

pGAPZ α B MCS

361 GATTATTGGA AACCACCAGA ATCGAATATA AAAGGCGAAC ACCTTTCCCA ATTTTGGTTT
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 *Pst*I *Eco*R I *Pml*I *Sfi*I

736 CTC GAG AAA AGA GAG GCT GAA GCT GCAGG AATTCACG TGGCCCAGC CGGCCGTCTC
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

792 GGATCGGTAC CTCGAGCCGC GCGGCCGCC AGCTTTCTA GAA CAA AAA CTC ATC TCA GAA
Glu Gln Lys Leu Ile Ser Glu

polyhistidine tag

852 GAG GAT CTG AAT AGC GCC GTC GAC CAT CAT CAT CAT CAT CAT TGA GTTTTAGCCT
Glu Asp Leu Asn Ser Ala Val Asp His His His His His His ***

907 TAGACATGAC TGTTCTCAG TTCAAGTTGG GCACTTACGA GAAGACCGGT CTTGCTAGAT

3' *AOX1* priming site

967 TCTAATCAAG AGGATGTCAG AATGCCATTT GCCTGAGAGA TGCAGGCTTC ATTTTTGATA

1027 CTTTTTTTATT TGTAACCTAT ATAGTATAGG ATTTTTTTTG TCATTTTGTT TCTT

* 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).