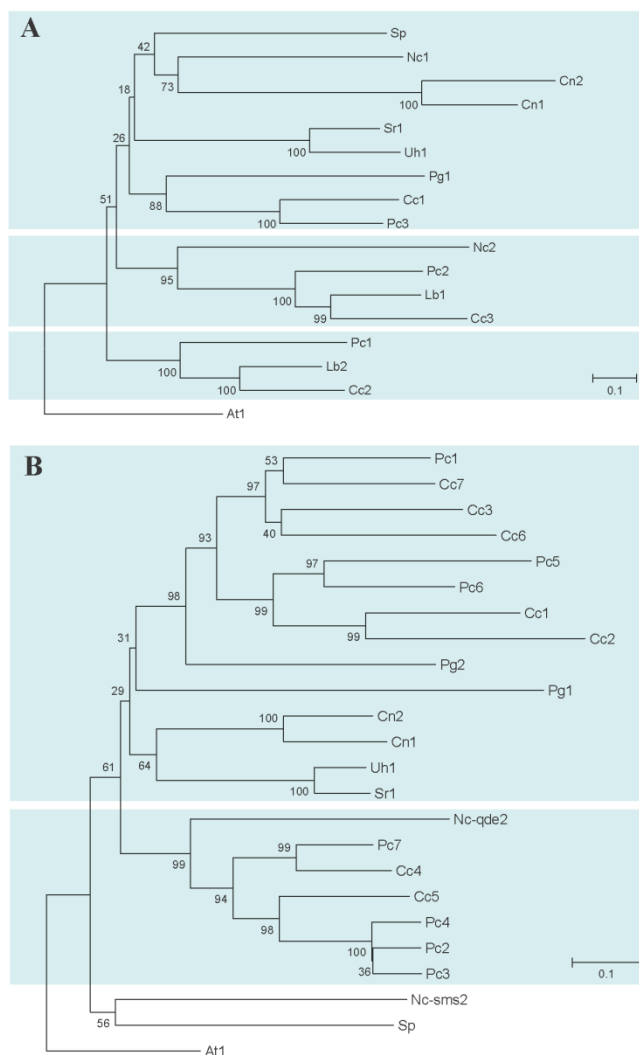
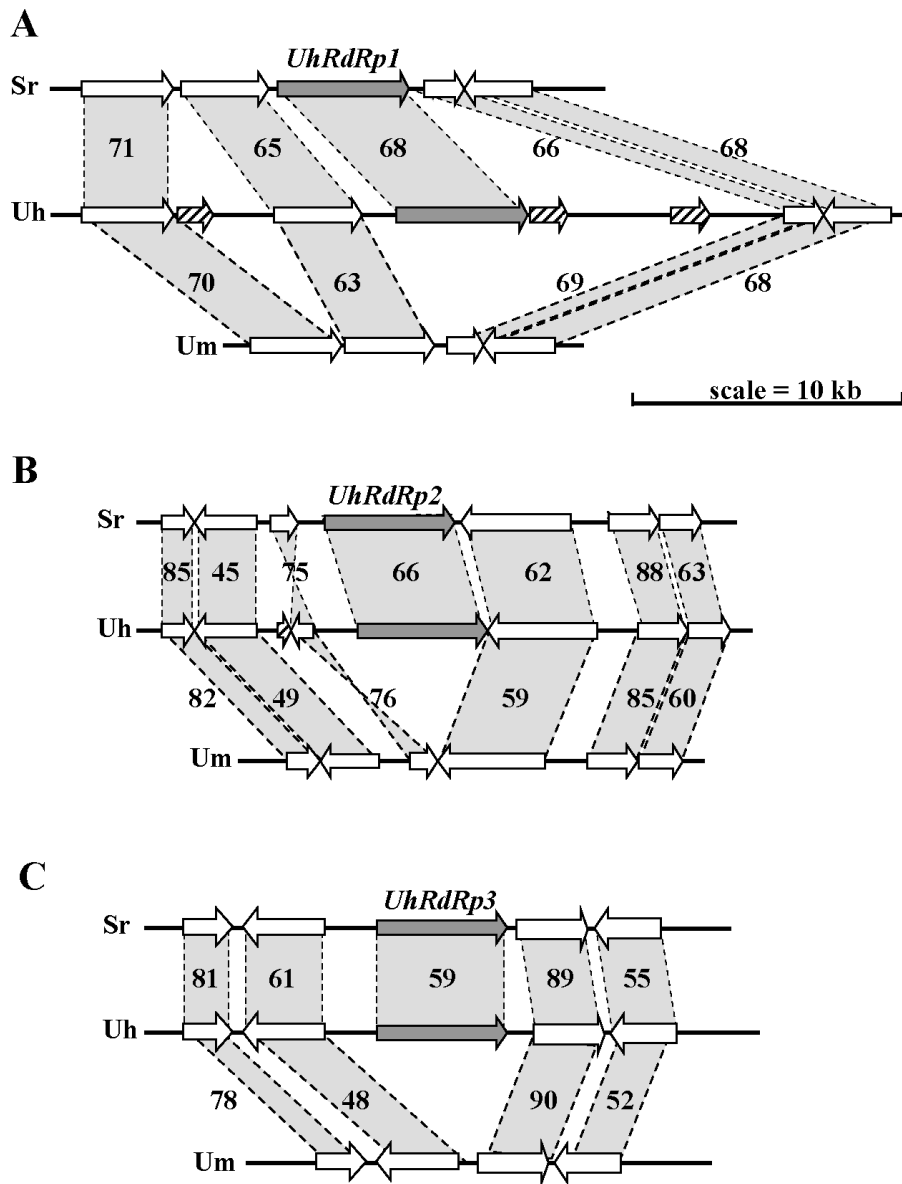


Supplemental Figure 1. Heat map revealing distribution of various features on the *U. hordei* chromosomes. Chromosome numbers are given by Roman numerals and chromosome ends are indicated by vertical bars. Rows a, b and d to f represent the frequency of occurrence of the various elements over a 10 kb region of sequence. The color scale ranges from zero frequency (white) to 10 or more features (black) with red indicating a mid-range of 5. The mating-type locus *MAT-1*, the ribosomal DNA regions (see Supplemental Dataset 1) and names of cluster homology regions (see Supplemental Dataset 4) are indicated. The contents of the rows are as follows: (a) Called genes. Out of all 7113 called genes, 6879 genes are represented on the mapped supercontigs; 234 genes are located on assembled contigs that could not be mapped and may be located in the gaps. Interruptions indicate sequencing gaps. (b) Genes encoding small candidate secreted effector proteins (CSEPs). (c) Identified *U. hordei* CSEP cluster homology regions, named as defined in Supplemental Dataset 4; the colors represent regions with homology to *U. maydis* (black) and regions without such homology (red). (d) Small sequencing gaps within supercontigs. (e) All repetitive and transposable element sequences. (f) Family of 2752 variants of LTR2, LTR5, LTR13, and composite TE, Tuh3 and Tuh5 elements that are related to the Ty1/copia-type elements previously identified in the *U. hordei* *MAT-1* mating-type region (Bakkeren et al., 2006). (g) Family of 1377 variants of LTR1, LTR3, LTR6, LTR7, LTR8, LTR10, LTR12 and Tuh1-related sequences, which belong to a Ty3/Gypsy class. Only the two largest repeat families are shown. Note that since many of the TEs and repeat elements are located on many small contigs that could not be assembled into the larger genome contigs, only a partial distribution can be revealed.

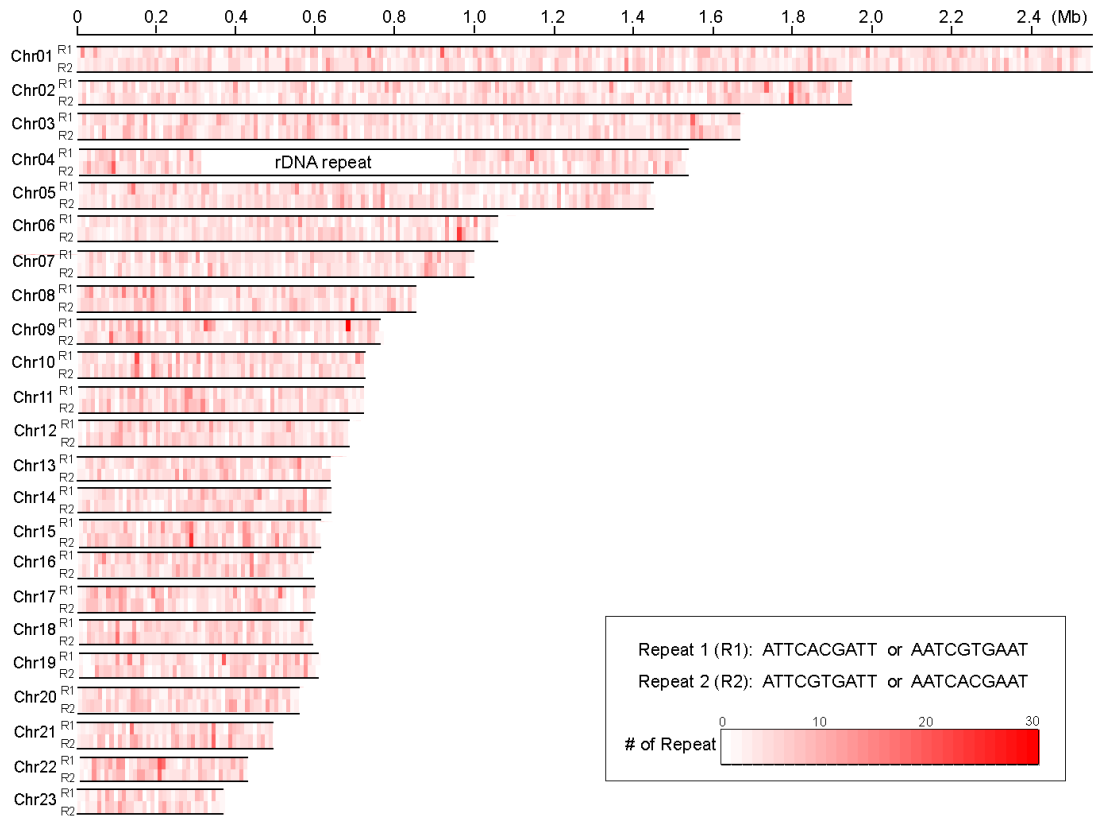


Supplemental Figure 2. Phylogenetic relationship of selected Dicer (A) and Argonaute (B) protein sequences. Trees were drawn from aligned protein sequences using MEGA5 (Tamura et al., 2011). Dicer protein sequences were trimmed to span the two RIBOc domains. The Neighbor Joining method was used to construct the trees and the values at the nodes represent % of 1000 bootstrap replicates. *Arabidopsis thaliana* proteins (At1) were used to root the trees. Cc, *Coprinopsis cinerea*; Cn, *Cryptococcus neoformans*; Lb, *Laccaria bicolor*; Nc, *Neurospora crassa*; Pc, *Phanerochaete chrysosporium*; Pg, *Puccinia graminis* f. sp. *tritici*; Sp, *Schizosaccharomyces pombe*; Sr, *Sporisorium reilianum*; Uh, *Ustilago hordei*.

Accession numbers were for the DICERs: At1, DCL1, AT1G01040; Cc1, D6RKZ5; Cc2, A8NX83; Cc3, A8PF80; Cn1, Q5KKA8; Cn2, Q5KKA7; Lb1, B0DAX9; Lb2, B0CY37; Nc1, DCL1, Q7S8J7; Nc2, DCL2, Q7SCC1; Pc1, Phchr1_1385; Pc2, Phchr1_4895; Pc3, Phchr1_890; Pg1, PGTG_12289.2; Sp, DCR1, Q09884; Sr1, sr16838; Uh1, UHOR_08937, and for the ARGONAUTE proteins: At1, AGO1, AT1G48410; Cc1, 1.108_5-1; Cc2, 1.108_5-2; Cc3, 1.198-10; Cc4, 1.213_11; Cc5, 1.224_12; Cc6, 1.258_15; Cc7, 1.325_24; Cn1, CNJ00490; Cn2, CNJ00610; Nc-qde2, Ago1, NCU04730; Nc-sms2, AGO2, NCU09434; Pc1, White_Rot 120; Pc2, White_Rot 148.1; Pc3, White_Rot 148.2; Pc4, White_Rot 148.3; Pc5, White_Rot 158; Pc6, White_Rot 330; Pc7, White_Rot 635; Pg1, PGTG_08429.2; Pg2, PGTG_11327.2; Sp, SPCC736.1; Sr1, AGO, sr15057; Uh1, UhAGO1, UHOR_06256. The amino acid alignment used to produce the tree is presented in Supplemental Dataset 5 online.



Supplemental Figure 3. Comparative microsynteny around loci present in *U. hordei* (Uh) and *S. reilianum* (Sr) but missing in *U. maydis* (Um). Genes implicated in the RNA silencing pathway indicated as dark arrows: (A) RNA-dependent RNA polymerase *UhRdRp1* (UHOR_08874), (B) *UhRdRp2* (UHOR_01631), and (C) *UhRdRp3* (UHOR_15740), are depicted. Synteny is indicated by shaded bars with percentage amino acid identity between the predicted flanking proteins. Note that the region surrounding *UhRdRp1* (A) is more expanded and contains three *U. hordei*-specific genes, UHOR_13400, UHOR_08875 and UHOR_13402. The encoded proteins match many related protein sequences in the genome. UHOR_13402 encodes a protein with a RVT_2 superfamily retrotransposon-like motif and UHOR_13400 codes for a protein with a putative integrase core motif. The region surrounding *UhRdRp2* (B) harbors a small gene with unknown function. Interspersed between the two genes is UHOR_01630, also a gene of unknown function, but found in an inverted orientation compared to both the *U. maydis* and *S. reilianum* homologs. These features point to the involvement of TEs in the evolution of these loci and might have caused the deletion events that occurred in the *U. maydis* genome.



