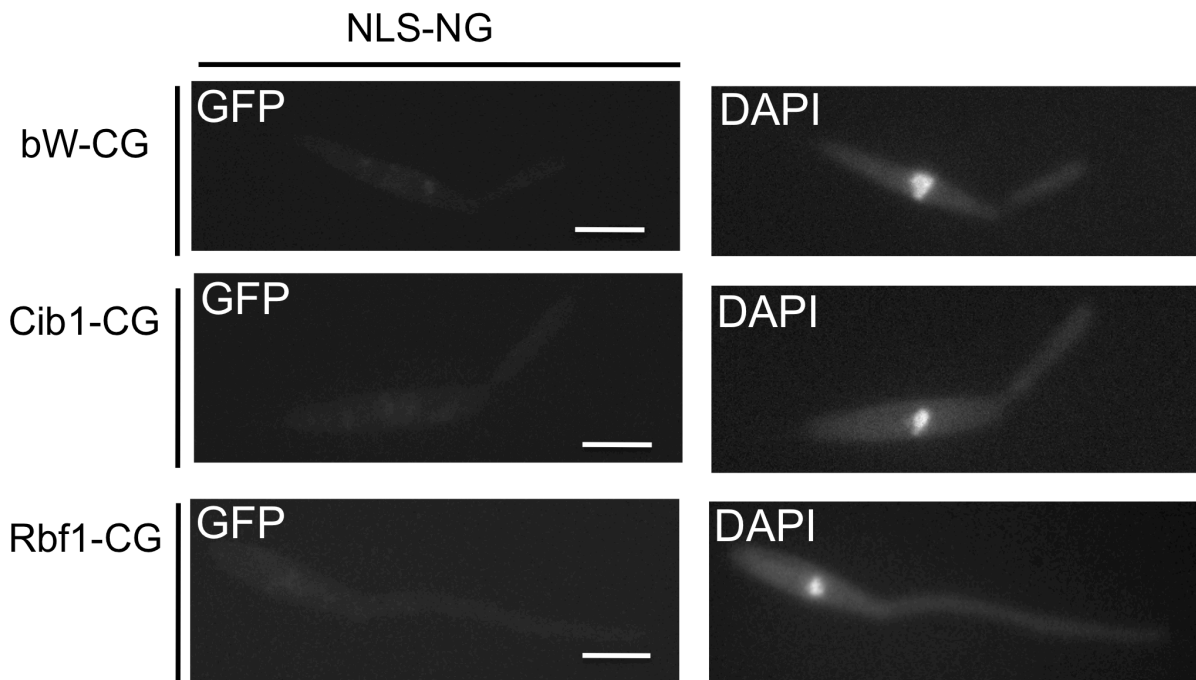


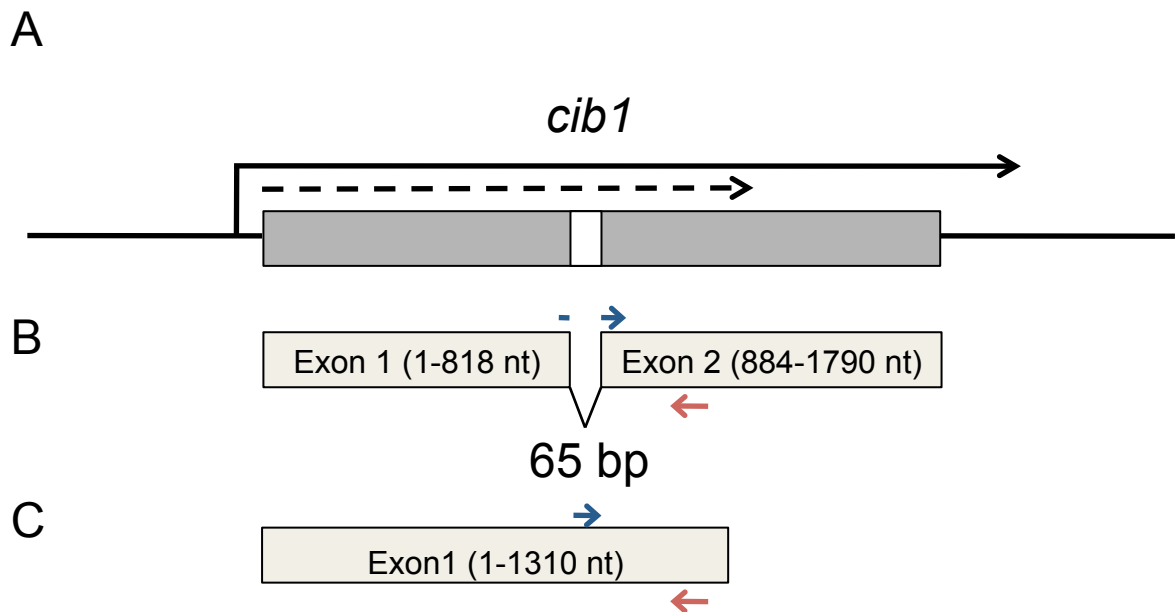
Supplemental Figure 1. Quantification of Clp1-binding to bW, Rbf1 and Cib1. Strength of Clp1-protein interactions were determined by quantification of β -galactosidase (β -gal) activity (Amberg et al., 2006) and 3-Aminotriazole (3-AT) mediated inhibition of yeast growth on selective medium (SD -leu-trp-ade-his). Yeast strain AH109 was co-transformed with pGBKT7-Clp1 and pGAD-bW, pGAD-Rbf1 or pGAD-Cib1, respectively. Binding of Clp1 to bW (24.51 U \pm 0.92 U) or Cib1 (79.52 U \pm 2.07 U), is approximately two- to six-fold stronger than Clp1 binding to Rbf1 (12.68 U \pm 1.01 U) as deduced from β -gal activity. In contrast, control strains, co-transformed with pGBKT7-Clp1, pGAD-bW, pGAD-Rbf1 or pGAD-Cib1 and the empty prey (pGADT7) or bait plasmid (pGBKT7) exhibited only basal β -galactosidase activity. Values represent the mean of three technical replicates of three biological replicates each. Similarly, strain AH109 transformed with pGBKT7-Clp1 and pGAD-bW or pGAD-Cib1, rendered the yeast cells insensitive to 3-AT concentrations >30 mM, whereas growth of strain AH109 co-transformed with pGBKT7-Clp1 and pGAD-Rbf1 was inhibited by addition of 5 mM 3-AT.

