Supplementary Information

A sex-inducing pheromone triggers cell cycle arrest and mate attraction in the diatom *Seminavis robusta*

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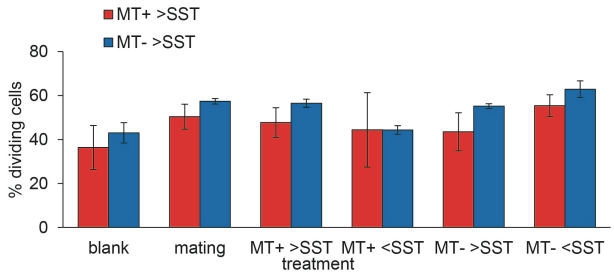
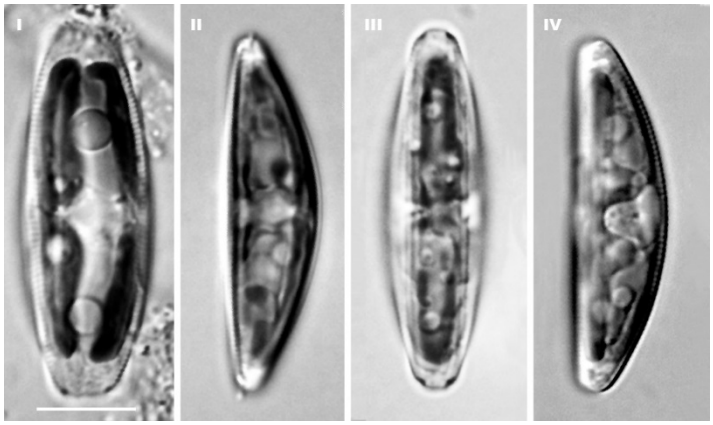
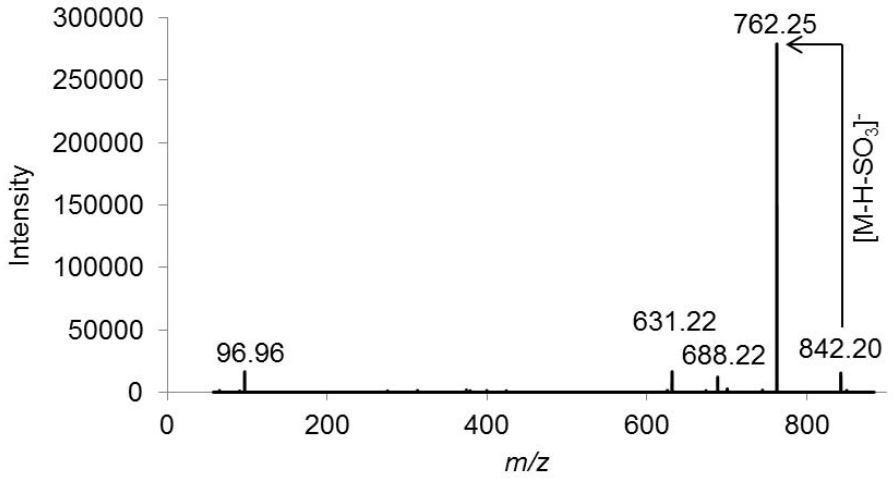