Supplemental Figure 4. Distribution of the 10-bp repeats in the *U. maydis* genome. The two simple repeat sequences R1 and R2, as well as their complementary sequences (Schirawski et al., 2010), were searched across the 23 chromosomes of the genome and their occurrence was counted within each 10-kb window. Red indicates a high density of the repeats while white indicates a low density.

>um06396-um06397 (ex-Dc11)

GAGTGCACACTACAACATCTTTTTCAGATACGCCGGTCTTGACCTTCCGGCCACAATTCAGGATGAATTCAGGGCGAACTTTTACTCCGCAATCGTTTGCCAAAG
CCCTTGGCCATCGCGCCGTTGCAATCGGCGCAGCCAAAGCAACGGCGGCATCGATGACAATGCTTACAGCAGCACCACCGGTAGCGATGACAGTAGAAAAACATG
GCAGTGTGGATTCGATCGATAGCATACCCGATGAGAGCGGCTCCGGTCTTTATAGCACAGAGTCTGTTCCGTGAGGACGGGGAAAAATCATCTTGTCAT
GTTGTGGCTTGAAGAGTTGGGGTTCATATCTCGTATACCCATCATCCCTCACAAACCGAGACAGAAACAGGTAGATAGTCTAACCCACCACAGACGCTATA
CCCCTCCGGATGTCACGCTCGCGCCTCACGCTCTCGCTGTATCCCACCGCCATGCTTTCCACCAGCTTCGATCACGGTATGGCTGATGCGATGCTG
ACGCTGAACCGGGCAGAGCATGGTCCGCTGATCGCGCCGAGTTGCGCAATCAAGCGATCACCTGGCCGCGCATAACACACACAGTCGGCA (**ΔUHOR_**
08937) CCACTTGATGGCGGATGCTTTGCGTTTTGATCGCATTACACAATGATCCGTTTTTGGCGTCGTCGAGCCACAAGCTGCCATAGCTTAGCCAAC
ACGGTTCAGTTGACAAGCAAACTCCAACCACGATACTTTGCGATTGTGCGCAAGATGCACAACGAGCAGCACTGGCTCCTTGTCTGTGCAATTCAGCTTTC
ATCATGATGCTCAACCTGCGCAGAGACAGTACGAGTGTGTTGGCTGGCGGCTAGGATACAAAGTCGTGAGTGTATGCCAAGTGGCGCTGTGCGGTATGTTATC
GAGTTCGGGTGGATTTGTCACACGTCAGAGCAGAAACGGCACAGGTTGAGAGAGTACGAGTGGTGTGAGTGTACGTGAGGTGAAA**ATTCGTGATT**GACGATT
GTGAAGATCAAGACGCTGAGGTTGTGATGCTGGCCGATCACGGATGTCGTCTGGTCCGAGTCTGACCACGGACCGCCCGGTAGTCCGCTATGAGTCCGCTTC
CAACCGATCTGCATTACGACGAGCACTACGACTAGCGAATCATACGATTGAAGCAACACTGGACAGACGCTCGAGC**ATGTACAACGGTATTGGACTCAAGA**
CGGCACGTGGAACGGGCACGAATGGGTACGTGCAACGCAACCTCTCCAACCTTCGAGGCTGGAAAGAACGGGTGGAACAAGCGTGTGCGACCGATGAGGTCGG
GTCGGATACACGCTTTGGTCCCGACGACGATTTGGAGCACGAGCGAAAGCGAGCGGTGGAAGTGAAGTGCATGGAGCTGCGGCTCGAGCT

>um04177-um10893/um04178 (ex-Ago1)

CGTGAAGAGCAGGTTGAGCCAAGTGTGCGGACATTTTGGCGGCAAGTCAACTTCTGGATGCAACAACCTTGGCGTCGCATCTTTTGGATGCATTCGACCG
GCTCGAGAGGTTGGTGGTGTGCCAGATGATGAAGAGTGAAGCAAACTCTTTTGGACAGGGCGCTCGAGCTCTGCCTTCGCTGCGCCCTTGTTCAGCA
GCATAGCGCGCGCTGGTCCCTCTGTGACATGGCTGTAGTCGGTGAAGTAGTCAATACCGTGTAGTAGCGGTGTTCAATGCTAGTGTATTTGGTGAAGCAA
AGCAAAATCAAGACGCTGAGGTTGTGATGCTGGCCGATCACGGATGTCGTCTGGTCCGAGTCTGACCACGGACCGCCCGGTAGTCCGCTATGAGTCCGCTTC
TGCACAGCGCAGCTCGAGTTAGATTAAAGTAAGCAGCAAGTCTCGAGTTCAGACCATGATACCGAGCCACAGTTGAAACGAATCGTGAAGGGTGAACGAGG
GGGATGGATGTTGATGAGAGACAAGATGAGGAGATGCTGAATTTTGTAAACACTCACGACTGGCTCTCTGTGCGGCGTGTGGACGACTCACTCGCC**AAATC**
GTGAATCAGGAATTTAAGCGAAGTCTAAAAATTTGTAATTTGTAATTTGCTCTTTCTGAGTGGGATTCGCG**ATTCGTGATT**CTTGCTTGATTACCA**ATTC**
CGATTCCGCGCAGTCAAGAGACGCGCAGCATTCCCAGATCCGCTCAGCCATCGATCTGAGGATGCAACTGTGATCGCACTGCCCTGTCTTCAACATG
AGAGCTTTGCAAGAGAGAGAGTACCCTTGCAATTTGAAAGAGGGGGTGAAGAATGGTCTGATTACAGATCTGCCTGCAAGTTTTAACAGCAACTGTGTGAT
TCTCTTTCTGGATCGCATATCAGAACCACTCACACTCGTGA (**ΔUHOR_06256**) CTGACGACTGAAACGGAGGAGCACACGGACATACAGTCAGC
AGTACATCCTCGAGCGAA**ATTCACGATT**GACACACAGGATGCTTTACGCTTCTGTCCAGGTGCGACTCGTGACTGGATGGTGTCTCAATCCAATAGCCGGT
CACAAACAGCAATCGTGAACCAAAATGATACTGTACAGTACATGTAGGAAAAAATAAAAAAAAAAACAAGAAAAATCTGTAGTAAT**ATTCGTGAAT**CGCAT
TCAGAAATATTAATGTTATAATCGACAAGAGCGGACAAGCAGATCCGCTTCTATCAGCTTAACAAGTGGACTTTTGCAGCTTCAATTTGCACCGTAAATTTGC
AATTTGCAGCATCGATTTCCGTGCTCTGTGCGTA**ATTCACGAAT**CACAAATTTAGTACAGAGTCTGTGAGTCTCGAATAGTATGGAAGAGTGGAGCTAAC
GTACAGGTTACACATACAGCATGCGGTGCGGTTGACGGTTGACAT**ATTCGTGATT**CGTATTGTTGATCTGTGTCGCTCGGTTACAAATGTCTCAGCTGA
GCAGCAAAAGCAGATCTATGTGAGAACGGCGCACCACTCGTCCCATCTCTGACGGTCTTCTGTAATCGGTGAAAGTCAATTTGGCGGCTTGGGCAATCTTCTG
CGATCTTTGCTTGAACAGGACAGTCTGCATCAGTTGTTGTTGTTGTAATAATTTAGCAATTCAGATTCGCGCTCGCGCAGGCTGAT**ATTCGTGCGGAAGT**
CTGCAAGGCTCGGTAGGCAAGCGCTCAGCTACCGAGAAGTCTGTACAAGACTCAACAGCTGATTTGACCGAAGCAGTACCAAGCAAGAGCTAACAGCAAGCAGC
ATCCACAGCACAGAGATGGTGGGTGGCTGAGGATGAACCTCCGATGAGGCGAGCGAGGACAGCCAGGCTGGCAAGCGCAGGGCGGACGCTAACAGCAGC
AAGTTGAACCTGATCGGTGCCATCAACACACTGCAGCAAGAG

>um06257-um06259 (ex-RdRp1)

CTGGCGTGAAGTTCACCGGAAGTGGGGCAGACCCGCGTCTGTTGAGCGAACTCGACATTGGACTCTTGATGGGAGGAGTAAGTGTATGGAAGGGCGCACTCA
TCTCAGTGGCAACAACACTGCGGTGCGGATGGCGCAATGCGGGTCTGCTGAGCGCAAATCTCTTCTGATGTTGTCTATCTATCTGTCAACAAGCGTTCG
TTGATATTAGTCTGTCAGGTGACACCTGGGGTCTGTGATGTGTAAGAACAGTGCAGTAACTGTCCTTGGCAG**ATTCACGAAT**CGATCGTGGTTC**ATT**
CGTGATTGACCTCGTGAATCGCAATCGTCCCGATCTGATTTTTTCAGGCGAG**ATTCACGATT**TACG**ATTCACGATT**TGTGCCATGAAG (**ΔUHOR_13**
400) CGCTGCTAAGCAC**ATTCACGAAT**TAATCCTGAAT**ATTCGTGAAT**CTCGGCTTGGCGTCTCGTCCGCGAGGCTGTGGGGAGCCTGTCTGTGCACAGC
CATAAAGACACACAC**ATTCGTGATT**CATATTAGTCTGTGAGACCTGAAGACCGTCCAACCGTTACCTTTGCTCCCTCATCTTGGAGCTCGACCTGCCT
CTATCACTACTTCTCTTTCCGAGGCTCACAACACTACATCAAAGCTTGCATCTGGCAGGTTACCACCTTTTACTGAGTGCAGC**ATGGACGGCGCGGCTGGA**
AGCTGTAGCGGAAACCGCGCGGATCTTTGGCGGTTCTTCCAGCATGTCGAGCATGGGATGGGAGCGACATCTGCTTTTGTCTGACAGCAGCCACCCCTCATC
ACCTCCACCACAGTGCAGTGTAGCAGTATGCCTCGACCTCGCGCATCCGCTGCGACCAATGCATCTTCAATCCAGGCCATCACTGCATCGACTCAAGCAAC
CACAGCAAAATGATGAGGCACAATGGTTCGCTAAAGGACATCGTTTGCAAGGGCGTGAAGTGCATCAACAGAACCAACGGACCATGCTCGCTCATC
CGCTTTGCAACGTTCTGCTTTGAGGGGCGAGCTTCAAATCACACTCCCGCTCGGCGGTGGTCCAGTACAGCTACCTCAGTCAACTGCTTCCGCGAGCAT
TGCTACCAAAGTGAACAATGACCGAATGGAGGAGAAGAACTGGAAGCGCGCTCAGCATCTTGCCTCGCAGCAGTACGGTTTGGACGTGATGCTCGGTTT
CGACTCGATCACTTCTTTGCGCTACCGCAGGGAACGATGGAGGCGCAGGGAGCTCGCCCTGTTTGGCTGTGCGGTGTGCAGCTTGTGCATGGCTGGCTA
CCCATCCAGCGGATGACAGACCTATCAGGCGATACAGGAAGCGCGCAGTACAACAAGGCTACTGACGTGGTGGTCAAGGGTGAACGGTGGCAGATGGTG
CGTGTGCGCGATCGAGGTGTCGGCGCCCTGGCAGCAGAGCTTGAAGTCAAGGCTGAAGTCCAATGGCAAGCGGCGGAACGACGCGCCTGGACCGACGA
TCAACGTGCAACGATACGTCAGGCACTAGCTCTGCAATCATTTCTGGACAGCACTCAACTCAACTCACATATCACGGCTTATTTTGTGCTGGCGCAAGAGATT
CCTGCGGGCCAGCCGATTGCGCTTTTCCGCAATTCACATCTCTCGGTGCTGTACAAGCGGCTGCCACAGAAAGCGTGAAGCGCAGGACTCAAGCGCAGCAC
CTATGTCGCCGCCACCGCCACCGCGCAACCTCTTCACTCTGGTACCAGCGGAGTCTTGTGAGGAGTGTAGATGTTTGGGAGAGTCTGGTGGATGTGGA
TGGTGAAGCAGCGAGTTTTTCGACGGAAAGTTTCAACAAGTGCATCTGCGCAAGGCGATTAACGTTAGGAGAACCGCGGACCGCTTGGAGCCGATGGAGCC
GATAGGCGGGCTATCAACAGCAAGAGTCCGACTACCGCTTGGATGCGAGTATTACCAATGACAGGATCGATTTGACCGAGGATCGATTTGGAGGACAGCAGAGGGA
GGAACAGACAGTCACAATCTCAGCAGACAATGGTGCAGGCGAGCGCAGCCACAGCCAGCTGCGCTGAGCTGATGTTAGAGACGCCCCAACGAGGTGTTAC
CACCATGCGATTTCGAGACGGTGCAGTAAAGACGAAGGAGATGCATTGATCGTGTGAGCTTGTATCCATTAACAATGCGCAACGATCTTGCAGATTCGCTT
AGCAGTCTGCAGGATCTGCTGATCGGAGGATCAGAGGCTGTGCACTCGGTTGCCGTTAGCAAGTCAATCGACTAACCCATCTCTCAATGCTTCAGAGACGGCTT
CAACACCTCATCCAACGCAACCGTCTCTTGTCAATGCGAGGACTCCGCTCGGCTCAGGATGACAGTACCACTCAACTTCCATTTGCTGGCGCAAGAGATT
CAAGCTATCGGCTGGTGCATTTGCCGTGCCATCTCTGCCGTCTGGTGCATGCGCTGCTAGAGCAAGAGAAATCGCTAGAGCCAGAATCTATCTGGCAGCC
ATTGAGACGGCTTTGGCATCTGGTGCACCTCTCGAGAACCGGAGGGTCAAGTCAAGGGAATTCGAGTGGCAATTCGAAGGGATGGATTGATCAGGGTGAAGT
AGCGCAACATCACAGCGTTCGAGCACCCCTGGACAAGGGAATAGAAGCGCTCCACCACCGAGCGTGGCGCTCGATTGCAACACCGCTGCGCAACTTT
GGATCTGGAGCGCTGTTTCAACAAGACGGGACGCGAGGATCTACGAAGCGGAGCAGGCGGTTGGAGGCGGATGGGAGTGGTCTAGTGGAGTGGCG
AAGGGGACGAGAAGTGTCTCGATGTGATACTGTGGAACGCAAGCAGGACCAAGTGTGAGCGGATCAATTTGTGATGGCTACTTCTGTCGCAAGGCTGGTGA
CCGAGTGCAGTCTGGCGAATGTGTTGGTTCGAGGAGTGGATGCTGTTGGAGGCACATCTCGCTTTGTGACGCCGCAACGACAGCAGGATGCTGGATGGTCT
GTTACGCCATTTGGCTGGTCAAAAAGGACTAGTACAGGACGAGCAGTGTGTTGACGACTTGTGGTGTGAGCTCTGGAGCTGCGAACATCTGGCTT

