Name	Genotype	Parent Strain	MAT type	Reference
FY4	*S288C prototroph*		A	Brachmann et al (1998)
DBY19054	*ura3D::NatMX, bud9::ACT1pr-Z3EV-ENO2term-URA3-Z3EVpr(P4)-GFP-Gal80term*	CEN-PK113-7d	α	McIsaac et al (2014)
LBCY197	*ura3D::NatMX, bud9::ACT1pr-Z3EV-ENO2term-URA3-Z3EVpr(P4)-GFP-Gal80term, his3::KanMX-Z3EVpr-mCherryLinker*	DBY19054	α	this work
LBCY200	*ura3D::NatMX, bud9::ACT1pr-Z3EV-ENO2term-URA3-Z3EVpr(P4)-GFP-Gal80term, Puf3::KanMX-Z3EVpr-mCherry-Puf3*	DBY19054	α	this work
LBCY201	*ura3D::NatMX, bud9::ACT1pr-Z3EV-ENO2term-URA3-Z3EVpr(P4)-GFP-Gal80term, Pub1::KanMX-Z3EVpr-mCherry-Pub1*	DBY19054	α	this work
LBCY203	*Puf3::HPH, ura3D::NatMX, bud9::ACT1pr-Z3EV-ENO2term-URA3-Z3EVpr(P4)-GFP-Gal80term*	DBY19054	α	this work
LBCY209	*ura3D::NatMX, bud9::ACT1pr-Z3EV-ENO2term-URA3-Z3EVpr(P4)-GFP-Gal80term, Puf3:: KanMX-Z3EVp-mCherry-Puf3-Cox17-3'U*	LBCY203	α	this work

Name	Sequence	Selectable Markers	Reference	Notes
PKT174	CaURA3-Amp-yECFP	Amp, URA	Sheff & Thorn (2004)	
PSR101	CaURA3-Amp-mCherry	Amp, URA	Sharad Ramanathan	pKT174 CFP replaced with mCherry
PYMN25	NAT-GAL1p-yeGFP-ployGA linker-Amp	Amp, NatMX	Janke (2004)	
PYMN14	KanMX-GDPp-Amp	Amp, KanMX	Janke (2004)	
PAG34	HPH-Amp	Amp, HPH	this work	
PLBC80	KanMX-Z3EVpr(P4)-mCherry-ployGA linker-Amp	Amp, KanMX	this work	
PLBC94	KanMX-Z3EVpr(P4)-mCherry-ployGA linker-PUF3(ORF) -Amp	Amp, KanMX	this work	
PLBC95	KanMX-Z3EVpr(P4)-mCherry-ployGA linker-PUB1(ORF) -Amp	Amp, KanMX	this work	
PLBC96	KanMX-Z3EVpr(P4)-mCherry-ployGA linker-PUF3(ORF)-COX17 3'UTR -Amp	Amp, KanMX	this work	

ID	Name	Sequence	Features
24	ho::GALprGFPCOX17OK_rv	AATTTTTATGGCCTTCTATCGTAAGCCCATATACAGTACTCTCACCCTGGAAATCATCCGAGTCCTTTTCTGGTCACGTGGTCTTA	To check by colony PCR correct PUF3(ORF)-COX17(3'UTR) genome integration
70	HTA2__C	CAGAAATGATGATGAATTGAACAAG	Positive control for Colony PCR of yeast HTA2 locus_FWD
71	HTA2__D	CCACAAATTTCTGCTGATAAAAAGT	Positive control for Colony PCR of yeast HTA2 locus_RV
97	His3_rv (25bp)	ATGCTGCAGCTTTAAATAATCGGTG	To check by colony PCR correct Z3EVp-mCherry genome integration
104	KanB_rev	CTG CAG CGA GGA GCC GTA AT	To check by colony PCR KanMX constructs_FWD
105	KanC_fwd	TGATTTTGATGACGAGCGTAAT	To check by colony PCR KanMX constructs_RV
149	prURA3-PKT174-fw	ATGATGTGACTGTCGCC	To check by colony PCR TEFpromoter constructs_FWD
196	his3::NAT-GALpr-GFP_fwd	GGGTGGTCCCCTAGCGATAGAGCACTCGATCTTCCCAGAAAAAGAGGCAGCGTACGCTGCAGGTCGAC	Transform Z3EVp-mCherry to his3 locus_FWD
197	his3::NAT-GALpr-GFP_rev	AACCGGCAAGAGCCTTGAACGCACTCTCACTACGGTGATGATCATTCTTGCGCTTATCGAAATTAATACGACTCA	Transform Z3EVp-mCherry to his3 locus_RV
308	Fwd: KanMX_Z3EVpr	AGTGTCGAAAACGAGCTCAGTTATATTGAATTTTCAAAAATTCTTACTTTTTTTTTGGA	To check several sequence fragments of PLBC80
309	Rev: Z3EVpr_mCherry	TCCTCGCCCTTGCTCACCATTATAGTTTTTTCTCCTTGACGTTAAAGTATAGA	To check several sequence fragments of PLBC80
310	Fwd: Z3EVpr_mCherry	AACGTCAAGGAGAAAAAACTATAATGGTGAGCAAGGGCGAG	To check several sequence fragments of PLBC80
311	Rev: mCherry_mutDELYK	TTTGTACAATTCATCCATGCCGCCGGTG	To check several sequence fragments of PLBC80
312	Fwd: mutDELIK_spacer	ATGGATGAATTGTACAAAGGTGCTG	To check several sequence fragments of PLBC80