Reference:

Amberg, D.C., Burke, D.J., and Strathern, J.N. (2006). Assay of β -Galactosidase in Yeast: Assay of Crude Extracts. Cold Spring Harb Protoc **2006**, pdb.prot4157-.

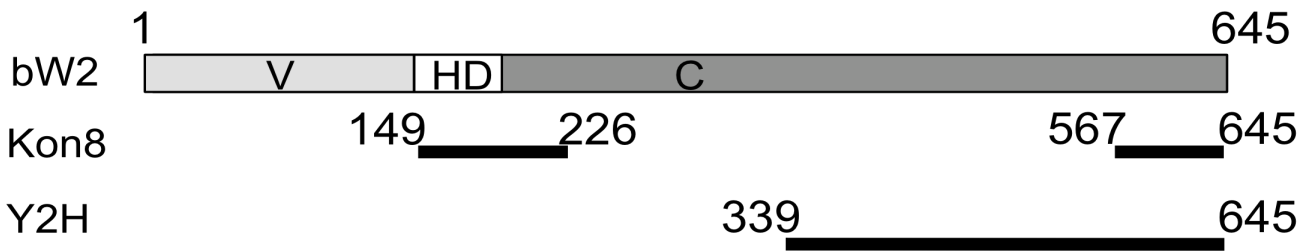


Supplemental Figure 2. bW-CG, Cib1-CG and Rbf1-CG do not display nonspecific interactions in BiFC analysis. bW-CG, Cib1-CG and Rbf1-CG were co-expressed with the nuclear localized N-terminal GFP-fragment (NLS-NG). Only background fluorescence was detected, indicating that bW-CG, Cib1-CG, and Rbf1-CG do not interact nonspecifically with nuclear localized NG. For visualization of nuclei cells were stained with 4',6-diamidino-2-phenylindole (DAPI). Scale bar =5 μ m.

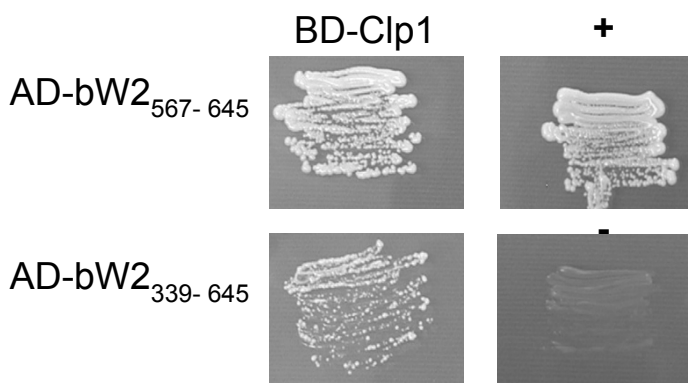


Supplemental Figure 3. Schematic overview of the *cib1* locus and transcribed mRNAs. **(A)** Transcription of the different *cib1* mRNA derivatives. Transcription of the spliced variant is depicted by a solid line, transcription of the unspliced variant by a dotted line. **(B)** Primers used for analysis of gene expression and absolute quantification of gene expression. The forward primer used for the quantification of the spliced transcript binds to the intron/exon borders and is therefore specific for the spliced *cib1* transcript. **(C)** The forward primer used for the quantification of the unspliced transcript binds to the intron region and is therefore specific for the unprocessed *cib1* mRNA transcript. The reverse primers used for quantification of the spliced or unspliced *cib1* mRNA are identical.