TGCAATTCCTTAGCGGGAGTGTGGAAGGTAGAGTTGGTTCCGTTTGGCGCAACACCACGGCGGAGCTTCTGGAAGCGCTGCTGGGGCCGATGCAGGTGGGCCAC
 CAGCGCGAGTCAAAAAGACGGCTTCTCTTCGCTCGTCCGGGGCCCTTCTCGATCCGACTCGACCGCGCAGCAGCTAGTTCGCAAGACAAGCTGCAGA
 ACCGCCAGCAGTGGGAAGAACAGTACCGCAACAAGTCCGTGACGATCTCTACGGTGACCGGAAAGCAAAGCAACCTTGGCAACGCCACCAAGTTCAA
 GGCAAGAAGGCGAAAAGGGCAAGGACGACAAGAAGGATTGCTGCATCATGTGACGTAGATATTGCGTCAAAGGCTTTGCTACCTGTTGCAGCCAATCTAAG
 AAGTGTTCGTTCAAGGGTCAGAGCAATTTGGCACGCTGTCTCGACGCAAGAATGAGTATTTGCTTTGCTATTCACAATTGTGCCAGGCCAGGGCCTCGACT
 ACGCATCTTGAATCGTGACTGAGCTGGATATACG**ATTCTGTGATT**GTCAAAGTTCCACTGGAACTTACAGAGCAGTCAATCCCGTCCGCGTGTCCAACGGC
 TCACAAATGCGGGCAGGTCACATGCACGAG**ATTCTGTGATT**TCTAATGAGCCGCCGTCGTTGCGTGGCCG**AATCTGTAAT**CGT**AATCTGTAATCAGCAAT**CG
 TAGT (**ΔUHOR_08874**; **ΔUHOR_08875**; **ΔUHOR_13402**) CACGAGTGGTAGATTATACCGAGTCAAGGAGTGTGAGGTTGGAGA
 AAGTACACGGCTATACGCTAAAGCAGGGATCT**AATCTGTAAT**CACGGGAAGAAGCGCGCTCGGAGAAGCTTCGTGCTTTTGTGTTGGGCAAGCGCAGAAA
 GCGGAGATGTGCGCCGACAGTCGCGAGTTGGAGA**AATCAGCAATCAGCAATCTGTAATCAGCAAT**GTGAATCGTTTCGGCGCAGCTGACGGTAGAAAGTGC
 GAGAACGTGGAACCCTTTTTTAAGTAATGGCCAAACATTCACGATCAGTTAACCGAGTCAACAGTCACAGTCACGACACTACATATAACCGAGTGCATCTC
 TTCCCCCTCTCTCTCGTCTCCTACACGCAAAACACCCAGAGTAGACAGAAAACAGCAGCAATCCGACATCCAGCGACTGCAACC**ATGTCTGAGCAACAACA**
 CGACGCTAAACAGGCAACCCGATCGTCTACCTCGATCTCGCCTTTGGTTGCTCGCCTGCGTCTCGCCCCGGATCAACCGCATCGTCTCGAGCTGTACGC
 GGATCGTGTCGCGCGCACCGCGAGA**AATCTGTAAT**CTGCACCAACACTCTC

>um01077-um01079 (ex-RdRp2)

TGGATACCTGAGTGGAGCAGCGTCCAGTAGCGAGGTCAAGGAAGAAGGGATGGCAGATCTAAGGGAGAAGCCGGCCTCGTCCGACCGGGTTCGAAACGCTTGC
 GAGCAGAGTATCGTCTGACTGAGTGGATGAGTTGGCAAATGCGGAT**TTTATCAGAGGAGGGCGTGTGGCAAGTTGACGTCAGAAGCGGGAGAGGGA**
 GAGTGGAGAACTGTAGCAGTTGCTCAGTGGCATGTGTGATAGAGCGAAGAAGCAGTCCGATCAGCAGAGCATGGTGTGGATGGGAGCAAGAAAGTCGTTGA
 CAGAAAGAAATGAAACGGTACGAGGATCAAAAAAGTAAACCGGATACTTGGTTGGGATAACGGTCAAAGTGTGTGAGGCCTGAGGCGCTCGAGGAAGCA
 CATTCGTCTCTCTCGGTATCATGAACCAAGCCAACTTGTGTGTCTGTGCGGCCAGACGGTGGGTAGATGCGCGCGTAACCCAACCTCTCTGTAAG
 ACAAGCCACGGCAGAGACTCACAGAACGATCACGGATGTTGGCGTGGCTCAGCTATGTTATCACG (**ΔUHOR_16687**) **AATCTGTAAT**GTGCTGA
 GTTCAGGATCCCTCGCACGACTGGTCCAGCAGTGCACGCCAGCAGTGCACGGATGGCTCTGATACTTTTTTAATGTGGATGCACCTTGCAGCGCTCACCCAC
 GACTTTAGCTTTGAACCTTGGACCTTATGCTGGACAAGCGCCGCTCAGCTTTCGCGCATTCA**AATCAGCAAT**GT**AATCAGCAATTCGTGATT**CGTGA
 TTACAGTCCCGGGACG**ATTACAGATT**TTTACAAGATCATAATGTGAAACGAACGGCGTAAACATCTGTATTTTAAACAACAAACGTTCAAGAGACGAAAAGTA
 GGAAACGTGAAGC**ATTACAGATTACAGATT**CACGCTCGTTTTGCTGTTTGACATGATGCAGCTTACGACGCTCTGGCTCGCATGCCTATTTTCCCCCTTTT
 TCTCTCCAACTCGGGACTGAGTCACTGTGTCTCGCGTCTGAGCTTACAGTGGACATGTAACTTAAAGTTAACTCACACTCGTGACTTAGGTGAGCTCCAGC
 TTTGGCCGCTCCTCCGCAATCCAGATCCAGACCCTGGTGGACTCTCTCTGTATTGACTGCAGCCGATTCTGAGCAGATGCGACAGTCGTGAGTGTCTCGAG
 CTTGGCAGACTTTCTCCGCAATTTGGTGTCTTCGCGGAGCTCGCTGCTGCCAACAGCTCTGTGTACAGCAGCTCTACCTGAGCAGCTGAGCTGC
 AGATTCACGCGATCGGTCTGACTAAGTTAGCCCTCTTTCTTCTGACATCCATCGACTCAAATCACGCGACTCTCAGAAATCAACGGCGACTTGTATC
 ACCTAGCACC**ATGCTCAAACCGGAGAGCGAATGAAGGCTGAGGCCACCGAGGCCCTCGACGCCAGGATGAACTCAACTGTCCAGGCTTTGAAATCGGACCGC**
AGTTTTGCGGCTCTCGGCGACTGCTCGCCAACTCGCCCTGCGGGTTCATCTCGTAAGCGCTCTGCGACTCGTCAGGAGCTCTACCTCTTTTCCATC
AGCCATCCACCCTATTGATCCCTCCAACCTCGCACCAAGCCAGTGCAGGTTACCGTCCACGTCTGGTGGTGCCTTCGACCGGCTCTGGTTCCGCG
ACATGAAGAACAAGGCGTCAATCGGTGAGGCCAGCCACCAAGACGGTCTGGTCGAAACGTAAGGCTGACGTCGTGATCGAGTCAGAGACAGGACTT
TGTAGATCTTGTACCGAAAGTTCAAGCCAGCGACTCTACAACGAAGGAAGGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
GCTATTCAGTTGATCAAGCGTCAAGCGAATGCATCAATATTGTGACAATTAGATGGTGACCGTGGACTTTCGGCATTTTTCTGCCCCGATTGCGAG
ATCAAGATCAAGGCTGACTCGATCGCATCGCAGCTTCGAGTCTGCTCGCTTTCTCGCACAGCGTTCAAGATCTACGGAACCTCTCCTACCCAGAGCGCG
AGACCAAGGTCGACGCGTCAATATCAGCGCGAGGAAACGATGCTCGTATACCGACTACGGCTCTGGTCTCCGCTCCGCTCCCGATCGCGCAAGGCT
TTGAGTTCGGCATGCTGTCTGCTGCACTGTACACCACAGCTTTGGTCCCACCCAGCATCAAGCCGCTTAGCTTGAATGACCTGAGTGCATAGTGGTGGCTTT
 AGGACGTAGTTCATAGCATGCTGTGTGGGGTAACCTCATACTTCTTTTTCGGTAATGAATCTATTTACATCTCAACAGAGTGTGAAAAGAACCGACTAAA
 CAAAAGGCGCAAATGGAATCAGACTTTGTGGGCGGATAAATAAGAAACAGAGCAAACGAGCGTATAAAGTTGAATAAGGACTGTGAGAAATCATAAAGA
 CGGAGACTTGAACAAAGAGAGACAAAACGACCAAGTCCGTTGTACGTAG (**ΔUHOR_01631**) **AATCTGTAAT**ACGAGTATCACTTACGAGGGG
 AGCGCAGACTAGGATTGCTTTCGCAAAAGTCCGGTGGACTTTCGGCTTTAGCAACGCTCCTTTGGCGGCTACCCACCCGCAATTGGTTCGCGTGGTACCGG
 CGCAACACTCGCTCGAGTAACAGATTCTCGAGTGCAGCGACTTGTGTGCTAGCGAAAAGAGAGCTGCCAGCGAGGA

Supplemental Figure 5. Sequences of the loci in *U. maydis* deleted for RNA silencing genes.
 Compare Figure 4 and Supplemental Figure 3. The sequences flanking the deletion site are largely conserved between *U. maydis* and *U. hordei* and are depicted in red, and those of the intergenic “empty” site are in black, in which also the estimated position of the deleted gene present in *U. hordei* is indicated (Δ UHOR_0xxx). The numerous 10 bp-repeats found in the *U. maydis* genome (Kamper et al., 2006; Schirawski et al., 2010) and their location, are depicted in pink (ATTCGTGATT or AATCAGCAAT) and green (ATTCACGATT or AATCTGTAAT).

