

## SUPPLEMENTARY FILE A: METHODS

### 1. Genome assemblies and annotation

All of the genome assemblies used in this study are publicly available from either the National Centre for Biotechnology Information (NCBI) or the Joint Genome Institute (JGI) (Table S1). All 14 genomes were subjected to gene annotation using the web-based gene annotator AUGUSTUS (Stanke and Waack, 2003). For the *Neurospora* genomes, the *N. crassa* species-specific gene model parameters were used. The *F. graminearum* parameters were used for all three *Huntiella* genomes, while the *Byssochlamys*, *Thermoascus* and *A. flavus* genomes were annotated using *A. nidulans* specific parameters. These species-specific parameters were chosen based on the closest relative that could be found in the AUGUSTUS gene model parameter library. In addition to these genome-wide annotations, the contigs on which the target genes (*MAT*, pheromone and pheromone receptor genes) were identified were also subjected to Fgenesh annotation (Salamov and Solovyev, 2000). The RNA sequence mapping described below was also used to confirm or correct the predicted gene models.

### 2. RNA-seq data

The majority of the RNA sequence data used in this study were obtained as raw reads from the Sequence Read Archive (SRA) and Gene Expression omnibus (GEO) databases of the NCBI (Table A.1).

Table A.1: The species used in this study, their sexual strategies, the genome assemblies used and, where relevant, the raw RNA reads used.

Species	Sexual Strategy	Isolate	Source	Accession Numbers	Reference / Submitter
<i>Neurospora crassa</i>	Heterothallic	OR7A FGSC4200 / 2489	NCBI	DNA: AABX00000000.3 RNA: GSE41484	Galagan et al., 2003 Wang et al., 2014
<i>Neurospora discreta</i>	Heterothallic	FGSC 8579	NCBI	RANX00000000.1	University of California, Berkeley
<i>Neurospora tetrasperma</i>	Pseudohomothallic	FGSC 2508	NCBI	AFBT00000000.1	Ellison et al., 2011
<i>Neurospora terricola</i>	Primary homothallic	FGSC 1889	NCBI	CAPR000000000.2	Gioti et al., 2013
<i>Neurospora pannonica</i>	Primary homothallic	FGSC 7221	NCBI	CAPQ000000000.2	Gioti et al., 2013
<i>Neurospora africana</i>	Unisexual (MAT1-1)	FGSC 1740	NCBI	DNA: CAPO000000000.2 RNA: ERS213531	Gioti et al., 2013 European Bioinformatics Institute
<i>Huntiella bhutanensis</i>	Heterothallic	CMW 8217	NCBI	MJMS00000000.1	Wingfield et al., 2016
<i>Huntiella omanensis</i>	Heterothallic	CMW 11056	NCBI	DNA: JSUI00000000.1 RNA: SRP108437	van der Nest et al., 2014 Wilson et al., 2018
<i>Huntiella moniliformis</i>	Unisexual (MAT1-2)	CMW 10134 CMW 36919	NCBI	DNA: JMSH00000000.1 RNA: SRP108437	Van Der Nest et al., 2014 Wilson et al., 2018
<i>Byssochlamys spectabilis</i>	Heterothallic	NBRC 109023	NCBI	RCHW00000000.1 SRP138004	Prefecture, 2014 Joint Genomes Institute
<i>Byssochlamys fulva</i>	Primary homothallic	BYSS01	NCBI	NIXA00000000.1	University of Dayton Research Institute
<i>Byssochlamys nivea</i>	Unisexual (MAT1-2)	CO 7	NCBI	QEIL00000000.1	Cornell University
<i>Thermoascus aurantiacus</i>	Unisexual (MAT1-1)	ATCC 26904	JGI NCBI	DNA: 405671 RNA: PRJNA681677	Singer, n.d. This study
<i>Thermoascus crustaceus</i>	Unisexual (MAT1-2)	JCM 12817	NGBI	BCIC00000000.1	RIKEN Center for Life Science Technologies
<i>Aspergillus flavus</i>	Primary homothallic	NRRL 3357	NCBI	AAIH00000000.2	Yin et al., 2018

## 2.1 RNA-seq data for *Thermoascus aurantiacus*

*T. aurantiacus* ATCC 26904 was grown in a modified glucose-preculture medium as previously described (Schuerg et al., 2017). Accordingly, ascospores from 7-day-old potato dextrose agar plates were harvested and  $1 \times 10^6$  spores per ml were used to inoculate glucose pre-cultures (2% glucose [w/v], McClendon, pH = 5.25, 0.8% soy meal peptone [w/v]). 50 mL pre-cultures were incubated for 48 h in 250 mL Erlenmeyer flasks at 50 °C and 180 rpm. These cultures were filtered under vacuum, using a Buchner funnel and Whatman paper #1, each washed with 100 mL defined McClendon's medium without peptone (McClendon's salts pH = 5.25, 0.25 mM ammonia nitrate) (Mcclendon et al., 2012) and shifted to four new flasks containing the same medium and either 2% beechwood xylan (Megazyme) or no carbon source. All cultures were grown under constant incandescent light for 48 hours in a rotary shaker at 50 °C and 180 rpm. From these shift cultures, samples were taken 1, 4, 6 and 8 hours after shifting. The sampling procedure involved taking an aliquot of 8 ml culture and vacuum filtering and washing it on a Whatman paper with immediate freezing in liquid nitrogen.

Total nucleic acids were extracted by grinding the frozen culture samples with a mortar and pestle in liquid nitrogen and resuspending this in TRIzol® Reagent (Thermo Fisher Scientific). RNA was isolated with Phenol:Chloroform:Isoamyl Alcohol, ethanol precipitation and subsequent DNaseI treatment. RNA quantity was determined on a Qubit (Thermo Fisher Scientific) and RIN values were determined using a Bioanalyzer (Agilent RNA 6000 Nano). Samples of suitable quality (RIN values > 8) from all time points of xylan and no carbon cultures were taken for cDNA synthesis and library

construction with the TruSeq® Stranded Total RNA Library Kit (Illumina®). For this study, only one biological replicate for each condition and time point was sequenced on a MiSeq (Illumina®).

### 3. Gene identification

#### 3.1 *MAT* genes

*MAT* genes for which reference sequences were available were downloaded from NCBI (Table A.2) and used in BLASTn queries against their respective genomes in order to identify the *MAT* loci. For example, the sequences for *matA-1* (*MAT1-1-1*), *matA-2* (*MAT1-1-2*) and *matA-3* (*MAT1-1-3*) from *N. crassa* were downloaded and used as a BLASTn query against the *N. crassa* genome. In order to identify the *B. spectabilis* *MAT* locus, the *MAT1-1-1* protein sequence was downloaded from NCBI and used as a tBLASTn query against the *B. spectabilis* genome. For species whose *MAT* genes were not available from NCBI (Table A.2), various BLASTn and tBLASTn searches were conducted against their genomes using *MAT* genes from closely related species. For example, to search for the *MAT* locus of *N. discreta*, the three *MAT* genes from *N. crassa* were used in BLASTn searches.

Table A.2: The accession numbers or Gene IDs for all genes used in this study.

Species	Gene	Accession Number/Gene ID
<i>N. crassa</i>	<i>matA-1</i> ( <i>MAT1-1-1</i> )	3880391
	<i>matA-2</i> ( <i>MAT1-1-2</i> )	3880488
	<i>matA-3</i> ( <i>MAT1-1-3</i> )	3880489
	<i>mfa-1</i> (a-factor pheromone)	XM_011396530.1
	<i>ccg-4</i> ( $\alpha$ -factor pheromone)	XM_960001.3
	<i>pre1</i> (a-factor receptor)	3872329
	<i>pre2</i> ( $\alpha$ -factor receptor)	3875871
<i>N. discreta</i>	<i>matA-1</i> ( <i>MAT1-1-1</i> ) <sup>a</sup>	Appendix B
	<i>matA-2</i> ( <i>MAT1-1-2</i> ) <sup>a</sup>	Appendix B
	<i>matA-3</i> ( <i>MAT1-1-3</i> ) <sup>a</sup>	Appendix B

	<i>mfa-1</i> (a-factor pheromone) <sup>a</sup>	Appendix B
	<i>ccg-4</i> ( $\alpha$ -factor pheromone) <sup>a</sup>	Appendix B
	<i>pre1</i> (a-factor receptor) <sup>a</sup>	Appendix B
	<i>pre2</i> ( $\alpha$ -factor receptor) <sup>a</sup>	Appendix B
<i>N. tetrasperma</i>	<i>matA-1</i> ( <i>MAT1-1-1</i> )	XM_009857139.1
	<i>matA-2</i> ( <i>MAT1-1-2</i> )	XM_009857138.1
	<i>matA-3</i> ( <i>MAT1-1-3</i> )	XM_009856640.1
	<i>mfa-1</i> (a-factor pheromone) <sup>a</sup>	Appendix B
	<i>ccg-4</i> ( $\alpha$ -factor pheromone)	XM_009858490.1
	<i>pre1</i> (a-factor receptor)	AM749905.1
	<i>pre2</i> ( $\alpha$ -factor receptor)	AM904749.1
<i>N. terricola</i>	<i>matA-1</i> ( <i>MAT1-1-1</i> )	HE600070.1
	<i>matA-2</i> ( <i>MAT1-1-2</i> )	HE600070.1
	<i>mata-1</i> ( <i>MAT1-2-1</i> )	HE600070.1
	<i>mfa-1</i> (a-factor pheromone) <sup>a</sup>	Appendix B
	<i>ccg-4</i> ( $\alpha$ -factor pheromone) <sup>a</sup>	Appendix B
	<i>pre1</i> (a-factor receptor) <sup>a</sup>	Appendix B
	<i>pre2</i> ( $\alpha$ -factor receptor)	HE861764.1
<i>N. pannonica</i>	<i>matA-1</i> ( <i>MAT1-1-1</i> )	HE600067.1
	<i>matA-2</i> ( <i>MAT1-1-2</i> )	HE600067.1
	<i>matA-3</i> ( <i>MAT1-1-3</i> )	HE600067.1
	<i>mata-1</i> ( <i>MAT1-2-1</i> )	HE600067.1
	<i>mfa-1</i> (a-factor pheromone) <sup>a</sup>	Appendix B
	<i>ccg-4</i> ( $\alpha$ -factor pheromone) <sup>a</sup>	Appendix B
	<i>pre1</i> (a-factor receptor)	HE861745.1
<i>N. africana</i>	<i>matA-2</i>	HE600066.1
	<i>matA-3</i>	HE600066.1
	<i>mfa-1</i> (a-factor pheromone) <sup>a</sup>	Appendix B
	<i>ccg-4</i> ( $\alpha$ -factor pheromone) <sup>a</sup>	Appendix B
	<i>pre1</i> (a-factor receptor)	HE861735.1
	<i>pre2</i> ( $\alpha$ -factor receptor)	HE861751.1
	<i>MAT1-2-1</i> <sup>a</sup>	Appendix B
<i>H. bhutanensis</i>	<i>MAT1-2-7</i> <sup>a</sup>	Appendix B
	a-factor pheromone <sup>a</sup>	Appendix B
	$\alpha$ -factor pheromone <sup>a</sup>	Appendix B
	<i>pre1</i> (a-factor receptor) <sup>a</sup>	Appendix B
	<i>pre2</i> ( $\alpha$ -factor receptor) <sup>a</sup>	Appendix B
	<i>MAT1-2-1</i>	KU950302.1
<i>H. omanensis</i>	<i>MAT1-2-7</i>	KU950303.1
	a-factor pheromone <sup>a</sup>	Appendix B
	$\alpha$ -factor pheromone <sup>a</sup>	Appendix B
	<i>pre1</i> (a-factor receptor) <sup>a</sup>	Appendix B
	<i>pre2</i> ( $\alpha$ -factor receptor) <sup>a</sup>	Appendix B
	<i>MAT1-2-1</i>	KU950299.1

	<i>MAT1-2-7</i>	KU950298.1
	a-factor pheromone <sup>a</sup>	Appendix B
	$\alpha$ -factor pheromone <sup>a</sup>	Appendix B
	<i>pre1</i> (a-factor receptor) <sup>a</sup>	Appendix B
	<i>pre2</i> ( $\alpha$ -factor receptor) <sup>a</sup>	Appendix B
<i>B. spectabilis</i>	<i>MAT1-1-1</i>	GAD92179.1 <sup>b</sup>
	<i>MAT1-1-9</i> <sup>a</sup>	Appendix B
	<i>ppgA</i> ( $\alpha$ -factor pheromone) <sup>a</sup>	Appendix B
	<i>preA</i> (a-factor receptor) <sup>a</sup>	Appendix B
	<i>preB</i> ( $\alpha$ -factor receptor) <sup>a</sup>	Appendix B
<i>B. fulva</i>	<i>MAT1-1-1</i> <sup>a</sup>	Appendix B
	<i>MAT1-2-1</i> <sup>a</sup>	Appendix B
	<i>MAT1-2-4</i> <sup>a</sup>	Appendix B
	<i>ppgA</i> ( $\alpha$ -factor pheromone) <sup>a</sup>	Appendix B
	<i>preA</i> (a-factor receptor) <sup>a</sup>	Appendix B
<i>B. nivea</i>	<i>preB</i> ( $\alpha$ -factor receptor) <sup>a</sup>	Appendix B
	<i>MAT1-2-1</i> <sup>a</sup>	Appendix B
	<i>MAT1-2-4</i> <sup>a</sup>	Appendix B
	<i>ppgA</i> ( $\alpha$ -factor pheromone) <sup>a</sup>	Appendix B
	<i>preA</i> (a-factor receptor) <sup>a</sup>	Appendix B
<i>T. aurantiacus</i>	<i>preB</i> ( $\alpha$ -factor receptor) <sup>a</sup>	Appendix B
	<i>MAT1-1-1</i> <sup>a</sup>	Appendix B
	<i>MAT1-1-9</i> <sup>a</sup>	Appendix B
	<i>ppgA</i> ( $\alpha$ -factor pheromone) <sup>a</sup>	Appendix B
	<i>preA</i> (a-factor receptor) <sup>a</sup>	Appendix B
<i>T. crustaceus</i>	<i>preB</i> ( $\alpha$ -factor receptor) <sup>a</sup>	Appendix B
	<i>MAT1-2-1</i> <sup>a</sup>	Appendix B
	<i>MAT1-2-4</i> <sup>a</sup>	Appendix B
	<i>ppgA</i> ( $\alpha$ -factor pheromone) <sup>a</sup>	Appendix B
	<i>preA</i> (a-factor receptor) <sup>a</sup>	Appendix B
<i>Aspergillus flavus</i>	<i>preB</i> ( $\alpha$ -factor receptor) <sup>a</sup>	Appendix B
	<i>ppgA</i> ( $\alpha$ -factor pheromone)	7919755
	<i>preA</i> (a-factor receptor)	7912518
	<i>preB</i> ( $\alpha$ -factor receptor)	7914252

<sup>a</sup>This study

<sup>b</sup>Protein sequence

### 3.2 Pheromone genes

#### 3.2.1 $\alpha$ -factor pheromone

Pheromone genes for which reference sequences existed were downloaded from NCBI (Table A.2) and used in BLASTn queries against their respective genomes in order

to identify the gene's location as previously described for the *MAT* genes. For species where the pheromone genes were not available from NCBI (Table A.2), tBLASTn searches were conducted against their genomes using pheromone genes of closely related species. This method successfully identified all the  $\alpha$ -factor pheromone genes in the *Neurospora* and *Huntiella* species.

Identification of the  $\alpha$ -factor pheromone genes in the *Byssochlamys* and *Thermoascus* genomes was achieved using a microsynteny approach based on the location of the  $\alpha$ -factor pheromone gene in the *A. flavus* genome. The proteins encoded by the genes directly flanking the *A. flavus*  $\alpha$ -factor gene were used in local tBLASTn searches against the genomes of the *Byssochlamys* and *Thermoascus* species. The region between the identified flanking genes in these species was subjected to Fgenesh (Salamov and Solovyev, 2000) and manual annotation in order to identify the pheromone gene.

The predicted  $\alpha$ -factor pheromone genes of all species considered in this study were translated and analyzed using the hydrophobicity and signal peptide predicting software programs, ExPASy ProtScale (Gasteiger et al., 2005) and Phobius (Krogh et al., 2007). Hydrophobicity was measured using the Kyte & Doolittle measure, with a window size of 9, a relative weight of window edges compared to window centers of 100%, a linear weight variation model and no scale normalization. Probability outputs from both programs were used to generate plots using the *ggplot2* package in R (Wickham, 2010; Wilkinson et al., 2005) (Figs S1 and S2). The potential mature  $\alpha$ -factor repeats were manually annotated (Table A.3).

Table A.3: Structure and repeat sequence of the  $\alpha$ -pheromones from each species.

<sup>a</sup> The gene sequence for the  $\alpha$ -pheromone from *N. pannonica* was split across two contigs and had to be manually assembled. It is likely that sequence data is missing and thus there may be a peptide repeat missing from this schematic.

Species	Pheromone Structure	Repeat Sequence
<i>N. crassa</i>	---■■■■■■---	■ QWCRIHGQSCW
<i>N. discreta</i>	---■■■■■■---	■ QWCRIHGQSCW ■ QWCCHIHGQSCW
<i>N. tetrasperma</i>	---■■■■■■---	■ QWCRIHGQSCW
<i>N. terricola</i>	---■■■■■■---	■ QWCRIHGQSCW ■ QWCQIHGQSCW
<i>N. pannonica</i> <sup>a</sup>	---■■■■■■---	■ QWCRIHGQSCW ■ QWCQLHGQSCW
<i>N. africana</i>	---■■■■■■---	■ QWCRIHGQSCW ■ QWCRIRGQSCW
<i>H. bhutanensis</i>	---■■■■■■■■■■■■---	■ DSNGGLPGELL ■ NSNGGLPGELL
<i>H. omanensis</i>	---■■■■■■■■■■■■---	■ DSNGGLPGELL ■ NSNAGLPGELL ■ YSNAGLPGELL
<i>H. moniliformis</i>	---■■■■■■■■■■■■---	■ DANGGLPGELF ■ DAWGGLPGELF
<i>B. spectabilis</i>	---■---	■ WCRRPGQPC
<i>B. fulva</i>	---■---	■ WCVDPGQVC
<i>B. nivea</i>	---■---	■ WCRRPGQPC
<i>T. aurantiacus</i>	-----	N/A
<i>T. crustaceus</i>	---■---	■ WCSLNGQGC

### 3.2.2 $\alpha$ -factor pheromone

In order to identify the  $\alpha$ -factor pheromone genes from the *Neurospora* and *Huntiella* genomes, we used the same method as was used for the  $\alpha$ -factor pheromone gene

identification (Table A.2). These genes were all translated into their predicted proteins to confirm the presence of the conserved C-terminal CaaX domain (Table A.4)

Table A.4: Sequence of the a-pheromones from the *Neurospora* and *Huntiella* species. The C-terminal CaaX domains have been indicated in red.

Species	Pheromone Sequence
<i>N. crassa</i>	MPSTAASKVPQTTMFNGY <b>CVVM</b>
<i>N. discreta</i>	MPSTAASKVPQTTMFNGY <b>CVVM</b>
<i>N. tetrasperma</i>	MPSTAASKVPQTTMFNGY <b>CVVM</b>
<i>N. terricola</i>	MPSTAASKVPQTTMFNGY <b>CVVM</b>
<i>N. pannonica</i>	MPSTAASKVPQTTMFNGY <b>CVVM</b>
<i>N. africana</i>	MPSTAASKVPQTTMFNGY <b>CVVM</b>
<i>H. bhutanensis</i>	MAAIKNITSSKNAARGVDQSNPCNVMRGVDQSNPCAVMRGVDQSNP <b>CTVM</b>
<i>H. omanensis</i>	MAAIKNNTTSKNAARGVDQSNPCAVMRGVDQSNPCAVMRGVDQSNP <b>CTVM</b> RGVDQSNP <b>CTL</b> M
<i>H. moniliformis</i>	MPSIKNHTPSTKTSGNETIQPPTSNAGRAIQSPINPITRGVTQAPPNV MRGVTQAPP <b>CNVM</b>

A similar approach was not conducted for the *Byssochlamys* and *Thermoascus* genomes, because no a-factor pheromone has been identified in the genomes of any other Eurotiomycetes species and thus no pheromone sequences were available from closely related species. Thorough tBLASTn searches using all the a-factor pheromone sequences from (Dyer et al., 2003; Pöggeler, 2002) yielded no significant results. A method similar to the microsynteny-based approach used above also failed to produce usable results. Instead, all of the predicted coding sequences in the *Byssochlamys* and *Thermoascus* genomes were translated into putative protein products. These proteins were then filtered for those harboring the terminal CaaX

domain. These proteins were then screened to identify proteins with other similarities to previously identified a-factor pheromones.

### *3.3 Pheromone receptor genes*

The receptor genes were identified using the same method as was used to identify the *MAT* genes (Table A.2). Thus, where sequences were available from NCBI, they were used to identify the genes in the genomes. Where sequences were not available, sequences of closely related species were used in BLASTn and tBLASTn searches as necessary. The a- and  $\alpha$ -factor receptor genes from each of the 14 species were translated and subjected to functional domain discovery using the NCBI Conserved Domain Search (Marchler-bauer et al., 2015) to confirm their identity. These proteins were also subjected to hydrophobicity analysis using Phobius (Krogh et al., 2007) in order to identify putative transmembrane domains. Probability outputs from Phobius were used to generate plots using the *ggplot2* package in R (Wickham, 2010; Wilkinson et al., 2005).

## 4. Gene, protein and functional domain comparisons

All nucleotide and amino acid comparisons were conducted using the *Create Alignment* and *Create Pairwise Comparison* functions in CLC MainWorkbench V8.1 (CLC bio, Aarhus, Denmark). The gene, protein and functional domain alignments were conducted using the default settings, which includes gap open and gap extension costs of 50 and the "Very accurate (slow)" alignment setting. Pairwise comparisons were also conducted using the default settings and included gap, differences, distance, percent identity and identity comparisons.

