

pGAPZα A MCS

361 GATTATTGGA AACCAACGAGA ATCGAATATA AAAGGCGAAC ACCTTTCCCA ATTTTGTTTT

pGAP forward priming site

421 CTCCTGACCC AAAGACTTTA AATTTAATTT ATTTGTCCCT ATTTCAATCA ATTGAACAAC

481 TATTTTCGAAA CG ATG AGA TTT CCT TCA ATT TTT ACT GCT GTT TTA TTC GCA
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala

532 GCA TCC TCC GCA TTA GCT GCT CCA GTC AAC ACT ACA ACA GAA GAT GAA ACG
 Ala Ser Ser Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr

α-factor signal sequence

583 GCA CAA ATT CCG GCT GAA GCT GTC ATC GGT TAC TCA GAT TTA GAA GGG GAT
 Ala Gln Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp

634 TTC GAT GTT GCT GTT TTG CCA TTT TCC AAC AGC ACA AAT AAC GGG TTA TTG
 Phe Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu

685 TTT ATA AAT ACT ACT ATT GCC AGC ATT GCT GCT AAA GAA GAA GGG GTA TCT
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val Ser

*Xho*I* Kex2 signal cleavage *Eco*R I *Pml*I *Sfi*I

736 CTC GAG AAA AGA GAG GCT GAA GCT GAATTCAC GTGGCCCA GCCGGCCGTC TCGGATC
 Leu Glu Lys Arg Glu Ala Glu Ala
 Ste13 signal cleavage

*Asp*718 I *Kpn*I *Xho*I *Sac*II *Not*I *Xba*I *myc* epitope

793 GGTACCTCGA GCCGCGGCGG CCGCCAGCTT TCTA GAA CAA AAA CTC ATC TCA GAA GAG
 Glu Gln Lys Leu Ile Ser Glu Glu

polyhistidine tag

851 GAT CTG AAT AGC GCC GTC GAC CAT CAT CAT CAT CAT CAT TGA GTTTTAGC CTTA
 Asp Leu Asn Ser Ala Val Asp His His His His His His ***

905 GACATGACTG TTCCTCAGTT CAAGTTGGGC ACTTACGAGA AGACCGGTCT TGCTAGATTC TAAT

3' AOX1 priming site

969 CAAGAGGATG TCAGAATGCC ATTTGCCTGA GAGATGCAGG CTTCAATTTTT GATACTTTTT TATT

1033 TGTAACCTAT ATAGTATAGG ATTTTTTTTTG TCATTTTGTT TCTTCTCG

* The *Xho*I site upstream of the Kex2 cleavage site is used to clone the gene of interest flush with the Kex2 cleavage site (see page 14).