

Supplementary Table S4:

Distribution of DNA with similarities to transposable elements within the *U. maydis* genome

Sequence ^a	Chromosome	Alignment length	Mis-matches	Query start	Query end	Subject start	Subject end
um00820_3	0	214	36	378	591	95458	95671
hobS_ORF	0	2859	1	1640	4494	124296	127154
um00820	1	813	0	1	330	18481	19321
tigR_ORF	1	4109		1	4109	1024917	1028545
tigR_rep	1	315	2	104	418	1024519	1024908
tigR_rep	1	418	2	1	418	1028865	1029278
tigR_rep	1	62	8	12	73	1054652	1054801
um00449	1	1004	0	1	882	1205724	1206728
hobS_rep	1	61	3	1	61	1804924	1805201
hobS_rep	1	304	16	411	706	1805204	1805621
tigR_rep	2	25	1	1	25	12538	13017
hobS_rep	2	66	8	492	556	142222	142405
hobS_rep	2	199	2	1	194	145196	145813
hobS_ORF	2	4503	13	1	4494	145821	150321
hobS_rep	2	749	7	1	743	150963	151711
tigR_rep	2	27	1	332	358	154672	154698
um01135	2	943	0	1	879	895113	896056
um01901_2	3	224	21	6	224	60341	60563
um01901	3	537	0	1	537	333332	333868
tigR_rep	3	37	1	334	370	1110151	1110187
hobS_rep	3	749	5	1	743	1141415	1142163
hobS_ORF	3	2455	2	2050	4494	1142804	1145257
gap	3					1145257	1145358
hobS_rep	3	751	7	1	743	1145768	1146518
hobS_ORF	3	4515	19	1	4494	1147160	1151670
hobS_rep	3	750	5	1	743	1151679	1152428
um01587	3	1564	0	1	1335	1152896	1154460
um11504_2	3	372	16	50	420	1154342	1154713
hobS_rep	3	644	16	107	743	1154838	1156260
hobS_ORF	3	1958	8	2544	4494	1156906	1158862
gap	3					1158867	1158968
hobS_rep	3	749	8	1	743	1160033	1160781
hobS_ORF	3	4509	8	1	4494	1161424	1165929
hobS_rep	3	751	6	1	743	1165937	1166743
hobS_rep	3	78	3	652	728	1166863	1166940
hobS_rep	3	37	5	687	723	1167239	1167275
hobS_rep	3	102	7	1	102	1167275	1167440
hobS_rep	3	42	2	365	406	1167476	1167737
hobS_rep	3	99	7	4	102	1168299	1168692
gap	3					1168692	1168793

um11686	3	1792	0	1	1620	1172648	1174440
tigR_rep	3	418	0	1	418	1438888	1439301
tigR_ORF	3	4109	0	1	4109	1439310	1443418
tigR_rep	3	418	0	1	418	1443737	1444154
hobS_rep	4	381	19	366	738	74286	74666
hobS_rep	4	102	7	1	102	74751	74852
hobS_rep	4	376	23	371	738	75365	75737
hobS_rep	4	752	4	1	752	75813	76564
hobS_ORF	4	1190	2	1	1188	76569	77758
gap	4					77758	81849
pCM5	4					81849	82768
hobS_rep	4	120	1	3	752	81851	83159
TigR_ORF	4	2439		479	2917	568487	570810
um06265	4	3831	0	1	3831	574877	578707
TigR_rep	4	154	12	149	302	741007	741158
TigR_ORF	4	609	36	3498	4106	741378	741982
TigR_rep	4	116	3	1	399	870585	870957
hobS_ORF	5	81	9	1	81	148438	148518
hobS_rep	5	71	10	662	732	148533	148774
um02312	5	1324	0	1	900	559535	560859
hobS_rep	5	461	29	275	732	754102	755555
hobS_ORF	5	4503	6	1	4494	756196	760697
hobS_rep	5	748	7	1	741	760708	762526
hobS_rep	5	99	7	4	102	763088	763668
pCM14	6					103829	106412
hobS_rep	6	36	3	67	102	104469	105727
hobS_rep	6	41	3	6	46	108881	109291
hobS_rep	6	97	4	468	557	109805	110064
tigR_rep	6	31	1	334	364	198372	198402
tigR_ORF	6	164	26	1509	1672	198481	198642
um02565	6	1726	0	1	1482	846263	847989
um02817	7	731	0	1	732	5249	5980
tigR_rep	7	31	2	334	364	16630	16660
hobS_rep	7	38	3	518	555	842502	842539
hobS_rep	7	107	7	1	100	843117	843448
hobS_rep	7	31	2	6	36	844580	845171
um03249	8	813	0	1	636	445890	446703
hobS_rep	8	70	9	515	584	630482	630551
hobS_rep	8	307	13	427	732	633843	634149
hobS_rep	8	328	12	1	321	634695	635521
hobS_ORF	8	4502	8	1	4494	635529	640030
hobS_rep	8	328	12	1	321	640670	641496
hobS_rep	8	32	3	16	47	641903	642260
hobS_rep	8	104	7	1	102	642268	642518
hobS_rep	8	449	21	285	732	643162	643694
hobS_ORF	8	1336		36	957	645880	647246