## 5. RNA-seq mapping

Expression analysis was conducted using CLC Genomics Workbench V7.5 (CLC bio, Aarhus, Denmark). The raw data were filtered to retain only reads with a Phred score of at least 20 ( $Q \geq 0.01$ ). The filtered reads were then mapped to the contigs containing the various genes of interest using the NGS Core Tool *Map Reads to Reference*. No masking was included, and the mapping settings were maintained at default. To ensure maximum mapping, the minimum length fraction and minimum similarity fraction values were set at 0.5 and 0.8, respectively. These relatively lenient mapping parameters ensured that reads spanning introns could successfully be mapped. This also ensured that successful mapping occurred despite the genome and transcriptomes originating from different isolates, as is the case for the majority of the species considered in this study. The resulting gene mappings were used to: 1) confirm or correct the gene models predicted by the various gene annotation programs and, 2) determine whether the various genes of interest are expressed in the two different sexual systems.

## 6. References

- Dyer, P.S., Paoletti, M., Archer, D.B., 2003. Genomics reveals sexual secrets of *Aspergillus*. *Microbiology* 149, 2301–2303.
- Ellison, C.E., Stajich, J.E., Jacobson, D.J., Natvig, D.O., Lapidus, A., Foster, B., Aerts, A., Riley, R., Lindquist, E.A., Grigoriev, I. V, Taylor, J.W., 2011. Massive changes in genome architecture accompany the transition to self-fertility in the filamentous fungus *Neurospora tetrasperma*. *Genetics* 189, 55–69.
- Galagan, J.E., Calvo, S.E., Borkovich, K.A., Selker, E.U., Read, N.D., Jaffe, D., Fitzhugh, W., Ma, L., Smirnov, S., Purcell, S., Rehman, B., Elkins, T., Engels, R., Wang, S., Nielsen, C.B., Butler,

- J., Endrizzi, M., Qui, D., Ianakiev, P., Bell-pedersen, D., Nelson, M.A., Werner-washburne, M., Selitrennikoff, C.P., Kinsey, J.A., Braun, E.L., Zelter, A., Schulte, U., 2003. The genome sequence of the filamentous fungus *Neurospora crassa*. *Nature* 422, 859–868.
- Gasteiger, E., Hoogland, C., Gattiker, A., Duvaud, S., Wilkins, M.R., Appel, R.D., Bairoch, A., 2005. Protein identification and analysis tools on the ExPASy Server, in: Walker, J. (Ed.), *The Proteomics Protocols Handbook*. Springer: Humana Press Inc., Totowa, NJ, pp. 571–608.
- Gioti, A., Stajich, J.E., Johannesson, H., 2013. *Neurospora* and the dead-end hypothesis: Genomic consequences of selfing in the model genus. *Evolution (N. Y.)* 67, 3600–3616.
- Krogh, A., Sonnhammer, E.L.L., Ka, L., 2007. Advantages of combined transmembrane topology and signal peptide prediction - The Phobius web server. *Nucleic Acids Res.* 35, W429–W432.
- Marchler-bauer, A., Derbyshire, M.K., Gonzales, N.R., Lu, S., Chitsaz, F., Geer, L.Y., Geer, R.C., He, J., Gwadz, M., Hurwitz, D.I., Lanczycki, C.J., Lu, F., Marchler, G.H., Song, J.S., Thanki, N., Wang, Z., Yamashita, R.A., Zhang, D., Zheng, C., Bryant, H., 2015. CDD: NCBI' s conserved domain database. *Nucleic Acids Res.* 43, D222-226.
- Mcclendon, S.D., Batth, T., Petzold, C.J., Adams, P.D., Simmons, B.A., Singer, S.W., 2012. *Thermoascus aurantiacus* is a promising source of enzymes for biomass deconstruction under thermophilic conditions. *Biotechnol. Biofuels* 5, 1–9.
- Pöggeler, S., 2002. Genomic evidence for mating abilities in the asexual pathogen *Aspergillus fumigatus*. *Curr. Genet.* 42, 153–160.
- Prefecture, K., 2014. Draft genome sequence of the formaldehyde-resistant fungus *Byssochlamys spectabilis* No. 5 (Anamorph *Paecilomyces variotii* No. 5) (NBRC109023). *Microbiol. Resour. Announc.* 2, e001162-13.

- Salamov, A.A., Solovyev, V. V, 2000. *Ab initio* gene finding in *Drosophila* genomic DNA. *Genome Res.* 10, 516–522.
- Schuerg, T., Prahl, J.P., Gabriel, R., Harth, S., Tachea, F., Chen, C.S., Miller, M., Masson, F., He, Q., Brown, S., Mirshiaghi, M., Liang, L., Tom, L.M., Tanjore, D., Sun, N., Pray, T.R., Singer, S.W., 2017. Xylose induces cellulase production in *Thermoascus aurantiacus*. *Biotechnol. Biofuels* 10, 1–11.
- Singer, S.W., n.d. Genome assembly of *Thermoascus aurantiacus*. Joint Genome Institute.
- Stanke, M., Waack, S., 2003. Gene prediction with a hidden Markov model and a new intron submodel. *Bioinformatics* 19, 215–225.
- van der Nest, M.A., Beirn, L.A., Crouch, J.A., Demers, J.E., de Beer, Z.W., De Vos, L., Gordon, T.R., Moncalvo, J.-M., Naidoo, K., Sanchez-Ramirez, S., Roodt, D., Santana, Q.C., Slinski, S.L., Stata, M., Taerum, S.J., Wilken, P.M., Wilson, A.M., Wingfield, M.J., Wingfield, B.D., 2014. Draft genomes of *Amanita jacksonii*, *Ceratocystis albifundus*, *Fusarium circinatum*, *Huntiella omanensis*, *Leptographium procerum*, *Rutstroemia sydowiana*, and *Sclerotinia echinophila*. *IMA Fungus* 5, 472–485.
- Van Der Nest, M.A., Bihon, W., De Vos, L., Naidoo, K., Roodt, D., Rubagotti, E., Slippers, B., Steenkamp, E.T., Markus Wilken, P., Wilson, A., Wingfield, M.J., Wingfield, B.D., 2014. Draft genome sequences of *Diplodia sapinea*, *Ceratocystis manginecans*, and *Ceratocystis moniliformis*. *IMA Fungus* 5, 135–140.
- Wang, Z., Lopez-giraldez, F., Lehr, N., Common, R., Trail, F., Townsend, J.P., 2014. Global gene expression and focused knockout analysis reveals genes associated with fungal fruiting body development in *Neurospora crassa*. *Eukaryot. Cell* 13, 154–169.
- Wickham, H., 2010. A Layered grammar of graphics. *J. Comput. Graph. Stat.* 19, 3–28.
- Wilkinson, L., Anand, A., Grossman, R., 2005. Graph-Theoretic Scagnostics. *Proc. EEE Symp.*

Inf. Vis. 1, 21.

Wilson, A.M., van der Nest, M.A., Wilken, P.M., Wingfield, M.J., Wingfield, B.D., 2018.

Pheromone expression reveals putative mechanism of unisexuality in a saprobic ascomycete fungus. *PLoS One* 13, e0192517.

Wingfield, B.D., Duong, T.A., Hammerbacher, A., van der Nest, M.A., Wilson, A., Chang, R., Wilhelm de Beer, Z., Steenkamp, E.T., Markus Wilken, P., Naidoo, K., Wingfield, M.J., 2016. Draft genome sequences for *Ceratocystis fagacearum*, *C. harringtonii*, *Grosmannia penicillata*, and *Huntiella bhutanensis*. *IMA Fungus* 7, 317–323.

Yin, G., Hua, S.S.T., Pennerman, K.K., Yu, J., Bu, L., Sayre, R.T., Bennett, J.W., 2018. Genome sequence and comparative analyses of atoxigenic *Aspergillus flavus* WRRL 1519. *Mycologia* 110, 482–493.

## SUPPLEMENTARY FILE B: SEQUENCES OF INTEREST

Note: Because these sequences were extracted and predicted from publicly available genome and transcriptome data, they could not be resubmitted to a publicly available database.

*N. discreta*, matA-1, MAT1-1-1 protein

Gene sequence:

```
ATGTCGGCGTCGACCAAATTGTCAAGACATTGCTGACCTCGCTGAGGACGACCGCGAACGCGAAGCGGCA  
ATGAGAGCTTCTCAACGATGATGCGTACCGAACCTGTCGCCAATCCCCGCGACAAAGAAGAAG  
GTCAACGGCTTCATGGTTTCAGATGTAAGTTAAATCTGAATCTGTCGATAATCCATGCTGACTG  
CTCTTCATTCAGCGTACTATTCCCCGCTCTCTCAGCTCCGAAAAGGAGAGATCGCCCTTT  
ATGACCATTCTCTGGCAGCACGATCCCTCCACAACGAATGGGATTTCATGTGCTCGGTGTATTG  
TCAATCCGTACCTATCTTGAGCAGGAGAAGGTTACTCTGCAACTTGGATTCACTATGCTGTTGGC  
CATCTGGGAGTGATTATCCCGCGACAACATACATGGCATCGTTGGCTGGAACCTCGTCCGTCTGCC  
AACGGCACACACGACCTCGAGCGCACCGCTTCCCTTGATTAGGCACAATCTCCAGCCCAGAAC  
GGCCTATGCCTGCTCACAAAGTGCCTCGAGAGCGGATTGCCTCTGCCAATCCTCACTCTGT  
GCCAAGCTTCAGATCCTAGCTACGACATGATCTGGTTCAACAAGCGTCCTACAGTCAGCAGAAA  
CATTGGTCAAACGTGACGATTCTGAACCTCGAAGTGTGGCGATGTTCCCTCGCAATTACGCAGTC  
GCCGCAGAGGCAGATGGTATACCAATCTCCTCTCCCATTGGATTCAAGCAGGGAGATTCGGT  
ACTGAGTCCGGTACTCAGCTCATTTGAGACTTGGATTCTATTCTCGAGAATGGACACGCC  
TCCAGCAATGACCCCTACAAACATGGCTCTGGCTATGGATGTTCTATGATGGGTTAG
```

CDS annotation:

```
join(1..157,212..915)
```

Protein:

```
MSGVDQIVKTFADLAEDDREAAMRAFSTMMRTEPVROIPATKKVNGFMGFRSYSPFLSQLPQKE  
RSPFMTILWQHDPFHNEWDFMC SVYSSIRTYLEQEKVTLQLWIHYAVGHLGVIIRDNYMASFGWNL  
VRLPNGTHDLERTALPLIRHNLQPMNGLCLLTKCLESGLPLANPHSVIAKLSDPSYDMIWFNKRPY
```

SQQKHFGQTDDSELEVSAMFPRNYAVAAEADGITNLPLSHWIQQGDFGTSGYSAHFETLLDSILE  
NGHASSNDPYNMALAMDVPMMG\*

*N. discreta*, matA-2, MAT1-1-2 protein

Gene sequence:

ATGGATCTCATCAACATGCAACCTAGAAAGTCAGAGCAACCAGTTAGGTTGAAGAAAACCGTGTC  
TCTAGCCAGGAAGGCCAGGATCTCGAAGTGATGTACAAGGTAACTATTTCTGACTCAAAAAAAA  
CTCATTACTTGTCACTGATGAATTGGTCAGAAACTCCATCAGCTACAGGCTAGGCTTCCCGTTC  
AGTTCTTCAGAGGCAATCAAGGAGTTCGAAGAGAATCTCGGTGTCTCTATGAAGCCAAGCT  
CTTACTATGCACAACACGAACGAAGTATGCCAACAGCTGGTTCGGTTCTAGCAACGAGTTGGGTC  
TATCGACGAGAGCAGGATTATCAAGGCATCGTGTATCATTGAGTCGGCAACACAATTCTCAA  
TTTTCTCTCATTATTGAGAAGAACGAGGATTGCCATCAGGCAGGAGATCAAAGACTCCAACAAGC  
TGCCTACAAAGGCCAGCAGTTGCCTTCGCCTCGCTCACCTACATGCCACAAAGATGCTCA  
GGAGGCTCCGGAAAGGAATTGGCTTGGCTACGGAAAAGAGGTGTATGTAATGGATGGCCATCT  
TTTGCACAGGTCAAAGCAAGAGGTCGTGGGCAGGCAGGAAAGAAACTGGCATATGACCATA  
TCTCCACCCCTTGAGGCGCGTCCCAGGCACCCATGGCACAAGTTCTTGGCAATCTGAAGTCGA  
CGCCGACAAGCAACTTCGCCTTCGATGATGGTACGTCTGTCACAATGATCGAGTCGGACCTCG  
GAAGTTCTTGAGTTGGCTCGAAACTGCTGAATTCAATTGGACAAATCAGGAGCGAGCATCA  
GAGAGTCGCTACGATTCACACAGAGGTGATTACTCAACGCGTCGAAACAGACCAAAACTCGCAC  
ACTGACTTATGGTAGAGTGGACATGCCAGCCAGTACCGACATCTATTCAAGAGGTAAGT  
TCCTTGGCCCGTCTAACGTCATGCTATCCATCGTCAGAGCACAAATGCACGCTTTGACTC  
ACTAATGATGACTGACATTATTGAAGGCTCTCCTCAGGAAGTTGGACTTGCCATGACAACACCGT  
TCCATGGTTACGGTAGAAGGACAACCTGAGATTGTGTTCCATCATGAAGGCTTGCAGGTT  
GTATGATCCTGCCACTGCTCACGGATGATAATGTGCTAACAACTGATCAACAGGTCCCCATTGAC  
TACAGCCAGGAGCGCCAACTCAGCATCCTCTCCATGTTTCACTCGACCCGCACTTGGGGGAA  
GGTCTGGAGCTTGCAGATAACTTGAACCGCGAGACGGTGTGCAGCAAGAAGAGCACATCTATTAC  
ACCTGA

CDS annotation:

```
join(1..105,164..883,940..984,1083..1184,1243..1392)
```

Protein:

```
MDLINMQPRKSEQPVRFEENRVSSQEGQDLEVMYKKLHQQLQARLSRSVLSEAIKEFEENLRCLFYEA  
AKLLLCTTRTKYRQSWFGSSNEFGSIDESRIKASCCIIESANTILNFLSFIEKKRGLPSGGDQRL  
QQAAAYKGQQFAFRLLRSLTCHKDAQEAPGKEFGLAYGKEVYVMDGHLLHRSKQEVVVGQAGGRNWHI  
DHTLHPLRRVPGTPWHKFFGNLEVDADKQLRFDDGTSVDNDRVGPRKFFFVVVPETAEFILDEIRS  
EHQRVATIHTESGHAQPPVPTSQQEALLRKLDFAMTPFHGYVVEGQPEIVFHHEGLRQVPIDYS  
QERQLSILSHVFTRPALWGEGLELADNFDP RDGVQQEEHIYYT*
```

*N. discreta*, matA-3, MAT1-1-3 protein

Gene sequence:

```
ATGTCTGCCTTAGACGTTGATGCAATCAGCGACATCGCACCCGGTCTCAGCCCTGTAACGCCCTT  
CACTATGGCAGGATCCAGGAATGCTGTTAGATCCCCTCTGGCCGATTTGCTGAAGAGGATCTT  
GTCTATGCGATGGACAACTCAGCGTGAGTCTGCCCAAGGAAAGCTTCTTCAGATCTCATAGCT  
GACTCGTTGAGTGTGTATTGGCGAAGAGGGCTTGCTTATGGTTGCCCGATGAGACAAGCAT  
CGCGATTGACGTATCCAGTTGGACTCATGATGGTGAATGGGAAACTGGGACATACTCGCGT  
TTGCCCTCGTAAGTTCTCAAACATTGGCGCCCTGCACTCAAGCTAATGAGACATTCCAGCGC  
AAACTCCTACCATTCCGGCGAGAACACCTTGAGCATCTCAAATCAAGGAGGTGCTAATCCGAGC  
AGCAAGAGCAAAGCTCCATACCGTCGACATGACTCTGCCATCAACTTTTGAAACAGAGTCGG  
TAACCCAGAGCAATGGTACTAGCCGCCCCGCAACCAGTTGCTTCTATATTACCAATGGCTTTGG  
ATACTCTGTTCTCGAAGATCCAAGTCTATCAGCTCGCGATATTGTATGTGAACGAACACTCTCCG  
TCCTGTATGGCATTTATTGACAATATCTACACAGCTCAAGTTGCGGGCTTGTGGAACAAACGAG  
CACCCCGGGAAAAGCTCGCTCATGGAACCTGGCGGAAATGGAGGTTCAGCGTCACCGAGCTGAG  
AATCCTCACCTTACCCGACCAGTCGCGATTCCCACGACTGACCCGTTCTCCTCGCATGAGA  
TATCCTTGCCTGAAGATCGGCAACGAATTCTGCGGATGCTGACTTTGTCTGGAA
```

GAGTCGAACGGTCAGCTGGCTGCCGAAGAAGCCGCATTAACGATAACGAACAAACCCAAGAACCG  
GAAGAGGTCGACCCTTCCCCGACTACGAGTGGGAGGAGCCAACCAGATTATTGACATGTCGACC  
GACCTGTCCGTAGCGCAGGACCCGGACTTCATGATGACGGAGGACGACTCCATGGGATTCTCTC  
AAGCAGGCGTGCTGA

CDS annotation:

join(1..155,211..341,394..639,695..1137)

Protein:

MSALDVDAISDIAPGLSPVTALHYGRIQVMLFRSHLADFAEEDLVYAMDNSAVVFGEEALLMVAPD  
ETSIAICTYPVGLMMVEWGNWDILAVSPPPQTPTIPGENTLSISNQGGANPEQQEQSSHTVDMTLPI  
INFFEQQSSVTQSNGTSRPRNQFVLYYQWLDTLFSEDPSSLARDISQVVAGLWNNEHPAAKARFME  
LAEMEVQRHRAENPHLYPDQSRFPTTDPPVPPRMRYPCVISPEDRQRILRMLDFVWEESNGQLAEE  
AAFNDTEQTQEAEEVDPFPDYEWEEPNIIDMSTDLSVAQDPDFMMTEDDSMGFLLKQAC\*

*N. discreta*, mfa-1,  $\alpha$ -factor pheromone

Gene sequence:

ATGCCTTCCACCGCTGCTTCCACCAAGGTCCCCAGACCACCATGAACTTCAACGGTTACTGCGTT  
GTTATGTAA

CDS annotation:

(1..75)

Protein:

MPSTAASKVPQTTMFNGYCVVM\*

*N. discreta*, ccg-4,  $\alpha$ -factor pheromone

Gene sequence:

ATGAAGTTCACTCTCCCTTTGTCATCTTCGGCCGCGTGGCCTCCGCCACCCGGTCGCCAGCCA  
AACGCTGAGGCCGAAGCCCAGTGGTGCGAATCCACGCCAGTCCTGCTGGAAGGTCAAGCGTGT

GCCGATGCCTCGCCAACGCCATCCAGGGCATGGTGGTCTCCGCCTCGCATGAGTCGGCAC  
CAGCCCGCTCAGGTCGCCAACGCCAGGTTGACGAGCTGCCGCATCATTGCCCTCACTCAGGAG  
GACGTCAACGCCTACTACGACTCGCTTGGCCTCCAGGAAAAGTCGCCCATCCACCGAGGAGGAG  
AAGAAGACCGAGAAGGTCGCCAACCGTGAAGCCGAGGCCAGTCAGTGCCACATCCACGGC  
CAATCGTGTGAAAGAAGCGTGAGGCCGAAGCCCAGTGGTGCCGCATTCACGGTCAGTCCTGCTGG  
AAACGTGACGCCCTCCCCGAGGCCGAGCCCCAGTGGTGCCGCATTCACGGCCAGTCCTGCTGGAG  
AAGCGTGACGCCCTCCCAGGCTGCTCCCAGGCTGCTCCCAGGCTGCTCCCAGGCTGAGGCCAACCGCAATGG  
TGCCGCATCCACGGCCAGTCCTGCTGGAAAGCCAAGCGCCGCCAGGCCGTATGACCGCCATC  
CAGTCGCCAGGCCAGTCCTGCTCCCAGGCTGCTCCCAGGCTGCTCCCAGGCTGAGGCCAACCGCAATGG  
GGCAAGCGCGATACTTGCTGGAACGTCAGGCTCCCGGTGGTGTCAAGAGCTCCTGCTGGAAAGCGT  
GATGCCTCCCCAGAGGCCGGCTTGCAATGCTCCGACGGCGTGCACCAAGGCCACCGTGACTTG  
CACGCCATGTACAACGTCGCTCGCATCCTCACTGCTCACTCCGATGAGAACTAG

CDS annotation:

(1..915)

Protein:

MKFTLPLVIFAAVASATPVAQPNAEAEAQWCRIHGQSCWKVKRVADAFANAIQGMGLPPRDESGH  
QPAQVAKRQVDELAGIIALTQEDVNAYYDSLGLQEKFAPSTEEKKTEKVAKREAEEAQWCHIHG  
QSCWKREAEAQCRIHGQSCWKRDALPEAPEQWCRIHGQSCWKRDAAPEAAPPEAEANPQW  
CRIHGQSCWKAKRAAEAVMTAIQSAEAESALLRDNTFSPVDRVGKRDTCWNVRLLPGGVKSSCWKR  
DASPEAACNAPDGACTKATRDLHAMYNVARAILTAHSDEN\*

*N. discreta*, *pre1*, a-factor pheromone receptor

Gene sequence:

ATGAACAAACACTGATTCTGGCAAGTGTGCCAACATCACCAACCTCCTACACCACACCTGAA  
GAACGACTTGGCCTCCGCTCCTACACCAATATTGGTCTTCAGGTCAACCTCTTCAGAGTC  
TTTCTGGATTCTCGGAATACTCATTCTTGTGCCTGCAAGGCTGTTATGGATCAATGGCGAA  
TTTCTGCCACGGTACATTGCATGTCAACAGTCACGCTCAACTCTTTACGTCGTCAACTCGCTC