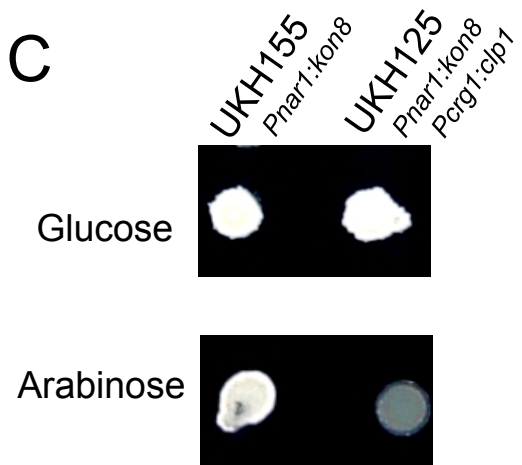
A



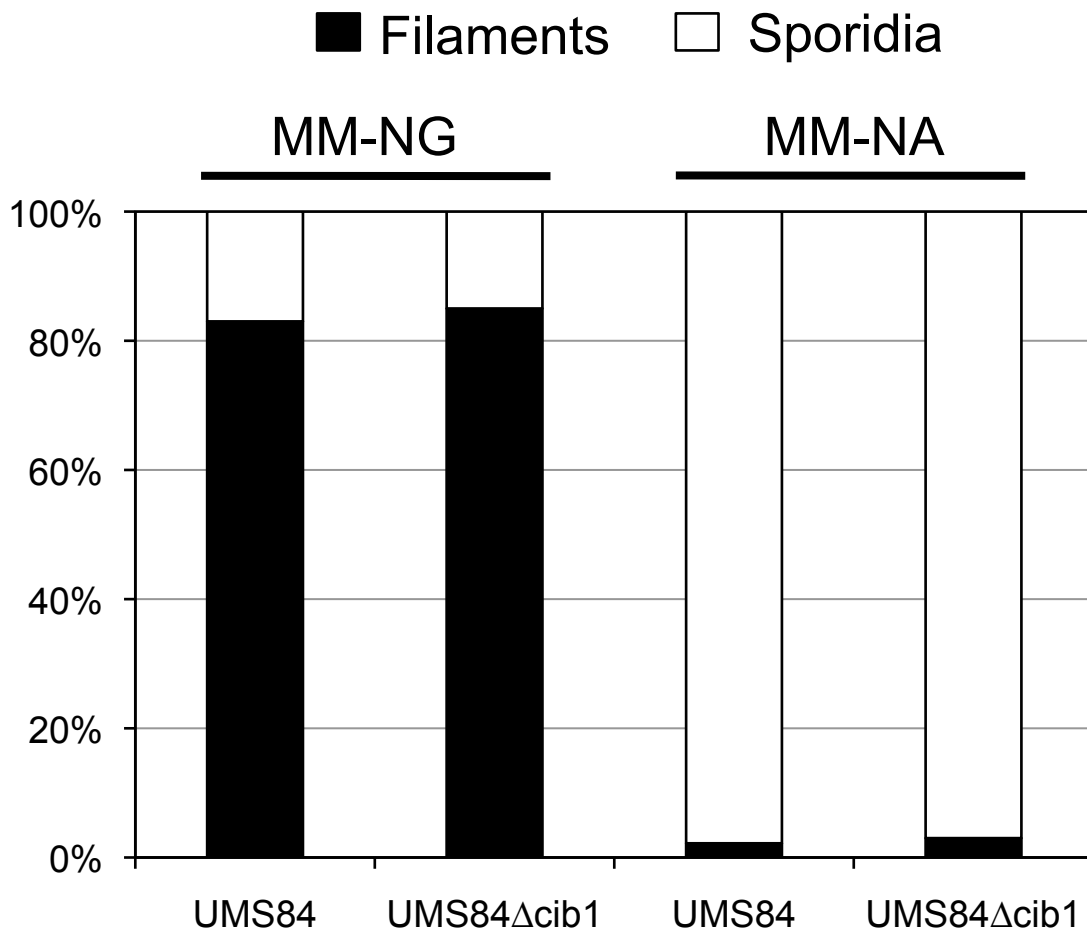
B



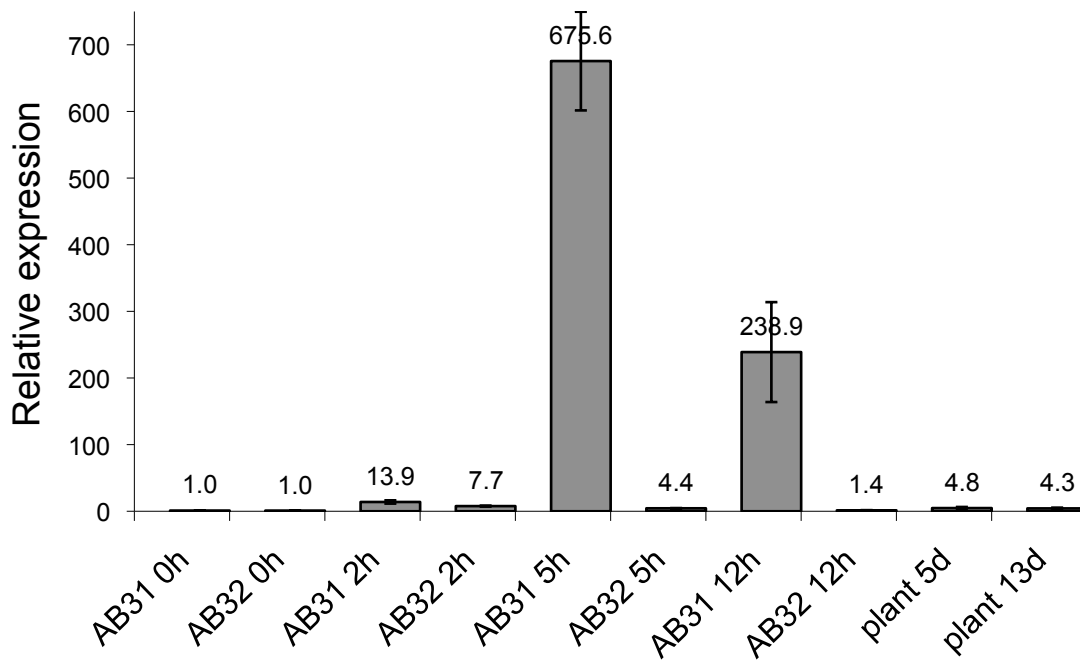
C



Supplemental Figure 4. Kon8 dependent filament formation is suppressed by induced expression of *clp1*. **(A)** Overview of bW2, the bW fragment isolated in the Y2H screen and the bW2 fragments required for Kon8 function. **(B)** The overlapping region of the fragments (aa 567-645) is sufficient for Clp1 interaction in Y2H system. Positive and negative controls were strain AH109 transformed with pGBKT7-p53 and pGADT7-T or pGBKT7-lam1 and pGADT7-T (Clontech), respectively. **(C)** *kon8*-dependent filamentation on charcoal-containing nitrate minimal media is abolished by arabinose-induced co-expression of *clp1*. Strain UKH155 (*a2 b2 P_{nar1}:kon8*) displays filamentous growth when spotted on charcoal containing nitrate minimal media irrespective of the carbon source used. In contrast, filamentous growth in strain UKH125 (*a2 Δb::P_{crg1}:clp1; P_{nar1}:kon8*) is abolished when the arabinose-inducible *clp1* gene is co-expressed on charcoal containing nitrate minimal media supplemented with arabinose.



Supplemental Figure 5. *Cib1* is not required for Clp1-mediated inhibition of *b*-dependent filament formation. Strains UMS84 ($a2 P_{nar1}:bE1/bW2 P_{crg1}:clp1$) and UMS84Δ*cib1* ($a2 P_{nar1}:bE1/bW2 P_{crg1}:clp1 \Delta cib1$) were grown in minimal media with glucose (MM-NG) or arabinose (MM-NA) as sole carbon source for 12 h and relative