

Supplementary Table S7: Map based cloning assembly of the *U. maydis* genome (BayerCropScience assembly)

Chromosome ^a	Size in bp	Number of Bacs	Number of Contigs	Description of breaks and gaps
I_a	1.477.548	22	4	Contig-break: Position 701346 (Bac UM242-17f14 position 2511) Mapping-break (Sublibrary): $\approx$ 13kb Position 814839 (Bac UM123-17b5 at position 26152) one direction sequencing failure, other direction $\approx$ 500 bp missing Position 1210754 (Gap between UM165-12f11 and UM166-18f10, covered by Bac UM289-13g15), Size of gap $\approx$ 20kb
I_b	555.428	8	2	Contig-Break: Position 95880 (Gap between UM209-13j5 and UM171-23i21, covered by Bac UM296-14n18), Size of gap $\approx$ 9kb
I_c	148.752	3	1	
II	1.830.909	29	3	Contig-break: Position 343026 (Gap between UM139-14k7 and UM124-24g11, covered by Bac UM293-24d16, Size of gap $\approx$ 3kb) Position 1069600 (UM95-22b6 position 18657) Size of gap $\approx$ 1.1kb Remark: Bacs UM251-13f6 and UM18-9c8 are connected via their restriction site used for cloning. To validate this, Bac UM246-24d3 was sequenced; it covers no new sequence. Bacs UM72-9h13 and UM90-14d20 9c8 are connected via their restriction site used for cloning. To validate this, Bac UM238-15l3 was sequenced; it covers no new sequence
III_a	1.038.714	13	1	
III_b	321.849	4	1	
IV_a	501.834	7	2	Contig-Break: Position 457746 (UM196-22g10 position 5003) Size of gap $\approx$ 0.5kb
IV_b	206.458	3	1	
IV_c	62.705	1	1	Remark: rDNA-Bac; contains two cluster
IV_d	42.743	1	2	Remark: rDNA-Bac; Contig-Break: Position 32563: gap $\approx$ 2kb
V	1.313.125	19	1	Remark: Bacs UM70-11m10 and UM33-9c8 are connected via the restriction site used for cloning. Bac UM180-22k7 was sequenced to check this. It covers no new sequence Position 1308185 (UM287-6k18 position 988) poly-C; number of C's not determined exactly
VI	1.020.931	16	1	Remark: Bacs UM174-9d6 and UM175-18h2 are connected via the restriction site used for cloning. Bac UM292-15g19 was sequenced to check this. It covers no new sequence
VII_a	329.701	4	1	
VII_b	584.184	8	1	
VIII	734.638	12	1	
IX	415.229	6	1	
X	578.171	9	3	Contig-break: Position 243235 (Bac UM140-22g19 at position 37251) Size of gap not known Position 509492 (Bac UM143-13j11 at position 20559: one direction sequence failure; from the other site $\approx$ 30kb are missing

XI	601.237	8	2	Contig-Break: Position 381577 (Gap between UM27-9j16 and UM66-24k17 covered by Bac UM294-24e10, Size of gap $\approx$ 26kb) Remark: Position 268049 (UM96-19e8 position 68465) poly-GGA number of GGA's is variable
XII	501.587	8	3	Contig-Break: Position 235709 (Gap between UM55-12i10 and UM118-10c11 covered by Bac UM290-13h8, Size of Gap $\approx$ 18kb) Position 400872 (UM65-15b11 position 33648) Gap $\approx$ 0,5 kb
XIII	510.451	7	2	Contig-Break: Position 151404 (UM15-B1b6 position 69826) Transposon repeat could not be resolved
XIV	590.558	9	1	
XV	596.344	9	1	
XVI	539.260	9	2	Contig-Break: Position 409470 (UM257-10p16 position 14786) Repeat: size of gap $\approx$ 0.5kb
XVII	519.932	7	1	Remark: Position 48640 (Bac UM259-17i10) poly-TA, number of TA's is variable
XVIII	409.659	6	4	Contig-break: Position 1210754 (Gap between UM182-13k20 and UM183-12f16 covered by Bac UM291-10m23, Size of gap $\approx$ 16kb) Position 87291 (UM183-12f16 position 7071) Size of gap cannot be determined Position 358571(UM284-20j20 position 26784) Repeat; Size of gap cannot be determined
XIX	464.657	7	2	Contig-Break: Position 289296 (UM125-10h20 position 843) Size of gap $\approx$ 2.6 kb
XX	454.761	6	1	
XXI	420.014	7	1	
XXII	386.956	7	1	Remark: Bacs UM86-17j6 and UM231-6i3 are connected via the restriction site used for cloning. Bac UM295-19o11 was sequenced to check this. It covers no new sequence
XXIII	267.596	3	2	Contig-Break: Position 210054 (UM214-17n5 position 7401) Stop of sequencing in both directions Size of gap cannot be determined
Sum	17.425.931	247	50	Gaps in contigs are marked with 20 n. In the entire sequence 400 n's (20 times 20 n's are contained)

^a Sequence assembly is accessible at http://www.broad.mit.edu/cgi-bin/annotation/fungi/ustilago_maydis/download_license.cgi. as
Bayer_chromosomes.fasta.gz