um11504	9	455	0	1	420	125871	126326
tigR_rep	9	56	8	1	56	229817	230187
hobS_rep	9	37	2	1	37	587396	587892
hobS_rep	9	34	3	672	705	588296	588329
hobS_rep	9	383	24	355	732	589279	589839
pCM7	9					589282	592095
hobS_rep	9	43	2	468	510	590567	590781
um03801	10	1067	0	1	1068	224665	225732
hobS_rep	10	26	1	76	101	559800	559992
hobS_rep	10	239	17	495	732	560657	560895
hobS_rep	10	100	6	1	100	561510	562256
hobS_rep	10	22	1	687	708	562420	562441
hobS_rep	10	750	17	1	743	562575	563324
tigR_rep	10	115	2	1	115	681943	682316
tigR_rep	11	418	8	1	417	311	725
um03882	11	1232	0	1	1233	39576	40808
hobS_rep	11	16	0	561	576	258505	258520
hobS_rep	11	340	20	411	732	267982	268473
pCM22	11					269234	269605
hobS_rep	11	83	6	1	83	269571	270242
hobS_rep	11	25	1	78	102	270243	270326
hobS_rep	11	35	0	371	405	270344	270885
tigR_rep	11	269	28	149	417	446810	447215
tigR_rep	11	314	6	104	417	686288	686676
tigR_rep	12	116	4	1	116	3001	3391
um11295_2	12	348	14	259	606	356650	356997
hobS_rep	12	21	1	696	716	558596	558616
hobS_rep	12	170	7	1	169	559849	560435
hobS_rep	12	98	1	646	743	560614	561230
hobS_ORF	12	3841	5	658	4494	561871	565711
gap	12					565711	565812
hobS_ORF	12	2271	3	1	2260	565812	568081
hobS_rep	12	748	8	3	743	568089	568836
hobS_rep	12	338	13	396	732	569867	571207
hobS_ORF	12	157	24	48	198	576170	576326
hobS_rep	12	27	2	538	564	576464	576490
tigR_rep	13	251	18	156	404	5111	5487
um11764	13	591	0	1	591	6483	7172
pCM9	13					208842	212975
pCM30	13					209356	209859
um04731_3	13	335	45	158	487	210137	210465
hobS_rep	13	100	12	1	100	210972	211569
hobS_rep	13	97	4	468	557	212590	213721
hobS_ORF	13	4514	13	1	4494	214362	218874
hobS_rep	13	730	6	17	740	218885	219614
hobS_ORF	13	4520	7	1	4494	220272	224791
hobS_rep	13	563	9	183	743	224799	230681

hobS_ORF	13	3752	4	757	4494	226931	230681
gap	13					230681	230782
hobS_ORF	13	338	1	1	338	230782	231118
hobS_rep	13	749	8	1	743	231127	232900
hobS_rep	13	26	2	5	30	235822	235924
hobS_rep	13	97	13	482	578	236501	236597
hobS_rep	13	25	1	79	103	237635	237659
um04491	13	2244	0	1	2244	592383	594908
tigR_rep	13	418	8	1	417	605725	607906
um10521	14	963	0	1	909	211316	212279
hobS_rep	14	33	3	14	46	238944	239466
hobS_rep	14	102	8	1	102	241923	242492
um03882_2	14	473	55	766	1230	243257	243720
pCM20	14					243527	244025
hobS_rep	14	327	15	1	321	243870	244692
hobS_ORF	14	4499	17	1	4494	244703	249201
hobS_rep	14	334	15	1	321	249842	250671
hobS_rep	14	121	14	431	551	251243	251588
tigR_rep	14	69	8	296	364	427434	427501
um00820_2	14	261	34	350	610	466664	466924
pCM43	15					266748	270268
hobS_rep	15	52	5	67	118	266966	267581
hobS_rep	15	40	4	67	106	268971	269383
hobS_rep	16	201	8	511	710	416320	416519
gap	16					416523	419599
hobS_ORF	16	2458	5	2044	4494	419599	422056
hobS_rep	16	756	7	1	743	422698	423453
hobS_rep	16	54	2	652	705	424334	425018
tigR_rep	16	274	6	145	418	543033	543438
tigR_rep	16	21	1	96	116	543347	543367
hobS_rep	17	47	3	1	47	92469	93041
hobS_rep	17	42	2	675	716	93070	94497
hobS_rep	17	250	3	1	244	95163	95831
hobS_ORF	17	4510	4	1	4494	95842	100351
pCM12	17					100475	104163
hobS_rep	17	250	2	1	244	100992	101660
um04731	17	2045	0	1	1740	103352	105397
hobS_rep	17	47	5	481	527	105810	105856
um04867	17	1158	0	1	1077	490231	491389
tigR_rep	17	115	3	1	115	558567	558955
tigR_rep	17	419	7	1	418	573847	574261
tigR_ORF	17	3002		1	2800	574580	577582
hobS_rep	18	38	0	668	705	475973	476010
um06204_3	18	236	13	500	735	477392	477627
um05462	18	509	0	1	510	477877	478386
pCM19	18					478729	479348
hobS_rep	18	45	3	1	45	479615	480555