ATATGGCGAGACAACAATGTCAAGAAATGGTATGCCGGCTATGGGTGGTGCATTTCATACTTAC  
GTCTTCTTGC GGTTGAAACTATCTCCACACCCTCTTCGACATCATGCTCGGTCTGCCATC  
AAGATCGGTAGCCCCGGAGTCACCAAGCCTCAGTCCTAAGGAAAAGAAACGCAAGGACCGAGTTCG  
GCCCTCATCATCTCGCCAATCCGGTCTTACAGGTCTGCTCACCTACTTCTCATTACGCAACGG  
TACGACGTCTTCACTCTGCCGGTTGCAATGCCATCTCGATCCAATGGGTCTTCTCGTTTC  
TTCATTCTCCCATGCCAGTCTCACGCTTGGGGCGGCTGGCTGGCAGGTAAAGATAACAAACCAA  
GTCCATGGCATGTTCGCAATCGCTCACAATGTACACAGGGTTTTACAAGTACCGGCAG  
TGGAGAAACTCACCGCGAAGTCTTACCAAGTGATGACAGTATAACGAACCGCGAGACAAAAACGCC  
TGAGGAGAAAGCTCTACTTCTCACTCTCTATTCTCGTCTAGTCGTGCCGACTGTTGCGTCT  
TCTTCGTCTTCAACCTCATTCAAGGTTGCCGTGGTCACTGCCGTTGACCTCCATCGCATTACG  
CCAACATCAACTTGTCTCGTCAACACGACGGAAAGAATGAAAGTCTCCGAGTCCTTACCAACT  
ATGTGCCAGTGGTGAGCTAGCGGCAATTGCATCACCTCGGCACAACAGTCGAGGCATATAACC  
AATACCGCTTAGTTCTCGTCTTCCCTGGCTTAGGAAAGTTGCCCAAGCTGTATCAGGAATATG  
ACCCCGATGAGTCTGGACCACCATCTGAGCTAGCACGCAAACAAGTTGAAATCGTGGTGGTCAT  
CCATAACGACAAACAACAAAAGGGTACAGTCACAAGGTATAAGATCACACACCTCACAACATAAC  
TATCACATTGGATCATCTGGATGCTGACGTACAGTTGAATAAGCAGCCAGTGTGGAAATGACTTCT  
CTATCCTCCCTATTACTGAGGACATACCACTCACAAACCAATCTAACCTGCACAAACGGGTGAAG  
GCTCCTATACCGTCCC GGTTATGCATACGATGAACTCGGAAAAGAAATCTGAACCAGTATTCTA  
CCCAGTCCTCAGCCACAGCAAACCGACCATATCCATGGCCGATCTGTCAAGACAATCACCCCC  
CTCCAGCACGCAACCCATGGTATTCCGACCGAATGCTTCCACGTCCCACATTGCCAATGC  
CACTGTCGCCATTACATACCGTCTCTGCATGCCGTCAAGCAAAGCAGACGGAGGGAACGCAGA  
AACGGACGACAGTCAACAGGCTTCTCAAGGCTACACCGCACTCAGTAGCTCCTCCACAACAATCC  
TACCCCCCTGAATTCACCTACCTGCCCTCTCCCCGATTCCAATCTCACATCCTCCTCAAGAC  
ATTCAACCACAGGAGGAACGACACTGGCGACGAGAAAGACACAAAAACAGAAAGAACAGACACGC  
AAAATAGCACAAGCAATGGACAACCAAGAACCCATTGACACCCAGCGGATCCATGGAGTCCCTTG  
CTTCCAGTCACACCAACACTACCTGGAGTTGACACACGCGTGTGGTCCAGAAGGATAACGACG  
ACTCTGCCGGTCTACCCAAAGACTCACCGATCTCCATGCTCTCGTTCAATCACGGACCCAGC  
TCTCACCGCCGCATCATACAGTGTGCTGTTGGTCAAGAATCCTCCTTGCTCCGCTGCCGATC

AATCGGCAGGATTGAAATCAGTCGGCTGAAATCAACAGATTGGACGGCGTTAGGACATCCAC  
CGAGAGGCAGGGTGGTTAGAGTAGAGACCCATATAGCGAGTGAGATTGAGGTCAATTAGCAGTCTG  
GGCGTGATGATGGTAATGATCGTGTGGTCAACGAGGTGGAAGGGGTGGTAG

CDS annotation:

join(1..643, 700..1225, 1301..2300)

Protein:

MNNTDSWASVANITTSYTTPEERLGPPAPYTNIGLQVNLFFRVFLGILGILIPARLLWINGE  
FSATVHCMSTVTLNFFYVVNSLIWRDNNVKWYAGYGWCDFHTYVFAVETIFHTTLFDIMLGLAI  
KIGSPRVTSLSPKEKKRKDRVSALIIFANPVLQVLLTYFLITQRVDFTLAGCNAIFDPNGVFV  
FILPSPVFTLGAAGLAGVCFYKYRQLEKLTVLPSDDSIRTARQKRLRRKLYFLTLSILVLVVPT  
VCVFFVFNLIQGWPSLPFDLHRIHANINFVSFTTERMKVSAVLTNYVPVVSSAACITFGTTVE  
AYNQYRLVLVFLGLGVWPKLYQEYDPDESGPPSELSTQTSSKSWWSSITTNNKRGTVTSQCGND  
SILPITEDIPLTNQSKPAQTGEGSYTVPGYAYDELGKEISNQYSTQSSATAKSDHNPWPDLSDNHP  
PPARNPWYFRPNNAFHVPITLPMPLSPIYIPSLHAGQAKQTEGTQKRTTVNRLSQGYTALSSSTTI  
LPPSNSPTCPLPPIPISTSSSRHSPQEERHWATRKTQKQEPDTQNSTSNGTTKNPLTPADPWSPF  
ASSHTNTTLGVDTRVWSQKDNNDSAGPTQDSPISHASRSITGPQLSPPPSYSVAVGQESSFASAAD  
QSAGFEISRPNQQIGTALGHPPRGGVVRVETHIASEIEVISSLGRDDGNDRVGDQRGGRGW\*

*N. discreta*, pre2,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGGCCTCCTCCGTCGACATCTACAGCGGCATAACCCAATCCCTCAACTCCACCCACGCCACTCTC  
ACCCTCCCCATCCCCCGCCGACCGCGACCACCTCACGAACCAAGTCCTCTTCTCGACAAC  
TACGGCCACCTCCTCAACGTAACCACCAACCGAAGTCGACACCCTCACCGACATGGTCATCTCCACC  
GCCATCAACTACGCCACCCAAATCGCGCCACCTCATCATGCTGCCATCATGCTTCTCATGACG  
CCCCGCCGCCGTTCAAGCGTCTACCCACCATCATCGCTTGGCCCTTGATGAACCTGATC  
CGCGTCGTCCTGCTTGCCTTCTGCCGTCGCACTGGACCGATTCTACGTCTGTACTCGGGC  
GACTGGCATTCCGTGCCCGCAGCGACATGCAAATCAGCGTGGCAGCCACGGTGCTCAGCATCCCC

GTCACGGCCCTGCTGCTGTCGGCGCTCATGGTGCAAGCGTGGAGTATGATGCAGCTGTGGACACCG  
CTATGGCGGGCCCTGGTCGTGTTGGTCTCTGGTCTGCTTCGTCGACCGTGGCGCTTCGTT  
GCCAATTGCATTTCAAGCCAAGAATATCCTGTATGCGGACCCGTTCCCGCCGTATTGGGTGCGC  
AAGCTGTACCTGGCGATGACGACGGGTCGATTCGTGGTTACCTTCTTGTTCATGATTGCGTTG  
GTCATGCATATGTGGACTAACAGGAGTATCTGCCGAGTATGAAGGGTTGAAAGCCATGGATGTG  
TTGATTATTACTAACTCCATCTGATGCTGATTCCGGTCTTGTGCCCCGCTGGAGTTCCCTGGAC  
TCGGCCAGTGGTTGAGAGCGGTTCGCTTACGCAGACGAGCGTCGTATTGCTTGCCGCTTGGC  
ACGCTGGTTGCCAACGGATTGCTACGAGGGATAACATGCCGTACTCTGGAGGCTCTGGACCT  
AACGGAAGTTGCCGTGAGCAATTGAGTCTTACCGGTGGCGGTGGTGGTGGAGGTGGTGG  
CACCAAGATAAAGGAAATGGAGGAGGAGGAGGAGGTAGACAAAATGGCACCACCCCTCCCACCACC  
ACCAATAACAACAACATAGCAACCACCTTCTCCTCCATCGCGTGCAGCGGCATCAGCTGC  
CTGCCAAGGCAAAGCGCATGACGCCAGCTCGCATCTCCAGTCAACGACCCCTTGACAACG  
ACCAACTCGACCATAGCCAGCAATGACTCGTGGTTCCCGAGTCCAAGCGTCCACAATGCCACG  
CAATACCAATATGCGATGAACATGAACATGAACATGCCCACTACCACCCACCTGTTCTTATCCT  
GGGTACAACAGCCGTAACACGGCGTTACCTCTCACATTGCCAGCGACGGGGACACCACCGGG  
ATGAACCGACATCCGAGCGTCGACCACTTGATCGCGAGCTGGCGAGGATAGATGATGAAGATGAT  
GTGGACAACCAAGATGTGTACCCCTTGCGTCATTGAGAAGGCGGTATGGATGGCGATGATAAT  
GATGATGATGTAGAGAGGGGGAGGGGGAGAGCCCTACCTCCGCCGCTGGGGAGTGAGAGTG  
GAGAGAAGGATTGAGACTAGGAGTGAGGAGAGGATGCCGTCGCTTAATCCGTTGGAGTCACAAAG  
CCGAGGTCTTGAGTAG

CDS annotation:

(1..1734)

Protein:

MASSVDIYSGITQSLNSTHATLTLPIPPADRDHLTNQVLFFFNDNYGHLLNVTTTEVDTLTDMVIST  
AINYATQIGATFIMLAIMLLMTPRRRFKRLPTIISVLALCMNLIRVVLALFCPSHWTDFYVLYSG  
DWHSPVPRSDMQISVAATVLSIPVTALLSALMVQAWSMMQLWTPLWRALVVLVSGLLSFATVALSF  
ANCIFQAKNILYADPFPPYWVRKLYLAMTTGSISWFTFLFMIRLVMHMWTNRSILPSMKGLKAMDV  
LIITNSILMLIPVLFAGLEFLDSASGFESGSLTQTSVVIVLPLGTLVAQRIATRGYMPDSLEASGP

NGSLPLSNLSLTGGGGGGGGHQDKGNGGGGGRQNGTIPPTTNNNNNIATTFSSSIACSGISC  
LPKAKRMTASSASSSQRPLLTTNSTIASNDSSGFPSPSVHNATQYQYAMNMNMNMPHYHPPVPYP  
GYNSRNTGVTSHIASDGHHQGMNRHPSVDHFRELARIDDEDDVDNQDVYPFASFEKAVMDGDDN  
DDDVERGRRALPPPPLGGVRVERRIETRSEERMPSPNPLGVTKPRSFE \*

*N. tetrasperma*, mfa-1, a-factor pheromone

Gene sequence:

ATGCCTTCCACCGCTGCTTCCACCAAGGTCCCCAGACCACCATGAACCTCAACGGCTACTGCGTT  
GTTATGTAA

CDS annotation:

(1..75)

Protein:

MPSTAASKVPQTTMFNGYCVVM\*

*N. terricola*, mfa-1, a-factor pheromone

Gene sequence:

ATGCCTTCCACCGCTGCTTCCACCAAGGTCCCCAGACCACCATGAACCTCAACGGCTACTGCGTT  
GTTATGTAA

CDS annotation:

(1..75)

Protein:

MPSTAASKVPQTTMFNGYCVVM\*

*N. terricola*, ccg-4,  $\alpha$ -factor pheromone

Gene sequence:

ATGAAGTTCACCTCCCTTGTATCTCGCCGCCGTGGCCTCCGCCACCCGGTCGCCAGCCT  
AACGCTGAGGCCAAGCCCAGTGGTGCAGATCCACGCCAGTCCTGCTGGAAGGTCAAGCGTGTT  
GCCGATGCCTCGCCAACGCCATCCAGGGTATGGGTGGTCTCCGCCCGACGAGTCGGCCAC  
CAGCCGCCAGGTGCCAAGGCCAGGTGACGAGCTGCCGGCATCGCCCTCACCCAGGAG  
GACGTCAACGCCACTACGACTCCCTGCCCTGCACGAGAAGTCGCTCCCTCACCGAGGAGGAG  
AAGAAGACCGAGAAGGTGCCAAGCGCGAGGCCGAGGCCGAGGCCAATGGTGCCGCATCCACGGC  
CAGTCGTGCTGGAAGAAGCGTGAGGCCAAGCTCAGTGGTGCCGCATCCACGCCAGTCCTGCTGG  
AAGCGTGACGCTCTCCCCGAGGCCGAGCCCCAGTGGTGCCGCATCCACGGTAATCTGCTGGAAG  
AAGCGCGATGCTGCTCCCGAGGCTGCTCCGAGGCCGAGGCCAACCCGCAATGGTGCCGCATCCAC  
GGCCAGTCCTGCTGGAAGGCCAAGCGCGCCGCCGAGGCCGTATGACCGCCATCCAGTCGCCGAG  
GCCGAATCTGCTCTCCTCCGTGACACCACCTTAGCCCCGTCGACCGCGTCGGCAAGCGCGAT  
GCCCAAGTGGTGCAATGTCAAGTCGCTCCCGATGGTGCACCAAGGCCACCCGTGACTGCACGCCATG  
TACAACGTCGCTCGGCCATCGTCACTGCTCACTCCGATGAGAACTAG

CDS annotation:

(1..906)

Protein:

MKFTLPLVIFAAVASATPVAQPNAEAEAQWCQIHGQSCWKVKRVADAFANAIQGMGLPPRDESGH  
QPAQVAKRQVDELAGIIALTQEDVNAYYDSLGLHEKFAPSTEEKKTEKVAKREAEAEAQCRIHG  
QSCWKKREAEAQCRIHGQSCWKRDALPEAEPQWCRIHGQSCWKKRDAAPEAPEAEANPQWCRIH  
GQSCWKAKRAAEAVMTAIQSAEAESALLRDTTFSPVDRVGKRDAQWCNVKFPGGVKGNCKRDAS  
PEAACNAPDGACTKATRDLHAMYNVARAIVTAHSDEN\*

*N. terricola*, *pre1*, a-factor pheromone receptor

Gene sequence:

ATGAACAAACACAGATTCTGGCAAGTGTGCCAACAGTACCACTCCTACACCACACCCGAA  
GAACGACTTGGCCCTCCGCTCCTACACCGATATTGGTCTCCAAGTCAACCTCTTCAGAGTC

TTTCTAGGAATCCTCGGAATTCTTATTCCCTCGTCGAAAGCTATTATGGATCAACGGCGAA  
TTTGGGCCACGGTACATTGCATGTCAACAGTCACACTCAACTTCTTTACGTCGTCAACTCGCTC  
ATATGGCGAGACAACAATGTCAAGAAGTGGTATGCTGGCTATGGGTGGTGCATTCCATACTTAC  
GTCTTCTCGCGGTTGAAACCATCTTCACACCACTCTTCGACATCATGCTCGGTCTGCCAAC  
AAGATCGGTAACCGCGAGTCACCAAGCCTCAGTCCAAGGAAAAGAAACGCAAAGACCGAATCTCG  
GCCCTGATCATCTCGGCAATCCGGCCTACAGGTCTGCTCACTTACTTGTCAATTACTCAACGG  
TACGACATCTCAACCCTGCCGGTTGCAATGCCATCTCGACCCCAATGGCGTCTTCGTTTC  
TTCATTCTCCCATGCCAGTCTCACGCTTGGTGGCAGGCTGGCAGGTAAAGATAACAAAGCAA  
GTACATGGTATTTCGTAATCGTTACAATATACGAGGAGTTGTTTACAAGTACCGACAGC  
TGGAGAAACTCACTCGGAAGTCATACCAAGTGATGATAGTATACGAACCGCGAGACAAAAACGCC  
TGAGGAGAAAGCTCTACTTCTCACTCTCTATTCTCGTAGTTGTGCCGATTGTTGCGTCT  
TCTTCGTTCAACCTCATTCTGGGTTGGCGTGGTCGCTGCCGTTGACCTCCATCGCATTACG  
CCAACATCAACTTGTCTCGTCACAACGACGGAAAGAATGCAAGTTACCGCGTCCTACCAATT  
ACGTTCCAGTGGTGAGCTGGCGGCCATTTCATCACCTCGGCACAACAGTTGAGGCATATAACC  
AGTACCGTTGGTCTCGTTCTCGGCTTGGAAAGATTGGCCAAGCTGTATCAAGAATATG  
ACCCCGATGACTCTGAGCCACCATCTGAGCTAGCACGAAACAAGTTGAAATCGGGTGGTCAT  
CCATGACGAAGAACAGCAAAGGGGTACAGTCACAAGGTATGAGACTCGCAAGCTCCAACATAA  
CCATCACATTGGACTATCTGGATGCTAACGACAATTGAATGAACAGCCAGAGCGGAAACGATTTC  
TCTATCCTCCCTATTACTGAGAACATACCTCACGAACCGATCAACACCTGCACAGACAACGGT  
GAATGCTCCATACCGTCCATGTTCTCCATACGATGAGCTCAGAAAAGAATTCCGGACCTGTAC  
CCTACCCAGTCCTCACCCACAGCAAAGCCAACCATAACGCCTGGCCGATCTGTCAAGACGACCC  
CCTGCTCCAGCAGCAGCCCCATGGTATCTCCGACCGGATGTTCCATGTCCGATCAAACGCC  
ATGCCACTGTCACCCATTACATACCATCCCTGCACGCGGATCAAGAAAAGAAGACGGAGGGAAAG  
CAGAAACGAGCCAGTGTCAACAGGCTCTGCAGGCTACACCGCGCTCAGTGGTCCCTCCACAACA  
ATCCTGCCGTCCTCGCAGTCACCCACCTGCCCTCTGCCCTCCACCCACATCCTCCTCA  
AGATATTCAACCACAGGAGGAGCGCCACCGCCAACAAGAAAAGAAACAAAACAGAAAGAACAG  
ACGCAAACAGCACAAGCAATGGGACACATAAGAAGAAACTCATTGACGCCAGCAGCACCATGGAGT  
CCCTTCGTTCTACCCACACCCACACCACACTAGGAGTTGACACTCGCGTATGGTGTCCAGAAG

GATAACAAACGGAAAAGACCATGCTGCTCACCCACAAGACTCGCCAGTCTCCCATTTCTCGC  
TTAACCTCAGGACCTCAGCTTCACCGCCGCATCGTACAGCGTCGCTGTCGGTGAATCCTCCTT  
GCTTCCGCTTCCGATCGATCGACGGGACTCGGAATCAGTTGCCGAACAACAACAGATCGGAGC  
GCGTTGGGACACCCGCATCCGCTAAGGGCCCTCGGGTGAGGGTTGAGACGCATATAGCGAGC  
GAGATTGAGGTTATTGGTGGTCTGGACGTGATGATGGTAATGATGGTATGGTCAACGGGT  
GGAAGGGAGTGA

CDS annotation:

join(1..643, 700..1225, 1302..2322)

Protein:

MNNTDSWASVANSTSYTTPPEERLGPPAPYTDIGLQVNLFRRVFLGILGILIPLVPAKLLWINGE  
FGATVHCMSTVTLNFFYVVNSLIWRDNNVKWYAGYGWCDFHTYVFFAVETIFHTTLFDIMLGLAN  
KIGNPRVTSLSPKEKKRKRDRISALIIFGNPVLQVLLTYFVITQRYDISTLAGCNAIFDPNGVFV  
FILPSPVFTLGAAGLAGVCFYKYRQLEKLREVIPSDDSIRTARQKRLRRKLYFLTLSILVLVVP  
VCVFFVFNLILGWPWSLPFDLHRIHANINFVSFTTERMQVTAVLTNYVPVVSSAAIFITFGTTVE  
AYNQYRLVLVFLFGKIWPKLYQEYDPDDSEPPSELSTQTSSKSWWSSMTKNSKRGTVTSQSGND  
SILPITENIPLTNRSTPAQTTGEC SHTVPCSPYDELRKEFPDLYPTQSSPTAKANHNAWPDLSD  
PAPARSPWYLRPDAFHVPIKLPMPLSPIYIPSLHADQEKKTEGKQKRASVNRLSAGYTALSGS  
ILPSSQSPCTCPLPPLPTTSSRYSPQEERHRPTRKKQKKEPETQNSTSNGTHKKNSLTPAAPWS  
PFASTHTHTTLGVDTRVSSQKDNNNGKDHAAPQDSPVSHFSRLTSGPQLSPPPSYAVGE  
ASASDRSTGLGISSPEQQQIGTALGHPHPLRALGVVRVETHIASEIEVIGGSGRDDGNDGDQ  
GRE\*

*N. pannonica*, mfa-1, a-factor pheromone

Gene sequence:

ATGCCTTCCACCGCTGCTTCCACCAAGGTCCCCAGACCACCATGAACTTCAACGGCTACTGCGTT  
GTTATGTAA

CDS annotation:

(1..75)

Protein:

MPSTAASKVQTTMFNGYCVVM\*

*N. pannonica*, ccg-4,  $\alpha$ -factor pheromone

Gene sequence:

ATGAAGTTCACCCCTCCCTTGTATCTCGCCGCCGTGGCCTCCGCCACTCCGGTCGCCAGCCC  
GCCGCCGAGGCCAACGCTCAGTGGTGCCAGCTCCACGCCAGTCCTGCTGGAAGGTCAAGCGTGTC  
GCCGAGGCCTCGCCAACGCCATCCAGGGCATGGTGGTCTCCGCCCGACGAGTCCGGCAC  
CAGCCCGCCAGGTCGCCAACGCCAGGTCGACGAGCTGCCGGCATCGCCCTCAGCCAGGAG  
GACGTCAACGCCTACTACGACTCCCTCGCCCTCCACGAGAAGTTGCCCTCCACCGAGGAGGAG  
AAGAAGACCGAGAAGGTGCCAACGCCAGGCGAGGCCAGGCCAGGCCAATGGTGCCGCATCCACGGC  
CAGTCGTGCTGGAAGAAGCGTGAGGCCAGGCTCAATGGTGCCGTATCCACGCCAxxxxGCCAG  
CCCCAATGGTGCCGCATCCACGGTAATCTGCTGGAAGAACGCGTACGCCGCTCCGAGGCTGCT  
CCCGAGGCTGAGGCCAACCGCAATGGTGCCGCATCCACGCCAGTCCTGCTGGAAGGCCAACGCG  
GCCGCCGAGGCCATCATGACCGCCATCCAGTCCGCCAACGCCAGTCCTGCTGGAAGGCCAACGCG  
ACCACCTTCAGCCCCGTCGACCGCGTCGGCAAGCGCGATCCCCAGTGGTGCCGCATCCACGCCAG  
TCCTGCTGGAAGCGTGATGCCTCCCCGAGACGGCTTGCAACGCCCGATGGTGCTTGCACCAAG  
GCCACTCGTGACTTGCACGCCATGTACAACGTTGCTCGTGCATCGTCACCGCTCACTCCGATGAG  
AACTAG

CDS annotation:

(1..864)

Protein:

MKFTLPLVIFAAVASATPVAQPAEANAQWCQLHGQSCWKVKRVAEAFANAIQGMGLPPRDESGH  
QPAQVAKRQVDELGIITALSQEDVNAYYDSLGLHEKFAPSTEEKKTEKVAKREAEAEAQCRIHG  
QSCWKKREAEAQCRIHGxxxxxxxxxEPQWCRIHGQSCWKKRDAAPEAAPEAEANPQWCRIHGQSC  
WKAKRAAEAIMTAIQSAEAESALLRDTTFSPVDRVGKRDQPWCRIHGQSCWKRDPASPETACNAPD

GACTKATRDLHAMYNVARAIVTAHSDEN\*

Note: This protein was encoded by a gene that was found on the ends of two scaffolds and thus could not be fully assembled. This is why the **xxx** is found in the middle of the gene and predicted protein.