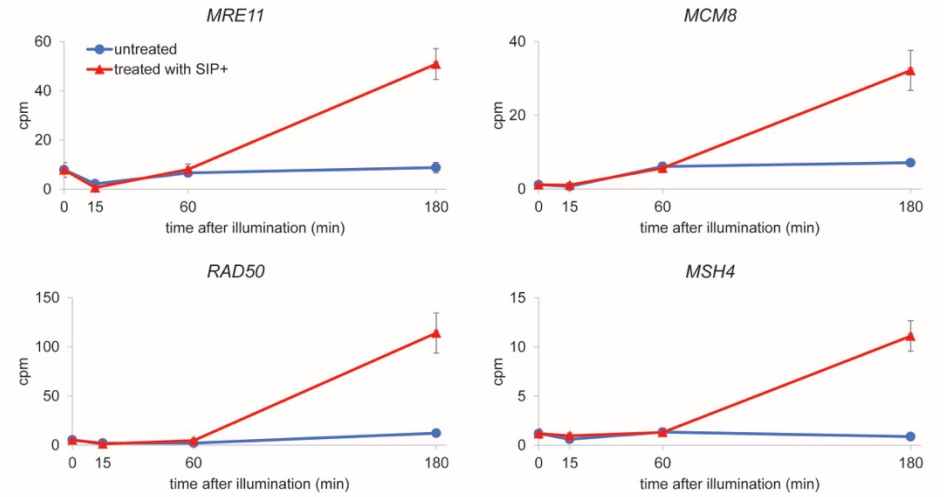
Supplementary Figure S1. The cytostatic pheromone has no effect on cells above the SST. Means ± s.e. (n = 3) of proportions of mitotically dividing MT^+ or MT^- cells above the SST, 9 h after illumination, depending on the administration of fresh medium (blank), medium from a mating culture or medium from the opposite mating partner (above or below the SST).



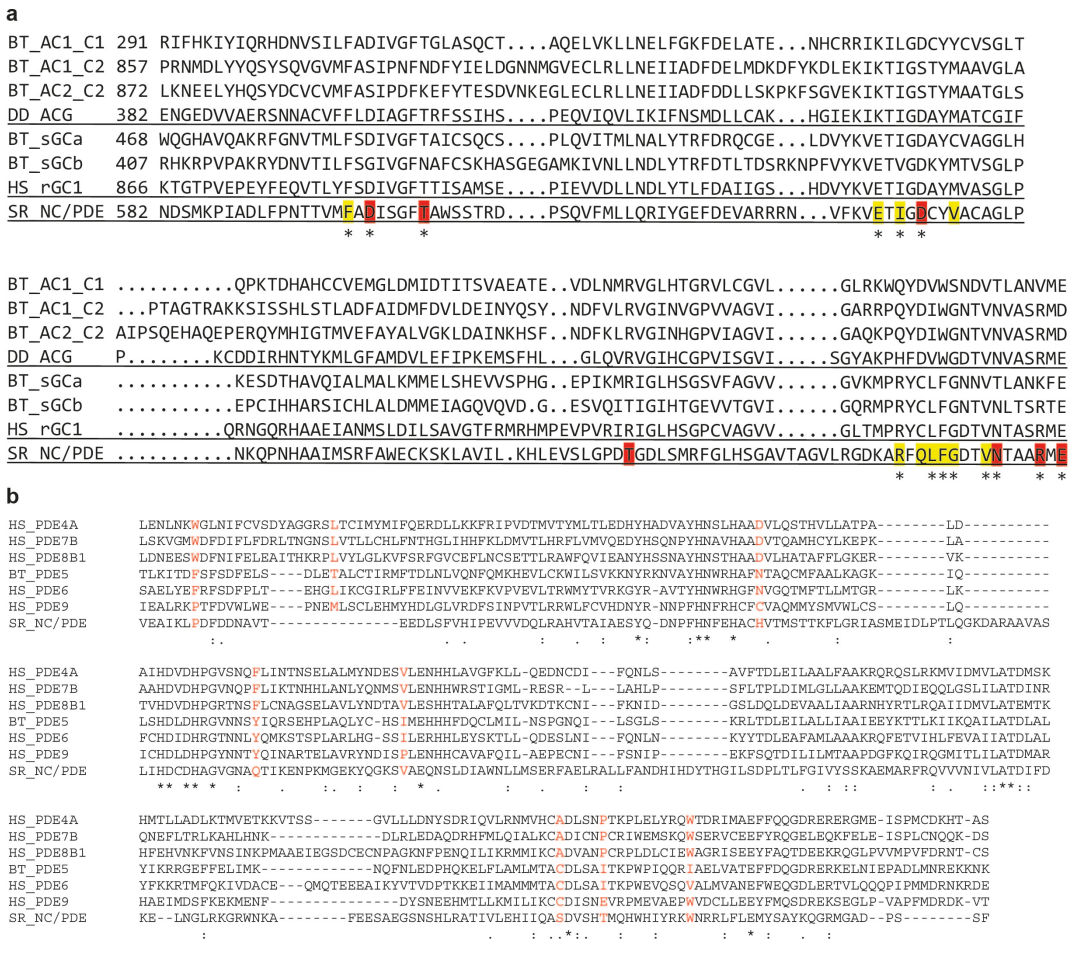
Supplementary Figure S2. Cytostatic effect of MT^- medium. Light microscopy images of MT^+ (85B) cells treated for 8 h with control medium (i-ii), or with filtered medium of MT^- (85A) cells below the SST (iii-iv). Cells are shown in the girdle (i, iii) or valve (ii, iv) view. Scale bar = 10 µm.



