTAACTGGCTTA-3'
pLEICS-83-Seq-R	5'-CCAATTATGTCACACCACAG-3'
pLEICS-85-Seq-F	5'- CGATAGTACTAACATACGCT -3'
pLEICS-85-Seq-R	5'-TTGGCGTCTTCCATGGTGGC-3'
pLEICS-89-Seq-F	5'-CTGCCTAACTGCAAGGCTGTGGACAT-3'
pLEICS-90-Seq-R	5'-TGCCATCGCGCGGACCAACATCGACGTAGT-3'
pLEICS-91-Seq-R	5'- TCACTTCTGAGTTCGGCATGG -3'
pLEICS-94-Seq-F	5'-CGGCATCGCAGCTTGGATACA-3'
pLEICS-94-Seq-R	5'- GGAATTTACGTAGCGGCCGC -3'
pLEICS-95-Seq-F	5'-GAGCCTATGAAAAACGCCA-3'
pLEICS-95-Seq-R	5'- TCAGCCAGGCGGGCCATTTA -3'
pLEICS-98-Seq-F	5'-TTACGTGCCGATCAAGTCAA-3'
pLEICS-98-Seq-R	5'- AGCAGCAGATTACGCGCAG -3'
pLEICS-106-Seq-F	5'- GCAACAGACATACAACTAA -3'
pLEICS-106-Seq-R	5'- GATGTGCGCTCTGCCCACTGA -3'
pLEICS-107-Seq-F	5'- AAGAATCCTGGCTGTGGAAA-3'
pLEICS-107-Seq-R	5'- CACTCCTTTCAAGACCTAGA -3'
131-EGFP-Seq-R	5'-TGAACTTGTGGCCGTTTACGT-3'
131-APEX2-Seq-R	5'-ATGAAGCCTCTGAGCTTCTTCTTCGCCTTCTCAA-3'

CMV-P-F	5'-GTCTATATAAGCAGAGCTCTCTGGCTAA-3'
132-mCherry-Seq-R	5'-ATGTGCACCTTGAAGCGCAT-3'
133-miniSOG-Seq-R	5'-TCTCTGGAATACTCGGTCAGCTCCA-3'
pLEICS-135-Seq-F	5'-GTACGGTGGGAGGCCTATATAA-3'
pLEICS-135-Seq-R	5'-TGAGGAGTGAATTCCTCGAGGA-3'
pLEICS-144-Seq-F	5'-GCAATTAATGTGAGTTAGCT-3'
pLEICS-151-Seq-F	5'-TGGCAAATATTCTGAAATGAGCTGTTGACA-3'
pLEICS-151-Seq-R	5'-CACGATGATCGTGCCGTGATCGAAATCCAG-3'

Family A vectors homology region:

N-ter: GTATTTTCAGGGCGCC...
C-ter: GACGGAGCTCGAATTTCA...

Family B vectors homology region:

N-ter: AGGAGATATACATATG...
C-ter-His or GST tag: GAAGTACAGGTTCTC...
C-ter-no tag: GAAGTACAGGTTCTCTCA...

Family C vectors homology region:

N-ter: TACTTCCAATCCATG...
C-ter: TATCCACCTTTACTGTCA...

Family D vectors homology region (with TEV site):

N-ter: GTATTTTCAGGGCGCC ...
C-ter: GTCGACTGCAGAATTtca ...

Family E vectors homology region (without TEV site):

N-ter: TCCGGACTCAGATCT ...
C-ter: GTCGACTGCAGAATTtca ...

Family F vectors homology region:

N-ter: CGAAACGAGGAATTCTCGATG ...
C-ter: CAGGTTCTCACTAGT ...

Family G vectors homology region:

N-ter: GCTCGAGAATTCTTCG ...
C-ter: CAGGTTCTCACTAGT ...

Family H vectors homology region:

N-ter: TACGTAGAATTCTCGATG ...
C-ter: CAGGTTCTCACTAGT ...

Family I vectors homology region:

N-ter: TACGTAGAATTCTCG ...
C-ter: CAGGTTCTCACTAGT ...

Family J vectors homology region (with TEV site):

N-ter: GTATTTTCAGGGCGCC ...
C-ter: CAATGCCAATAGGATATCtca ...

Family K vectors homology region (without TEV site):

N-ter: TCCGGACTCAGATCT ...
C-ter: GTGGTGGTGGTGGCTCGAGtca ...

Family 29T vector homology region (with TEV site):

N-ter: TAGCGCTACCGGACTCAGATCTCGAGATG...
C-ter: CTGAAAATACAGGTTCTCGAG...

Family 29 vector homology region (without TEV site):

N-ter: CTACCGGACTCAGATCTCGAGATG...
C-ter: TACCGTCGACTGCATGAATTC...

Family 35 vector homology region:

N-ter: ATGGCCATGGAGGCCGAATTC...
C-ter: TCGACGGATCCCCGGGAATTC...

Family 36 vector homology region:

N-ter: GCCATGGAGGCCAGTGAATTC...
C-ter: ATGCCACCCGGGTGGAATTC...

Family 37 vector homology region:

N-ter: CTACTCTAGAGCTAGCGAATTC...
C-ter: GGATCCGATTTAAATTCGAATTCtca...