*N. africana*, mfa-1,  $\alpha$ -factor pheromone

Gene sequence:

ATGCCTTCCACCGCTGCTTCCACCAAGGTCCCTCAGACCACCATGAACCTCAACGGCTACTGCGTT  
GTGATGTAA

CDS annotation:

(1..75)

Protein:

MPSTAASKVPQTTMFNGYCVVM\*

*N. africana*, ccg-4,  $\alpha$ -factor pheromone

Gene sequence:

ATGAAGTTACCTTCCTTGTCACTTCGCCGCTGTGGCCTCCGCCACCCGGTCGCCAGCCC  
AACGCCGAGGCCAAGCCCAGTGGTGCGCATCCACGCCAGTCCCTGCTGGAAAGTCAAGCGTGT  
GCCGATGCCTTCGCCAACGCCATCCAGGGTATGGGTGGTCTCCGCCCGCGACGAGTCCGGCAC  
CAGCCCGCCAGGTCGCCAAGGCCAGGTCGACGAGCTGCCGGCATCATGCCCTCACCCAGGAG  
GACGTCAACGCCACTACGACTCCCTGGCCTGCACGAGAAGTCGCCCTCCACCGAGGAGGAG  
AAGAAGACCGAGAAGGTCGCCAAGCGCGAGGCCGAGGCCGAGGCGCAATGGTGCCGCATCCACGGC  
CAGTCGTGCTGGAAGAAGCGTGAGGCCGAAGCTCAGTGGTGCCGCATCCACGCCAGTCTTGCTGG

AAGAACGTGATGCTGCTCCGAGGCTGCTCCTGAGGCCAACTCGCAATGGTGCCGCATTCGCGGT  
CAGTCCTGCTGGAAGCGTGATGCCTCCCCGAGGCGGCTTGCAACGCTCCGATGGTGCTTGCACC  
AAGGCCACCCGTGACTTGCACGCCATGTACAACGTGGCTCGTGCCATTGCCACTGCTCACTCCGAT  
GAGAACTAG

CDS annotation:

(1..669)

Protein:

MKFTLPLVIFAAVASATPVAQPNAEAEAQWCRIHGQSCWKVKRVADAFANAIQGMGLPPRDESGH  
QPAQVAKRQVDELAGI IALTQEDVNAYYDSLGLHEKFAPSTEEEKKTEKVAKREAEAEAQWCRIHG  
QSCWKKREAEAQWCRIHGQSCWKKRDAAPEAAPEANSQWCRIRGQSCWKRDASPEACNAPDGACT  
KATRDLHAMYNVARAIATAHSDEN\*

*H. bhutanensis*, MAT1-2-1, MAT1-2-1 protein

Gene sequence:

ATGGAAAACCTCCTCATTGATCCCACCTTGATGGGCCAGCTCATCTTGAGACTTCGGCTTGAA  
ACTGCAGGTCTTGATCCATTGGTATACTTCACAGTCCAACAACAACAGATTCTCCAATCTGCATGG  
GCAGCAGCAACAGTCAAATATCACCATTTCAAAGTCGCAGCATTACATGCGAACATGGTACTA  
GCCCTCAGCGAGGACTCCAAAAGTCATTGCTGGCTGATTCACGTACGAATATTACTTCAAACC  
AATTTTAGTACTGACATCATTCTCCAGGAACGTGATAGGCGCCCCGGCCTTATTGGTTAGAG  
ATTCTCCGATCTGATCGCTTTTATCGGATCCTTACAAGAATTTCGTCCATCAACCAGTCGC  
TCATCATGATGCCAGGATATGATCATTCTTGGTTGACTGGAGATGCTTCATCCAAAGTG  
GTCTCCCTCTCCAATAAGCGTTCAAGGTACGAATCCGACGACAGTAATAAGATGACGTCAAAC  
AAAAACTACCTCGCCCCGCTAATGCGTACATATTGTACCGTAAAGAGCGCCACCATTCCGTCAAAG  
ACGAGTTCCGGGGATCTGTAACAACGAAATTGTGAGTCCTAATTATCATACAACCCCTCACTGAT  
ATAAGGCTTACTAACATAGCTATTAAGCGCGAATTCTGGCCGCCATGGAAGGAAGAAAGCGAGA  
CAGTTCGGGCGTTCTACAAAGAGCAATCTGAAAACCTACAAACAAACTTCATGAACACCCACCCAG  
ACTATCAATACAGACCGCGCAAGGCAGGAGAAAGAAGAAGAGAACAGGGGTGTTCAACCCAAAG

ACTCCGAGAACACTGGGTTACAATACCCGTTCTGCTAGGGAAACCCAAAGGTGTTGTCGCTG  
AGAGCCCTATTTAA

CDS annotation:

join(1..242, 296..627, 688..938)

Protein:

MENFLIDPTLMGPAHLETSALTAGLDPLVYFTVQQQQLQSAWAAATVQISPFSKVAALHANMVL  
ALSEDSQKSLLADFTNVIGAPALLVRDSSDLRFFIGSLQEFSINQSLIMMPGYDHFLLVSTGDA  
SIQSGLPSPISVGHESDDSNKDDVKQKLPRPPNAYILYRKERHHSVKDEFPGICNNEISRILGRR  
WKEESETVRAFYKEQSENYKQNFNMNTHPDYQYRPRKAGEKKRNRRVQPKDSENTGLQSPVSARGT  
PKVLFAESPI \*

*H. bhutanensis*, MAT1-2-7, MAT1-2-7 protein

Gene sequence:

ATGGACATTGACGCCGTGCGACACCTCCAGCACCTTGTTGGTAACCTGTCGCAAAAACCAAAATGG  
CAGATGCTGGCGTCTCTCATTCTTATCATTACACCACCATCCAGACTCAGGAAGGAGTACCCCTCATC  
CATCCTTGCATTGATAACCATCAGCCGCCTTTGCTCGAAGTTATCCCCCAAATCGATATCTC  
CAGAACTGCTTCAAACAGCCACCTTCCTTACAATGGACCTCCCTTCTTCAAGAGACTAGCT  
TTTGAGAAAGGCTTCATGGGATTCCGGCCGATACATGTACCGATACTATGTCTGTCTACATG  
AACGCCATGCTTGTCTCCCAGAAGATGCAGTTTCAATTGCATGGAGTCAGTGCCTTGCACATCAA  
ATTCACGCCTCACATCCGAAGCTCTCGCGCATACTTCATCGAACTGGCAACGGAGTTCTCTGG  
GCATAA

CDS annotation:

(1..468)

Protein:

MDIDAVRHLQHLWVTCREKPKWQMLASLILIHTIQTQEGVPLIHPCALIPSAASLLEVIPPNRYL  
QNCFQQPPSFTMDLPLLFKRLAFEKGFMGISGRYMYRYYVSVMNAMLDLPEDAVSLHGVSFAHQ  
ISRLTSRSSRAYFIELGNGLWA \*

*H. bhutanensis*,  $\alpha$ -factor pheromone

Gene sequence:

```
ATGGCCGCTATCAAGAACATCACCTCCTCCAAGAACGCCGCCGGCGTCGACCAGTCCAACCCG  
TGCAACGTCATGCGTGGTGTGACCAGTCCAACCCGTGCGCTGTCATGCGCGGTGTTGATCAGTCC  
AACCCCTGCACCGTCATGTAA
```

CDS annotation:

(1..153)

Protein:

```
MAAIKNITSSKNAARGVDQSNPCNVMRGVDQSNPCAVMRGVDQSNPCTVM*
```

*H. bhutanensis*,  $\alpha$ -factor pheromone

Gene sequence:

```
ATGAAGTTCTCTACCATCCTGGCTGTTGCCTCTGGTCTCGCTGCCGTGAGGCCGCTGCCATCACC  
CCCGTCGAGGCCCGCGATAACGCCCTACTGTTGAAGCTCGCGCAAGTTCTGAAGAACTCCAAC  
GGCGGTCTCCCCGGTGAACCTCCTCCGCCGCTCTGGACGACTCCAACGGTGGTCTTCCCGGTGAG  
CTTCTTCGCCGCGAGGAGCCTACTCTTGAGGCTCGCGCAAGTTCTGAAGAACTCCAACGGTGGT  
CTCCCCGGTGAGCTCTCCGTCGTGAGGAGTCCATCGAGGCCGTGATGAGGCTACTCTTGAGGCT  
CGTGGCAAGTTCTGAAGAACTCCAACGGTGGTCTTCCCGGTGAGCTTCTCCGCCGCAAGTTCTC  
CAGAACTCCAACGGTGGTCTTCCCGGTGAGCTCCTCCGCCGTGAGGAGGCTACCTTGAGGCCG  
GGTAAGTTCTGAAGAACTCCAACGGTGGTCTTCCCGGTGAGCTTCTCCGCCGTGAGGAGCCTACC  
CTTGAGGCTCGTGGCAAGTTCTGAAGAACTCCAACGGTGGCCTTCCCGGTGAGCTTCTCCGCCG  
TTCTTGAGCAGACTCTAACGGTGGCCTTCCCGGTGAGCTTCTCCGCCGTGAGGAGCCTACCTTGAG  
GCTCGTGGCAAGTTCTGAAGAACTCCAACGGTGGTCTTCCCGGTGAGCTTCTCCGCCGTGAGGAG  
TCCATCGAGGCTCGCGATGAGGCTACCCCTGAGGCTCGCGCAAGTTCTGAAGAACTCCAACGGT  
GGTCTTCCCGGTGAGCTTCTCCGCCGTGAGGAGCCTACTCTTGAGGCCGCCGTGAGGAGCCTAC  
AACTCCAACGGCGGTCTCCCCGGTGAGCTTCTGTAA
```

CDS annotation:

(1..894)

Protein:

MKFSTILAVASGLAAVEAAAIPVEARDTAPTVEAR GKFLKNSNGGLPGE LLRREEPTLEARGKFLKNSNGGLPGE LLRREEESIEARDEATLEARGKFLKNSNGGLPGE LLRRKFLQNSNGGLPGE LLRREEATLEARGKFLKNSNGGLPGE LLRREEPTLEARGKFLKNSNGGLPGE LLRRREESIEARDEATLEARGKFLKNSNGGLPGE LLRRFLDDSNNGGLPGE

*H. bhutanensis*, pre1, a-factor pheromone receptor

Gene sequence:

ATGAGTAATTCTCAAACAGCAATCCGGCCCTCCGCATAGTCGATGGCATGTCTGTTATCGACTTC  
TCATAACCTCATGACGAGCCC ATCAAACCCCAACCAAATAATTCCAACAGCGATGGCGTCGAAGCT  
TACCCCGGCCATGTATATACTGATCGAATCCTCGACTCACACTCGGCCCTTGCCATTCTCCTT  
TACTTATGCCACTCGTATCCTCTACAGACACAATGAGTTCTGCGCCTTCATCATGGTGTGTTGC  
TGGTTGATAAACACCGTGT TTTCACTCTAGCGCTATACTGTGGCCGTCGCATGATACCAGTAAT  
TGGTGGTCTGGAAAAGGGTATTGTGATGTTCAATTAAACATTCTACGCGCTGTTCCATTACCATGGCC  
ATGTCTGCTCTACATCATGTTAGCTACCCTTCTCGCTCCATAACACTCGCCAGTGAGGGTCCG  
TTATTACGGGCTGAAGCTGCCGTAAAGCTCAAACAAGGCCTTTCAACACCCGCTATC  
ATCGTTGGCCTTTATCAAATCTCGCTGCCCTCAACCGGTTGTTATATCCTATAGCCGGCTGC  
GTACGCCTCTGGGATACGTCAATGGCCTACCCCTGCCGTCAACATCATTCAAGAGATATTCTGCCTC  
ATGGCTGGTTTACAGCTGGTAAGTAACAAAGATTCCGCACGTCAACTGCTACAAATCTTACTGAC  
ACTACTTTACTAGTCACAACTTTGTGGACTTATTACAGGTCTAACGGAGAAACAAATCTGCCACC  
GCCCTGATGAACAATCCGCTAGCCGCCAATCCAGTAACCGTGCCGTGCGTAGTCATGCT  
GCAGTAACCATTCTAGTACCCCTACGTCCCCATATCGACATACATTATCATCACAAACATCAAGGTT  
CTTATACCCTGAATGCGTATTCCCTCGCCGGCTCCATAAGAACATAGATTAGGCTTGTTGAG

ATTCATGGCAGGCAATATATTCATGACAGCGAATGGTAAATAACCGTGCTGTATTGAACACA  
TGGATTCCAATAGCTGCAGTTATCCCATGTTGGGTTCTACGGGCTCTCAACCGAAGCTATAAAC  
TCCTATCGGAGAGGTCTCCTCAACCTCGGTCTGGCCCCCGGTATCCAATTCTCTACACGGAATAC  
ACACCCGGTCGTCGACATCATCAACGCCCTCATGGCTCGCCTATTGTTCTCGCGGCCCTGGA  
GAGATCTCCAAGAATAAACCATCTGAATTAAGTTGGGGAGCGCATGCGCATCATTACAAGGACTT  
GAAAGCCCAGCAGTTGCCACATTAAAACAGAAAGTGGTAGACCAATGGTATGGGACGGTCTTCT  
CGAGCAACAGGTGGAGAGGCTGGTGTAAACCCTGATTGTTATGGCGAGGGAGTCTACAGAGA  
GTAGGCACCGGTGACGGAACGTGACGGTGATGACGGAGATTGACCTGAGAAAGTACCCGAGGCGAG  
CGGGCTCAAGAAGAAGTATAG

CDS annotation:

join(1..679, 740..1539)

Protein:

MSNFSNSNPALRIVDGMSVIDFSYLMSPSNPQIIPNSDGVEAPGHVYTDRILRLTLGPLAILL  
YFMPLRILYRHNEFCAFIMVFCWLINTVFFTLSAILWPSHDTSNWSGKGYCDVHLTFYAAVPTMA  
MSALYIMLATLSRSITLASEGPLLRAEARRVKLQGLFIFTPAIIVGLLSNLAASNRFVLVPIAGC  
VRLWDTSWPTLAVNIIQEIFCLMAGFTAVKLLWTYYRSQRNNKSATALMNNPLARQSSNRARRLV  
MLAVTILVPYVPISTYIIITNIKVLIPNAYSFAGLHNIDLGFGEISWQAIYFMTGEWVNNAVL  
NTWIPIAAVIPCFGYGLSTEAINSYRRGLNLGLPRYPILYTEYTPGRRTSSTPSWLASFVSSR  
PGEISKNPSELSSGSACASLQGLESPAVAHIKTESGRPMVWDGLSRATGGEAGAVTDCYGEGL  
QRVGTGDGNVTVMTEIDLSTRGERAQEEV\*

*H. bhutanensis*, pre2,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGACCGATTCACTTTATTCTTCATACAATATCCACTTTCAGAGCCACTTGATGGCTCGTGAT  
GATAGTAACCAGACCATCGACTTCGACCCGAAAGTGTACCGTTAACATCACCAACTCCAAGTGTT  
GGAGTCGTGACAGTAACTATGCATGTCGTCGAATACTACTCTCGGTATCTGGTTAACTACTCTATA  
TCACGCGGGCTACAAACTGGAATGTTAGCCATGACATTAATGGCTTGATATTTCAAGCCCCAAG

GACCGCATCCTCAAAAGAACATCGTCATTCAAATCATCACTTATGCGTGCATCATCAAAAGC  
GTCCTCCTACTCAGATGGGCTACATCGGGTGGGATCGATGTACAGCATCATCACCGGAGATTAC  
TCCAACCTGAAGGCTTCAGACTCCAACAACCAAATCGTTCTATCAGTCGCTAGCATTCTACTCATT  
CTTTTGTTGAAGTGTGCTGCTACACAGCTGGACTATCTTCGCATGTGGAGGCCGACCATA  
AACTACATTGTTGGTTTATCAGTGTCTAGGAACCTCCACAGTCGCTATGCGAACAGTATAT  
CAGGCAATAGGACTGAAATCTGTGTTAGATGTGGCGGCTGACAGGAATCATCAGAGTCTACCGAC  
TTGTTACTCGTAAGTGTATTGTTCTCAAACCTGGCTCTCGCTATTCAACCGTTGGTTACA  
GCGATCTTCAATGTCAAATTAATTAGTCATATGTGGAAGACTAAACGGCTGCTACCCAGTCGTA  
GGCATGACGCCGATGGAGATTAACTGCAACTAATGGTTCTCATGATTGCACCATGTAAGTGT  
AATTGAATTGTCCTGTCATTAGATACTAATCTCCTTCAGTGTACCTTGTTGCT  
TCCAGCTCGAAGCTCTCACACACAGTAGACTTGCTACATGGACCACCTGCCATTCTATGATT  
CTGCCATTGGTCCCTCATTGCTCAAAGACTTATCAGCGGCCAAAAGTCTCTTCACTTGTTCAC  
ATCTCAGCCGTGTCAAGCAACAGCAGCAATACCCAACACTCCATTGTTAACGGAGGACAAGAC  
CTTACCATGACTGCAGCAACTAACAGACAATGGTCGAGACCGGGCGACTGGCGAGTTCCAGAT  
GATCGCGATGATTGTCATATTACAGAGATGTTGACCAAGAAGTGAGCGTCGTAGCTCAA  
AATTGA

CDS annotation:

join(1..850, 908..1260)

Protein:

MTDSLFLHTISTFQSHLMARDDSNQTIDFDPKSVPFNITPSGGVVTVMHVVEYYRSYLVNYSI  
SRGLQTGMLAMTLMALIFFSPKDRILKKNIVIQIITLCVAIIKSVLLRWATSGWGSMSIITGDY  
SNLKASDSNNQIVLSVASILLLFLVELMLLLHSWTIFRMWRPTIKYICLVLGVFLGTSTVAMRTVY  
QAIGLKSVDVAADRESSESTDLLTVLFFSNLALAISTVWFTAIFNVKLISHMWKTKLRLPSRK  
GMTPMEILTATNGFLMIAPLIFVCLSSSKLSHTVDFATWTTAIPMILPFGSLIAQRLISGKVSS  
LVHISAVSSNSNTPLPLFNGGQDLTMATAATNKTMVETGATGEFPDDRDDCVNIHRDVDQRSERR  
VAQN\*

*H. omanensis*,  $\alpha$ -factor pheromone

Gene sequence:

```
ATGGCCGCTATCAAGAACACCACCATCCAAGAACGCCGCCGGCGTGACCAGTCCAACCCC  
TGCGCCGTCATGCGCGGCGTTGACCAGTCCAACCCCTGCGCTGTCATGCGCGGCGTGCACCAGTCC  
AACCCCTGCACTGTCATGCGCGGTGTTGACCAGTCCAACCCGTGCACCCTCATGTAA
```

CDS annotation:

(1..189)

Protein:

MAAIKNNTTSKNAARGVDQSNPCAVMRGVDQSNPCAVMRGVDQSNPCTVMRGVDQSNPCTL\*

*H. omanensis*,  $\alpha$ -factor pheromone

Gene sequence:

```
ATGAAGTTCTCTACCATCCTGGCTGTCGCCCTCTGGTCTTGCGCCCGTCGAGGCCGCCATGCC  
CCCGTTGAGGCCCGCGATGCCACCCCGCTGTTGAGGGTCGTCACTTCCTGGACGACTCCAACGGT  
GGTCTCCCCGGTGAGCTTCTCGCCCGAGGAGTCTACCGTCGAGGCTGCCACTTCTGGAAAAC  
TCTAACGCTGGCCTCCCCGGTGAGCTTCTCGCCGCTTCTGGAGGACTCCAACGGTGGTCTTCCT  
GGTAGCTTCTCGCCGCTTCTGGAGGACTCTAACGGTGGTCTTCCCGGTGAGCTTCTCGCCGT  
GAGGAGCCTACCGTCGAGGCTGCCACTTCTCGCTTCTGGAGGACTCCAACGGTGGTCT  
CCTGGTGAGCTTCTCCGTGCTTCTGGAGGACTCCAACGGTGGTCTTCCCGGTGAGCTTCTCCGC  
CGCGAGGAGCCTGCCGTGAGGCTCGTCACTCCTGAAGTACTCCAACGCCGGTCTCCCCGGTGAG  
CTTCTCCGCCGTGAGGAGCCTGCCGTTGAGGCTGCCACTTCTGAAGTACTCCAACGCTGGTCTC  
CCCGGTGAGCTTCTGTAA
```

CDS annotation:

(1..612)

Protein:

MKFSTILAVASGLAAVEAAAIAPIVEARDATPAVEGRHFLDDSGNGLPGEELLREESTVEARHFLEN  
SNAGLPGEELLRRFLEDSNGGLPGEELLRRFLEDSNGGLPGEELLRREEPTVEARHFLRRFLEDSNGGL  
PGEELLRRFLEDSNGGLPGEELLRREEPAVEARHFLKYSNAGLPGEELLRREEPAVEARHFLKYSNAGL  
PGEELL\*

*H. omanensis*, *pre1*, a-factor pheromone receptor

Gene sequence:

ATGAGTGATTCTCAGGCAGTAATCCGGCTTCGCATGGTCATGGCATGTCTGTCATCGACTTC  
ACATACTCATGACAAGCCCACAGACCCAATCAGATAATTCCAACAGCGATGGCGTTGAAGCT  
TACCCCGCAATGTATATACTGATCGAACCTCGACTTACACTCGGCCCTTGCCATTCTTCTT  
TACTTATGCCACTCGTATCCTCTACAGACACAATGAGTTCTGCGCCTCGTCATGGTGTGTTGC  
TGGTTGATAAACACTGTGTTTTCATTCTAACGCTATAATGTGGCGTCACATGATACCAGAAAT  
TGGTGGTCTGGAAAAGGGTATTGTGATGTTCAATTACATTCTACGGCTGTTCTACCATGGCC  
ATGTCTGCTCTACATCATGTTAGCTACCCCTTCGCTCCATAACACTCGTCGCCAGGGTCCG  
TTATTACGGGCTGAAGCTCGTGTAAAGCTCAAACAAGGCCTTCATTTCACACCCCGGAATC  
ATCATTGGTCTTTATCAAATCTCGCTGCCCAATGGTTGTTTATATCCCATAGCCGGCTGC  
GTGCGCCTCTGGGATACGTATGGCCTACCCCTGCCGTCAACATCATTCAAGAGATATTCTGCCTC  
ATGGCTGGTTTACAGCTGGTAAGTGATACAGATCCGCAAATCAACTGCTATAAATCTTACTGAC  
ACTACTTTACTAGTCAAACTTTATGGACTTATTACAGGTCCAACGGAGAAACAAATCTGCCACT  
GCCCTAATGAACAATCCGCTAGCCGCCAGTCCAGCAACCGTGCTCGTCTCGTCATGCTC  
GCAGTAACCATTCTAGTGCCTACGTCCCCATATCCACATACGTCATCATCACAAACATCAAGGTC  
CTTATACCCATGAATAACGTATTCTCGCCGAGCTCCATAAAGACAGAGATATAGGCTTAGTGAG  
GTTTCATGGCAGACAATATATTCTACGACAGGCGAATGGTAAATAACCGTGCTGTATTGAACACA  
TGGATCCCAGTAGCTGCAGTTGTCCATGTTGGTTCTACGGGCTCTCAACCGAAGCTATAAAC  
TCCTATCGGAGAGGTCTCCTCAACCTCGGTCTGGCCGGCGGTATCCAATTCTACACGGAATAC  
ACACCCGGTGTACACATCATCAACACCCATGGCTCGCCTATTGTTCTCGCGGCCCTGGA

GAAATCTCTAAGAACCATCGGAATTAAAGTTCAGGGAGCGTATGCGCATCATTACAAGGACTT  
GAAAGCCCAGCAGTTGCCATGTTAGAACGGAAAATAGTAGACCAATGGTATGGGATGGTCTTTCT  
CGGGCGACAGGTGGGGAGGCTGGTGCTGTGACCACTGATTGTTATGGTGAGGGCAGTCTACAGAGA  
GTAGGCACCGGGCACGGAACGTGACGGTGATGACGGAGATTGATCTGAGAAGTACCCGAGGCAGG  
CGGGCTCAAGAAGAAGTATAG

CDS annotation:

join(1..679, 815..1539)

Protein:

MSDFSGSNPALRMVDGMSVIDFTYLMTSPSDPNQIIPNSDGVEAPGNVYDRLRLTLGPLAILL  
YFMPLRILYRHNEFCAFVMVFCWLINTVFFILNAIMWPSHDTRNWWSGKGYCDVHLTFYTAVPTMA  
MSALYIMLATLSRSITLVAEGPLLRAEARRVKLKQGLFIFTPGIIIGLLSNLAASNRFVLYPIAGC  
VRLWDTSWPTLAVNIIQEIFCLMAGFTAARQSSNRARRLVMLAVTILVPYVPISTYVIITNIKVL  
IPMNNTYSFAELHKDRDIGFSEVSWQTIYFMTGEWNNRAVLNTWIPVAAVVPCFGFYGLSTEAINS  
YRRGLLNLGLGRYPILYTYTPGRHTSSTPSWLASFVSSRPGEISKNQSELSSGSVCASLQGLE  
SPAVALHVRTEENSRPMVWDGLSRATGGEAGAVTTDCYGEGLQRVGTGDGNVTVMTEIDL'RSTRGGR  
AQEEV\*

*H. omanensis*, pre2,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGAGCGATTCACCTTTTTCTTCATACGATATCCACTTTCAGAGCCACTTGATGGCTCGCGAT  
GATAGTGACCAGACCATAGGCTTCGACCCGAAAAGTGTACCGTTCAACGTCAACCACTCAAGCGGT  
GGAGTCGTGAAAGTAACTATGCATGTCGTAATCCTACTCTCGGTATCTGGTCAACTACTCTATA  
TCACGCGGGCTACAAACTGGAATGTTAGCCATGACATTAATGGCCTTGATATTTTCAGCCCCAAG  
GACCGCATCCTAAAAAGAACATCGTCATACAAATCATCACTTATGCGTTGCCATCGTCAAAGC  
GTCCTCCTACTCAGATGGGCTACATCGGGATGGGATCGATGTACAGCATCATCACTGGAGATTAC  
TCCAACTTGAAGGCTGCAGACTCCAATAACCAAATCGTTATCAGTCGCTAGCATTCTACTCATT  
GTTTTGTTGAACTAATGCTGCTACTACACAGTTGGACTATCTTCGCATGTGGAGACCGATCATC

AAGTACATTGTTGGCTTATCAGTGTGTTAGATGTGGCGGCTGACAGGGCATCGTCAGAGTCTACCGAC  
CAGGCAATAGGACTGAAATCTGTGTTAGATGTGGCGGCTGACAGGGCATCGTCAGAGTCTACCGAC  
ATGTTACTTGTAACTGTATTCTTTCAAACCTGACTCTCGCTATTCAACTGTTGGTTCACAGCCATATTCAATGTCAAGCTGATTAGTCATATGTGGAAGACTAAACGGCTGCTACCCAGTCGTAAGTGA  
GCCATATTCAATGTCAAGCTGATTAGTCATATGTGGAAGACTAAACGGCTGCTACCCAGTCGTAAGTGA  
GGCATGACGCCGATGGAGATTTAAGTAACTGTAAGTAACTGGTTCTCATGATTGCACCAAGTAAGTGA  
AATTCACTCCTGCTTGCGTTATTATAACAATACTAATCTTCTTTGTTCACTGGTATTGTTGTCT  
GTCCAGCTCGAACGCTCTCACACGTAGCAGACTTGCTACATGGACGACCAGTGCCTATGAT  
TCTGCCATTGGTCCCTCATTGCTCAAAGACTCATCACCAGCCAAAAGTCTCTTCACTGTTCA  
CATCTCAGCTGTGTCAAGCAACAGCAGCAATAACCAACACTTCCATTGTTAACGGGGACAAGA  
CCTTACCATGACTGCAGCAACCAACAAGACAATGGTCGAAACCGGGCGACTGGCGAGTTCCAGA  
TGATCGCGATGATTGTGTCAATGTTACAGAGATGTTGACCAAAGAAGCGAGCGCCGTTAGCTCA  
AAGCTGA

CDS annotation:

join(1..850, 909..1261)

Protein:

MSDSPFFLHTISTFQSHLMARDDSDQTIGFDPKSVPFNVTSSGGVVKTMHVVESYSRYLVNYSI  
SRGLQTGMLAMTLMALIFFSPKDRILKKNIVIQIITLCVAIVKSVLLRWATSGWGSMSIITGDY  
SNLKAADSNNQIVLSVASILLIVFVELMLLLHSWTIFRMWRPIIKYICLALSVLLGSSTVAMRTVY  
QAIGLKVLDVAADRASSESTDMLLTVFFF SNLTLAISTVWFTAIFNVKLISHMWKTKRLLPSRK  
GMTPMEILTNGFLMIAPMVFCLOSSKLSHVADFATWTTAIPMILPFGSLIAQRLLTSQVSS  
LVHISAVSSNSNTPLLFNGGQDLTMTAATNKTMVETGATGEFPDDRDDCVNVHRDVDQRSERR  
LAQS\*

*H. moniliformis*, a-factor pheromone

Gene sequence:

ATGCCTTCCATCAAGAACACACTCCGTCTACCAAGACCTCTGGCAATGAGACCATCCAACCCCC  
ACTAGCAACGCCGGCGTGGAGCGATTCAAGTCTCCCATCAACCCGATCACCCGGCGTCACCCAG  
GCTCCGCCGTGCAATGTGATGCGTGGAGTTACTCAAGCCCCCCTTGCAATGTCATGTAA

CDS annotation:

(1..192)

Protein:

MPSIKNHTPSTKTSGNETIQPPTSNAGRGAIQSPINPITRGVTQAPPNVMRGVTQAPPNV\*

*H. moniliformis*,  $\alpha$ -factor pheromone

Gene sequence:

ATGAAGTTCTCCACCATCTGGCTGTTGCCCTCGTTCTGCCGCCGTTGAGGCCGCTGCCATTGAG  
CCCCGCCGCGACATCTGAAGGACGCCAACGGTGGTCTCCTGGCGAGCTTTCCGCCGCGAGGAG  
TCCGTCATTGAGCCCCGCCGCAAGATCCTCAAGGACGCCAACGGTGGTCTCCCGGTGAGCTCTC  
CGCCCGGAGGAGGCTGCTGTTCTCGAGCCCCGCCGCAAGATCCTCAAGGACGCCCTGGGTGGTCTC  
CCTGGCGAGCTTTCCGCCGTGAGGAGTCTGTCATTGAACCCCGCCGCAAGATCCTCAAGGACGCC  
AACGGTGGTCTCCCTGGCGAGCTCTCCGCCGAGGAGGCTGCCGTTCTCGAGCCCCGCCGCAAG  
ATCCTCAAGGACGCCCTGGGTGGTCTCCCTGGCGAGCTTTCCGCCGTGAGGAGTCTGTCATTGAA  
CCCCGCCGCAAGATCCTCAAGGACGCCAACGGTGGTCTCCCGGTGAGCTCTCTAA

CDS annotation:

(1..519)

Protein:

MKFSTILAVASVLAAMEAAAIEPRRDILKDANGGLPGELFRREESVIEPRRKILKDANGGLPGELF  
RREEAAVLEPRRKILKDAWGLPGELFRREESVIEPRRKILKDANGGLPGELFRREAAVLEPRRK  
ILKDAWGLPGELFRREESVIEPRRKILKDANGGLPGELF\*

*H. moniliformis*, pre1,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGAGCAATCTCTCAGCCAACAACCCGGCCTCCGTACGGTGAATGGAATGTCTATTCTCGACTTT  
TCATATCTCATGACGGACGCAGCAAACCCAAACTACATAACAATGAACGCCGACGGTGTCCCTGCT  
TATCCCGGCCATTGTATACTGATCGAATACTCCGACTTATATTGGGCCCTTGTCTACTCCTT  
TACCTTATCCCACCTCCATATCCTCACAGACACGATGAGTTCTGCGCCTTCATAATGGTTCTTGC  
TTTGTGGTATACGCCATATTTTACCCCTCAACGCTATAATGTGGCCGTACAGGACACTAGCAAT  
TGGTGGTCTGGTATCGGGTATTGCGACATCCAGTTAACATTCTATACTGCCGTTACAGTAGGT  
ATGGCGGCACTTACATGATGTTGGCTGCTCTGTCGTTCTATAACACTCGCCACAGAGGGCCCT  
TTGCTACGGGCTAAGCTGCCGGTAAAACCAAGCAAGGACTCTTCATTTCACACCTGGTGT  
TTTGTGGCCTTCTATCAAACCTCGCTGCCTACAATCGGTCGCTATATATCCTACCGCTGGCTGC  
ATCGTATCTGGATGCATCATGGCCTGTCTTGTCGTCACATTACCAAGAGTTATTTGCCTC  
ATGGCCGGGTTCACAGCTGGTAAGTTACACAGAACCCGATGCATGTCAACCACCAATCTTAC  
TGACATTTATTCACTAGTCAAAATTACTGGACTTATTCAAGTCTCAACGAAGGAACAGCTCAG  
CTACAGCCCTGATGAATAATCCTCTAGCCCCAATCCAGTAACCGGCTCGTCTAC  
TGCTCGCAGTAACCATTCTGGTGCCTACGTCCCTCTGTGCACATACCTGATCACCATAAACATTA  
AAGCTCTTGTACCCATGAATTCATATTCTCAAACAGCTCCATGCCCAAAGATTAGGCTTG  
GTGAAGTTTATGGCAGACCCTATTTATGGCAGGGGAATGGGTGAATACCGTACTGCATTCT  
ACACATGGTTCCAATATTGCAATTCCCAGTTGGCTACGGTCTTCAACGAAGCTA  
TAAACTCTTATCGGAGAGGTCTACTTAAACTCGGCCTGGCTCCGGTATCCAATTCTTACACGG  
AATACACACCCGGTCGCGCGTTATCAAATCCTCATGGCTTGCTCATTTGTACATCACAGC  
CTAGAGATGTTCCAAGACTCAACAATGTGAATTAGTTCTGGAAGTCCTCGTACGTCACTCCAAG  
GACTTGCACCCAGGAGTTGCTATGTCAGACCAGATGATGACAGACCAATGGTATGGACGGTC  
TTGCTCGAGCAACAGGTGGTGGGCTGGTGCAGTAACTACTGATTGTTATGGTGGAGGTAGTATAC  
AGAGAGTAAGCACCGGTGACGGAACGTCAAGGTGATGACGGAGATTGACCTGAGAACGACCCGAG  
GCGGACGGGATCAAGAAGAAGTATAG

CDS annotation:

join(1..679, 745..1544)

Protein:

MSNLSANNPAFRTVNGMSILDPSYLMFTAANPNYITMNADGVPAYPGHLYTDRILRLIFGPLVILL  
YLIPLHILHRHDEFCAFIMVSCFVVYAIFFTNAIMWPSQDTSNWWSGIGYCDIQLTFYTAVPTVG  
MAALYMMALAALSRSITLATEGPLRRAQARRLKLKQGLFIFTPGVFVGLLSNLAAYNRFIAIYPTAGC  
MRISDASWPVFVNIIQELFCLMAGFTAVK1YWTYFKSQRRNSSATLMNNPLARQSSNRARRLY  
MLAVTILV ру VPLCTYLITINIKALVPMNSYSFKQLHAPKDLGFGEVSWQT1YFMAGEWVNTRTAF  
YT WVP1FAIFPCFGFYGLSTEAINS YRRGLLKLGLGSRYPILYTEYTPGRRALSNPSWLASFVTSQ  
PRDVPKTQQCEFSSGSPRTSLQGLATPGVAHVRPDDDRPMVWDGLARATGGAGAVTTDCYGECSI  
QRVSTGDGNVKVMTEIDL RSTRGGRDQEEV\*

*H. moniliformis*, pre2,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGACTTATCCACCTTCTTGATCATACTATCCACTTCCACAGCTACTTAATGGCTCGTGAT  
GAGAGTAACCAGACCATAGACTTCGATCCAAAGATATAACATTCAACATCACCAACAGAGGGT  
GAAGTTCTGACCATCAATATGTATACCATCGAATACTACTCTCGATATCTGGTCAACTACTCTATA  
TCACGCAGGGCTCCAACCGGAATGTTAGCCATGACATTGATGGCTTGATATTTTCAGTCCAAA  
GACCGCATTCAAGAAAAACATCGTTACCAAATCGTTACCCCTGTGCATTGCTGTCAAGAGC  
GTCTTCTGCTCAGATGGCTACGTCGGGTGGGTTCAATGTACAGCATCATCACTGGAGATTAC  
TCGTATCTCAAAGCTTCAGATTCCAACAACAAATTGTTCTGTCAGTCGCTGGCATCTTTGGTT  
CTTTCATCGAGATAATGTTGTTGCTCATGGCTGGACTATCTTCGCATGTGGAAGCCCATCATC  
AAAGTACATCTGTTGGTTCTGTCGGTGTCTCGCCATTGCAACAGTCGTATGCGAGCTGTATAT  
CAAGTAATAGGACTGAAATATCTTTGACCAACGGCGCTGGCAAGCTGATGTCACAGGCTCCGAC  
GATTTAGTCGTGGTTCTGTCAGTCGCTGGCTTCAGTCGCTGGCATCTGGTACCGTAA  
GCAATCTTAATGTCAAATTGGTTAGCCACATGTGGAAGACTAAACGAATATTGCCTACCCGTAAA  
GGTATGACACCGATGGAGATTAAACCGTCACCAATGGTTGCTCATGATTGTACCATGTAAGTCT  
CAATTCTCGTCTCTGCCACGTTAGATACTAACCTCCTGTCAGTTGTTGCTGT  
CAAGTACAAAGCTTCACATCAAATAGACTTTCTACATGGACCATAACTGTAATCCCCATGATT  
TGCCATTGGATCCCTCATTACCCAGAGGCTATCGGCAACCAAAAGTCTCTCACTGCTCACA

TATCAGTTGCGTCGAGCAGCACAGAACACACCAACGCTTCCATTGTTAATGGGGACAGGACC  
TGACCATGACTCCAGCAACCAACAAGACCATGGTAGAAACTGGGGCGGCTGGCAAATTCCGAATG  
ACTGCGATAATTGTGTCAATGTTACAGAGATATTGACCAGAGAAGCGAGCGTCGGTTGGCTCACA  
ATTGA

CDS annotation:

join(1..850,1063..1259)

Protein:

MTYPPFDHTISTFHSYLMARDESNQTIDFDPKDITFNITTGEVLTINMYTIEYYSRVLNVSI  
SRGLQTGMLAMTLMALIFFSPKDRILKKNIVIQIVTLCIAVVKSVFLLRWATSGWGSMSIITGDY  
SYLKASDSNNQIVLSVAGIFLVLFIEIMLLLHGWTIFRMWKPIIKYICLVLSVFFAIATVVMRAVY  
QVIGLKYLTTAACAGKLMQSASDDLVVVSLFFANLALVISTIWFTAIFNVKLVSHMWKTKRILPTRK  
GMTPMEILTVDNGLLMIVPFASSSTSNTPLPFLNGQDLTMTPATNKTMVETGAAGKFPNDCDNC  
VNVRDIDQRSERRLAHN\*

*B. spectabilis*, MAT1-1-9, MAT1-1-9 protein

Gene sequence:

ATGAAGTCGAAGAACCTTGTTCATGCCTGAAATGCGACAGAGGGCAGCTAGATGGTATG  
GATATCTCGGCATCTGAAATACGTGGATGCTGACTATACTCAGAGAACGGTCAGGTGCTCCGGAAG  
AGTTCTGAGCTATTCTACTCGAACTGGAAGATACCGTGGAAAGATGCCTATGCGCAAGTCTTCAG  
TTTGTCTCCTGAGCATCCAGGAATCTGATAGGCCAATCCATAGAATTATCCCTAGCCAGAACTC  
CTGAGCTTATTTGGATGATATTACCTTCTATCGAGGAAGCTACATCTACTCTGTTAGTGGT  
GTTCCCGAGCTCCGTCGACTCCAGCGCCAGCAACATCTTATCCATCCTAGACTCAGCAAAGAGA  
TTCCTCTGTTCTATGAAAAGCAAAATTAGCATCAACCATAAGAGAACCCCTCTCAGCCGCCAAAAG  
ATGCACGAAAGTCTCTGCTGGAAAGAACATAGAGCGGAAGAACAGATAAGTTCTAGCTATTCAA  
CATCCTACTTACGACCCACATCTGCGTCCGTGGCAACAGTTCTGATGGATGGGGCTCCGGTAGT  
GGTCTCAATGCTCGAGACATATTCTACAACAGAAAGCCAGACTCTATTACTAGCCCCTCCAAGGAT  
TCGTCGTTCGCATACTCCCCCTGGGCTGTATGTCTCCTAAGGAAATTACATTCAAATGCAAGA

GAGATGGAGAGAAAATGCAGAGAGGTAAATTCTGAATTAAACAGAAAGCAATCGTGTGATACCA  
ATGTGTAGGGAAAGACCGCAATGCCAGGGATCCTTCGTCTGGTCCGTCGAGATAACATACACATA  
CAATCCAGGTACGCCAGTAGACCTCAGTATTCAATTGGTATTATTGATGAATATTGCTTACTTCTA  
GAAGGTTCCAACGACCAAAGATCAGGTTCTCTTCGGTCTACGACACGAAATGGTCGAGTATG

A

CDS annotation:

join(1..43,140..724,773..819,929..991)

Protein:

MKSKKPCFCHAWKCEFLLELEDTVEDAYAQVFQFVFLSIQESDRPIHRIIPQPELLSFILDDIYL  
SIEEATSTLLVVVPELRRILQRQQHLYPSLDSAKRFLCSMKS KISINHKRTLSAAKKMHESLCWERI  
HRAEEQIVLAIQHPTYDPHLRPWQQFLMDGAPGSLNARDIFYNRKPDSITSPSKDSSFRILPPGA  
VCLLRELHSNAKSNRVIPMCRERPQCQVPTTKDQVPSFGLRHEMVRV\*

*B. spectabilis*, *ppgA*,  $\alpha$ -factor pheromone

Gene sequence:

ATGAATTCTCTTGTCTTGTACTGCTGGCAGTATCCGTGCAGACAATAGCCAGTCCT  
CTAGATCGATGGTGCCGT CGTCCCAGCCAGCCATGTATAAAGATCAAGCGGGAAATCCA ACTCTGG  
AAGTCGGAAC TTGGACATCAGAACCTAGAGAGAAGGAGACTCTCGCTTTGGACTCTAACAGT  
CGACCGCCGGAGTTCTGGTCGATCTATTCAAGAGAGACGTCGAGTCTAGTTCCG  
TACGCATCGCATACGAGTATAGCTTGA

