

Name	Sequence
pCAP05-1_5121F	AGCTCCAATTCGCCCTATAGATCACGAGCAATAAACCCGC
pCAP05-1_5121R	CTGGAAAGCGGGCAGTGAGCGGCCTTTTGCTCACATGTTC
pCAP05-2_3943F	GAACATGTGAGCAAAGGCCGCTCACTGCCCGCTTTCCAG
pCAP05-2_3943R	CCTATTTGTTTATTTTTCTAACGATTGATGGCGGTCCTGG
pCAP05-3_2024F	CCAGGACCGCCATCAATCGTTAGAAAAATAAACAAATAGG
pCAP05-3_2024R	GGGTTAATTCGAGCTTGGCTATTTTACACCCGCATATGAT
pCAP05-4_1639F	ATCATATGCGGTGTGAAATAGCCAAGCTCGGAATTAACCC
pCAP05-4_1639R	GCGGGTTTATTGCTCGTGATCTATAGGGCGAATTGGAGCT
vio2ta16-1_3121-40F	CTCGGTTTGACGCCTCCCATGGTATAAATAGTGGCTCGAGCCTAACTAACCGCCAT GTG
vio2ta16-1_3121-134R	CTGTAGTAGCTGCGTATGTCCAGTGACTGT
vio2ta16-2_3058-134F	TGCTCAGAGCGGCACACTTG
vio2ta16-2_3058-108R	TCTGGCGGGTAATGATCTGG
vio2ta16-3b_3027-482F	GCGGTTTGCCTTCCTTATACGGGTCAAGTG
vio2ta16-3b_3027-40R	AGTAGCAGCACGTTCCCTTATATGTAGCTTTTCGACATCGATCCGCGGGTTTCCTAAAT TAC
vio2ta16check_402F	CTCGGGAGATGCCAGAAGTC
vio2ta16check_402R	GCTCGCCCAATGCCATAAGG
pET28a-vioE-F	TGAAATTTTTCAACCGACTCCATTAACAACCTGAGTAAGCACTCGAGCACCACCA CCA
pET28a-vioA-R	CCGCTCCGATGATTGAGATGGTGTGTTTTCTTAACCGTCATGTATATCTCCTTCTTAAA GT
PLR1(NcoI)_669F	ACCTGCCCATGGGC TTTTTTGGGCTGCACAAAAGA
PLR1(HindIII)_669R	GGCCGCAAGCTT TTAGCTAAAGCTCAGCTCTTTG
PLR2(NcoI)_684F	ACCTGCCCATGGGCA AACCTACCGAACAAGATAG
PLR2(HindIII)_684R	GGCCGCAAGCTT CTAAATAAGGTTGTTTATTAAACT
PLR3(NcoI)_654F	ACCTGCCCATGGGCA ATCAGTTTTTAATTGCGGATGA
PLR3(HindIII)_654R	GGCCGCAAGCTT CTACTTTGCCGCCTCGATT
PLR4(NcoI)_657F	ACCTGCCCATGGGC AGCAGTACTGCATTTTTATTG
PLR4(HindIII)_657R	GGCCGCAAGCTT TTAACGTATCTCGTCAGGGA
PLR5(NdeI)_642F	CGGAATTCATATGGGTA ACGGAAAAGAAAATAG
PLR5(XhoI)_642R	AACCGCTCGAG CTACACAAGTCCCTTCTT
PLR6(NcoI)_717F	ACCTGCCCATGGGCA AAGCGATTCAAAGTAGCAA
PLR6(HindIII)_717R	GGCCGCAAGCTT TTAATGACGCTGTATTGAGA
PLR7(NdeI)_600F	CGGAATTCATATG AAAATTTTAGTTGTAGAAGATCAA