Family 39C-Tag vector homology region:

N-ter: AGGGAGACCCAAGCTTGGTACCATG...
C-ter: TCGAGACGGAGCTCGAATTC

Family 39NC-Tag vector homology region:

N-ter: GTATTTTCAGGGCGCC...
C-ter: TCGAGACGGAGCTCGAATTC

Family 40C-Tag vector homology region:

N-ter: AGGGAGACCCAAGCTTGGTACCATG...
C-ter: ACGGTGTTGTCCTTCATCTCGAG

Family 40NC-Tag vector homology region:

N-ter: GTATTTTCAGGGCGCC...
C-ter: ACGGTGTTGTCCTTCATCTCGAG

Family 49 vector homology region:

N-ter: ACCCAAGCTTGGTACCATG...
C-ter: AAAATACAGGTTCTCGAG...

Family 69 vector homology region:

N-ter: TTCCAGGGGCCCCTGGGATCC...
C-ter: CTCGAGTCGACCCGGGAATTCtca...

Family 72 vector homology region:

N-ter: CATCATTTTGGCAAAGAATTCATG ...
C-ter: GGAGGGAGAGGGGCGGAATTCtca ...

Family 73 vector homology region:

N-ter: ACCTGTGGGTACCCGCTCGAGATG ...
C-ter: TATCGATACCGTCGACCTCGAGtca ...

Family 74 vectors homology region:

N-ter: TCTGCTACCACAGCCGCGGATCC ...
C-ter: TCCTTCACAAAGATCCTCTAGAtca...

Family 76 vector homology region:

N-ter: CATCATCAGACCACGCGGATTC ...
C-ter: TCCTTCACAAAGATCCTCTAGAtca ...

Family 77 vector homology region:

N-ter: CATCATTTTGGCAAAACC ...
C-ter: GACGGAGCTCGAATTtca ...

Family 79 vector homology region:

N-ter: TTCAGGCGGCCGCGGCTCGAGC ...
C-ter: TTCTCCTTTACTCATGGATCCtca ...

Family 80 vector homology region:

N-ter: TCCAAGTTTGGTCTAGAGCTAGCATG ...
C-ter: CCGCGGATCCGATTTAAATTCGAAtca ...

Family 81 vector homology region:

N-ter: CTGGAATTCCCGGGGATC ...
C-ter: CTGCAGGTCGACGGATCC ...

Family 82 vector homology region:

N-ter: GGTGGGATCGATTGGATC ...
C-ter: CTCGGTACCCGGGGATCC ...

Family 85 vector homology region:

N-ter: TATCGATAGGTACCGAGCTC ...
C-ter: ATCGCAGATCTCGAGCCCGGG ...

Family 89vector homology region:

N-ter: ATTTCCGGTCATGGGATG ...
C-ter: GACGGAGCTCGAATTCA ...

Family 90 vector homology region:

N-ter: AGGAGATATACATATG ...
C-ter: CAGTACCGATTTCCGGATCC ...

Family 94 vector homology region:

N-ter:TAGCTAGTTAATTAAGGATCC ...
C-ter: CGTACCACCACACTGGGATCC ...

Family 95 vector homology region:

Forward Primer:GNNNNNNNNNNNNNNNNNNNNNNgnttttagagctagaaatagca
Reverse Primer: nnnnnnnnnnnnnnnnnnnnnCGGTGTTTCGTCCTTCCACA

N: 20-nt guild sequence; n: Reverse complementary of N.

Family 98 vector homology region:

Forward Primer:GNNNNNNNNNNNNNNNNNNNNNNgnttttagagctagaaatagca
Reverse Primer: nnnnnnnnnnnnnnnnnnnnnCCTATAGTGAGTCGTATTA

N: 20-nt guild sequence; n: Reverse complementary of N.

Family 118 vector homology region:

Forward Primer: NNNNNNNNNNNNNNNNNNNNNNNNtttttagagctagaaatagcaag
Reverse Primer: nnnnnnnnnnnnnnnnnnnnnATCTACACTTAGTAGAAATTGGT

N: 24-nt guild sequence; n: Reverse complementary of N.

Family 131-A homology region (Tag: N-His₁₀-3xFlag, C-EGFP/mCherry-APEX2/miniSOG):

N-ter:AGGGCGCGATATCTAAGCTAGC ...
C-ter: GCCCTTGCTCACCATGAATTC ...

Family 131-B homology region (Tag: N-His₁₀-3xFlag, C-APEX2/miniSOG Tag):

N-ter:AGGGCGCGATATCTAAGCTAGC ...
C-ter: GTCGAGCCCGAGCCCTTGGCGCGCCC ...

Family 131-C homology region (Tag: C-EGFP/mCherry-APEX2/miniSOG Tag):

N-ter: TATAGGGAGACCCAAGCTTGGTACCATG ...
C-ter: GCCCTTGCTCACCATGAATTC ...

Family 131-D homology region (Tag: C-APEX2/miniSOG Tag):

N-ter:TATAGGGAGACCCAAGCTTGGTACCATG ...
C-ter: GTCGAGCCCGAGCCCTTGGCGCGCCC ...

Family 135 vector homology region:

N-ter: GTCGAGTTAATTTGTTAACATG ...
C-ter: TGGTTAGCAGAGGGTAACTCA ...

Family 136 vector homology region:

N-ter: GTATTTTCAGGGCGCC ...
C-ter: GCCCTTGCTCACCATGAATTC ...

Family 144 vector homology region:

Forward Primer:GNNNNNNNNNNNNNNNNNNNNNNggttttagagctagaaatagca
Reverse Primer: nnnnnnnnnnnnnnnnnnnnnCAATCGCTATGTCGACTCTAT

N: 20-nt guild sequence; n: Reverse complementary of N.

Family 151 vector homology region:

N-ter: TTCACACAGGAAACAGAATTC ...
C-ter: TCCGCTAGTCCGAGGCCTCGAG ...