CDS annotation:

(1..291)

Protein:

MNFSLVFLVLLAVSVQTIASPLDRWCRRPGQPCIKIKRGIQQLWKSELGTSEPREKETLAFLFNS  
RPPEFSGRSIHSSRETSSLVPYASHTSIA\*

*B. spectabilis*, *preA*,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGGCTGACATTGAGTATAAACGTGCTCCTGAGGCCATTATTATTCCGTTCTATCCCTCCTCTCA  
ATAATACTGAGCATCACTCCGTTGATGTGGCACTTGAGAAACTCCAACCTCCCCGCTGTCTGTCTC  
GTCTGTTGGTCCTCATCAATAATCTGTTAACATCGAATGCCTCATCTGGCTACTGACAAT  
ATTGATTCCCTGGTGGAGCGCGTCGGACTCTGCGATATCGAAGTCAAATTGATGGTGGCAAGCTAC  
GTTGGCATACCGGGAGCTGTTGTATCTCCGCCATCTGCGGAAGTCTGGACACAGATCGT  
ACAGTTCTTGTCCCTCTGGAAGTCAGCGTCCAAGAAGCTTGCCATTGAGATAGCATTCTGCTTA  
GTCGTGCCCTGCTTGGCCATGATCACACACTACTTGTCCAGAAAACCGTTACATGCTCTACACG  
ATTTCAAGGTGTGAACAACTTTGACGAAAGCTGGTTACGTTGTTCTATCTTACCTGTGGCCG  
ACTGTGATATGCGTCATTGCAGCTTACTACTGCTGTACGGATATCCTATGCCAATTACCAATGAT  
TGCAAGATGCTAACTACTTCCTAGGTCTCGTATGTACGGATTATCAAGTACAACAGAGAGTTG  
GAGCTATCCTGAGTGGTTCTGGGGAGTAGTCTTAACAAAACGAGGTTCTACGCCCTGTTGCA  
TGGCATCTGTGATGCTGTTGGCGATACTTCCTACCCAGGCCTACGTCTATGTTGATATCCAAC  
TGTCACTGCCATGGCACGATTACTCCTTACCAAGGATGCACGGCTGAATGGAACACAATTATCA  
AGGTTGCGACCCATGGACAGAGCTTTCGATCGTTGGATACCAATTGGTGGAAATACTGTTCTGT  
TCGTTTCTCGGTTGGAAAGGATGCGACTCGATGTACCGTTGATCTCACCAAGCTTGGAG  
TTGATCGCTGGCTCCCAGCAAAGTCACATTCCGATATCTACTCCGGAAAACGAGCTCTTCAG  
GTAGTCGAATGAGTAAACTAGGGAAAATGTTACCTGGAGTCTCCAGTCCAACACCACAAGGTCA  
TGCCGGATTTCGCCGGATTCCCTTTGTAAGAAAACCGTCTCCCGCTAACTGAGAAGCAGAATT  
CACGAACTAGCTCTGTTCCCATGATCCTCCAGCAGTTCTACTTCTACTACCGACCTGGAAA  
AAGGATCCGGCATCCACTCCGTAGACAGGAACATGACCAATGAATTGTCGTTCTCAGTAGACTCG  
CCCGTCTGAGGATGTGGACGGCTTCCGCACCGAACAGGAAATGCCCTGCTGGACCTCTAATA  
ATAACAGTGTGGGCCACGCGGGATGGCGATACTCATCCAGATGCTGGTCTTCAGTAGACTCG  
TAGAGTCGGGCATCAAGGTCAAGCACGTCACTGCCAGACCAAGGTGTCCATCTGCCACATTGCG  
GTGACGAGATCGTGTCTTACGAGCCTTGA

CDS annotation:

join(1..562,619..1117,1181..1547)

Protein:

MADIEYKRAPEAIIIPFLSLLSIILSITPLMWHLRNSNFPAVCLVCWFLINNLNFNIVNAFIWPTDN  
IDSWWSGVGLCDIEVKLMVASYVGIPGALLCIFRHLAEVLTDRTVLVPSGSQRRKKLAIIEIAFCL  
VVPVLAMITHYFVQKTRYMLYTISGCVNNFDESWTFVLSYLWPTVICVIAAYYCCLVMYRIIKYN  
REFGAILSGSRGSSLNKTRFLRLFCMASVMLLAILPTQAYVLYVDIQLSLPWHDYSFTRMHGPEWN  
TIIKVATHGQSFFDRWIPIGGILVLVFVFFGFGKDATSMYRSIFTKLGVDRWLPAKSHSDIYSGKTT  
SSSGSRMSKLGKMFWSLQSNTTSRISRTSSVSHDPSSSSSTSTDLEKGSGIHSVDRNMTNELSF  
FSRLARLRMWTVFRTATGNAPAGPPNNNSVGAPRGMDTHPDAGPSPKIESGIKVKHVIRQTKVSI  
CPHCGDEIVSYEP\*

*B. spectabilis*, *preB*,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGCAGAAATCTTCGACCCCTTCACGCAGAGCGTGACCTCCATCTGGCAGATGGATCTCCTCTC  
CCAGTTCCGTCGGAGAGCTGGACGACTTCGTTCACTATGGTATCAAGATCTGCATCGTCTACAGC  
TCTCAGCTTGGTGCCTGCCCTGGCTTGCTGGTTCTCCTCTTGACGAAGAGAGACAAGCGA  
CTGTCCCCGGTTTCCTGCTCAATGGCTCTGCTTAATCTTCAATGCGTCCGCTTGATCTGCAAT  
TCCGTCTATTCACTACCGAGTTCTCCAAGGTGTATCCTTACTTTCAAGGAGACTACTCCGAGTT  
CCAGCCAGTGCTTATGCGAACTCCATTCTGGCTGTTCTCCAGGTGCTGCTGGTTGCCATT  
GAGTGCTCCCTCATCTGCAGACTCAGGTTATCTGTGTCACTCTCGTCAGCTTACAAGAACATA  
CTTCTGGGTATCTGTGGTTATCTTTGCTTGCCTGGATTCCGCCTGGCTCTGGCTGTTGAG  
AATTGATCGCTATCGTCAAGCGGCCAACTTGATGCTGTCTGGTAGAAAGCGCCACCAATATT  
ACTACCACATTAGCATCTGCTTCTCAGCTGCATTTCATGCCAAGTGGGACATGCCATTCA  
CGACGCAAGAGGATGGGAATCAGGCGGTTGGCGATGCAGGTGATTTCATCATGAGCTGCCAG  
ACACTGATTGTTCCATGTATGTTATCCGTACCGATATCACGATGGATTCTGCTAACTCATGATA  
GCCATCTTGCGATCCTGCAGTATTGTGTCAGGTTCCGTGAAATCGACTCCTCGTTCACTCTC  
GTCGCGATCTCTCCCTGTGACCTCCCTGTGGCGACGTCTTGACCAGCAATGGTAGCCAAGCA  
TCCAGCGGGTCAACTGAACGTAACAGACTTTGGAAGCCGATTGCTTGGAAAGCGCAGAGAAGCTT  
AAGCAGTCTTCTACGCAAGGCCGTCCAGTTGGCTCTGTAGCTACTTCAAGCCGACTGGGGCA

GCGCATATGAATTCCCTTGCCCTGACCTTGAGGCTGGAACAGCGATTGGGGTGAAGCACGATGTT  
ACAGTTGCTTCTAACAAACATGTAG

CDS annotation:

join(1..742, 794..1146)

Protein:

MQKSFDPFTQSVTFHLADGSPLPVSGELDDFVQYGIKICIVYSSQLGASLALLVLVLLTKRDKR  
LSPVFLNNSALIFNACRLICNSVYFTTEFSKVYPYFSGDYSRVPASAYANSILAVVFQVLLVAI  
ECSLILQTQVICVTLRQLYKNILLGISVVISLLAVGFRLALAVENSIAIVQAANFDAVWLESATNI  
TTIISICFFSCIFIAKLGHAIQRRKRMGIRRGAMQVIFIMSCQTLIVPSIFAILQYCVEVPEIDS  
FVLTLVAISLPLTLSLWATSLTSNGSQASSGSTERNRLWKPIRLGSAEKLKQSSTQGPSSLASVATS  
SPTGAAHMNSLCPDLEAGTAIGVKHDVTVASNNM\*

*B. fulva*, MAT1-1-1, MAT1-1-1 protein

Gene sequence:

ATGGCCGCCGTACGACTCCCCTCCAGCAGCGTTAACAACTTTTGTGACTATGCCGCCTGAT  
CGTCTGGAAGAGCTGCTCAGGTATCTCAATGAAGCCAGAGAGGGTTCAGACAATGAAACTCATGGG  
GACAATACTGGGCCCGAATCCATTGGTACGCTTCCTCGCCTATCTGCCGACAACGTGCA  
GCCCTCGCTCACCAGCTTGTGGAGACGTCCGCGAAGGGAAAGCTAAGGCCTCTAACAGC  
TTTATTGCCTTCAGAAGTAAGTTAGATAATCCAGACAGAATTGAAATACTGAGCTAAACCATGAG  
CAGGCTCTATTGAACATCTCCCCGACTTGACTCAAAGGCGAAGTCCGGATTCTCAAATTTC  
TCTGGCAGAACGACCCTTCAAGGCCAATGGCTGTACTCGCAAAGCATATTCCATTGTTCGCG  
ATTCTCATATTGGCGAGGTCTCTTTGATTGCTTGAATTGAACCTCCGGTTCTTGACATCG  
TGGACCCTGCCATTACCTTGAAGCTATGGATGGAGTTGACCAACCAGGGACAGAGTCAGTACA  
CCATGGCTAAGGTCAGATCAGTCCCTATTGTCGAGGTCGAGGTTCTACCATTCGGTGAACG  
ATATTGTCACTCGTTTACGAACCTGGCTACGTGTGGAGAAAAGCGTAACCATACTGAGTC  
GGGGCAATGACGGCCAGCTTCTAACATGGCATTGTCGCTCAGCCAACATTGATTGTCAACGAGA  
ACAACGCAGTCCAGATCTCTGGACCTGACAACAATGTGGTCATTGACCTCGATGCGAAAGCTGACG

CTGAAGTTTCCCCAATAACGCTCCAGCAGGAACCTCCGTCTCCGGCTCCTAGCGACTTGAGTCGA  
TGGTTCACGATAATT CGGGACGGAGCCTGAAGTACACCATGTGATGCCTCAGTCTAAGGTTGACA  
ACGGCTTCAATGCCAATGTGCAGTTGCTGATGCGCATGACCCCTGAAGTCTTCTTCCTCTGGAAG  
TGCTTCATACTCCCCTATGCCCTACGATCCTCTCATCTCAGGGCCATGGAGAACTACGACATTG  
ACAGATT CCTGAATCTTAA

CDS annotation:

join(1..280,334..1142)

Protein:

MAAVTTPLQQAFNNFLLTMPDRLELLRYLNEAREGSDNETHDNTGAANPFFDALPRPILPTTA  
APRSPALRGRRPREGKLRPLNSFIAFRSFYSNIFPDLTQKAKSGILKFLWQNDPFKAKWAVLAKAY  
SIVRD SHIGEVSLDSFLNLNSGFLDIVDPAHYLEAMGWELTNQGQSQYTMAKVRSVPIVEVEVSTI  
HSVNDIVTRCYELGYVSGEKRNH TLSRGNDGPASNMAFVAQPTLIVNENNNAVQISGPDNNVVIDLD  
AKADAEVFPNNAPAGTPSPAPS DLSMVHDNFGTEPEVHVMP QSKVDNGFNANVQFADAHDPEVF  
FPLEVLHTPLMPYDPLISGPMENYDIRFLNL\*

*B. fulva*, MAT1-2-1, MAT1-2-1 protein

Gene sequence:

ATGGCGATGATA CCTATTG CAGTGAAGGCAGCTGCCAACCTACGGACAAAGTCACGGAGTTGATC  
TGGCAGGATGCTT GCGTCACCTCGAATCTACGAACAA CGAACAGTCCTGCTCCAACGAACATCACC  
GACATGATCGGCCAGGACAATCTCGACAAGATAAAAGTCTCGTCTCAGGTAAGATGCCGTTGGAT  
TACAGAGAATGGACAAGCTAATACGCAGACAGCGCCCTCATTGATGCTCCGGTTCTGGCCTTCGTC  
GACA ACTCGATCAATGCTCTCGTGT CATGCGTATT CCTGCATTGCGGGACTGTGATCTCTG  
TCGTCTCATACC ATGATTCCCAATTG CAGAACGAGCCGCCGAA CGCCGATAAGTCCGATGAA  
AAATCCATCCGTGCGAGAATT CGAGAGTTCCACGACCCCGAATGCTTTATCTTGATCGCCAG  
CATCATCACCCGAAAATTAGAGCTGCGTACCTGAATT CACAATAACGATATT GTGAGTATACT  
TAATAC CCTGATA CCTGGGAAGTACCGCTAATGGAGATAGCAAAATGCTGGAAAAGTGGAAAC  
GCTGAGTCCGATGAAGTCAAAGCCCATTACAAGTTGCTCGCGACGACATCAAGCGCAGACACGCC

GC GGAGAATCCGGGATACCAGTACGCACCTCGCAAATCATCTGAAAAGAACGCGTCGGATGGCATCG  
CGCCAGTTCAAAATGGCAGAAAGCCTAGTACAACACTGC GTGGCCGACTCCCCGGATCCAATGCG  
ACGGCCGTCTCATCCATCGTGACGACCCCCATTCCCTTCATCCAGCTTGCTGAAAGAGCAAGA  
AATACCGGGGCAAACGGAACATATGTGACCTAGAACATGTGAACGTTGCCATCGGTCAAAATGAT  
GTCGTGGCGACCTGAACCTCGACTCTGGCACCTCGACGATTTGATCCAGCGAGCCGAA  
AGCGACCAGGAAAAGGCCATGCTGTGTCAGCATATCAGTCACAAGAGTCATCAGGAACTGGAGAC  
TCTTTTAACCTCTCGAATTATTACTGACTGCTACTGA

CDS annotation:

join(1..179, 231..517, 569..1095)

Protein:

MAMPIAVKAAAEPDKVTELIWQDALRHLESTNNEVLLPTNITDMIGQDNLDKIKSRLSALIDAP  
VLAFVDNSINALRVMRIPAFAGTVISLSHTMIPNLQNEAAANADKSDEKSIRARISRVPRPPNAF  
ILYRQHHHPKIRAAYPEFHNDISKMLGKQWNAEDEVKAHYKLLADDIKRRHAAENPGYQYAPRK  
SSEKKRRMASRQFQNGRKPSTTALADSPGSNATAVSSIVTTPIPFHPALAERARNTGANGNICDLE  
HVNVAIQONDVVVGDLNFDFDSGTFDLIIQRAESDQEKA MLCQHISHKSHQGTGDSFN FSEFITDCY

\*

*B. fulva*, MAT1-2-4, MAT1-2-4 protein

Gene sequence:

ATGGACTTGTACTGCCGCACTGTTGTGAGAGTTCTGGGCCATGGCTCAGGACGCGACTTGGCC  
TCTGAGCAAAGACACCAGGCCCTGTACGCGGCTGTCTCGTCTTCAGTCACCGTAACCCCTTCGG  
CTTATGGCCCAGGTATCTGCTATAAACGATGGCAGATCGTGATCCAGCCTCCCCTCAGACTACA  
GCGGTGGCGGAGAATGGCGACTCCCCAGTCACCGCTACGGAATGTTATCAATGCCATTATTACC  
GACTCTCGTGTGTCGTCCCCACGAATGCGGACTTCGAAGGCCACCGATTGAAC TGTTAGTACACTG  
GACCCCTCGTATTGAAAATGCGTTGAATGGTGCCAGAAATTCAAGTTCACCGGGCCTTGCTTTCT  
TTGGAGCAGGATGCCAATCAAGACCTCGTCAGATGTACCGAGAAGTACGGCTATCACTACATCTTC  
AGGGCTGGATTGAGGCAATATTACATGACGTAAGTTCAAGGAACAATGAATATTGAAGTTGCTCA

CGCTTAGCAGAAAATTGTCGGAGAACTGAATTCTGGAGAGCGGACGCGTGGCAATGAG  
TACAGAGTCAGCGCACAGAAACTCTGCTATGAAGCAATGGAAAAGCAGGTCAAGCTGAATGCTACT  
GAAAAAAGAATTCTCATACAGGCGCTGGTGCTCGGCAGAGGACGCGCACAGATTCTGTGAGTAC  
CTCTGAATTAGACATGTCGAACGCGCTAACGCTAGTAACCAGGGAGCTGGCTAGAGAGGAATCGAG  
GCGCCTACATTGCAATGAAGACTTGCATTCTGCTAGAGCACCTCAACTGTAACGATTCCACAC  
AGGACACATAG

CDS annotation:

join(1..491, 540..718, 769..869)

Protein:

MDLYCRTVVRVLGAMAQDATLPSEQRHQALYAAVSFFSHRNPFRMAQVSAINDGRSLIQPPHQTT  
AVAENGDSPVNRYGMFINAIITDSRVVPTNADFEGHPIELFSTLDPRIENALNGAQKFQVHRALLS  
LEQDANQDLVRCTRKYGYHYIFRAGLRQYYMTKIVAENLFWRADARGNEYRVSAQKLCYEAMEKQ  
VKLNATEKRILIQALGCSAEDAHRFWSWLERNRGAYIAMKTCISLLEHLNCNDSTQDT\*

*B. fulva*, *ppgA*,  $\alpha$ -factor pheromone

Gene sequence:

ATGAGGCTCTCTCAATTCTTCTGACCCTGGCTGCCGCCAGTCAGGCTCTCCAACCGGC  
CTCGAACGCCAGCCACCGAGAGCGATATCACATTGGATGCCGTAACCATCCTCGTCCTAAA  
GGCTCCTACGGATACAAGAATTGGTGTGTAGACCCGGGTCAAGTTGTGAACCGCTCAAGGTCAA  
CGCACCCCCGACGCTCTGAGGAACGCGAGATACTTACGGAGCGCAGACGGATCTACAGCTTAG

CDS annotation:

(1..264)

Protein:

MRLSSILLTLAAAQALPTGLERPATESDITLDARNHPPRKGSYGYKNWCVDPGQVCEPLKVK  
RTPDALEEREILTERETDLQL\*

*B. fulva*, *preA*, a-factor pheromone receptor

Gene sequence:

```
ATGGGCCCTCCGATCGCTAAATTGAGGCCAATCCGCACGCACCGCTAGAGACACATCCCTTGCT  
ATCGCTAGGCCATACCGGCTCTGGCCTGTGCTCTATTCGTCACTATCCAACTCTGATCTTA  
CACCTGAAAAACCGCAACTGGCCCCTACGTGCATCACCGCTTGGTTATTATAGCCAACCTCTTC  
TCTATGGCAAACGCCCTGATCTGGAGCACGAACGATCTGGATTCTGGTGGAGCGCGAAGGGCTT  
TGTGATGTTGAAACCAGACTCATGGCAGCCAGCTACGTTGGTGTGCCAGGCGCTTGGTCTGTCTG  
TTTCGAAATCTGGCCGCCGTGCTAGATAACGAGCCGTACTACTCTCGTCCCTAGTCAGGCACAAC  
CGGCGCAAGATTTCTGGAGATTGTGTTCTGCCTGGTGAATTCCGGCATGTTGATGGTTACCAGC  
TACATGGTGCAGACGAATCGGTATCGATCTCGAGATCTCAGGATGCACCTCCCTGTGCGATCAA  
AGCTGGGTGAGCATCGTGCTGCTCTATATGTGGCCCGGGATAATCTGCCTGATAGCCATCTACTAC  
TGTTGTAGGTCCCCGTCTACGAAAACCAACACCTTGCTGCTTGACTAATGAGACTGTCCAGGCC  
TAGTACTGCTCCGTGCCTACAAATACCGAGCCAATTGGAGATATCCTCAGGGCGTCTGGTACCA  
GTTGGACTAAGTCCAGGTTCTTCGTTCTCGACTCGCCCTCTGATCCTGCTCGCAATCACCT  
CATTTCAGACATACTTCCTTACGACAATGTACGGTGGCTCGTCCGGCTGGCACGGTTTTCTT  
GGCGCGGAGTTCACGGGCCTGAATGGAAGATTGTTCTCATGGTCTCCACGGATGGCAATAGTTCCA  
TCGACTGCTGGGTGTTCATTATTGGCGGTTATTGTCTCGTCTCCGGATTGGCGAGATG  
CCATTCACTGACGCTCTGCGCTTCTGCCCTGGATGCGAGCGTTCTGTGATTGTCTATCGC  
GTCTATTCGCCAGCGGAAGGCGTACTCCCCATTCAAACCTTCAAAAAATAAAATACCAGAT  
CGACACGGGAACAAAATGGCAATATCACAGTATGTTCTATTGGTTTTTTGTTTATAT  
ATTTGTTTGTGGATCTCTGCCGGCGTGAAGTGCTAACACGTAACACCAGGAACCTTCCAGA  
CCGGCTCCAGATACTCTGACCCAATACGTCAAGACTCCGGATACCGCATTCCATCAAGGCAAAC  
GAGACGAATGCGAATAATACTCCTCCTGGCCAAGAAGAGCGTGGAGTCCTCCGAACACCCTG  
TCTTCTTCTCCCTGCATACAGTGACAACCTCAGGCCACAGCTGCTTCCAGGCTTCATCCCACA  
TTGAACAGTGTCTCTGCCAGTGCCTGGCAGATAGAAGCCAAAAGAGCCACGGCAGTAGCACCTTG
```

CGTTCCCTCGTCGCTTCTGCAGAAGAGGGATTATCAGGTGAGGCAAATGATCAGTCAGAACAGC  
GATGTTGCGAACCGTGATGTCTAG

CDS annotation:

join(1..598, 658..1180, 1257..1608)

Protein:

MGPPIAKLRPNPHAPLETHPSAIARAIPALACVSIFVTIPTLILHLKNRNPVTCITAWFIIIANLF  
SMANALIWSTNDLDSWWSGEGLCDVETRLMAASYVGVPGLVCLFRNLAAVLDTSRRTLVPSQAQL  
RRKIFLEILFCLVIPAMLMVTSYMQTNRYAIFEISGCTSLCDQSWVSIVLLYMWPGIICLIAIYY  
CCLVLLRAYKYRAQFGDILRASGTSWTKSRFFRLFALALLILLAITSFQTYFLYDNVRWLVPGWHG  
FSWRGVHGPEWKIVLMVSTDGNSSIDCWVFIIGGFIVVFSGFGRDAIQMYRSALSRLGCERFCDC  
LSRLFRQREGVLPISNSSKKNTRSTREQKWPISQYVLFLFFFWAPDTLDPIRQDGYRIPSRQNE  
TNANNTPSWPRAWKSFRTPLSSPSAYSDNFRPTAASRLHPTLNSVSASAWADRSQKSHGSSTLR  
SSSSSAEEGIIQVRQMISQKSDVANRDV\*

*B. fulva*, *preB*,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGGCATCTGAATCATTGACCCGTTGAAGCAGAACATGCACTTCCATTACGATGATGGACTCCG  
TTCGACGTGCCGATGGACCAATTGGACAAGTTCTCCAGTACAACATTGGATGTCCATCAACTAT  
GGAGCCCAGCTGGTGCAGTCTTATCGCCTGGTCGCTTCGTTACTTGACCAAGCCGGATAAA  
CGCAAGTCAGCTATCTTCTTGCTAACGTCTGCATTGCTCTCCAATATTGGCCGGCTGTTTGT  
CAACTCTTCTATTCGTGGCCCTGGCATGAAATATACCTATTCGCGTATGACTATTCAAGG  
ATCCCGGACAGCGCCTACGCCAACCTGTCTTACCGTTATCTCAGCATCGCCTGCTAACATT  
ATCGAGCTCTCGTGGTCTTCAGCTCGGCTCTGTGTGCGACGCTCCGGCGTACCGGCTC  
CCACTTCTCATTGTGTCGTCGGCCTGGTTCTTCAGTTGGCTTCGGATTGGCTCGGTGTC  
CTCAATTGCTTGAATATCGTGCATCGGTGTACTCGACGGATTGATATGGTTGCAGAGAGCGAAC  
AATATCGTTCTGACCGTCAGCATCTGCTTCTTCAGCGGCTTCGTCGTCAAACGGCTATGCG  
ATCAAGGCTCGGAAGCGACTGGGTATAACGGATCTGGCCGACGAAAGTTCTGTTATTGTCGGA

TGTCAGACCATGCTTGTCCAGGTAGGAGCATTCTTCCTTGCTCTATGTCTCT  
CCCCCCTTCTACTCCAAGTTCAACTACAAATGATCCAGACCAAACACATCCGCATAATCACCA  
AACTCGTTCTAATACCAATGACAGTGCTATTGAGACCATAACATGGCACCACCTCCCAGAA  
ATATCCGCCAACACTGCCTGACAATTATCTCGATCTCGCTTCCTCTTCCTCGCTCTGGCCAAGCAC  
AGTCTCGACAGCAATCTCGAAAAAGGAAAGCTGCTCTTCCCCGCATCGATGGCATGGGCAC  
TCATATAACTCCAACGCTACGTGCTTTCAGGGAAGAATCACCCGCGCCACTATGACCTGGAATCC  
GGACAGGAGAAGGGCATTCTATGCCCGCGACATTTCAGTCCTAGCTTAAGAACAGTAATAAC  
AGCCAGCCTAGTGGCACCGTGTGGATATCCATCAGCCCATTAG

CDS annotation:

join(1..748, 884..1233)

Protein:

MASESFDPKQNVTFHYDDGTPFDVPMQLDKFSQYNIRMSINYGAQLGASLIVLVAFVTLTKPDK  
RKSAIFLLNVSALLSNIGRLFCQLFYFVGPWHEIYTYFAYDYSRIPDSAYANSVLTIVIFSIVLLIF  
IELSLVFQLRALCATLRRRYRLPLLIVSSGLVLLSVGFRIWLGVLNCLNIVRSVYSTDLIWLQRAN  
NIVLTVSICFFSAAFVVKLGYAIKARKRLGITDLGPTKVLFIVGCQMLVPVLFETIQYGTTFPEI  
SANCLTIISISLPLSSLWAKHSLDNLAKRAALSPPSMGHHSYNSNATCFSGKNHPRHYDLESG  
QEKGISIARDISVLSFKNSNNSQPSGHRVDIHQPI\*

*B. nivea*, MAT1-2-1, MAT1-2-1 protein

Gene sequence:

ATGGCCACAGTTCTGCGGCCGTATAAAATCCGTTCTGAATCGATGGACCAGGTAACCGAATTA  
CTCTGGCAAGACGCTCTGCATCACCTTGGTGTACTAACAAACGAGGTTCTGCTGCCAATCAACGTC  
ACCGATCTGATCGGTCAAAGCAATGTCAACAAAGCTCAAGGCGCTTTGGTAGGATGCCGAACC  
TCTATAGCTAGAAAGGATACTAAAGCATGAGAGTAGTGCCCTTATTGCGCCCTGTTGTGGCATT  
TGTTGACGAATCTATCAACCGCTTCGCATCGTACTCCAGCTTCGCCGGCTGGCTGCTTC  
TGCAGCTTGTCTGACTCCGGCTCTAACGTACCCATGATGAAGCTGGCTCAATGT  
GGTGAAGAGCTGGAGATTCGGGACCAATTCAAAGGAGCCAAGATTCCCTCGCCTCCCAATGC

GTTCATCCTTACCGTCAGCACCAACCATCCGATCGTCAAAGCGGCATCCTGAGTTCTAAACAA  
TGATATCTGTAAGGTGTCACATCACCTATAATAGTTGAAGTAATGCTAAAATTATAGCTGTCGTT  
TTAGGAGAACAGTGGAAACAAGAGCCTCAGCATGTCAAAGCTCAGTCCAAGCCCTGCAGAGGAG  
ATAAAGCGCAAACATGCTGAAGCCTATCCAAACTACCAATACAGTCCTCGCAAGTCTACCGAGAAA  
AGCGTCCGGACTCTTACTCCGCGCCAGCCTCTGCAGGCCAGTGTCAAACAGTCCATTAGAACGCCATGCCT  
GACACGTCGCCATTGAGTCGACCACCGCAGCTCTGTCAAACAGTCCATTAGAACGCCATGCCT  
ATTCAGATTGATTGATTCCCTTCAGGATCTGACTCTCACGTGGAGAGCCAGGTGTCCGATTTT  
TTTTTCCGGAAATGATTGACTACGAAAACATCGAGTTGACGAAGAAGAATTGAATCTATGATT  
CAGCAGGCTGAGAGCGCACAGGACAGGGCAGCACTGTTGAAGAAATCACCATCGTCCCAGCTGCC  
ACTCCTGACCCCTAACGACTGGATGAACATTCAATTATGTAA

CDS annotation:

join(1..182, 235..536, 587..1095)

Protein:

MATVSAAVIKSASESMDQVTELLWQDALHHLGATNNEVLLPINVTDLIGQSNVNKLKARLCALIRA  
PVVAFVDESINALRIMRTPAFAGSAASAACHVLTPALNVPIHDEAGFNVVKEAGDFGTNSKGAKIP  
RPPNAFILYRQHHHPIVKAHPEFHNDISVVLGEQWKQEPQHVKAHFQALAEIKRKHAEAYPNY  
QYSPRKSTEKRRRTLTPRQPLCRPSDLMSIPQDTSPIESTTAASVKQSIRTAMPIQIDSIPFQDLD  
SHVESQVSDFFFGEMIDYENIEFDEEEFESMIQQAESAQDRAALFEEITIVPAATPDPNDWMNFIM

\*

*B. nivea*, MAT1-2-4, MAT1-2-4 protein

Gene sequence:

ATGTACATATCAGCCTTTCAATGTTCATCACAAACGCCACTCGTCTGCCAAGTTCAAG  
TTCACAGCTGGAGATATGGATATCGCTCATTGCCATGGACTAGGAAATACAACCAGAATGAAGGAT  
AAGGCAGTAGACTACCATTGAACTCCTCAGTCGATTCTACAGATTCGGGTTGTTCTTAAT  
ATCGCAGACTTGAGGGCCATGCTATAGAGTTGATTAGCACTCTCCTGCAGGAATTGAAAATTAA  
CTTGGCCCTGAGAAAAGGCTGATTTCATAGGGATCTACTTCATCTCGAAAAAGAACAAATGAA

AATCTAACGAATATAACGAACAAGTATGGTTACTATCTTCAGAACCGGACTTCGAAATTAC  
TGCACGACGTTTTTACAAAACCTGATCCATAATCAACATAAAACAGACGCGAAATAGGAGGGG  
TGTCTCAAGCATATCAATTCTGGAGGCCGACCCCTCGCGGTCCAGGATATCGAGAGTCGCTCA  
GAGACTATACTATGAAGCTATCGAAAAACACCCGGCACTCAATCCTGCAGAAAAGCGTGTATCAT  
TATAGCAATAAGGTGTTCCCAGAGGACGCTTGAGATTTGTGGGTATGATCCTCCACTAGTTCT  
CAGTTGTCTAACACGTGTATCAGGAACTGGATCACTAAACACCGTATGGCGTATTATGCGATGA  
AACATGTACCGTGTACTTGAAGAGCAGCAATGCTGAATTGTACGTACAGAGAGTTACAATGC  
TGATTTACTGAGGAACCCAGAACTATTCGATGA

CDS annotation:

join(1..404, 451..635, 685..827)

Protein:

MYISAFNVHHNATRLVAQVSEFTAGDMIAHCHGLGNTTRMKDKAVDYHIELLSI LTDGFVVVPN  
IADFEGHAIELISTLPAGIENLLGPEKRLDFHRDLLHLEKEANENLNEYTNKYGYHYIFRTGLRNY  
CTTNRRGVVKHINFWRPDPRPGYREFAQRLYYEAIEKHPALNPAEKRVIIIAIRCFPEDALRFWN  
WITKHRMAYYAMRTCTVLLEEQQCLNCTYREFTMLILLRNPELFR \*

*B. nivea*, *ppgA*,  $\alpha$ -factor pheromone

Gene sequence:

ATGAAGCTCTGCCTTATCCATGTTCTCATGCTGCTGGGTGTATCTCTGAAGACGACAGCAAGCCCC  
CTAGTCATCTAAATCATTGGTGCCGTCGTCCCGGGCAGCCCTGTGCAGTGAGAAAACGTGCCGTT  
GAACATTGGCAGTCGGAGTCCGAGTCGCTAAAGCTTAATGACCGGCAGCCTTTACTTCGGACTT  
TTCAACAGTCAATCTCCAAGCTTCGAGTAGACCAATTGAAGGTATCTCCAGGGAAAGCATCGATA  
TCGTTGCGTAAGCATATGGACCATAATTGACGGGCATGTGGACCGACTGCCAGGCATAG

CDS annotation:

join(1..324)

Protein:

MKLCLIHVLMLLGVSLKTTASPLVNLNHWCRPGQPCAVRKRAVEHWQSESESSKLNDRQPFTFGL  
FNSQSPSSSRPIEGISREASISLRKHMDHQLTGMWTDCQA\*

*B. nivea*, *preA*, a-factor pheromone receptor

Gene sequence:

ATGGTTCCAGCAATTACGAGCGTGCTCCTGCGGTCAATTATCATCCCAGTCCTATCGCTCCTGTCA  
ATCATACTGAGCATGACGCCCTAGTCTGGACTTGAGGAACCTCCAACTTCCCTGCTGTGTGCG  
TTGGTTCTGGTCAA**TAA**CGTCTTCAACATTGTGAACGCCTCATCTGGCCTACGGATAATATTGA  
CTCATGGTGGAGCGGTGTTGCACTCTGCGATATCGAAGTCAAGCTGATGGTAGCCAGTTATGTTGG  
CATGCCTGGAGCCTGCTATGCATCTTGCCACCTGCGCAGGTTCTGGATAACGGACCACGTACAGT  
TCTCGTCACTAGTCACAGTCAGCGTCGGCAGGAACCTGTTATCGAGATAACTTTGCTTGGCCGT  
GCCTGCCATAACTATGATCACCCACTACTGTGTTCAGAACAGACTCGTTATATGCCCTACACGATTTC  
GGCGGGTGTAAACAACCTCGACGAAAGCTGGTCACTCTTATGCTTACCTGTGGCCAAGAGT  
GATTTGCAATAATTGCGGCTTACTATTGCTGTATGACTTCTATCCTGGTATGACGACCGAAAT  
ACTAACTACTACCAGGCCTCGTATACCGTATCGTCAAGTACAACAGAGAGTTGGAGGCCATCC  
TTAGTAGTTCCAGCGGAAGCAATCTGAACAGGACAAGGTTCTTACGACTGTTCTGCATGGTGTCTG  
TGATGCTACTGGCAATTCTCCCACACAGGTCTACGTCTTATGTTAATGCCAGCTATCACTGCC  
ATGGCACGAATACTCCTTGCCAAGATCCACGGTCCGACTGGAATATCATCATCAAGGTTGCAAC  
TCATGGCCAGATTCTTGACCGCTGGATACCAATTGGTGGCGCTTCTTATTTGTCTTCTT  
CGGCTTGGAAAAGATGCTACTTCCATGTACCGTTGATCTCGATCTCGTCAAGTTGGGATGGAGCATT  
CCTCCCATCTAAGTCAAATTCCGATATCTTCTCTGAGAACAGACTGAGCTCCCGGGAAACAAACT  
GGGTTCTTCTAGCATTGCTAAACGAGTGTACCTGGGACAATCCACCGTGTCAAGGTCAGT  
TTGTGCCTTCTGTGAGAAATCATTGCTCTAATTGAATGCAGCAGCATGAGAACGGATCT  
GTCTCTACTGATCCTCCACTCCCCCTGCTACCGATTGGAGAACAGGACCCGCATCCACTTCACA  
GAAAGGAACATGACTAAAGCTCTACGATCCAGAATGGCTCCTCCCGAATCTGGAGTCTTCCAT  
GCCCAACGAGGAAGCAGCTCTACTGTGCCTGAAAATAACAATCTGCTTACGGAAAACACTGTT  
TCTACCAGTGCCTGTGCAGGTCAAGTCCGTGTGAGATGGGTGATGCCGTCCATCACCGAAAACA

GAGGGGGCTATCAAAGTCAAGCATGTCATTGCCAGGCCAAGGTCTCCATCTGCCTATACTGCGGC  
TATGAGATCGTGTCTTACGAACCATGA

CDS annotation:

join(1..558,610..1116,1167..1545)

Protein (Truncated):

MVSSNYERAPAVIIIPVLSSIIILSMTPLVWHLRNSNFPAVCRLVSGQ\*

Note: The red stop codon is the in-frame stop codon that disrupts this gene and produces a truncated protein.

*B. nivea*, *preB*,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGGAGAGATCTTCGATCCCTCACACAGAACGATGTAACCTCTACTTAGCCAACGAATCTCCTCTT  
GAGGTCTCCGTCGGAGACTTGGACGATTTCATCCAATACGGCATCAAGATCTCCACCGTCTACAGC  
TCTCAGCTTGGTGCTCGCTGGCGCTGCTCGCCTCTACTCCTCCTGACCAAGCGTGACAAGCGA  
GAGTCTCCAGTCTCTTACTAACAGCTCAGCTCTGATTCTCAATGCTTGCATTGATCTGCAGC  
TGCCTCGATTTCACTACTGAATTCTCGAAGGTCTATCCTTACTTCTCCGGAGACTACTCTCGGGTC  
CCGGCCAGCGCTACGCCATTCCATTCTCGCGGTTGCTTCCAAGTGCTGCTGATCGTCATT  
GAATGCTCCATTCTTGCGAGACTCAAGCTATCTACGTACGATTGCGACGTCCAGAACATATA  
CTGCTGGGTGTCTCGTTCTGATCGCTCTCCTTGCAATAGGGTCCGCCTGGCCCTGGCTGTTGAA  
AACTCCATTGCTATTGTCCAGGCGGGAGTTCAACGCGGTCTGGTTGGAAAGCGCTACCAACATC  
ACCACAATTATCAGCATCTGCTTCTCTCGTCCTTTTATTTCAAGCTGGACATGCCATCCGA  
CGGCGCAAGATGCTGGGATCAAACAGTTGGAGGGATGCAGGTGATCTCATGAGCTGCCAG  
ACCTTGATTGTCCCAGTATGTCTCTCAGCTTAGGTTGATTGAAATGAACTGACTTGTACATAC  
AGCTATCTCGCGATCCTGCAGTACTCGCTGACGTCCTGAAATGGAGTCCTCGTTACTT  
TGTGCGATTCTCTCCACTTACCTCTGTGGCGACATCTTCAACCACCGTAGCGAGCC  
AGGAAGCGAATCTAGTAGACGCTATAGGTTGGAAGCCGCTCTCCAACGGAAGCTCAGAGAAGAA  
CGGACGGTCTTCTACGACGGAGTCTCTGCATCGGGTGCCTCAATACGACCTCTGTGGGTAGTTC

AAGCGCGACTATTGCGCAGATGAATACTCTACCCCTGACCTCGAGGCAGCACTGAGATCGGTATC

AAGCAGGATGTGA

CDS annotation:

join(1..742,795..1135)

Protein:

MERSFDPFTQNVTFYLANESPLEVSVGDLDDFIQYGIKISTVYSSQLGASLALLVLLLLTKRDKR  
ESPVFLNSSLALILNACHLICSCVDFTTEFSKVYPYFSGDYSRVPASAYANSILAVVFQVLLIVI  
ECSLILQTQAIYVTIRDVQKHILLGVSVLIALLAIGFRLALAVENSIAIVQAASFNAWLESATNI  
TTIISICFFCVLFIFKLGHAIRRKMLGIKQFGGMQVIFIMSCQTLIVPSIFAILQYCVDVPEMES  
FVLTFVAISLPLTLSWATSFTNRSEPGSESSRRYRLWKPLSNGSSEKNGRSSTTESSASGALNTT  
SVGSSSATIAQMNTLYPDLEAALRSVSSRM\*

*T. aurantiacus*, MAT1-1-1, MAT1-1-1 protein

Gene sequence:

ATGGCTGCGAACGTTCTCCTCTTCAGCGTGTTCACAACAATTTCCTTACGACAATCCCACAGAACAG  
GAGCTAGAAGAGCTGCTCGAGTACCTGCATAGCTTAATGCTGGAGGAAACAGTCCAATTCTCCG  
CATGCTGAAGGTGCTCCTCGGGCTATAGCCTCTGTTGAAAATAATAACCGTCGTCCAACCTCAGCC  
CTCAATGCTGGTATTCGACCGATGTCTCGCGTGGAAAGCGCTTCCCGAGGGGAAGCTTAGGCC  
CTTAACAGCTTCATTGCTTCAGAAGTTGTGACATCCCTACTAAACAATGAGAAAAAAAGAACT  
GACTAATCCCACAGACTTCTATTGGTTATCTTCCGGATCTCACTCAGAAGGCAAGGTCAAGGGAT  
TCTCAAGTTCTGGCAGAATGATCCATTAAAGGCCAAATGGGCCATTCTCGCGAAAGCTTACTC  
CATCATTGCGACAATCATGTGGCGAAGTTCTCTGATTCTCCTTAACCTGAATGGAAACTT  
CATCGGAATTCTGGAGCCAATCGCTATCTTGAGCTATGGCTGGAGCTCATTGTCGATGACCA  
GCACCAGTACACCATGGTGAGGGTCAATCCGACTTATCCAACCGAGACTGAGGCCGACCAATTA  
CTCGGTCAATGATATTGTTAATCGCTGCTACGAGACAGGTTATGTTCTGGTGATCCTCGTCCATG  
CAATATCAACTACCAGGAACTAGCCCTCTGATGGCGTTCGCTGCTCAGCCAATGTTGTCAATGG  
TAGCAGTGATATCCAGGCTACTGCACCCAAAGGAATCGTGGGTGGCACAGAAAACACAAGCATGGA

CTACAATGAAAATTCGATGCCATCAATCACGCTCACTACATTCTAGCGAGGTGGCACG  
CGCAGGTACTGATGAGGCTCGTCTGCAATTCTGAATTACTCAACGTCCGCAGTGGCCCGCATAC  
GCAGGAGGAGTTCATTGCTGAACTTGACGACGCAATTGAAATGCGAATCCAAATCCAAGGA  
CGACGAGTTGTCGTGCCATTCAATCCAGACATCCAGTCTCCAATTTGCGCTATGATCCAATGGC  
GCAGGAACCATTAGATGCCTTCGATATCAATGAATTGTCAATTGG

CDS annotation:

join(1..289, 345..1171)

Protein:

MAANVSPLQRAFNNFLTTIPKELEELLEYLHSLNAGGNSPIPPHEGAPAAIASVENNNRPTSA  
LNAGIRPMSSRGKRFREGKLRPLNSFIAFRNFYSVIFPDLTQKARSGILKFLWQNDPFKAKWAILA  
KAYSIIRDNHVGEVSDLFLNLNGNFIGILEPNRYLAAMGWELIVDDHQYTMVRVNPTYPTETEA  
ATNYSVNDIVNRCYETGYVSGDPRPCNINYQGTSPLMAFAAQPTVVNGSSDIQATAPKGIVGGNEN  
TSMMDYNENFDADAINHAHYIPSEVARAGTDEARPAIPELLNVRSGPHTQEEFIAELDDAIHEMRIP  
NPKDDELFPFNPDIQSPILRYDPMAQEPLDAFDINEFVN\*F\*

*T. aurantiacus*, MAT1-1-9, MAT1-1-9 protein

Gene sequence:

ATGGTAGAGGGCAGGTTAATGGTTAGTGTTCATTCATATCGACGAGTAAGTTACAGTAGATTAA  
CGGATCACTTAGGAGAACGGCCTCGTCTTGAGAAATGTGACGCTCTGTTCTATGGAGCTGGATG  
AAGCGGTGAAAATACCTACGAACAAAGATTTCAGTTCAATTGTCGATATCGAAGAGTCGACGGT  
CCTTATGGCAAATTCATCCTGACCCGGACAGTCGAGCTCATTCTCGAGGACATTATCTGCT  
ATCGAAGCTGCTACGTTCTCCTATCGTCGCTCTGAAATCCGTCGTATTCAACGATATCAAGAT  
CTGTACCCAACGGAAGAACTGTTGAAAAGTTCTGTCCATAAAGAACAGCCTACAGTGAAC  
CACAGACGCACTCTGGCTGCCGCAAAGAAGATGCGGGATGAGTCTTACTGGAAAAATCCATAGA  
GCTGAGCGTCTGGTTCTGGCAATTCAACGTCCAACGTTCTATCCCCACCTCAATCAGTGGCAG  
CAGTTCTTATCAGTGGTGCACCAGGAAGTGGCATTGACGTGCGCAATATGTTCTACAGCAGGTTA  
CCAGAAGAACGCTGGACGGCATCTGAAGCTTACCCAGATTCTGCGTTCCAGACCCTCCCAGTTGGC

GCAATGGCCTTTGGGAGAGTGGCGGGCTAGAGCAAGGGGCCTCGAGAGAAAATGCAGAGAAATG  
AGCCACATATATTGGACAAGTAAATTGAGGATGCAAGTTCTCACTCTATCCTCCTTCAGCCAGCT  
GTTCCGGAGAACATGCAGCAACATGATTCAACAAATACAGTAAGCTTCTAAACAATCTATTGAACA  
GCCATAATTGGAACACACATCCTAGAACAGTACATCTCTCGGATTCTCTCCATCCTTCGGG  
TCAAACATAAAACTCCGGTATGATTACCCCTCAAGAACATCACATAGTCGCTTCCACTAACAGTT  
ATTAGTTACTTATGATCCTAATATCTGGTCCCTGTATGTCGAGTCCTCTTACTCATTCC  
TCATAAAACTTGAGTTTGATTTCACATTAACTGACATCCCACAGCGTCAGCCAAAGATTCC  
AAATACCTCGTACTGTAAGGCTTGAAGATCTTCTGATGATCGGTATGCTCAAGCTCTACG  
TTCCAATTAAAAGTCTTCACTAACTTATATAACCTGCAGACCAAATAGAGGAATTGCAACCAAGG  
CGTGCATGCGATGCCACGCATATGGTGTGATCGAACGGAGTGGCTCTGATGGTAGG  
ATCATTCACTCATGAAGTCCTCTTCTGTGA

CDS annotation:

join(1..47,159..831,885..944,998..1027,1106..1169,1229..1350)  
(1..289,345..1171)

Protein (Truncated):

MVEGRLMVSFSHIDE \*

Note: The red stop codon is the in-frame stop codon that disrupts this gene and produces a truncated protein.