filament formation was quantified (N>100 cells). *b*-dependent filament formation is blocked by induced expression of *clp1* in MM-NA medium in UMS84 and UMS84Δ*cib1*, demonstrating that *clp1*-mediated inhibition of *b*-dependent filament formation does not occur in a *cib1*-dependent manner.



Supplemental Figure 6. qRT-PCR analysis of *rbf1* expression after *b*-induction in axenic culture and during pathogenic development. Expression analysis of *rbf1* was performed on RNA isolated from *U. maydis* strains AB32 ($a2 P_{crg1}:bE2/bW2$) and AB31 ($a2 P_{crg1}:bE1/bW2$), harboring incompatible and compatible combinations of *bE* and *bW* under the control of the arabinose inducible *crg1*-promoter. Strains were grown in glutamine medium supplemented with arabinose (MM-GA) to induce *bE*/*bW* expression for the time periods indicated. For analysis of *rbf1* expression during pathogenic development, RNA was extracted from leaf samples infected with a mixture of the compatible FB1 (*a1b1*) and FB2 (*a2b2*) strains 5 and 13 days after inoculation. Expression of *rbf1* is highly induced after induction of compatible combinations of *bE*/*bW*. During *in planta* development expression of *rbf1* is only marginally induced compared to the lowest expression value (AB32, 0 hours). Shown are the expression values of two technical replicates; error bars represent the standard deviation (SD). The *ppi* gene encoding the peptidylprolyl isomerase (*um03726*) was used for normalization.