Supplemental Data. Laurie et al. Plant Cell (2012). 10.1105/tpc.112.097261

A	CCCCCCTCAACAGCATATGTACCCTGTTTCATTATGCTGTTGTTTCAAGGTGTGACCTCTGTTCTTCAACACTGTCCGCAT	80
B	CCCCCCTCAACAGCATATGTACCCTGTTTCATTATGCTGTTGTTTCAAGGTGTGACCTCCGTTCTTCAACACTGTCCGCAT	80
C	CCCCCCTCAACAGTATATGTACCCTGTTTCATTATGCTGTTGTTTCAAGGTGTGACCTCCATTCTTCAACACTGTCCGCAT	80
D	CCCCCCTCAACAGCATATGTACCCTGTTTCATTATGCTGTTGTTTCAAGGTGTGACCTCCGTTCTTCAACACTGTCCGCAT	80
A	AGCTCGGGGACCCCGTTTCGTACACTGTGCTCCGGTATTTGCAGGTGTAGCCAGATCTTGCTTGCTGCATTGCCTGTCTC	160
B	AGCTCGGGGACCCCGTTTCGTACACTGTGCTGGTATTTGCAGGTGTAGCCAGATCTTGCTTGCTGCATTGCCTGTCTC	160
C	AGCTCGGGGACCCCGTTTCGTACACTGTGCTCCGGTATTTGCAGGTGTAGCCAGATCTTGCTTGCTGCATTGCCTGTCTC	160
D	AGCTCGGGGACCCCGTTTCGTACACTGTGCTCCGGTATTTGCAGGTGTAGCCAGATCTTGCTTGCTGCATTGCCTGTCTC	160
A	CCAATGGGCTTTGTGAGTACGCTCTGCCAAGTTTCTTGTGGTGTCTACGTAAGTGTGCTGCTGCTGGTTCCTTACTAACCTGTATGCAAC	240
B	CCAATGGGCTTTGTGAGTACGCTCTGCCAAGTTTCTTGTGGTGTCTACATACTTGATCTGCACCCTTCCCTCTTGGATGTT	240
C	CCAATGGGCTTTGTGAGTACATCTGCCAAGTTTCTTGTGGTGTCTACATACTTGATCTGCACCCTTCCCTCTTGGACATT	240
D	CCAATGGGCTTTGTGAGTACATCTGCCAAGTTTCTTGTGGTGTCTACATACTTGATCTGCACCCTTCCCTCTTGAACGTT	240
A	GTTACGGACGAAGTGATACTTGGTGTTCGATGTGCTTAAAGCTTCCAGTGTGTGCTGGTTCCTTACTAACCTGTATGCAAC	320
B	GTTACGGACGAAGTGATACTTGGTGTTCGATGTGCTTAAAGCTTCCAGTGTGTGCTGGTTCCTTACTAACCTGTATGCAAC	320
C	GTTACGGACGAAGTGATACTTGGTGTTCGATGTGCTTAAAGCTTCCAGTGTGTGCTGGTTCCTTACTAACCTGTATGCAAC	320
D	GTTACAGATGAAGTGATACTTGGTGTTCGATGTGCTTAAAGCTTCCAGTGTGTGCTGGTTCCTTACTAACCTGTATGCAAC	320
A	CAGTGTGTCCGAGTAGACCATCGGTGTCTGTGGCAATGCCAATTGAGCGTAGCAGCTGCTTGAGGAAGAGCACCTCA	400
B	CAGTGTGTCCGAGTAGACCGTTGGTGTCTGTGGCAATGCCAATTGAGCATAGCAGCTGCTTGAGGAAGAGCACCTCA	400
C	CAGTGTGTCCGAGTAGACCGTTGGTGTCTGTGGCAATGCCAATTGAGCGTAGCAGCTGCTTGAGGAAGAGCACCTCA	400
D	CAGTGTGTCCGAGTAGACCGTGGTGTCTGTGGCAATGCCAATTGAGCATAGTAGCTGCTTGAGGAAGAGCACCTCA	400
A	CATGTTGCTTCCATGGCTGCAATGAACCTGCTCCGACAGCGGACAATGACACGCATTTTTGTGTCCGCTGACTTCCAGGC	480
B	CGTGTGCTTCCGTTGGCTGCAATGAACCTGCTCCGACAGTGACAATGACACGCATTTTTGTGTCCGCTGACTTCCAGGC	480
C	CATGTTGCTTCCATGGCTGCAATGAACCTGCTCCGACAGTGACAATGACACGCATTTTTGTGTCCGCTGACTTCCAGGC	480
D	CGTGTGCTTCCATGGCTGCAATGAACCTGCTCCGACAGCGGACAATGACACGCATTTTTGTGTCCGCTGACTTCCAGGC	480
A	TACTGGATTCCCATACACTAACGCCACTGACCCCGATGTGCTCCTTCTCTGTATGGTGGCATCCGCTTCCCAGTTTGAT	560
B	TACTGGATTCCCGTACACTAACGCCACTGACCCCAATGTGCTCCTTCTCTGTATGGTGGCATCCGCTTCCCAGTTTGAT	560
C	TACTGGATTCCCGTACACTAACGCCACTGACCCGTAGTGTACTCCTTCTCTGTATGGTGGCATCCGCTTCCCAGTTTGAT	560
D	TACTGGATTCCCGTACACTAACGCCACTGACCCCGATGTACTCCTTCTCTGTATGGTGGCATCCGCTTCCCAGTTTGAT	560
A	CGCTGTGTGCAACCAAGTGGCTCTTGGGACTCACTTGCCTATATAAACCAATCCAACCTGCCTTGTGCTTTCGAGGTAGCGT	640
B	TGCTGTGTGCAACCAAGTGGCTCTTGGGACTCACTTGCCTATATAAACCAATCCAACCTGCCTTGTGCTTTCGAGGTAGCAT	640
C	CAGTGTGTGCAACCAAGTGGCTCTTGGGACTCACTTGCCTATATAAACCAATCCAACCTGCCTTGTGCTTTCGAGGTAGCGT	640
D	CGCTGTGTGCAACCAAGTGGCTCTTGGGACTCACTTGCCTATATAAACCAATCCAACCTGCCTTGTGCTTTCGAGGTAGCAT	640
A	AAGACCCTTTGTGCTGCTTGATAATGCTCCTGTGATGGTTCATGCATGTGCCTAGCGAGAACACCCATGGTGAGACTAAG	720
B	AAGACCCTTTGTGCTGCTTGATAATGCTCCTGTGATGGTTCATGCATGTGCCTAGCGAGAACACCCATGGTGAGACTAAG	720
C	AAGACCCTTTGTGCTGCTTGATAATGCTCCTGTGATGGTTCATGCATGTGCCTAGCGAGAACACCCATGGTAAAGGCTAAG	720
D	AAGACCCTTTGTGCTGCTTGATAATGCTCCTGTGATGGTTCATGCATGTGCCTAGCGAGAACACCCATAGTAAGGCTAAG	720
A	GTCGGGCCGGGTGCTGTTGGCAACCCAGAGCAGCTTGCCAACAATCACGATGACTCCCTCTGTTGTGCTGCGCTTGC	800
B	GTCGGGCCGGGTGCTGTTGGCAACCCAGAGCAGCTTGCCAACAATCACGATGACTCCCTCTGTTGTGCTGCGCTTGC	800
C	GTCGGGCCGGGTGCTGTTGGCAACCCAGAGCAGCTTGCCAACAATCACGATGACTCCCTCTGTTGTGCTGCGCTTGC	800
D	GTCGGGCCGGGTGCTGTTGGCAACCCAGAGCAGCTTGCCAACAATCACGATGACTCCCTCTGTTGTGCTGCGCTTGC	800
A	CAAGGGTTCCTCCAGTATGCTCTGCATTGGAACCATGGTCCGCTTCCGTACGTTTGTCCAGGTGCTTTGCCAGCACTGG	880
B	CAAGGGTTCCTCCGTTATGCTCTGCATTGGAACCATGGTCCAGCTTCAATATTGTCCAGGTGCTTTGCCAGCACTGG	880
C	CAAGGGTTCCTCCGTTATGCTCTGCATTGGAACCATGGTCCGCTTTCGATATTGTCCAGGTGCTTTGCCAGCACTGG	880
D	CAAGGGTTCCTCCGTTATGCTCTGCATTGGAACCATGGTCCGCTTTCGATATTGTCCAGGTGCTTTGCCAGCACTGG	880
A	TCAATGTACCCTGACTGACCAATCGTCAATGGTGTGCATCGCACGGTCTCAACTGATTTTGTATGCCCAAGAAGTGAGAGAC	960
B	TCAATGTACCCTGACTGACCAATCGTCAATGGTGTGCATCGCACGGTCTCGACTGATTTTGTATGCCCAAGAAGTGAGAGAC	960
C	TCAATGTACCCTGACTGACCAATCGTCAATGGTGTGCATCGCACGGTCTCGACTGATTTTGTATGCCCAAGAAGTGAGAGAC	960
D	TCAATGTACCCTGACTGACCAATCGTCAATGGTGTGCATCGCACAGTCTCGACTGATTTTGTATGCCCAAGAAGTGAGAGAC	960
A	CTCACCGTATCTTCCATCTTCCATCTCTGACCAATCTGCTTCTTAATCTTTAGGACCATTTCCAGCATGTTGCTATGA	1040
B	CTCACGCTATCTTCCATCTTCCATCTCTGACCAATCTGCTTCTTAATCTTTAGGACCATTTCCAGCATGTTGCTATGA	1040
C	CTCACCGTATCTTCCATCTTCCATCTCTGACCAATCTGCTTCTTAATCTTTAGGACCATTTCCAGCATGTTGCTATGA	1040
D	CTCACCGTATCTTCCATCTTCCATCTCTGACCAATCTGCTTCTTAATCTTTAGGACCATTTCCAGCATGTTGCTATGA	1040
A	ATCGACATAGATGACCACAATGGCCATATCTTACCCTGTCCCTTGGTGTCTAATGTATCAGATGACAGGGAGCACACTCT	1120
B	ATCGACGTAGATGACCACAATGGCCATATCTTACCCTGTCCCTTGGTGTCTAATGTATCAGATGACAGGGAGCACACTCT	1120
C	ATCGACGTAGATGACCACAATGGCCATATCTTACCCTGTCCCTTGGTGTCTAATGTATCAGATGACAGGGAGCACACTCT	1120
D	ATCGACGTAGATGACCACAATGGCCATATCTTACCCTGTCCCTTGGTGTCTAATGTATCAGATGACAGGGAGCACACTCT	1120
	*	
A	ACCTGGAAGAATCCCATGCGATCGCAAAGACCTGTCCAACTCTTGATTCCATTTCCGCCAGACTGCTTTAGGCCATATAG	1200
B	ACCTGGAAGAATCCCATGCGATCGCAAAGACCTGTCCAACTCTTGATTCCATTTCCGCCAGACTGCTTTAGGCCATATAG	1200
C	ACCTGGAAGAATCCCATGCGATCGCAAAGACCTGTCCAACTCTTGATTCCATTTCCGCCAGACTGCTTTAGGCCATATAG	1200
D	ACCTGGAAGAATCCCATGCGATCGCAAAGACCTGTCCAACTCTTGATTCCATTTCCGCCAGACTGCTTTAGGCCATATAG	1200

Supplemental Data. Laurie et al. Plant Cell (2012). 10.1105/tpc.112.097261

A ACCCTTGA**CT**ACCTTGTACACCTTGC**CA**GGTGTACTCCTGATCCTTCTGG**CG**GCTTCATGTAGATTGCTTCCTTTAACG 1280
 B ACCCTTGA**CT**ACCTTGTACACCTTGC**CG**GGTGTACTCCTGATCCTTCTGG**TG**GCTTCATGTAGATTGCTTCCTTTAACG 1280
 C ACCCTTGA**T**TACCTTGTACACCTTGC**TG**GGTGTACTCCTGATCCTTCTGG**TG**GCTTCATGTAGATTGCTTCCTTTAACG 1280
 D ACCCTTGA**T**TACCTTGTACACCTTGC**TG**GGTGTACTCCTGATCCTTCTGG**CA**GCTTCATGTAGATTGCTTCCTTTAACG 1280

A TGGAGTTCAAGTAAGCCATAGTGATGTCCAGAGCATGTACCTCCCAGTTGTTCTGCAC**CG**CTAGTGCTAAGATGGCTCTG 1360
 B TGGAGTTCAAGTAAGCCATAGTGATGTCCAGAGCATGTACCTCCCAGTTGTTCTGCAC**TG**CTAGTGCTAAGATGGCTCTG 1360
 C TGGAGTTCAAGTAAGCCATAGTGATGTCCAGAGCATGTACCTCCCAGTTGTTCTGCAC**CG**CTAGTGCTAAGATGGCTCTG 1360
 D TGGAGTTCAAGTAAGCCATAGTGATGTCCAGAGCATGTACCTCCCAGTTGTTCTGCAC**CG**CTAGTGCTAAGATGGCTCTG 1360

A **ATCA**CTCCGAGGGGTGCTACTGGAGAGAAGGTTTCTTGGTAGTCGATCCCCTCTCTGTGTGAAGCCCTT**GCG**ACCAG 1440
 B **ATCG**CTCCGAGGGGTGCTACTGGAGAGAAGGTTTCTTGGTAGTCGATCCCCTCTCTGTGTGAAGCCCTT**GCG**ACCAG 1440
 C **ATCG**CTCCGAGGGGTGCTACTGGAGAGAAGGTTTCTTGGTAGTCGATCCCCTCTCTGTGTGAAGCCCTT**GCA**ACCAG 1440
 D **ATCG**CTCCGAGGGGTGCTACTGGAGAGAAGGTTTCTTGGTAGTCGATCCCCTCTCTGTGTGAAGCCCTT**GCA**ACCAG 1440

A **TGC**CGCCTTGTGCTTAACAGGTACGCCATCAG**TG**TCAAGCTTCAGCCGAAGCACAACCTTAGAGTCCACAAGTGGTACTC 1520
 B **TGC**CGCCTTGTGCTTAACAGGTACGCCATCAG**CA**TCAAGCTTCAGCCGAAGCACAACCTTAGAGTCCACAAGTGGTACTC 1520
 C **TTG**CACCTTGTGCTTAACAGGTAC**AC**CATCAG**CG**TCAAGCTTCAGCCGAAGCACAACCTTAGAGTCCACAAGTGGTACTC 1520
 D **TGC**CGCCTTGTGCTTAACAGGTAC**AC**CATCAG**CA**TCAAGCTTCAGCCGAAGCACAACCTTAGAGTCCACAAGTGGTACTC 1520

A CTGGTGGTTGGTGCACCACCTCCCAAGTCCCATTGC**CTCA**AGTCCTTCTAGTCTCCT**TTCG**TATTGCCTCCTTCCAGAGC 1600
 B CTGGTGGTTGGTGCACCACCTCCCAAGTCCCATTGC**CTCA**AGTCCTTCTAGTCTCCT**TTCG**TATTGCCTCCTTCCAGAGC 1600
 C CTGGCGGTTGGTGCACCACCTCCCAAGTCCCATTGC**CTTGA**GTCTTCTAGTCTCCT**TTC**AATTGCCTCCTTCCAGAGC 1600
 D CTGGCGGTTGGTGCACCACCTCCCAAGTCCCATTGC**CTCA**AGTCCTTCTAGTCTCCT**TTCG**TATTGCCTCCTTCCAGAGC 1600

