**Supplemental material**

**Figure S1. Expression of some chimeric receptors in *S. pombe***

(A) Quantitative RT-PCR showing ectopic expression of some chimeric *map3* genes in *S. pombe* homothallic strains (TS1226 and TS1228–TS1231). (B) Quantitative RT-PCR showing ectopic expression of some chimeric *mam2* genes in *S. pombe* homothallic strains (TS1219, TS1221, and TS1222). Total RNA was collected from EMM2−N cultures (0 h, +N; 24 h, −N), and RT-PCR was performed. EGFP expression was normalized by expression of *act1+* as a control gene. The graphs in (A) and (B) show mean ± SD. *t*-test: \*P<0.05; \*\*P<0.01.

**Figure S2. Cellular localization of some chimeric receptors in *S. pombe***

A homothallic strain expressing SoMam2(IL1\_2\_3\_C)-EGFP (TS1221), Map3(IL1\_2\_3\_C)-EGFP (TS1228), or SoMap3(IL1\_2\_3\_C)-EGFP (TS1229) was grown on YEA overnight and incubated on SPA medium for 24 h at 30°. The cells were observed using fluorescence microscopy. SoMam2(IL1\_2\_3\_C)-EGFP and SoMap3(IL1\_2\_3\_C)-EGFP were partially localized to the cell surface, as indicated by the arrows. BF, bright field; GFP, GFP filter; scale bar, 5 μm.

**Figure S3. Analysis of dominant-negative phenotype in some chimeric receptor mutants**

(A) Effects on mating frequency of the coexpression of chimeric receptors and wild-type Map3 in homothallic strains. (B) Effects on mating frequency of the coexpression of chimeric receptors and wild-type Mam2 in homothallic strains. At least 1,000 cells were examined for each strain. Data are the mean ± SD of nine samples. *t*-test: \*P<0.05; \*\*P<0.01; \*\*\*P<0.001.

**Figure S4. Sequence alignment of M-factor receptors among four species of the genus *Schizosaccharomyces***

Shown are Map3 (365 aa), SoMap3 (Map3 of *S. octosporus*, 363 aa), ScMap3 (Map3 of *S. cryophilus*, 363 aa), and SjMap3 (Map3 of *S. japonicus*, 360 aa). Numerals to the right of each sequence indicate the length of the protein product. Identical amino acids among the four species highlighted by a white letter on a black background; amino acids conserved between at least two Map3 proteins are highlighted by a white letter on a gray background. Protein domains are indicated above the sequence. The alignment was generated with CLC Genomics Workbench.

**Figure S5. Sequence alignment of P-factor receptors among four species of the genus *Schizosaccharomyces***

Shown are Mam2 (348 aa), SoMam2 (Mam2 of *S. octosporus*, 348 aa), ScMam2 (Mam2 of *S. cryophilus*, 348 aa), and SjMam2 (Mam2 of *S. japonicus*, 348 aa). Numerals to the right of each sequence indicate the length of the protein product. Identical amino acids among the four species are highlighted by a white letter on a black background; amino acids conserved between at least two Mam2 receptors are highlighted by a white letter on a gray background. Protein domains are indicated above the sequence. The alignment was generated with CLC Genomics Workbench.

**Table S1. Strains used in this study**

**Table S2. Plasmids used in this study**

**Table S3. Primers used in this study**

**Table S4. Primer sets for construction of plasmids carrying chimeric receptor genes**

**Table S5. Primer sets for construction of plasmids carrying EGFP-tagged receptor genes**

**Table S6. List of sterility-suppressing mutations of Map3 obtained by screening**

**Table S7. Mutation primer sets for site-directed mutagenesis of the *map3+* gene by inverse PCR**

**Table S8. Numerical data for mating frequency experiments**

**Table S9. Numerical data for quantitative RT-PCR**

**Table S10. Numerical data for β-galactosidase assay**

**Table S11. List of mating frequency of some *S. pombe* homothallic strains**