Supplemental Table 1. Clp1 interacting proteins identified by Yeast Two hybrid screening

No	Accession ^a	No of		Description ^d
		Fragments ^b	isolation ^c	
1	um00168	1	1	related to Cell division control protein 15
2	um00241	1	1	putative protein
3	um00493	1	1	conserved hypothetical protein
4	um00523	1	1	related to CDC36 - transcription factor
5	um00578	1	1	b mating type locus, bW1 allele
6	um00769	1	1	conserved hypothetical protein
7	um01172	1	4	probable SDH1 - succinate dehydrogenase (ubiquinone) flavoprotein precursor, mitochondrial
8	um01228	1	1	related to eIF3I - translation initiation factor 3 subunit L
9	um01245	1	1	probable LEU2 - beta-isopropyl-malate dehydrogenase
10	um01640	1	1	related to GAS1 - glycosphospholipid-anchored surface glycoprotein
11	um01885	1	4	probable Alcohol dehydrogenase
12	um01886	1	1	related to carboxypeptidase
13	um02055	1	1	related to RNA14 - component of pre-mRNA 3'-end processing factor CF I
14	um02664	1	2	related to zinc finger protein white collar 2 (wc-2)
15	um02961	1	1	conserved hypothetical protein
16	um03013	1	1	related to CLU1 - translation initiation factor eIF3
17	um03172	1	1	Rbf1
18	um03416	1	1	carbon source-regulated protein (putative arabinase)
19	um03734	1	2	probable adenosylhomocysteinase
20	um03862	1	1	related to VPS27 - vacuolar protein sorting-associated protein
21	um04138	1	4	probable TAL1 - transaldolase
22	um04165	1	1	related to single-stranded dna binding protein 12k chain
23	um04531	1	1	conserved hypothetical protein
24	um04787	1	2	related to GLY1 - L-threonine aldolase, low-specific
25	um05339	1	1	probable 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
26	um05485	1	1	related to SWR1 - DEAH-box protein, putative RNA helicase
27	um06070	1	1	probable IPP1 - inorganic pyrophosphatase
28	um10243	1	1	related to DNA-damage inducible protein 2
29	um10466.2	1	1	related to MEU1 - multiple enhancer of UAS2
30	um10776	1	2	related to GCD2 - translation initiation factor eIF2B, 71 kDa (delta) subunit
31	um10787	1	3	probable FUM1 - fumarate hydratase
32	um10859	1	1	related to UV-induced protein uvi15
33	um11246	1	1	related to BZZ1 - Myo3/5p-Bee1p-Vrp1p actin assembly complex component
34	um11630	1	1	conserved hypothetical protein
35	um11761	1	1	related to RRP4 - 3'-5' exoribonuclease
36	um11782	3*	17	Cib1
37	um15099	1	2	conserved hypothetical protein

Legend:

^a= Accession according to MUMDB (<http://mips.helmholtz-muenchen.de/genre/proj/ustilago/>)

^b= number of independent fragments isolated in the screen

^c= number of times of isolation

^d= functional description/gene name according to MUMDB (<http://mips.helmholtz-muenchen.de/genre/proj/ustilago/>)

*individual Cib1 fragments isolated encompass amino acids 280-535; 350-550 and 374- 574. The overlapping region encompasses amino acids 374-535.

Supplemental Table 2. Pathogenicity of strain USA1¹

Strains inoculated	No. of Plants infected	Plants with Tumors
SG200	20	18 (90%)
USA1 (SG200 <i>cib1:3eGFP</i>)	28	25 (89%)

¹ Seven-day-old maize plants were inoculated with the strains indicated and tumor formation was scored seven days post inoculation

Supplemental Table 3: Differential gene expression upon induced co-expression of *clp1* and *rbf1* in *U. maydis*¹.

Gene (MUMDB) ²	Probe Set ³	Name ⁴	MUMDB Annotation ⁵	UKH156_1 ⁶	UKH156_2 ⁷	UKH156 mean ⁸	UKH156 SE ⁹	UKH164_1 ¹⁰	UKH164_2 ¹¹	UKH164 mean ¹²	UKH164 SE ¹³	fold change ¹⁴	difference of means ¹⁵
um02438	C115um033G_at	<i>clp1</i>	related to clp1, essential for A-regulated sexual development	7.9	8.7	8.3	0.4	4402.5	4751.2	4576.85	174.35	498.91	4568.55
um03568	C50um031G_at		related to regulatory protein alcR	109.2	99.8	104.5	4.7	292.8	244.1	268.45	24.35	2.15	163.95
um02383	W40um026G_at	<i>pra1</i>	a2-pheromone receptor Pra1	709.2	316.5	512.85	196.35	127.3	127.3	127.3	0	-4.03	-385.55
um02382	W42um026G_at	<i>mfa1</i>	a1-specific pheromone [mating factor a1]	3880.2	3223.2	3551.7	328.5	82.9	63.5	73.2	9.7	-37.51	-3478.5

1) The effect of Clp1 on *rbf1*-dependent gene expression was assessed by Affymetrix microarray analysis (UstilagoA) comparing strains UKH156 (a1 Δ b::Pnar1:*rbf1*; induction of *rbf1*) and UKH164 (a1 Δ b::Pnar1:*rbf1*; PcrG1:*clp1*; induction of *clp1* and *rbf1*) after 12 h growth under inducing conditions in minimal medium supplemented with nitrate and arabinose (MM-NA). dChip1.3 (Li, C., and Wong, W.H., 2003: DNA-Chip Analyzer (dChip). In: The analysis of gene expression data: methods and software., G. Parmigiani, E.S. Garrett, R. Irizarry, and S.L. Zeger, eds (New York: Springer), pp. 120-141) was used to calculate mean expression values and fold changes based on a 90% confidence interval ('lower bound of fold change'). Induced and repressed genes were filtered according to the following filter criteria: a change in expression of ≥ 2 and a difference of mean expression values > 100 was considered significant. All array data have been submitted to GEO (<http://www.ncbi.nlm.nih.gov/geo/>; accession number GSE21121)