A TGGGC**AT**CCTCACC**AT**TCA**TT**CATTGCTTCCCAAG**CG**TGGGTCCAGGTT**CAG**TATTGCTGTGTTGGCGG**CG**CCTACTGTGCT 1680
 B TGGGC**AT**CCTCACC**AT**TCA**TT**CATTGCTTCCCAAG**CA**TTGGGTCCAGGTT**CAG**TATTGCTGTGTTGGCGG**CG**CCTACTGTGCT 1680
 C TGGGC**AT**CCTCACC**GT**TCA**TT**CATTGCTTCCCAAG**CG**TGGGTCCAGGTT**CAG**TATTGCTGTGTTGGCGG**CA**CCTACTGTGCT 1680
 D TGGGC**GT**CCTCACC**AT**CC**AT**TGCTTCCCAAG**CG**TGGGTCCAGGTT**CAG**TATTGCTGTGTTGGCGG**CA**CCTACTGTGCT 1680

A GTCTAC**GG**CTGGTAGGAGATCCTCCACTGCGGCCTCTGATTTGGTCTCCTCCTCCAC**TG**TGGCTGG**TG**TGACACCCTCCT 1760
 B GTCTAC**GG**CTGGTAGGAGATCCTCCACTGCGGCCTCTGATTTGGTCTCCTCCTCCAC**TG**TGGCTGG**TG**TGACACCCTCCT 1760
 C GTCTAC**AG**CTGGTAGGAGATCCTCCACTGCGGCCTCTGATTTGGTCTCCTCCTCCAC**TA**TGGCTGG**CA**TGACACCCTCCT 1760
 D GTCTT**CG**CTGGTAGGAGATCCTCCACTGCGGCCTCTGATTTGGTCTCCTCCTCCAC**TA**TGGCTGG**CG**TGACACCCTCCT 1760

A CCTCGACCT**CG**CA**GT**CACCAC**GG**GCCTGACTGCCTCTTGTGGCGATCACTCCATCC**CTTG**TCTCATG**GA**CGTTGCT 1840
 B CCTCGACCT**TG**CG**GT**CACCAC**GG**GCCTGACTGCCTCTTGTGGCGATCACTCCATCC**CTTG**TCTCATG**GA**CA**TT**GCT 1840
 C CCTCGACCT**CG**T**GG**TCA**CA**CA**GG**GCCTGACTGCCTCTTGTGGCGATCACTCCATCC**TTTA**TCTCATG**GA**AT**GT**TGCT 1840
 D CCTCGACCT**CG**CG**GT**CACCAC**GG**GCCTGACTGCCTCTTGTGGCGATCACTCCATCC**TTTA**TCTCATG**AA**AT**GT**TGCT 1840

A GAGTTGCTCCATT**GA**ATTGACGC**AG**GGTGGTCC**GG**GTGCAAAACTTCCATGCTTT**GTG**TCT**TTCG**TCATACCCAATCAT 1920
 B GAGTTGCTCCATT**GA**ATTGACGC**AG**GGTGGTCC**GG**GTGCAAAACTTCCATGCTTT**GTG**TCT**TTCG**TCATACCCAATCAT 1920
 C GAGTTGCTCCATT**GA**ATTGACGC**AG**GGTGGTCC**GG**GTGCAAAACTTCCATGCTTT**CTG**TCT**CA**TCATACCCAATCAT 1920
 D GAGTTGCTCCATT**GA**ATTGACGC**CG**GGTGGTCC**AG**GTGCAAAACTTCCATGCTTT**GTG**TCT**ATCG**TCATACCCAATCAT 1920

A GATGGCTGGCTTTGCTCTAGCCCC**ATA**CTTGC**CT**GTGTTGCTTCTGTTGA**ATA**TGAACCCATGCCAAGCAT**CGA**AGA 2000
 B GATGGCTGGCTTTGCTCTAGCCCC**GT**ACTTGC**CT**GTGTTGCTTCTGTTGA**ATA**TGAACCCATGCCAAGCAT**TGA**AGA 2000
 C GATGGCTGGCTTTGCTCTAGCCCC**GT**ACTTGC**CT**GTGTTGCTTCTGTTGA**CA**TGAACCCATGCCAAGCAT**CGA**AGA 2000
 D GATGGCTGGCTTTGCTCTAGCCCC**ATA**CTTGC**T**GTGTTGCTTCTGTTGA**CA**TGAACCCATGCCAAGCAT**TGA**AGA 2000

A **CTC**TAGCTGCTGGCCAGCTTGT**CG**CGGTGGTTCATAAAAAGGCC**T**CGTGGGG**A**ATGGTTTTGGTGGCTGAC**AG**GGTA 2080
 B **CTC**TAGCTGCTGGCCAGCTTGT**CA**CGGTGGTTCATAAAAAGGCC**T**CGTGGGG**A**ATGGTTTTGGTGGCTGAC**GG**GGTA 2080
 C **CTC**GCAGCTGCTGGCCAGCTTGT**GC**AGTGGTTCATAAAAAGGCC**T**CA**T**GGGG**A**ATGGTTTTGGTGGCTGAC**GG**GGTA 2080
 D **CTC**GCAGCTGCTGGCCAGCTTGT**CG**CGGTGGTTCATAAAAAGGCC**T**CA**T**GGGG**A**ATGGTTTTGGTGGCTGAC**GG**GGTA 2080

A AGGTTATCA**T**GTGTGCTGCTGTGATTGCATA**TG**GCCACA**ACT**CTCTGGGGCAAGCTCGACCAATCAGCA**TCC**AG**TG** 2160
 B AGGTTATCA**CG**TGTGCTGCTGTGATTGCATA**CG**GCCACA**ACT**CTCTGGGGCAAGCTCGACCAATCAGCA**TCC**AG**CA** 2160
 C AGGTTATCA**CG**TGTGCTGCTGTGATTGCATA**TG**GCCACA**ACT**CTCTGGGGCAAGCTCGACCAATCAGCA**TCC**AG**TG** 2160
 D AGGTTATCA**CG**TGTGCTGCTGTGATTGCATA**CG**GCCACA**ACT**CTCTGGGGCAAGCTCGACCAATCAGCA**TCA**AG**CG** 2160

A CATCTTTTCTTGGAC**CA**ACTGATTGCTCTCT**CG**CC**GT**TCCATTTTGGAC**GT**GATCCCC**GG**GAC**CG**CTCTTTTGCCACT 2240
 B CATCTTTTCTTGGAC**CA**ACTGATTGCTCTCT**CG**CC**GT**TCCATTTTGGAC**CT**GATCCCC**GG**GAC**CG**CTCTTTTGCCACT 2240
 C CATCTTTTCTTGGAC**CA**ACTGATTGCTCTCT**CG**CC**GT**TCCATTTTGGAC**GT**GATCCCC**GG**GAC**CG**CTCTTTTGCCACT 2240
 D CATCTTTTCTTGGAC**CA**ACTGATTGCTCTCT**CG**CC**AT**TCCATTTTGGAC**GT**GATCCCC**AG**GAT**GT**CTTTTGCCACT 2240

A TGAAACCTCTT**GT**GTTTGGCAGTCTTCGGCTGCTATGCTGCACCATTCTCCTCCATT**GT**CGTGC**GG**AGTGT**TT**TGAGT 2320
 B TGAAACCTCTT**GT**GTTTGGCAGTCTTCGGCTGCTATGCTGCACCATTCTCCTCCATT**GT**CGTGC**GG**AGTGT**TT**TGAGT 2320
 C TGAAACCTCTT**GA**GTTTGGCAGTCTTCGGCTGCTATGCTGCACCATTCTCCTCCATT**GT**TGCTGC**GG**AGTGT**TT**TGAGT 2320
 D TGAAACCTCTT**GA**GTTTGGCAGTCTTCGGCTGCTATGCTGCACCATTCTCCTCCATT**GT**TGCTGC**GG**AGTGT**TT**TGAGT 2320

A TTCTGT**CT**GTTGCC**TG**TTCCATCCTGGCTATCCACCT**T**CTCAG**CA**CCGTGAGT**GC**GG**CG**CTCTTTGTGCAGAGTGGTTC 2400
 B TTCTGT**CT**GTTGCC**CG**TTCCATCCTGGCTATCCACCT**T**CTCAG**CA**CCGTGAGT**GC**GG**CG**CTCTTTGTGCAGAGTGGTTC 2400
 C TTCTGT**CT**CGTTGCC**CA**TTCCATCCTGGCTATCCACCT**T**CTCAG**CA**CCGTGAGT**GC**GG**CA**CTCTTTGTGCAGAGTGGTTC 2400

D TTCCTGCCTGTTGCCCGTTCATCCTGGCTATCCACCTCCTCAGCGCCGTGAGTGCACTCTTTGTGCAGAGTGGTTC 2400

A CATGTAGATCAGAGAGGAGAAGTCGCTCCACAGCAACTAGTGCCTAGTGGTAGTTGGCATGTCCTTTGAAATCTGTCATCA 2480
 B CACGTAGATCAGAGAGGAGAAGTCATCCACAGCAACTAGTGTGTAGTGGTAGTTGGCATGTCCTTTGAAATCTGTCATCA 2480
 C CACGTAGATCAGAGAGGAGAAGTCGCTCCACAGCAACTAGTGCCTAGTGGTAGTTAGCATGTCCTTTGAAATCTGTCATCA 2480
 D CACATAGATCAGGAGGAGAAGTTGTCCACAGCAACTAGTGCATAGTGGTAGTTGGCATGTCCTTTGAAATCTGTCATCA 2480

A GGTCTACGTGTACCAGCTCTAATGGTGCCTCCATTCTTTCGACTCTGATTGGCCATCCGTGCTCGAGTCTGTTTTCT 2560
 B GGTCTACGTGTACCAGCTCTAATGGTGCCTCCATTCTTTCGACTCTGATTGGCCATCTGTGCTTGAGTCTGTTTTCT 2560
 C GGTCTACGTGTACCAGCTCTAATGGTGCCTCCATTCTTTCGACTCTGATTGGCCATCCGTGCTCGAGTCTGTTTTCT 2560
 D GGTCTATGTGTACCAGCTCTAATGGTGCCTCCATTCTTTCGACTCTGATTGGCTCATCCGTGCTCGAGTCTGTTTTCT 2560

A TGACTGCACGCTGTACAGTGCTTCGACTCATGTTCCATTTCTGTGTCGTACCTAGGTAATGGCCCCGATTGTCTCGT 2640
 B TGACTGCACGCGTACAGTGCTTCGACTCATGTTCCATTTCTCGTCCGTACCTAGGTAATGGCCCCGATTGTCTCGT 2640
 C TGACTGCACGCGTACAGTGCTTCGACTCATGTTCCATTTCTGTGTCGTACCTAGGTAATGGCCCCGATTGTCTCGT 2640
 D TGACTGCACGCGTACAGTGCTTCGACTCATGTTCCATTTCTCGTCCGTACCTAGGTAATGGCCCCGATTGTCTCGT 2640

A TTTGTCTCGTCCCTGGGTGCCGAACCTCTCATGCCATAGGTAGCTGCTCGATGCTTCGTGTCTTATTGCCCTCCAGGG 2720
 B TTTGTCTCGTCCCTGGGTGCCGAACCTCTCATGCCATAGGTAGCTGCTCGATGCTTCGTGTCTTATTGCCCTCCAGGG 2720
 C TTTGTCTCGTCCCTGGGTGCCGAACCTCTCATGCCATAGGTAGCTGCTCGATGCTTCGTGTCTTATTGCCCTCCAGGG 2720
 D TTTGTCTCGTCCCTGGGTGCCGAACCTCTCATGCCATAGGTAGCTGCTTTGATGCTTTGTGTCTTATTGCCCTCCAGGG 2720

*

A CATTATCTAGTTTTCTGTGTTCTGGTGTCCACTGGGACATCATCTCGTGTTCCTCCAGTTCCAAAGCCAGTGCTTGC 2800
 B CATTATCTAGTTTTCTGTGTTCTGGTGTCCACTGGGACATCATCTCGTGTTCCTCCAGTTCCAAAGCCAGTGCTTGC 2800
 C CATTATCTAGTTTTCTGTGTTCTGGTGTCCACTGGGACATCATCTCGTGTTCCTCCAGTTCCAAAGCCAGTGCTTGT 2800
 D CATTATCTAGTTTTCTGTGTTCTGGTGTCCCTCGGGACGTGTCTAAGTGTCTTCCAACTCCAGGGCTAGTGCCCTT 2800

* * * * *

A CCTCACACTTTGAAGTGACCCTGCTTCTGTCCCTTTTGAATTGTACTTGGTACCCTCGTTCTGCTTTATGGTAGTTCC 2880
 B CCTCGCACTTTGAAGTGACCCTGCTTCTGTCCCTTTTGAATTGTACTTGGTACCCTCGTTCTGCTTTATGGTAGTTCC 2880
 C CCTCGCACTTTGAAGTGACCCTGCTTCTGTCCCTTTTGAATTGTACTTGGTACCCTCGTTCTGCTTTATGGTAGTTCC 2880
 D CCTGTACTTCGAACCGCCCTTTCTTCTGTTCCTCTGTATATGTAATTTGTGACCCTCAATTTGCTTATGATGGTTCC 2880