*T. aurantiacus*, ppgA,  $\alpha$ -factor pheromone

Gene sequence:

ATGAAACTTCATTCCGTCTCGCTGCCATCCTGGCAATGTCGTGGAGGCAGTAG

CDS annotation:

(1..54)

Protein:

MKLHSVLAAILAMSWRQ \*

*T. aurantiacus*, preA, a-factor pheromone receptor

Gene sequence:

```
ATGGCTGCCGGAACTTATGCCCTTCTGCTCAAGCTGGTCGTACCGGCCGTCTGTCTTTCG  
ATCATTCTGAGCATCCCTCCCTGGTCTGGACTCGAAGAACATACAACATTCTGCTTCATGCCTT  
GTCATCTGGTCCTTATCAACAACATTTCAACATCGAACGCCGCTATCTGGCCGACAGATGAT  
GTCGATTCTGGTGGAGCGCGTTGGCCTCTGCATATCGAAGTTAACGCTGATGATAGCCAGCTAT  
GTGGCGTACCAAGGAGCCCTGATGTATCTCCGTACCCTGCCATCTCCTGGACACGGACCGT  
GTCGTTCTGGTCCCTAGCCGAGCAGTCCCGCGCCTGCCTCGAAGTATTCTCTGCTTG  
GTTGTGCCAGCCATCTCCATGATCACGCACTACGTCGCCAGAACATGATTGCTCTACACG  
ATTGCCGGTTGCGTCAACTCCTCGACGAAAGCTGGTGACGCTCGTGCCTTCTTCATCTGGCCC  
ACAGTTATCTGCCTGATTGCCGGTACTACTGCTGTATGGCCTTTCCCCTTGATCTGAGT  
ATCCAATTCTGACGAGCCGTTACAGGTCTGGTGCTATTCCGCCTCTGGAGGTACAAGAACATT  
CGGGACGATCTCAGGTCTTGACAGCAGCCTAACGCAAATCACGCTCCTACGACTCTTCC  
CGCATTGACGCTCTCGTTATCCTGCCTGCGCAGGCTTACGTTCTACACCAACGTGGAATT  
CTCGCTTCCATGGCACTCGTACTCGTGGAGCAAGATAACGGACCGAGCTGGAACATGATAACCAA  
GATCGCGACGCACGCCAGATCTTCTCGACCGTTGGATTCCCGATTGCCGGCATCCTGCTATT  
CTTCTTCTCGGATTCGAACGGACGCAACCAGATGATGTACCGCTCGTCCCTGAGGCTGGACT  
GGGCCGCTGCTTCCCGCTCTGTCACACCCCTCACATCTGCAGTAGCCGTAGGACGAGTACAAGTTC  
TGTGAGCCAATAGTATCATTGACGAGCCGCGAAGCTGCTATTGAGTCCGACTCAATCTATCGT  
GTCGAGGTGAGACTCCCTCTTATCATCCTCTCGGATCCAATTAGGTATTACGTAGGAGTGGC  
AGGACAAACTCCGTATCCACTGAACCCCTCGGCCCTTCTTCTTCTTAAGGATCTC  
GAGAAAGGATTCCCTCCATTCCAATACCAACTACTACATTCCACGCCGTACCAACTCTGGGC  
CTCTTACCCCCAACCGCGAGCGTCCGTAGCCGTACCGTCACCGTGACATTCCATCCCTCGC  
CTCCCAAGGCTCAGAGAACGGTTCCACCACGGCTGGCAGGCAAGGGCGAGCGGGCTCGAGC  
GAGGCCGATACCGACACCATCCGTCTCCTCCAAGAACGGCATCATCAAGGTGAAGCAGATGATT  
CGGCAGACAAGCGAGAAGAGGTGA
```

CDS annotation:

```
join(1..562,621..1128,1182..1542)
```

Protein:

MAAGTYALSAQAVVVPALSVFSIILSIPPLVWHSKHNFPASCLVIWFLINNIFNIVNAAIWPTDD  
VDSWWSGVGLCDIEVKLMIASYVGVPGALMCIFRTLHLLTDRVVLVPSEQSRRRLADEVFFCL  
VVPAISMITHYVVQKNRFMLYTIAGCVNSFDESWTLVLSFIWPTVICLIAGYYCCLVLFRWLRYK  
NQFGTIFRSCDSSLSSRFLRLFFLAFTMILLVILPAQAYVLYTNVEFSLPWHSYSWSKIHGPSWNM  
ITKIATHGQIFFDRWIPIAGGILLFFFFGFGTDATMMYRSFLLRLGLGRCPALSHPHICSSRRTS  
TSSVSPIVSFSSRAKLLFSRTQSIVSRSGRTNSVSTEPFAPSSSFPSKDLKGFPSISNTTTFP  
RRHQLWGLFTPNRERRRSRHRHDIPIPRLPGSENTVSTTAWAGKGERRSSEADTDTIPS SKNGI  
IKVKQMIQTSEKR\*

*T. aurantiacus*, preB,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGGATATCAGTGACCCATATACTCAGAGTTTACTCTCATAGGCCCGATGGCACTACTTCAAT  
GCGACTTTGTACGAGATAGACGACTATCTCCAGTATAGCATCAAGATCTGCATCAACTACGGCTCC  
CAGATCGGTGCTTCATCGTACTCTTATCGCCTGCTGCTGTTGACAAGGCTTGACAAGCGTCAT  
TCTCCCGTGTCTTCCCCAACAGCTGCGCTCTTTTCAACATCTGCCGGCTAATCTGCATGGTC  
ACATATTTACCACTAACGATTTCAGGGCCTATCCCCTCCTCGGGCGACCTCTCGGAAGTCCA  
CTCAGCGCCTACGTCAACTCCATCCTGGGTGTTATCTTGACATTCTCCTGGTGGTCTGCTTGAT  
CCTGCAGACACAAGTCGTCGTACGACTCTCCGCAATGTTACAAACGCATCATCTCGTGATGTC  
AATCCTCATAGCTTGTCCAATCGGATTCCGTCTGGCTTGTAGTCGAAAACCTCAAAACCAT  
GGCGTCAGAGGGTTCTACTCGATATGCCTGGCTGCTAAATGCCACAAACATCCTCATAACCATCAG  
CATCTGCTTCTCAGCGCGATCTCGCAATCAAGCTGGTTACACCATTGGCAGCGCAGGCAGCT  
CGGACTGAAGCAGTTGGTCCAATGCAGGTAATCTCATTATGGGCTGTCAGACTATGATCGTCC  
TGGTAA

CDS annotation:

(1..732)

Protein:

MDISDPYTQSFTLIGADGTTFNATLYEIDDYLQYSIKICINYGSQIGASIVLFIVLLLTRLDKRH  
SPVFFPNSCALFFNICRLICMVTYFTTKIFRAYPLLSGDLSEVPLSAYVNSILGVILTFFLVVCFD  
PADTSRLYDSPQCLQTHHLRDVNPHSSCSNRIPSGVCSRKLKNHGVRGFYSICLAAKCHKHPHNHQ  
HLLLQRDLRNQAGLHHLAAQAARTEAVWSNAGNLHYGLSDYDRSW\*

*T. crustaceus*, MAT1-2-1, MAT1-2-1 protein

Gene sequence:

ATGGCGACTATCTCTTCCATTGCGATAAAATCAGCTGCCAATCCATGGACCAAGTGACAGAACATTG  
CTCTGGCAGGACGCTATGCGTCAACTCGGCTCTACCAACAACGAGATCCTTACCGACCAACGTG  
ATTGACTTGATCGGCCAGGCCAACGTCGACAAGATCAAAGCCGTGTTGGTAATGTTTTGTTCT  
ATTTTGATGACTCTAGCTCATTAATGCAGTGCTCTAATTGCTGCTCCTGTTGTGGCATTGATTGA  
CGAGTCGATCAATGCTCTCCGCATCATGCGTAGACCGGCGTCCGCAGGCTCAGCCAGTTCTGCAGC  
GTCCCCACGTCGTCGTTCCGCTGTATAGTGTGCCGGCCATAAAGACATGGCTCTGAGAATATGAC  
GGCTACACCTAAAATTGGAACTCCTGCAAAGGCTGCAAAATTCTCGTCCTCCGAATGCCTTCAT  
TCTCTACCGTCAACACCATCATCCCAGGTCAAGGAGGCGATCCGACTTCATAACAATGACAT  
CTGTATGTATTCTGTCTATCTCCCTCCTTATTAACAAGGAATTACTGACGAACAATTAGCAAT  
CATGCTCGAAAGCAGTGGAAAGAGGAGTCAGCCGATGTCAAAGCTCACTCAAAGCTTTGCAGA  
TGAAATCAAGCGAAACATGCTGCAGATTATCCAGACTATCAATATGCCCTCGAAAGCCGTCTGA  
AAAGAAACGCCGGTCGACTTCTCGCAATGCTCAACTAGAGAGCAGCGCAATCTACCCCCCTTGCC  
AGTGGCATTCTCATCTGCCCCATCCGCCATTGCGGCCAGCTGAGCAGTCTGCTCTGGCTTAGCAC  
GGATATCGATAATATTGATTGATGACATGACATGTTATCCTCAACGCTGCTCTGGCTTAGCAC  
TAATTATGAAAATGCTGAGTTGACAATGAAGAGTTGATGCTATGATCCAGCGCGTCCAGGACGA  
CCATGATCGAGTGGCATTCCATGAAAACCTCAACCTCACATCCAGCGCCCCGTTGGATACGCTGCA  
CTTCTCGGACTTTATCGTTGACTACTATTGA

CDS annotation:

join(1..182,229..530,591..1087)

Protein:

MATISSIAIKSAAESMDQVTELLWQDAMRQLGSTNNEILLPTNVIDLIGQANVDKIKARVCALIRA  
PVVAFIDESINALRIMRRPAFAGSASSAASHVVVPLYSVAGHKDMASENMTATPKIGTPAKAAKIP  
RPPNAFILYRQHHHPMVKEAHPDFHNNDISIMLGKQWKEESADVKAHFKALADEIKRKHAADYPDY  
QYAPRKPKSEKKRRSTS RNASTREQRNLPPLPVASSSVPSAISAPAEQSALTIGDIDNIDS MNDMLS  
FNAALGVSTNYENAEFDNEEF DAMIQRVQDDHDRVAFHENFNL TSSAPLDTLHF SDFIVDYY\*

*T. crustaceus*, MAT1-2-4, MAT1-2-4 protein

Gene sequence:

ATGGACCCATACGGCGCTATCCTCCTACAGTGGCTTCAAGAAATGGCTGCGGATGCAAACCTTGGG  
CCGGCCAAAAGAAGTAAGGCATCGTATATCGAACCTCATTCCATACTCATCGCAATACCATT CGC  
CTTTATGGCCAAGTTTAGCTCTTTAG

CDS annotation:

(1..162)

Protein:

MDPYGAILLQWLQEMAADANLGPAKRSKASYIATSFHTRNTIRLYGPSFSSF\*

*T. crustaceus*, ppgA,  $\alpha$ -factor pheromone

Gene sequence:

ATGAAGCTTCTTCATATCGCTGCCATTCTCGCAGTCATCGTTGTGGAGGCAGTT GCGATT CCT  
GGCGTCCATAACGGCGGT ATTGGTGCTTTAACGGCCAGGGCTGCAAGCTAACGTACTGCA  
GTCCCTGTCGAGGATTCCCTGCCAACCTGAACCCAATGCCGAGGCCGCCACAAACACGCTGCC  
TTCTGA

CDS annotation:

(1..204)

Protein:

MKLLSIFAAILAVIVVEAVAIPGVHNGGNWCSLNGQGCKLKRTAVPVEDSLAKPEPNAAEADKHAA

F\*

*T. crustaceus*, *preA*,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGGTCTCTGAAACTTACCCCTTCTGCTCAAGCAGTGGCATACCGTTCTGTCTTCCTTTCG  
ATCATTCTGAGTATCCCACCCTAGTCTGGCACTCGAAGAACATCGAACCTTCCTGCATCATGCCTT  
ATCGTCTGGTCCTTATCGACAACGTCTAACATAGTAACGCTGCTATCTGGCCGACTGACAAT  
ATCGATTCTGGTGGAGCGCGTTGGCCTCTGCGACGTCGAAGTTAACGCTGATGGTAGCCAGCTAT  
GTGGCGTACCTGGAGGCCCTGATGTGCATCTCCGTACCCCTGCCAACCTCCTGGACACGGATAGC  
GTCACTCTGGTCCAAGTCGCGAACAGTGCGGAAGGAGACTTGCTTCGAAATACTTTCTGCTTA  
GTCGTACCGGCTATCTCCATGGTACCCACTACGTCGCCAGAACATCGATTGCTACACG  
ATTGCTGGGTGCATCAAATCTTCGACGAAAGCTGGTGACGCTCGTGCCTTCATCTGGCCC  
ACGGTGATCTGCCTGACTGCCCGTACTACTGCTGTGGTTCTTCATTTGGATCTCC  
AAGACTGACGAGCCGTTAGGCATGGTGCATTCGCATCTGCAAATACAAGAACATCAATTGGGA  
CGATTCTCAAGTCTCTGATAGCAGCTTGAGCAAATCAAGATTCCCTACGACTTTCTCCTTGCAT  
TTCTGACGCTTCTCGTTATTCTCCCGCACAGGCTTGCCTCTCACACCAACGTGGCACTCTCAC  
TTCCATGGCACCGATACTCCTGGGCAATATAACACGGGCCAGCTGGTACGATAACCAAGGTGG  
CTACGCACGCCAGGCCCTCTCGACCGTTGGATTCTATTGCCGGTGGTATTCTGCTATTCTCT  
TCTTCGGTTTGGAACAGACGCGACCATGATGTACCGCTCGTCTTGAGACTGGACTCGGAC  
GTTGTTTCCGATCTGTCGCCCTCGTAAC TGCGCTCGCAGGATGAGTTCAATTCTGTAG  
GCCCGAGTAGAACATTCAAGCAGTCGCGCGAACAGACGCTATTCAAGTCGAAACGCAAGGCTATGGTTCAA  
GGTAAGGTGTTCTAACTGCACTGTGCAACTCTCCGATCATCCTAGACCGAATTATTACAAGCGT  
ACTAGGACCAATTCTATGCCACGGACCCCTTCACGCCCTCTTCCAGCGATATTGAGAAAGGA  
TTCCCCATTCAAACGGTCCATAAACACCACCCACATCGTCACCAACTTGGGTCTATTCACT

CCTAACGGCCAGCGTAACCGTAACATGTCCGTTCTCATCTTCCGGGCTCAGAGAATACGGTTCC  
ACCACAGCTTGGGCTGGGAAAGACCAGCGCCGCTCGAGCGAAACCGATGCAGAGACCATCCCGTCT  
TCTGTCAAAAATGACATTATAAAGGTGAAGCAGATGATCCGGCAGACGAGCGAGAAGAGGTGA

CDS annotation:

join(1..562, 616..1123, 1194..1515)

Protein:

MVSETYPLSAQAVVIPVLSFFSIILSIPPLVWHSKNRNFPAACLIVWFLIDNVFNIVNAIWPTDN  
IDSWWSGVGLCDVEVKLMVASYVGVPGALMCIFRTLAHLLDTSVTLVPSRGQCRRRLAFEILFCL  
VVPAISMVTHYVVQKNRFMLYTIAGCINSFDESWTLVLSFIWPTVICLTAAYYCCMVLFRICKYK  
NQFGTILKSSDSSLSSRFLRLFFLAFLTLLVILPAQACVLYTNVALSLPWHRYSGNIHGPSWYT  
ITKVATHGQAFFDRWIPIAGGILLFFFFFGFTDATMMYRSFLLRLGLGRCPDLSRPRNCSARRMS  
SISVGPVESFSSRAKTLFSRTQAMVSRTNSIATDPFTPSSSDIEKGFPISNGSINTIPHHRHQIWLWG  
LFTPNGQRNRNMSVPHPGSENTVSTTAWAGKDQRRSSETDAETIPSSVKNDIIVVKQMIRQTSEK  
R \*

*T. crustaceus*, preB,  $\alpha$ -factor pheromone receptor

Gene sequence:

ATGGTCCCTATTGACCCATATACTCAGAATGTTACTCTCCACCGCGCTGATGGCACTCCTTAGAG  
GTGCCTGTGGGCCAGGTGGACTACTCGTCAGTATGGCATCAAGATCTGCATCAATTACGGCTCG  
CAGATCGGTGCTCCATCATCCTCCTCATCGCCTGCTAATGTTGACCAAGCCTGAGAAGCGCTAT  
TCCCCCGTGTCTTCCTGAACAGCAGCGCTCTCGTCTTCAACATCTGCCGGCTGATCTGCATGGCC  
ACGTTTTCACCAACCGAGTTGCAAGGCCTATCCTTCCTCTGAACGACTTTCAAGCGTTCCA  
CTCAGTGCCTACATCAACTCCGTCTGGCGTTATCCTGACATTCCCTGCTGATCTGCATTGAG  
ATCTCCTTATCCTACAGACCCAGGTCACTGTTCCACCCCTCCGAACGACTTTCAAGCGTTCCA  
TTCTGGGCATCGATGTTATGGCTCTCGTCCAATCGGATTCCGTTCGCGTTGTCATCCAAAAC  
TCAATACTCATCATGGGAGCAGAGGCCTTACTTCATATACTGGCTGCAGAGCGCCACAAATATC  
GTCATAACCATCAGCATCTGCTTCTCAGCGCGATCTCGTCAAACGGCTACACTATTCGG

CAGCGCAGGAAGCTGGGTGAGGAAGTTGGTCCAATGCAGGTCACTTCATTATGGGCTGTCAG  
ACCATGATCGTCCAGGTAAGCATAGTATTCCGTGCGTATGCATAGGCAAACCTGGCTGACCTTGC  
CAGCTTCTTCATAATGCAGTATTATATCCCCGTGCCTGAAATGGAATCAAACGTTCTAACGC  
TCGTCGCGATATCTCTCCGCTTCCTCAATGTGGCTGCGCTGCTCTTCACAACCAATCTGAAT  
CAGCAGGCGATTCCATCGAACGCCGTAAGCTTGAAACCCATTTCATCTTCAGCCTCGATACGA  
GCAGACGGTGGTTGATATTCAAGAATTCCCTTCGACCGTCACCCACATCAGCAGCGTCTTGCT  
CGAACTCGACTATGCTTGACCGTCTCACCTGACGTGGAGGCTGGAAAGGGGATAGGAGTACACC  
GTGACTTCTCAGTGTCCAATCGCACTGCAAAGAAGTTCTGAATGCGTGA

CDS annotation:

join(1..742, 796..1172)

Protein:

MVPIDPYTQNVTLHRADGPLEVPVGQVDYFVQYGKICINYGSQIGASIILLIVLLMLTKPEKRY  
SPVFFLNSSALVNICRLICMATFFTTEFCKAYPFLSNDSSVPLSAYINSVLGVILTFLLLICIE  
ISFILQTQVICSTLRNVYQRIIFWASMLMALVPIGFRFAFVIQNSILIMGAEAFTSYTWLQSATNI  
VITISICFFSAIFVVKLGYTIRQRRLGVRKFGPMQVIFIMGCQTMIVPASFSIMQYYIPVPEMES  
NVLTLVAISLPLSSMWAASALHNQSESAGDSIERRKLWNPFSSFLDTSRWLIFKNSSSTVTHIS  
SVSCSNSTMLDRLYPDVEAGKGIGVHRDFSVSNSHCKEVLNA\*