2) Genes and annotations are derived from MUMDB (<http://mips.gsf.de/genre/proj/ustilago/>)

3) Probe Set on Affymetrix custom array UstilagoA defines region for detection of corresponding genes (<http://mips.gsf.de/genre/proj/ustilago/>)

4) Gene name as described in literature

5) Annotation according to MUMDB (<http://mips.gsf.de/genre/proj/ustilago/>)

6) Expression value UKH156_1 (experiment 1)

7) Expression value UKH156_2 (experiment 2)

8) Mean expression value UKH156 (baseline)

9) Standart error UKH156

10) Expression value UKH164_1 (experiment 1)

11) Expression value UKH164_2 (experiment 2)

12) Mean expression value UKH164 (experiment)

13) Standart error UKH164

14) fold change of mean expression (lower bound of confidence)

15) difference of mean expression values

Supplemental Table 4. Primers used in this study

Primer/Purpose	Sequence (5' to 3' direction)	Reference
Y2H analysis		
Clp1_Nde	CATATGTCACCCCGTCACCAG	This study
Clp1_Bam	GGATCCTCACTCGAGTTTGGTGGATTG	This study
pGAD-DS for	TACGACTCACTATAGGGCGAGCGCC	This study
pGAD-DS rev	TGGTGCACGATGCACAGTTGAAGTG	This study
<i>cib1</i> deletion		
<i>cib1</i> _lba	AGCTTGGACTAGTAAATGGGACCG	This study
<i>cib1</i> _lbi	GTTGGCCATCTAGGCCGAGGAGAAGGGATGCCAAGTG	This study
<i>cib1</i> _rbi	GTTGGCCTGAGTGGCCATGTTGAACACGTGCGTCAGTCC	This study
<i>cib1</i> _rba	ATTATCCCTTCGCCTTCCCTTC	This study
<i>cib1</i> _orf_f	TGTCAGAGACTCCTGTCAAGCAAG	This study
<i>cib1</i> _orf_r	GGGATTAGAGGAAGATGGGAGGG	This study
<i>cib1</i> _nested_f	ACGCCTGAATCGATGCAAAACTG	This study
<i>cib1</i> _nested_r	CAATCTCATTTCGTGTTCCGCGC	This study
<i>um02664</i> deletion		
<i>um02644</i> _lba	ATCCGCTACTCGCCACTGCTCATC	This study
<i>um02644</i> _lbi	GTTGGCCATCTAGGCCTCTCGAGTTGAAGTGCAGTGCAAG	This study
<i>um02644</i> _rbi	GTTGGCCTGAGTGGCCTCGACCTCATCATCCTGGCGTATC	This study
<i>um02644</i> _rba	GAAGAAGGCAACAATGGGAATGC	This study
<i>um02644</i> _orf_f	AAAGCATGTTGCAAGGCAATGTG	This study
<i>um02644</i> _orf_r	ATCTGCATAGGATTGATGGGCGC	This study
<i>um02644</i> _nested_f	ATCCAAACGCCGAATCACGAATAC	This study
<i>um02644</i> _nested_r	TTCTGGTCATACTCTGCGAGGTGG	This study
<i>cib1</i> RACE		
<i>cib1</i> _cDNA_3'	CCCTCCCATCTTCTCTAATCCC	This study
<i>cib1</i> _cDNA_5'	ATAGCCCTCGCCACAGATACAG	This study
<i>cib1</i> GFP fusion		
<i>CibGFP</i> _Lb_f	CAATCCTCAAATGAAGGCGTTCCG	This study
<i>CibGFP</i> _Lb_r	GTGGGCCGCGTTGGCCGACGCGATTGAGGCCATCAGAC	This study
<i>CibGFP</i> _Rb_f	CACGGCCTGAGTGGCCTGTTGAACACGTGCGTCAGTCCC	This study
<i>CibGFP</i> _Rb_r	CTCGCCACCTGTAGACAAACAAG	This study
<i>Pcib1</i> GFP fusion		
LB_as_Pcib1GFP	GGTGGCCGCGTTGGCCGTCATGATGAGAGACGAACGTGAA	This study
<i>cib1</i> _lba	AGCTTGGACTAGTAAATGGGACCG	This study
<i>CibGFP</i> _Rb_f	CACGGCCTGAGTGGCCTGTTGAACACGTGCGTCAGTCCC	This study
<i>CibGFP</i> _Rb_r	CTCGCCACCTGTAGACAAACAAG	This study
In vitro expression		
Y2H_ <i>cib1</i> _f	GGCCATTACGGCCATGACTAGCACCACCAGTCAACG	This study
Y2H_ <i>cib1</i> _r	GGCCGAGGCGGCCAGCGACGATTGAGGCCATCAGA	This study
BiFC analysis		
SplitGFPN5_Nde	GTGCATATGGGGACGTCGGCGGCCAACGCGGCCATG	This study
SplitGFPN3	GCCGGCGCGCCGGCCGCTTTAGGCCATGATATAGAC	This study
SplitGFPN5_Nde	GTGCATATGGGGACGTCGGCGGCCAACGCGGCCGAC	This study
SplitGFPN3	GCCGGCGCGCCGGCCGCTTTAC	This study
Leu2_lba_a	CCAACCATTGATGTAACCTCTC	This study
Leu2_lba_i	GCTGGCGATTGACGAGGC	This study
Leu2_rba_a	GCATCGGATCCGAATGGTACG	This study
Leu2_rba_i	TAGCTTGTTACTTGCTCACTTTATCAC	This study
Clp1_Nde	CATATGTCACCCCGTCACCAG	This study
Clp1_Sfi	GTGGGCCGCGTTGGCCGCTCGAGTTTGGTGGATTGGAGC	This study
<i>Cib1</i> _Nde	GGGCATATGACTAGCACCACCAGTCAAC	This study
<i>Cib1</i> _Sfi	GTGGGCCGCGTTGGCCGAGCGACGATTGAGGCCATCAGAC	This study
bW1_Nde	GGGCATATGACGCTACCACCACTACCAAG	This study
bW1_Sfi	GTGGGCCGCGTTGGCCGAGCGAAGAAAGAATTTGAGTAG	This study
rbf1_Nde	GGGCATATGGACATCTTGGGTAAGTCCAAG	This study
rbf1_Sfi	GTGGGCCGCGTTGGCCGGGCGCTCTGCAGTTGAGAGGAC	This study
NLS_Sfi_f	GTGAGCCTCCAAAAAAGAAGAGAAAGGTCAATTCGGCGGCCAACG	This study