*

A AAATTCGTCAAAAGATTACTCGTGCACCATTCTCGATCAAGCCTTGTACAGCAATAAATTAGCATTAGTTTCGGTACAT 2960
 B AAATTCGTCAAAAGATTACTCGTGCACCATTCTCGATCAAGCCTTGTACAGCAATAAATTAGCATTAGTTTCGGTACAT 2960
 C AAATTCGTCAAAAGATTACTCGTGCACCATTCTCGATCAAGCCTTGTACAGCAATAAATTAGCATTAGTTTCGGTACAT 2960
 D AAATTCGTCAAAAGATTACTCGTGCACCATTCTCGATCAAGCCTTGTACTGATAATAAATTAGATTAGTTTCGGTACAT 2960

*

A AAAGCACATCCAATAGTTGGATGGTGGCCTCACCGACCAGGAGGAGGCATCTCCTATAGCCTTACCTGAAGCTTTTCG 3040
 B AAAGCACATCCAATAGTTGGATGGTGGCCTCACCGACCAGGAGGAGGCATCTCCTATAGCCTTACCTGAAGCTTTTCG 3040
 C AAAGCACATCCAATAGTTGGATGGTGGCCTCACCGACCAGGAGGAGGCATCTCCTATAGCCTTACCTGAAGCTTTTCG 3040
 D AGAGCACATCCAATAGTTGAATGGTTACATCGCCAAACCTGAAGGAGGAGGCATCTCCTATAGCCTTACCTGAAGCTTTTCG 3040

* * * * *

A TCCCCAGCTGACTGATTGGCCGACCTTGTTCGTCGAGGTGAGCAGCATTCTCTCATCATTTACCAATATGATGGGTGTC 3120
 B TCCCCAGCTGACTGATTGGCCGACCTTGTTCGTCGAGGTGAGCAGCATTCTCTCATCATTTACCAATATGATGGGTGTC 3120
 C TCCCCAGCTGACTGATTGGCCGACCTTGTTCGTCGAGGTGAGCAGCATTCTCTCATCATTTACCAATATGATGGGTGTC 3120
 D TTTCCAGCTATACAGATCTGACCGTCTTGTGSCATCGAGGTGAGCAGCATTCTCTCATCATTTACCAATGATGGGTGTC 3120

*

A ACCTGAATCGATGATCCAGGTGTCGCATGCTGATTCGCTCGCCCTGTCGACTGCTAGAAAGGTGCACCCGAGTTCCTAGT 3200
 B ACCTGAATCGATGATCCAGGTGTCGCATGCTGATTCGCTCGCCCTGTCGACTGCTAGAAAGGTGCACCCGAGTTCCTAGT 3200
 C ACCTGAATCGATGATCCAGGTGTCGCATGCTGATTCGCTCGCCCTGTCGACTGCTAGAAAGGTGCACCCGAGTTCCTAGT 3200
 D ACCCGAATCGATGATCCAGGTGTCGAATGTTGCTTCAATCCCGCGATCGCTAGGAGGTGCACCCGAGTTCCTATC 3200

* * * * *

A GGTTCACCTCTTGTGTCGTATGAGCAACAGGTTCGCTTGTGCCTGGTGTG-----TTCGTGCAATTTTGA 3265
 B GGTTCACCTCTTGTGTCGTATGAGCAACAGGTTCGCTTGTGCCTGGTGTG-----TTCGTGCAATTTTGA 3265
 C GGTTCACCTCTTGTGTCGTATGAGCAACAGGTTCGCTTGTGCCTGGTGTG-----TTCGTGCAATTTTGA 3265
 D GACTCGCTTCTTGTGTCGTATGAGCAACAGGTTCGCTTGTGCCTGGTGTG-----TTCGTGCAATTTTGA 3280

A GCAATGTGATTCGGTCTCCACAAGCGTAGCACTTTGGAGGGGCAAGGGATTGCGAGGGTCGCGCCTGC CCTGGGTCC 3345
 B GCAATGTGATTCGGTCTCCACAAGCGTAGCACTTTGGAGGGGCAAGGGATTGCGAGGGTCGCGCCTGC CCTGGGTCC 3345
 C GCAATGTGATTCGGTCTCCACAAGCGTAGCACTTTGGAGGGGCAAGGGATTGCGAGGGTCGCGCCTGC CCTGGGTCC 3345
 D GCAATGTGATTCGGTCTCCACAAGCGTAGCACTTTGGAGGGGCAAGGGATTGCGAGGGTCGCGCCTGC CTTGGGTCC 3360

A TTGCCCAACCTGGTTGGCACTCCCTGTTCCGCGCTTGTGGCAACCCCTGCTGCTCCTCTAAATGCGGCCAGTGATCTCA 3425
 B TTGCCCAACCTGGTTGGCACTCCCTGTTCCATGCTTGTGGCAACCCCTGCTGCTCCTCTAAATGCGGCCAGTGATCTCA 3425
 C TTGCTCCGCTGGTTGGCACTCCCTGTTCCATGCTTGTGGCAACCCCTGCTGCTCCTCTAAATGCGGCCAGTGATCTCA 3425
 D TTGCTCCACCTGGT-----CGGTGCTTGTGGCAACCCCTGCTGCTCCTCTAAATGCGGCCAGTGATCTCA 3425

A CATCTGCTGTTTCTTGGCAAGTGCCTGGTAGGCTTCGTCATACTTACAGTCTGGTCTGGCCGTCTTCAGTGCATCAACG 3505
 B CATCTGCTGTTTCTTGGCAAGTGCCTGGTAGGCTTCGTCATACTTACAGTCTGGTCTGGCCGTCTTCAGTGCATCAACG 3505
 C CATCTGCTGTTTCTTGGCAAGTGCCTGGTAGGCTTCGTCATACTTACAGTCTGGTCTGGCCGTCTTCAGTGCATCAACG 3505
 D CATCTGCTGTTTCTTGGCAAGTGCCTGGTAGGCTTCGTCATACTTACAGTCTGGTCTGGCCGTCTTCAGTGCATCAACG 3505

*

A GTGTTGGCATAGAACCAATCTTGAAGCGTGCAGCGATAGAGAGTTGATTTCTTGAAGTCTCGTGCAGAAACGCTTCCGAG 3585
 B GTGTTGGCATAGAACCAATCTTGAAGCGTGCAGCGATAGAGAGTTGATTTCTTGAAGTCTCGTGCAGAAACGCTTCCGAG 3585

C GTGTTGGCATAGAACCAATCTT**AGCT**GTGCAG**CAA**TAGAGAGTTGATTTCTTGAGGTCCTCGTCGAAATGCTTTCCGAG 3585
D GCAATTGGCATAGAACCAATCTT**GGCC**GTGCAG**CGA**TAGAGAGTTGATTTCTTGAGGTCCTCGTCGAAACGCTTTCCGAG 3585

A GCATGCGGCATCGTTCCAGATCGAA**TCA**AGTTCCTTGCTAGCCTGA**CGACGCTCA**ATTGTGCAAG**TG**CACTGTGTGGA 3665
B GCGTGC**TG**CATCGTTCCAGATCGAA**TCA**AGTTCCTTGCTAGCCTGA**CGACGCTCA**ATTGTGCAAG**CG**CACTGTGTGGA 3665
C GCGTGC**CA**CATCGTTCCAGATCGAA**TTC**AGTTCCTTGCTAGCCTGA**CAACA**TCT**TCC**ATTGTGCAAG**CA**CACTGTGTGGA 3665
D GCGTGC**CA**CATCGTTCCAGATCGAA**TCC**AGTTCCTTGCTAGCCTGA**CGACGCTCA**ATTGTGCAAG**TG**CACTGTGTGGA 3665

A TACGATCCTGCAGTCCTGCTC**CG**CTTTACAGCA**TCCGTT****TAGT**GTTAGTGCCTTCTTGAGTTTGGCATAGAGTGTGC**TGCCA** 3745
B TACGATCCTGCAGTCCTGCTC**CG**CTTTACAGCA**TCCGTT****TAGT**GTTAGTGCCTTCTTGAGTTTGGCATAGAGTGTGC**TGCCA** 3745
C TACGATCCTGCAGTCCTGCTC**CA**CTTTACAGCA**TTCGTT****TAGT**GTTAGTGCCTTCTTGAGTTTGGCATAGAGTGTGC**TGCCA** 3745
D TACGATCCTGCAGTCCTGCTC**CG**CTTTACAGCA**TCCGTT****CAACG**TTAGTGCCTTCTTGAGTTTGGCATAGAGTGTGC**TGCCA** 3745

A **AGTTGAACTTCTTCATCCACCCCTCTGACGGTA**TAGGTGT**CGA**TGTGGCT**TATCCGGGCTGTATTCGC**CAGCAGGCGTGGAT 3825
B **AGTTGAACTTCTTCATCCACCCCTCTGACGGTA**TAGGTGT**CGA**TGTGGCT**TATCCGGGCTGTATTCGC**CAGCAGGCGTGGAT 3825
C **AGTTGAACTTCTTCATCCACCCCTCTGACAGTGTAGGTGTCAATGCGGCTATCCAGGCTGTATTCGC**CAGCAGGCGTGGAT 3825
D **AGCTGGACTTCTTCATCCACCTCCCTGACAGTGTAGGTGTCAATACGGCTGTCTGACTGTTCGCA**CAGCAGGCGTGGAT 3825

A GAGGCCACGAGTGCCT**TGCTAGGCTTCA****TCC**TATTCTCGCTCCAGG**TACAACGGTACC**CATACAGGAT**TTCCCTTCG** 3905
B GAGGCCACGAGTGCCT**TGCTAGGCTTCA****TCC**TATTCTCGCTCCAGG**TACAACGGTACC**CATACAGGAT**TTCCCTTCG** 3905
C GAGGCCACGAGTGCCT**TGCTAGGCTTCA****TCA**TATTCTCGCTCCAGG**TACAACGGTACC**CATACAGGAT**TTCCCTTCA** 3905
D GAGGCCACGAGG**GGCTTTATCCAA**GTCTTC**TCCG**TATTCTCGT**TTCCAGGCACTACCGTGC**CATACAGT**ATCTCCTTCG** 3905

A **CGTTGTGCACTCTCTGGAGGCAGT****CGATA**AAGGTGGGTTCCCA**AGGTGTGCCAATTGC****TATCGCTGAGCTTCTTGATGTGA** 3985
B **CGTTGTGCACTCTCTGGAGGCAGT****CGATA**AAGGTGGGTTCCCA**AGGTGTGCCAATTGC****TATCGCTGAGCTTCTTGATGTGA** 3985
C **CGTTGTGCACTCTCTGGAGGCAGT****TGATA**AAGGTGGGTTCCCA**AGGTGTGCCAATTGC****TATCGCTGAGCTTCTTGATGTGA** 3985
D **CATTATGTACTCTTTGGAGGCAGT****CAATGA**AAGGTAGGTTCCCA**AGGTGTGCCAGTTGC****TGTCGCTGAGCTTCTTGATGTGC** 3985

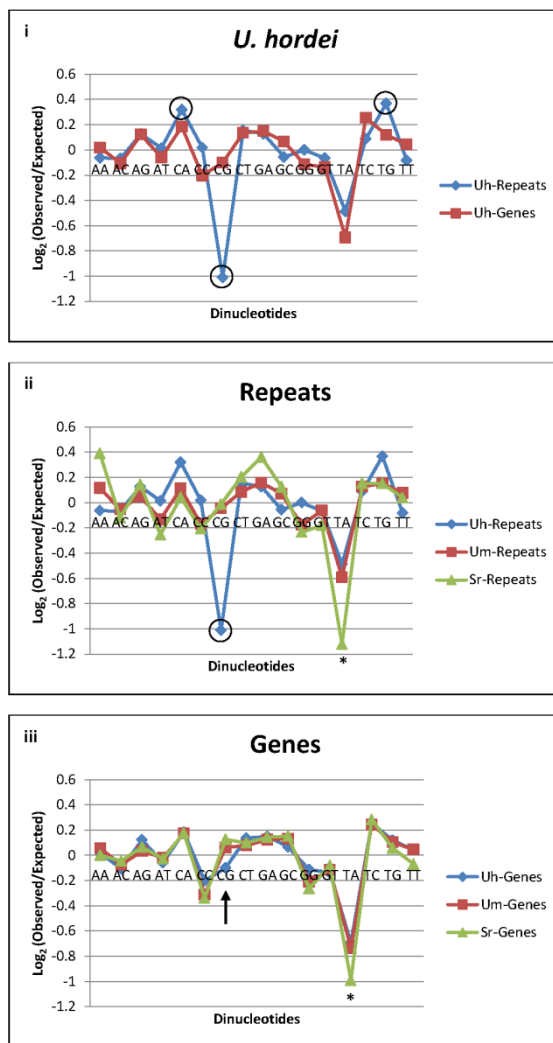
A GCAATGGAG**CTCGA**TACATCCTTGGGGATCTTT**TCGGTCTCCCGCGTGGAGCT**TGGTTGCTAATGT**TGACCAGACCCAT** 4065
B GCAATGGAG**CTCGA**TACGTCCTTGGGGATCTTT**TCGGTCTCCCGCATGGAGCT**TGGTTGCTAATGT**TGACCAGACCCAT** 4065
C GCAATGGAG**CTCGA**TAA**T**TCCTTGGGGATCTTT**TCGGTCTCCCGACA**TGGAG**CTTGGTTGCTAATGT****TGACCAGACCCAT** 4065
D GCAATGG**CACTTGA**ACCCTCCTTGGGGATCTT**CTCAGTTCCCTGCGTGGAGCT**TGGTTGCTAAT**GTCTGATGAGACCCAT** 4065