PLR7(XhoI)_600R	AACCGCTCGAG TTACAGCCAACCCTTTTGTC
qRT-cysG_126F	TCCACAGTTCACCGCATGGG
qRT-cysG_126R	CGCTGGTTAAGCGCGTCATC
qRT-vioA_140F	CTGACAATGCTGGCTATGAG
qRT-vioA_140R	CGCAGTATCAGCTTCTAGAC
csgD(NdeI)_651F	CGGAATTCATATG TTTAATGAAGTCCATAGTATTCATG
csgD(XhoI)_651R	AACCGCTCGAG TTATCGCCTGAGGTTATCGT
yhjB(NcoI)_603F	ACCTGCCATGGGCC AAATAGTCATGTTTGACAG
yhjB(HindIII)_603R	GGCCGCAAGCTTT CAGGAGGAGATATTTAACA
uhpA(NcoI)_591F	ACCTGCCATGGGCC ATCACCGTTGCCCTTATAGA
uhpA(HindIII)_591R	GGCCGCAAGCTTT CACCAGCCATCAAACATGC
sdiA(NcoI)_723F	ACCTGCCATGGGCC CAGGATAAGGATTTTTTCAGCT
sdiA(HindIII)_723R	GGCCGCAAGCTTT CAAATTAAGCCAGTAGCGG
PPR1(NdeI)_660F	CGGAATTCATATG ACCTGTAGACTACTGCT
PPR1(XhoI)_660R	AACCGCTCGAG TCAGTCATCCAGGCTGATGA
PPR2(NcoI)_666F	ACCTGCCATGGGCT TACAAAATTCTGATTGCCGAC
PPR2(HindIII)_666R	GGCCGCAAGCTTT CAACGGCGCAGATAATCA
PPR5(NdeI)_2718F	CGGAATTCATATG ACAGATCTGTCCCGTACCCA
PPR5(XhoI)_2718R	AACCGCTCGAG TCACGCCAGCAACCCAGG
PPRX(NcoI)_708F	ACCTGCCATGGGCC TTCACTGGAAACCCGA
PPRX(HindIII)_708R	GGCCGCAAGCTTT CAGATCCAGCCACGCAAGG
ATR1(NdeI)_1479F	CGGAATTCATATG GACGACAGCGTAAACAT
ATR1(XhoI)_1479R	AACCGCTCGAG TTATTTTTCCCTATGGCCGG
ATR2(NdeI)_930F	CGGAATTCATATG AGCGGGCAAGGCGCAG
ATR2(XhoI)_930R	AACCGCTCGAG TCACCCCTGATGCAAATATGCGCG
ATR3(NcoI)_717F	ACCTGCCATGGGCC CCGAAGACGGAGCGCCAGG
ATR3(HindIII)_717R	GGCCGCAAGCTTT CAGCTTATCAGGCCAAGGCG
ATRX(NcoI)_756F	ACCTACCATGGGCA AAGAACCGCTTCATGCA
ATRX(HindIII)_756R	GGCCGCAAGCTTT CTATTTAATCAGACCGACCC

Name	Description	Reference
pARS-VN	Plasmid used to amplify selective, counter-selective, and maintenance elements for yeast TAR cloning in construction of pCAP05	(1)
pRK442(H)	Plasmid used to amplify broad-host-range origin of replication and maintenance elements for Gram-negative bacteria in construction of pCAP05	(2)
pCAP05	TAR cloning and broad-host-range heterologous expression vector; CEN6_ARS4, HIS3, pAHD1, URA3, oriV, traJ, oriT, tetR, tetA, trfA, incC, korA	This study
pCAP05-vio2ta16	pCAP05 containing violacein gene cluster from <i>P. luteoviolcea</i> 2ta16; Tet ^R	This study
pET28a-vio2ta16	pET28a containing violacein gene cluster from <i>P. luteoviolcea</i> 2ta16 under control of T7 promoter; Kan ^R	This study
pACYCDuet-1	Commercial expression vector used for co-expression of LuxR homologs; Cm ^R	Novagen

1. Noskov VN, Kouprina N, Leem SH, Ouspenski I, Barrett JC, Larionov V. 2003. A general cloning system to selectively isolate any eukaryotic or prokaryotic genomic region in yeast. *BMC Genomics* 4:16.
2. Scott HN, Laible PD, Hanson DK. 2003. Sequences of versatile broad-host-range vectors of the RK2 family. *Plasmid* 50:74-9.