Supplementary Figure S3. Mass spectral analysis of SIP^+. The MS^2 spectrum of $[M-H]^-$ = 842 acquired by LC-ESI-Orbitrap mass spectrometry indicated a sulphated molecule.



Supplementary Figure S4. Differential expression of meiosis-related genes after treatment with SIP^{+}. Mean ± s.e. (n=3) counts per million (cpm) for *MRE11, MCM8, RAD50 and MSH4* in untreated (blue) and treated (red) cultures.



Supplementary Figure S5. Conservation of the cyclase and phosphodiestase domains of GC/PDE. (A) Sequence alignment of the catalytic core of the following adenylyl/guanylyl cyclases: BT_ACI_C1 (NP_776654.1), BT_ACI_C2 (NP_776654.1), BT_ACII_C2 (NP_112269.1), DD_ACG (Q03101.2), BT_sGCα (NP_786972.1), BT_sGCβ (NP_777066.1), HS_rGC1 (AAI48422.1) and SR_NC/PDE (BT = *Bos Taurus*, DD = *Dictyostelium discoideum*, HS = *Homo sapiens*, SR = *Seminavis robusta*).The first four proteins are adenylyl cyclases, the next three are guanylyl cyclases. Adenine/guanine binding residues are indicated in yellow in SR_NC/PDE and catalytic sites are indicated in red, conversed residues are indicated with * (adapted from Liu et al. (1997)). (B) Sequence alignment of part of the following PDE proteins: three cAMP-specific PDEs (PDE4, PDE7 and PDE8), three cGMP-specific PDEs (PDE5, PDE6 and PDE9) and the bifunctional *S. robusta* GC/PDE. The eight amino acids conserved only in cAMP-hydrolyzing PDEs are indicated in red.

Table S1: General statistics on the *S. robusta* transcriptome

total number of transcripts	50231
total transcriptome length	71.10 Mbp
minimal transcript length	501 bp
maximal transcript length	17339 bp
average transcript length	1416 bp
N50	1730 bp

Table S2: See file: TableS2.xlsx

Table S3: Primers used in the RT-qPCR on CYCA/B1, CYCB1, P5CS and GC/PDE.

gene	forward primer	reverse primer
V1[1]	CAAGGCAAGAAGGATGGCAAG	GCGACAAGCAAATTAGCAAACC
V4[1]	AGGCTACCGTGGGACTTGG	GATCTGGACTGCGCTGGTTC
CYCA/B1	GCTTGGGTCGATGCAATACT	ATCCGAGAGGGTCAAGAGGT
CYCB1	GGGATGTAACAAACGCCAAT	CCTCTCATCCATGACGGACT
P5CS	AATCGAAAACGGGGTAGCTT	CCCTCGACAATCTCAACCAT
GC/PDE	TCCTTCCCAAGTTTTCATGC	CATGGTTTGGTTGCTTGTTG

[1] Normalization genes.