A **GGCCATACTATTGCTTCCCTTGC****CGA**TAGTGTGGG**TTCGCCAGCTGGAGGATCCTGACTACCTGTGTGAGCCATCCTT** 4145
B **GGCCGTACTATTGCTTCCCTTGC****TGA**TAGTGTGGG**TTCGCCAGCTGGAGGATCCTGACTACCTGTGTGAGCCATCCTT** 4145
C **GGCCGTACTATTGCTTCCCTTGC****CA**TAGTGTGGG**TTCGCTA**CTGGAGGAT**TCTGACTACCTGCGTGAGCCATCCTT** 4145
D **AGCTCGTACGATTGCTTCCCTG****CCGT**TAGTGTGGG**TTCGCCAGCTGGAGGATCCTGACTACCTGTGTGAGCCATCCTT** 4145

A CCTC**CTG**TCC**ATTTC**CTG---**TG**TTTGATCATCAT**CC**CCCCTTCC**TG**CTGTCC**TG**CTCT**TTCG**ATGG**CGG**CATT**GCG** 4322
B CCTC**CTG**TCC**ATTTC**CTG---**TG**TTTGATCATCAT**CC**CCCCTTCC**CGT**CTGTCC**TG**CTCT**TG**ATGG**CAG**CATT**GCG** 4322
C CCTC**TCG**TCC**ATTTC**CTGCAG**TCG**CTTGATCATCAT**CTC**---**TTCC**ACCTGTCC**AG**CTCT**TTCG**ATGG**TGG**CATT**GCA** 4322
D CCTC**CTG**TCC**GTG**CTGTGG**TCATTT**GATCATCAT**CC**CCCCTTCC**CGT**CTGTCC**AG**CTCT**TTCG**ATGG**CGG**CATT**GCG** 4325

A **T****TGAGTTT**CAGACTCTTAATC 4243
B **T****TGAGTTT**CAGACTCTTAATC 4243
C **C****CGAGCTT**CAGACTCTTAATC 4243
D **T****TGAGTTT**CAGACTCTTAATC 4246

Supplemental Figure 6. Indication of RIP in *U. hordei*. DNA sequence alignment of four representative LTR-repeat sequences from cluster 2: (A) G_Tuh3_LTR.7822, (B) G_Tuh3_LTR.7853, (C) G_Tuh3_LTR.7876, (D) G_Tuh3_LTR.7874. The Clustal program, version 2.1 (Larkin et al., 2007) was used for this comparison. Indicated are G to A and C to T transitions (in red); many occurred at TCG triplets (or CGA on the opposite strand; highlighted in yellow) as found in the related smut fungus, *Microbotryum violaceum* (Hood et al., 2005), though they were not strictly limited to these triplets, as in *M. violaceum*. Classical repeat-induced point (RIP)-type CA to TA and TG to TA mutations (Clutterbuck, 2011) appear in grey boxes. The G-to-A mutation in the triplet TCA in bold type (or TGA on the opposite strand) introduces a stop codon in the putative transposase encoded on sequence A that may render this element inactive. Presence of mutations in both strands indicates multiple rounds of RIP activity at this locus. Mutations appear somewhat random with no particular target site preference, except when two mutations appear side-by-side, in which case a preference is seen at CpA (TpG) dinucleotides. Asterisks indicate alternative transitions (C to A, C to G and T to A) below.



Supplemental Figure 7. Analysis of dinucleotide frequency in three smut fungi. (i) In *U. hordei*, RIP targets repeats causing deamination of cytosine residues at CpG dinucleotides. This is evident by the depletion of CpG dinucleotides and the concomitant increase is both CpA and TpG (circles). **(ii)** RIP is evident at CpG only in *U. hordei* repeats (circle). All three fungi show depletion of TpA dinucleotides (asterisk). **(iii)** Dinucleotide frequency is nearly identical for the three smuts when comparing gene sequences. All three fungi show reduction in TpA dinucleotides, as was seen in the repeats (asterisk). A slight decrease in CpG dinucleotides can be seen in *U. hordei* only (arrow). After Zemach et al., 2010.

Supplemental Data. Laurie et al. Plant Cell (2012). 10.1105/tpc.112.097261

```

GROUP 1
SCORE=99, Nseq=5, Len=280

R17  AACCCGCAGGAGGAGGAGGAGGAGGTCGTAGCAGCGCCTCCGGCCGAGTCGCTGATGGCGACGAGCTTCAGAGGATGCAGAT
R135  -----GCGGAGTCCCTGATGCGGACGACGCTTCAGAGGATGCGAT
R149  -----GCGGAGTCCCTGATGCGGACGACGCTTCAGAGGATGCGAT
R198  -ACCGCCAGGAGGAGGAGGAGGAGGTCGTAGCAGCGCCTCCGGCCGAGTCGCTGATGCGGACGACGCTTCAGAGGATGCGAC
R248  -----GCGGAGTCCCTGATGCGGACGACGCTTCAGAGGATGCGAT
                *****

R17  GAAGCTCTTTTGCGTCAACAAAGCCCTCTCCACCGCCACGACAGTTCTGGACGAGCTCGACGAGCGTTC
R135  GAAGCTCTTTTGCGTCAACAAAGCCCTCTCCACCGCCACGACAGTTCTGGACGAGCTCGACGAGCGTTC
R149  GAAGCTCTTTTGCGTCAACAAAGCCCTCTCCACCGCCACGACAGTTCTGGACGAGCTCGACGAGCGTTC
R198  GAAGCTCTTTTGCGTCAACAAAGCCCTCTCCACCGCCACGACAGTTCTGGACGAGCTCGACGAGCGTTC
R248  GAAGCTCTTTTGCGTCAACAAAGCCCTCTCCACCGCCACGACAGTTCTGGACGAGCTCGACGAGCGTTC
                *****

R17  ACCACCATCGACGATGATGACCGGGGCTTCGGATTCCTTGTATACCTCCCTCAGGCCGCGCTTCTCGTACCAAGCATTGA
R135  ACCACCATCGACGATGATGACCGGGGCTTCGGATTCCTTGTATACCTCCCTCAGGCCGCGCTTCTCGTACCAAGCATTGA
R149  ACCACCATCGACGATGATGACCGGGGCTTCGGATTCCTTGTATACCTCCCTCAGGCCGCGCTTCTCGTACCAAGCATTGA
R198  ACCACCATCGACGATGATGACCGGGGCTTCGGATTCCTTGTATACCTCCCTCAGGCCGCGCTTCTCGTACCAAGCATTGA
R248  ACCACCATCGACGATGATGACCGGGGCTTCGGATTCCTTGTATACCTCCCTCAGGCCGCGCTTCTCGTACCAAGCATTGA
                *****

R17  TTCGGAATGTTTCTCATGTACCGTAGCG
R135  TTCGGAATGTTTCTCATGTACCGTAG-
R149  TTCGGAATGTTTCTCATGTACCGTAG-
R198  TTCGGAATGTTTCTCATGTACCGTAG-
R248  TTCGGAATGTTTCTCATGTACCGTAG-
                *****

GROUP 2
SCORE=100, Nseq=3, Len=238

R165  TCGCGGATCGAGCGTGCAGGAAGCGGTGAAAAGAAGCTTCGATTGCGGATATAAGCGGTGGGCGGTGAAAGCGGTGG
R257  TCGCGGATCGAGCGTGCAGGAAGCGGTGAAAAGAAGCTTCGATTGCGGATATAAGCGGTGGGCGGTGAAAGCGGTGG
R266  TCGCGGATCGAGCGTGCAGGAAGCGGTGAAAAGAAGCTTCGATTGCGGATATAAGCGGTGGGCGGTGAAAGCGGTGG
                *****

R165  TGGCGGCGAGTCCAGAAAGTCGGATGGTGGGGCTCAGGAACGGATAAGCTCAGGCCCTCAGCATCATGCACACTCACTCC
R257  TGGCGGCGAGTCCAGAAAGTCGGATGGTGGGGCTCAGGAACGGATAAGCTCAGGCCCTCAGCATCATGCACACTCACTCC
R266  TGGCGGCGAGTCCAGAAAGTCGGATGGTGGGGCTCAGGAACGGATAAGCTCAGGCCCTCAGCATCATGCACACTCACTCC
                *****

R165  ATCAAATGGTGGGACTTTCAAATTTTATTTCGCGTGGCGACTACAGATGCGTGGGAAGTAAATACGTTA
R257  ATCAAATGGTGGGACTTTCAAATTTTATTTCGCGTGGCGACTACAGATGCGTGGGAAGTAAATACGTTA
R266  ATCAAATGGTGGGACTTTCAAATTTTATTTCGCGTGGCGACTACAGATGCGTGGGAAGTAAATACGTTA
                *****

GROUP 3
SCORE=99, Nseq=3, Len=344

R143  -----CGCTTCAGGAAGTCCCGCTCCACGCTCAACTCGGC
R174  GCAACGCTACCCGCGGCTTCTACCGCAGCGAAGCTTCTAGAACGCCGCTTCAGGAAGTCCCGCTCCACGCTCAACTCGGC
R180  GCAACGCTACCCGCGGCTTCTACCGCAGCTGAAGCTTCTAGAACGCCGCTTCAGGAAGTCCCGCTCCACGCTCAACTCGGC
                *****

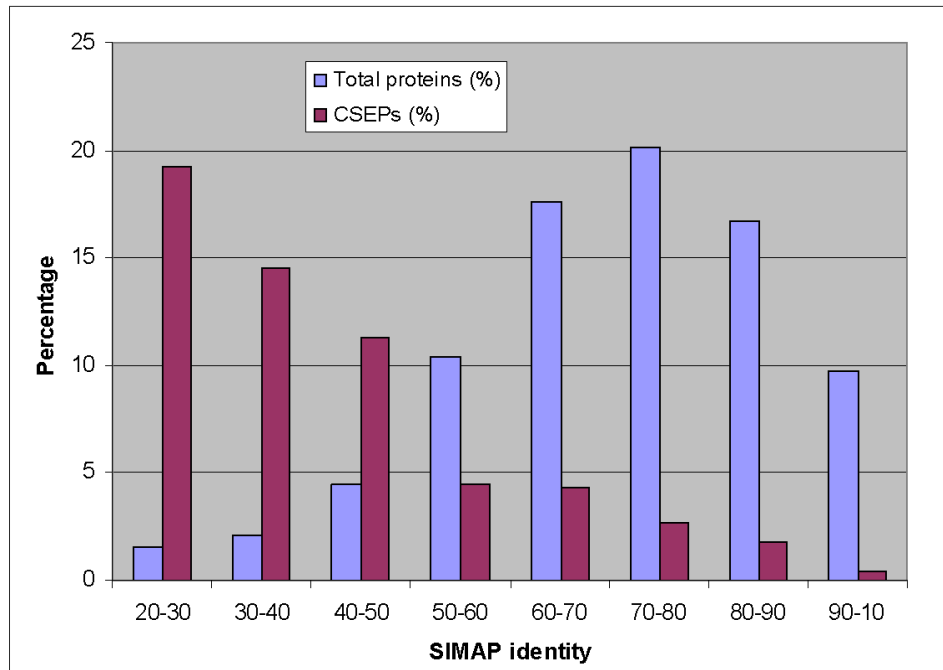
R143  TTTCAAGCCACGCTCGACGCCCACTCAACGCCACGCTCAGGAACCGGCTCAGAGGAAGTACAGACGCTCAAGCGCACGCT
R174  TTTCAAGCCACGCTCGACGCCCACTCAACGCCACGCTCAGGAACCGGCTCAGAGGAAGTACAGACGCTCAAGCGCACGCT
R180  TTTCAAGCCACGCTCGACGCCCACTCAACGCCACGCTCAGGAACCGGCTCAGAGGAAGTACAGACGCTCAAGCGCACGCT
                *****

R143  TCAACAACAAAACGCCGCGGCGCAGGCTTCTATTGTTGTTCTCAAAGCGAAGTCAACATGCTTCAAGCTCAACACGAGCGAAA
R174  TCAACAACAAAACGCCGCGGCGCAGGCTTCTATTGTTGTTCTCAAAGCGAAGTCAACATGCTTCAAGCTCAACACGAGCGAAA
R180  TCAACAACAAAACGCCGCGGCGCAGGCTTCTATTGTTGTTCTCAAAGCGAAGTCAACATGCTTCAAGCTCAACACGAGCGAAA
                *****

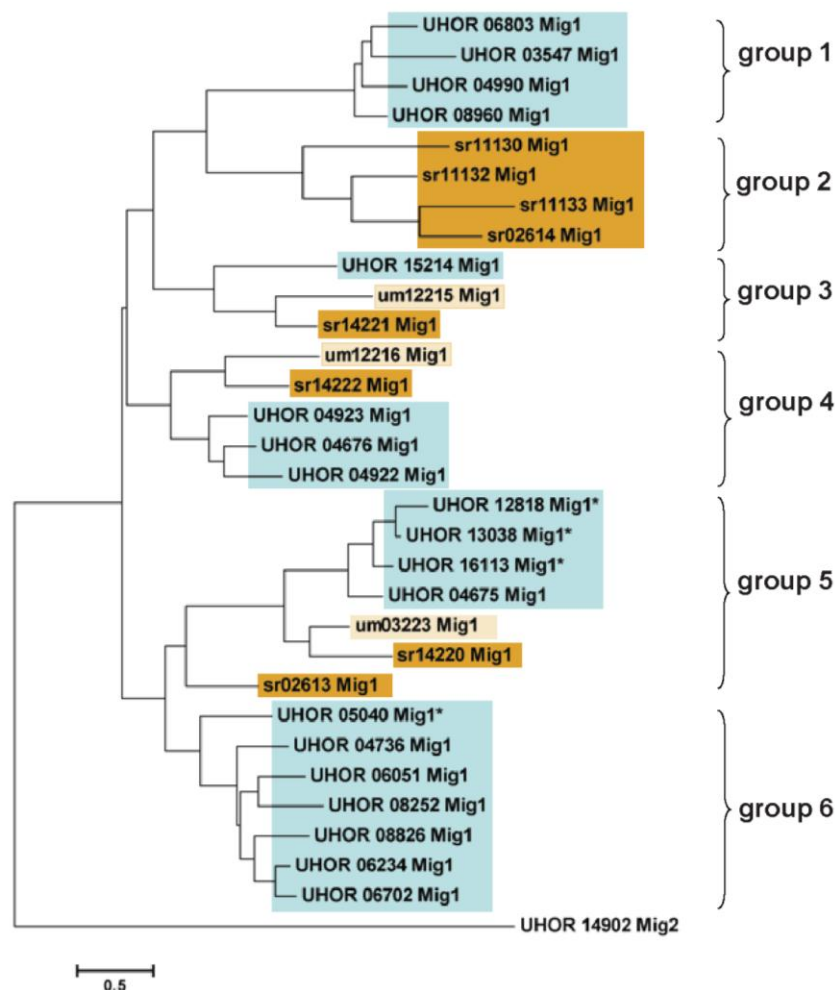
R143  GAGGAAAA
R174  GAGGAAAA
R180  GAGGAAAA
                *****