NLS_Sfi_r	ACGGTCGAGCCTCCAAAAAGAAGAGAAAGGTCGAATTCGGCGGCCA	This study
link1f	CGGCCCCGCCCCGCCTGCAAGATCCCCAACGACCTCA	This study
link1r	TGTGGTTCATCACCTTCTGCTTGAGGTCGTTGGGGA	This study
link2f	CGGCCCCGAGCATCGCCACCAACG	This study
link2r	TGGTGGCGATGCTGCGGGCCGCGT	This study
Y2H analysis bW2		
Y2G_bW567_Sfi_f	GTGGGCCATTACGGCCAACATGCAAAGCTTTGAGGAGATCGA	
Y2G_bW645_Sfi_r	GTGGGCCGAGGCGGCCTCAGGCAAGCGAGAAAGAGTTCGA	
qRT PCR		
RT_cib1_spliced_f	GCCTCCCTGCAGCGGATGC	This study
RT_cib1_unspliced_f	GGCGACCTGCTCTGATGCACC	This study
RT_cib1_r	CATCGACGTTGTTTCCGGCCT	This study
RT_mfa1_f	ATGCTTTCGATCTTCGCTCAGAC	This study
RT_mfa1_r	TAGCCGATGGGAGAACC GTTG	This study
RT_pra1_f	AACCGAAGGCATCTGC ACTGC	This study
RT_pra1_r	CCCGCATGTCGATGTCAGACT	This study
RT_prf1_f	TCGGTAGAACGAGCTGTGATG	Zarnack et al., (2008) ¹
RT_prf1_r	CTGTTGGACGATGTTGGAGTTG	Zarnack et al., (2008) ¹
RT_rbf1_f	AGTACGAGCTACGACGGATTC	Scherer et al., (2006) ²
RT_rbf1_r	GGGTAGGTGTTGGACACATTC	Scherer et al., (2006) ²
RT_eIF2b_f	ATCCCGAACAGCCCCAAC	This study
RT_eIF2b_r	ATCGTCAACCGCAACCAC	This study
RT_actin_f	CATGTACGCCGGTATCTCG	This study
RT_actin_r	CTCGGGAGGAGCAACAATC	This study
RT_ppi_f	ACGCCGATCACTTCGTC	Scherer et al., (2006) ²
RT_ppi_r	TCTTGGCAGTCTTGGGAAC	Scherer et al., (2006) ²
rbf1 deletion		
lb5'	CGACTTGTACCACAATGAGGC	This study
lb3'	CACGGCCTGAGTGGCCTCACGATTCGTGATTCGGTG	This study
rb5'	GTGGGCCATCTAGGCCTCGACACCGCATCTCGCC	This study
rb3'	TCCGAGTCCGACGACAGC	This study
Plga2 driven expression		
Plga2_EcoRV_5'	GGGTGATATCCGAAGGACTTACTCATCAAAGCGA	This study
Plga2_NdeI_3'	GGGGTCATATGGTTTCAGAGGAAAGGGAGGGAT	This study

1.) Zarnack, K., Eichhorn, H., Kahmann, R., and Feldbrügge, M. (2008). Pheromone-regulated target genes respond differentially to MAPK phosphorylation of transcription factor Prf1. *Mol Microbiol* **69**, 1041-1053.