313	Rev: spacer_S4	GATCTGATATCATCGATGAATTCTCTGTCG	To check several sequence fragments of PLBC80
316	URA3-Fwr	GGAAGAGGACTATTTGCAAAGGG	To generate an amplicon containing Z3EVpr
317	GFPDasher-Rev	ACCTGTGCCTTCTCCTTTTATGA	To generate an amplicon containing Z3EVpr
318	GR_PUF3_FWD	GTGCTGGTCCGACAGAGAATTCAATGGAAATGAACATGGATATGGA	To clone PUF3 and COX17 3'UTR in PLBC80
319	GR_PUF3_REV	AGTGGATCTGATATCATCGATGAATTCTCACACCTCCGCATTTTCAA	To clone PUF3 and COX17 3'UTR in PLBC80
320	PUF3_COX17_REV	GTCGGCAGACTGTCAGTAAGA TCACACCTCCGCATTTTCAA	To clone PUF3 and COX17 3'UTR in PLBC80
321	PUF3_COX17_FWD	TTGAAAATGCGGAGGTGTGA TCTTACTGACAGTCTGCCGAC	To clone PUF3 and COX17 3'UTR in PLBC80
322	GR_COX17_REV	AGTGGATCTGATATCATCGATGAATTC GTCCTTTTCTGGTCACGTGGT	To clone PUF3 and COX17 3'UTR in PLBC80
323	size check fwr	TTATGAAGAGGAAAAATTGGCAGTA	To check the Z3EVp number of binding sites in pCT001_FWD
324	size check rev	CTTCGCTGATTAATTACCCCAGAAA	To check the Z3EVp number of binding sites in pCT001_RV
325	FWD_PUF3_transform	GTGGAGAGGAAGATAATTTCCCAAATGTACCATTAGCACACTTGAGCGTACGCTGCAGGTCGAC	Transform Z3EVpr-mCherry-PUF3(ORF) in PUF3 locus
326	REV_PUF3_transform	TCACACCTCCGCATTTTCAAC	Transform Z3EVpr-mCherry-PUF3(ORF) in PUF3 locus
327	REV_COX17_transform	GCGCTCTTACGCTCTTCTTATTTCTGCAACAGATAGAGAATTTAACATTGTGGTCCTTTTCTGGTCACGTGGT	Transform Z3EVpr-mCherry-PUF3(ORF)-COX17(3'UTR) in PUF3 locus
328	FWD_PUF3_colony	GCAACAAGATCAGTTCACC	To check by colony PCR correct PUF3(ORF)-COX17(3'UTR) genome integration
329	GR_PUB1_FWD	GCTGGTCCGACAGAGAATTCAATGTCTGAAAATAACGAAGAACAAC	To clone PUB1 in PLBC80
330	GR_PUB1_REV	GGATCTGATATCATCGATGAATTCTTATTGTTGCTGCTGTTG	To clone PUB1 in PLBC80
365	FWD_PUB1_transform	GGCCGTCTTTCCTTGTCCTTCATTTTCCTCTCGTAATAATCATTCAACCGTACGCTGCAGGTCGAC	Transform Z3EVpr-mCherry-PUB1(ORF) in PUB1 locus
366	REV_PUB1_transform	TTATTGTTGTTGCTGCTGTTGC	Transform Z3EVpr-mCherry-PUB1(ORF) in PUB1 locus
369	REV_downPUF3_colony	GGGGAACATAAATGTTATGG	To check by colony PCR PUB1 and PUF3 constructs
370	FWD_PUB1_colony	GACACTCATGAACAGGCCGC	To check by colony PCR PUB1 and PUF3 constructs
371	REV_downPUB1_colony	GGTGCGCAGTGGTAGTGGC	To check by colony PCR PUB1 and PUF3 constructs
372	FWD_PUF3COX17_colony	GCGGAGGTGTGATCTTACTGACAG	To check by colony PCR PUB1 and PUF3 constructs
373	REV_PUF3COX17_colony	CATTTGGATACGCCCTAATCGGATGAAC	To check by colony PCR PUB1 and PUF3 constructs
374	PUF3::Hyg (only ORF) Fwr	AAACAAGAACTACGCATTTAAATTTCTTCTGAATAACGCAATATTGCGGGTATAAATGGGTAAAAAGCCTGAACTCACCG	Transform HPH for PUF3 KO, ORF replacement
375	PUF3::Hyg (only ORF) Rev	AGTAGATATCAAAATAAAACAAAATAAAATAGAGTAAGTGAAAGACAAATGGAGGTTATTCCTTTGCCCTCGGACGAGTG	Transform HPH for PUF3 KO, ORF replacement
384	PUF3 Fwr	CGAAGATCAGGAAAGCATTTTAAAC	To check by colony PCR PUB1 and PUF3 constructs
385	PUF3 Rev	TGTACCGTCAATCAAAGATTTTCCG	To check by colony PCR PUB1 and PUF3 constructs
386	PUB1 Fwr	ATATGAATATGAACAACAGCAGGGG	To check by colony PCR PUB1 and PUF3 constructs
387	PUB1 Rev	TAAATGTATCATCGGAGGAACTCTG	To check by colony PCR PUB1 and PUF3 constructs
399	5'UTR PUB1	GCCGTTACAAGGGAGGTGAA	To check by colony PCR PUB1 and PUF3 constructs
400	Internal HPH	GCCGATCTTAGCCAGACGAG	To check by colony PCR correct HPH genome integration