```

Supplemental Figure 8. Indication of RIP in *S. reilianum*. DNA sequence alignment of members representing three repeat families, using the CLUSTAL program (T-COFFEE Version_8.69; <http://www.tcoffee.org>).



Supplemental Figure 9. Diversity among *U. hordei* and *U. maydis* proteins. Depicted is the distribution of amino acid identities in 10 % increments (X-axis) among all *U. hordei* and *U. maydis* proteins (blue bars) as a percent of the total complement of 7,113 *U. hordei* proteins (Y-axis). The red bars represent the distribution of amino acid identities compared to *U. maydis* homologs of the predicted *U. hordei* candidate secreted effector proteins as a percentage of the 369 predicted secreted proteins.



Supplemental Figure 10. Molecular phylogeny tree depicting the relatedness among all Mig1-related proteins found in the genomes of *U. hordei*, *U. maydis* and *S. reilianum*. The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model (Jones et al., 1992). The tree with the highest log likelihood (-11797.2241) is shown. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was <100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise the BIONJ method with MCL distance matrix was used. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 31 amino acid sequences and one *U. hordei* Mig2 protein (UHOR_14902) was chosen to root the tree. There were a total of 309 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 (Tamura et al., 2011). Proteins with an asterisk are paralogs that were identified through protein sequence comparisons using BLASTp, or were identified based on similarity of cysteine residue patterns (Supplemental Dataset 3); they are not predicted to be secreted by SignalP. Expansions of homologs specifically in *U. hordei* (groups 4, 5 and 6) or also in *S. reilianum* (groups 1 and 2) are suggested, whereas some have one conserved member in each species (group 3). In *S. reilianum*, the 8 MIG1-related effectors are located within 17.7 kb on Chr 8, whereas in *U. maydis*, the 4 Mig1-related *Um* effectors and two pseudogenes (um12351 and um12352) are clustered within 6.5 kb on Chr 8. In *U. hordei*, among the 19 MIG1-related proteins, only five (UHOR_04922, UHOR_04923, UHOR_04990, UHOR_15214 and UHOR_05040) are found on Chr 8. UHOR_04736, UHOR_04675 and UHOR_04676 are found on Chr 7, and all others are spread out over the genome. The amino acid alignment used to produce the tree is presented in Supplemental Dataset 6 online.

Supplemental Table 1. TEs and repeat content among five basidiomycete genomes.

	<i>U. hordei</i>	<i>U. maydis</i>	<i>S. reilianum</i>	<i>S. roseus</i>	<i>M. globosa</i>
Genome Size (Mb)	20.01	19.68	18.47	20.98	8.93
Entropy (trinucleotides)	3.97	4.10	3.99	4.03	4.12
TEclass/RepeatMasker Prediction ^{1,2}					
DNA Transposons	627 (0.44)	220 (0.10)	106 (0.05)	268 (0.10)	13 (0.19)
DNA Transposons >200 bp	67 (0.21)	4 (0.01)	3 (0.01)	1 (<0.01)	5 (0.18)
LTR Retrotransposons	2242 (3.37)	407 (1.19)	89 (0.07)	455 (0.94)	29 (0.09)
LTR Retrotransposons >200bp	1237 (2.70)	201 (1.07)	12 (0.07)	218 (0.79)	20 (0.07)
Unclassified Retrotransposons	822 (1.00)	252 (0.17)	96 (0.07)	324 (0.40)	22 (0.04)
Unclassified Retrotransposons >200bp	329 (0.75)	59 (0.08)	15 (0.03)	92 (0.30)	3 (0.02)
LINES	636 (2.66)	70 (0.22)	31 (0.02)	53 (0.20)	25 (0.21)
LINES >200bp	634 (2.65)	70 (0.22)	10 (0.02)	53 (0.20)	25 (0.21)
SINES	17 (0.01)	27 (0.01)	12 (<0.01)	9 (<0.01)	7 (0.01)
SINES >200bp	10 (0.01)	4 (0.01)	2 (<0.01)	1 (<0.01)	0 (0.00)
Unclassified nonLTR Transposons	46 (0.19)	17 (0.02)	8 (<0.01)	13 (0.01)	7 (0.03)
Unclassified nonLTR Transposons >200bp	33 (0.18)	6 (0.01)	2 (<0.01)	3 (0.01)	3 (0.03)
Unclassified Repeats	152 (0.23)	52 (0.07)	15 (0.01)	43 (0.06)	7 (0.02)
Unclassified Repeats >200 bp	47 (0.19)	14 (0.05)	15 (0.01)	9 (0.05)	1 (0.01)
Small RNAs	41 (0.01)	55 (0.03)	26 (0.03)	96 (0.11)	29 (0.07)
Simple Repeats	3288 (0.75)	2080 (0.48)	3471 (0.76)	3677 (0.56)	724 (0.37)
Low complexity	971 (0.3)	414 (0.10)	777 (0.20)	1799 (0.55)	209 (0.13)
Total Repeat Coverage in kb	1560 (7.8) ³	401 (2.0)	143 (0.8)	532 (2.5)	80 (0.9)

¹ An estimate of the genome coverage in percent between parentheses is shown for each element type.

² TE Class Classifications for RepeatScout repeats of 200 bp or more are also reported.

³ Total coverage in the assembled *U. hordei* genome; this value increases to ~10% if the 1241 repeat-containing, small (<500 bp) contigs are included that could not be placed on the genome.

Supplemental Table 2. Number of clusters of TEs and repeat elements in four basidiomycete genomes.

Clustering parameters	<i>U. hordei</i>	<i>U. maydis</i>	<i>S. roseus</i>	<i>M. globosa</i>
75% alignment length, 80% identity	709	245	366	37
90% alignment length, 80% identity	1344	355	489	46
no alignment threshold, 90% identity	258	142	250	26
no alignment threshold, 80% identity	142	117	226	23
no alignment threshold, 65% identity	142	117	226	23

Supplemental Table 3. Conservation between *U. hordei* and *S. reilianum* proteins involved in transcriptional gene silencing and chromatin remodelling but absent from *U. maydis*.

Tentative protein name	<i>U. hordei</i> ID	<i>S. reilianum</i> ID	% Identity ¹	E-value ²
RNA-dependent RNA polymerase, UhRdR1	UHOR_08874	sr16789	68	0
RNA-dependent RNA polymerase, UhRdRp2	UHOR_01631	sr12376	66	0
RNA-dependent RNA polymerase, UhRdRp3	UHOR_15740	sr05666	59	0
Argonaute (UhAGO1)	UHOR_06256	sr15057	66	0
Dicer (UhDCL1)	UHOR_08937	sr16838	60	0
Chromodomain protein UhCHP1 (HP1-like) ³	UHOR_05116	sr14286	55	8e ⁻¹⁰⁴
Chromodomain protein UhCHP2 (HP1-like)	UHOR_07750	sr15731	60	2e ⁻¹⁰²
Chromodomain protein UhCHP3 (no chromoshadow domain)	UHOR_16420	sr10127	52	0
Cytosine5-specific methyltransferase UhDNAme (<i>Dim-2</i> , <i>Masc1</i> , <i>Masc2</i>)	UHOR_08509	sr16612	56	6e ⁻²²⁴

¹ Amino acid identities² BLASTx³ For review of the HP1 family see (Lomber et al., 2006)

SUPPLEMENTAL REFERENCES

- Bakkeren, G., Jiang, G., Warren, R.L., Butterfield, Y., Shin, H., Chiu, R., Linning, R., Schein, J., Lee, N., Hu, G., Kupfer, D.M., Tang, Y., Roe, B.A., Jones, S., Marra, M., and Kronstad, J.W.** (2006). Mating factor linkage and genome evolution in basidiomycetous pathogens of cereals. *Fungal Genet. Biol.* **43**: 655-666.
- Clutterbuck, J.A.** (2011). Genomic evidence of repeat-induced point mutation (RIP) in filamentous ascomycetes. *Fungal Genet. Biol.* **48**: 306-326.
- Hood, M.E., Katawczik, M., and Giraud, T.** (2005). Repeat-induced point mutation and the population structure of transposable elements in *Microbotryum violaceum*. *Genetics* **170**: 1081-1089.
- Jones, D.T., Taylor, W.R., and Thornton, J.M.** (1992). The rapid generation of mutation data matrices from protein sequences. *Comp. Appl. Biosciences* **8**: 275-282.
- Kamper, J., Kahmann, R., Bolker, M., Ma, L.-J., Brefort, T., Saville, B.J., Banuett, F., Kronstad, J.W., Gold, S.E., Muller, O., Perlin, M.H., Wosten, H.A.B., de Vries, R., Ruiz-Herrera, J., Reynaga-Pena, C.G., Snetselaar, K., McCann, M., Perez-Martin, J., Feldbrugge, M., Basse, C.W., Steinberg, G., Ibeas, J.I., Holloman, W., Guzman, P., Farman, M., Stajich, J.E., Sentandreu, R., Gonzalez-Prieto, J.M., Kennell, J.C., Molina, L., Schirawski, J., Mendoza-Mendoza, A., Greilinger, D., Munch, K., Rossel, N., Scherer, M., Vranes, M., Ladendorf, O., Vincon, V., Fuchs, U., Sandrock, B., Meng, S., Ho, E.C.H., Cahill, M.J., Boyce, K.J., Klose, J., Klosterman, S.J., Deelstra, H.J., Ortiz-Castellanos, L., Li, W., Sanchez-Alonso, P., Schreier, P.H., Hauser-Hahn, I., Vaupel, M., Koopmann, E., Friedrich, G., Voss, H., Schluter, T., Margolis, J., Platt, D., Swimmer, C., Gnrke, A., Chen, F., Vysotskaia, V., Mannhaupt, G., Guldener, U., Munsterkotter, M., Haase, D., Oesterheld, M., Mewes, H.-W., Mauceli, E.W., DeCaprio, D., Wade, C.M., Butler, J., Young, S., Jaffe, D.B., Calvo, S., Nusbaum, C., Galagan, J., and Birren, B.W.** (2006). Insights from the genome of the biotrophic fungal plant pathogen *Ustilago maydis*. *Nature* **444**: 97-101.
- Larkin, M.A., Blackshields, G., Brown, N.P., Chenna, R., McGettigan, P.A., McWilliam, H., Valentin, F., Wallace, I.M., Wilm, A., Lopez, R., Thompson, J.D., Gibson, T.J., and Higgins, D.G.** (2007). ClustalW and ClustalX version 2.0. *Bioinformatics* **23**: 2947-2948.
- Lomberk, G., Wallrath, L., and Urrutia, R.** (2006). The heterochromatin protein 1 family. *Genome Biol.* **7**: 228.
- Schirawski, J., Mannhaupt, G., Münch, K., Brefort, T., Schipper, K., Doehlemann, G., Di Stasio, M., Rössel, N., Mendoza-Mendoza, A., Pester, D., Müller, O., Winterberg, B., Meyer, E., Ghareeb, H., Wollenberg, T., Münsterkötter, M., Wong, P., Walter, M., Stukenbrock, E., Guldener, U., and Kahmann, R.** (2010). Pathogenicity determinants in smut fungi revealed by genome comparison. *Science* **330**: 1546-1548.
- Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., and Kumar, S.** (2011). MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol. Biol. Evol.* **28**: 2731-2739.
- Zemach, A., McDaniel, I.E., Silva, P., and Zilberman, D.** (2010). Genome-wide evolutionary analysis of eukaryotic DNA methylation. *Science* **328**, 916-919.