2.) Scherer, M., Heimel, K., Starke, V., and Kämper, J. (2006). The Clp1 protein is required for clamp formation and pathogenic development of *Ustilago maydis*. *Plant Cell* **18**, 2388-2401.

Supplemental Table 5. Strains used in this study

Strain / Name	Genotype	Reference
FB1	<i>a1 b1</i>	Banuett and Herskowitz (1989) ¹
FB2	<i>a2 b2</i>	Banuett and Herskowitz (1989) ¹
SG200	<i>a1 mfa2 bE1bW2</i>	Kämper et al., (2006) ²
SG200 Δ <i>cib1</i> / UKH6	<i>a1 mfa2 bE1bW2 Δcib1</i>	This study
FB1 Δ <i>cib1</i> / UKH7 UKH8	<i>a1 b1 Δcib1</i>	This study
FB2 Δ <i>cib1</i> / UKH9 UKH10	<i>a2 b2 Δcib1</i>	This study
SG200 Δ <i>clp1</i>	<i>a1 mfa2 bE1bW2 Δclp1</i>	Scherer et al. (2006) ³
SG200 Δ <i>um02664</i> / UKH77-79	<i>a1 mfa2 bE1bW2 Δum02664</i>	This study
FB1 Δ <i>um02664</i> / UKH81 UKH82	<i>a1 b1 Δum02664</i>	This study
FB2 Δ <i>um02664</i> / UKH83-85	<i>a2 b2 Δum02664</i>	This study
SG200 <i>cib1::3xeGFP</i> / USA 1-2	<i>a1 mfa2 bE1bW2 cib1::3xeGFP</i>	This study
FB1 <i>Pcib1::eGFP</i>	<i>a1 b1 Pcib1::eGFP</i>	This study
UKH50	<i>a2 b2 leu2::Pcrg1:clp1:NG</i>	This study
UKH71	<i>a2 b2 leu2::Pcrg1:clp1:NG ip^s Pcrg1:bW1:CG ip^s</i>	This study
UKH73	<i>a2 b2 leu2::Pcrg1:clp1:NG ip^s Pcrg1:cib1:CG ip^s</i>	This study
UKH74	<i>a2 b2 leu2::Pcrg1:clp1:NG ip^s Pcrg1:rbf1:CG ip^s</i>	This study
UKH75	<i>a2 b2 leu2::Pcrg1:clp1:NG ip^s Pcrg1:NLS:CG ip^s</i>	This study
UKH155	<i>a2 ip^s Pnar1:kon8 ip^s</i>	This study
UKH125	<i>a2 Δb::Pcrg1:clp1 ip^s Pnar1:kon8 ip^s</i>	This study
UKH156	<i>a1 Δb::Pnar:rbf1</i>	This study
UKH164	<i>a1 Δb::Pnar:rbf1 ip^s Pcrg1:clp1 ip^s</i>	This study
JB1	<i>a1 Δb</i>	Scherer et al. (2006) ³
UMS84	<i>a2 Pnar1:bE1/bW2 ip^s Pcrg1:clp1 ip^s</i>	Scherer et al. (2006) ³
UMS84 Δ <i>cib1</i>	<i>a2 Pnar1:bE1/bW2 ip^s Pcrg1:clp1 ip^s Δcib1</i>	This study
UKH214	<i>a2 b2 leu2::Pcrg1:NLS:NG ip^s Pcrg1:bW1:CG ip^s</i>	This study
UKH215	<i>a2 b2 leu2::Pcrg1:NLS:NG ip^s Pcrg1:cib1:CG ip^s</i>	This study
UKH216	<i>a2 b2 leu2::Pcrg1:NLS:NG ip^s Pcrg1:rbf1:CG ip^s</i>	This study
UVO151	<i>a1 Δb ipr Pcrg1:clp1 ips</i>	Scherer et al. (2006) ³
UVO151 Δ <i>rbf1</i> / UKH172	<i>a1 Δb ipr Pcrg1:clp1 ips Δrbf1</i>	This study
UKH178	<i>a1 Δb::Plga2:rbf1 ip^s Plga2:clp1 ip^s</i>	This study
UKH180	<i>a2 Δb::Plga2:rbf1 ip^s Plga2:clp1 ip^s</i>	This study
UKH184	<i>a1 Δb::Plga2:rbf1</i>	This study
UKH186	<i>a2 Δb::Plga2:rbf1</i>	This study
UKH178GN	<i>a1 Δb::Plga2:rbf1 ip^s Plga2:clp1 ip^s Pmig2_5:NLS3xeGFP</i>	This study
UKH180GN	<i>a2 Δb::Plga2:rbf1 ip^s Plga2:clp1 ip^s Pmig2_5:NLS3xeGFP</i>	This study
UKH184GN	<i>a1 Δb::Plga2:rbf1 Pmig2_5:NLS3xeGFP</i>	This study
UKH186GN	<i>a2 Δb::Plga2:rbf1 Pmig2_5:NLS3xeGFP</i>	This study

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