hobS_ORF	18	4351	2	1	4344	480563	484913
gap	18					484913	485971
hobS_ORF	18	919	0	3578	4494	486041	486959
hobS_rep	18	749	3	1	743	487601	488616
hobS_rep	18	118	0	626	743	488499	488616
gap	18					488616	490720
hobS_ORF	18	3861	3	1	3854	490720	494578
hobS_rep	18	749	3	1	743	494586	495334
um05427	19	554	0	1	555	18648	19202
hobS_ORF	19	4503	13	1	4494	22962	27463
hobS_ORF	19	4491		3	4494	31114	33456
hobS_rep	19	250	8	1	244	32658	33331
hobS_rep	19	107	0	1	106	38481	38781
hobS_rep	19	16	0	76	91	39767	39782
hobS_rep	19	396	24	338	723	40289	40847
hobS_rep	19	110	17	476	585	44050	44159
um05316	19	819	0	1	741	387167	387986
um11686_2	20	344	22	11	860	2254	2855
hobS_rep	20	640	17	110	743	45269	46171
hobS_ORF	20	270	1	4226	4494	46811	47079
gap	20					47079	53659
hobS_rep	20	322	1	422	743	53659	53980
um03882_4	20	704	75	285	991	94300	95021
um05946	20	716	0	1	717	94637	95353
tigR_rep	21	416	7	3	418	8	418
um03249_4	21	509	71	91	600	312169	312984
hobS_rep	21	403	25	338	731	323292	323742
hobS_rep	21	643	17	107	743	324680	325582
tigR_rep	21	252	20	149	399	325654	325902
gap	21					325904	329177
hobS_rep	21	303	11	1	297	329177	329507
hobS_rep	21	642	15	110	743	330629	331456
tigR_rep	21	252	15	149	399	331528	331942
tigR_ORF	21	21	0	3971	4109	331944	332104
tigR_rep	21	22	0	5	26	332338	332359
um03882_5	21	719	73	241	1230	332835	333799
um06204	22	1302	0	1	735	219799	221101
hobS_rep	22	29	3	78	106	220952	221026
hobS_rep	22	393	28	340	723	221705	222269
gap	22					222317	222982
hobS_rep	22	251	8	1	244	223622	224295
hobS_ORF	22	4502	15	1	4494	224303	228803
hobS_rep	22	250	7	1	244	229443	230121
um11295	22	606	0	1	606	394447	395052
tigR_rep	22	26	0	333	358	395815	396188
hobS_rep	23	25	2	1	25	238398	238507
um06435	23	616	0	1	471	238918	239534

hobS_rep	23	23	1	80	102	240897	240919
um06436	23	1551	0	1	1161	241293	242844
hobS_rep	23	478	25	266	728	244714	244768
hobS_rep	23	563	4	183	743	245312	245983
hobS_ORF	23	4508	5	1	4494	246627	251134
hobS_rep	23	563	5	183	743	251142	251813
gap	23					252369	252470
hobS_ORF	23	3729	7	1	3719	252470	256198
hobS_rep	23	557	5	183	737	256214	256879
hobS_rep	23	17	0	85	101	257531	257916

^a Queries for the retroelements TigR (indicated in yellow) and HobS (indicated in red) were the ORFs and terminal repeat sequences of the respective elements (HobS: GenBank Acc. No. DQ370139; TigR: GenBank Acc. No. DQ370140). Elements consisting of ORF and associated repeats are outlined with double-lined borders. Within the Broad whole genome assembly, no functional HobS or TigR element is present. Within the BayerCropScience map-based genome assembly, one potentially functional HobS copy is present. For other DNA transposons and retrotransposons, DNA sequences of *U. maydis* genes with similarities to transposases (indicated in blue) or polyproteins (indicated in green) were used to search for sequences within the genome (minimum length: 200 bp; cut off E-value: 10^{-30}). Gene designations of these genes refer to the MUMDB (<http://mips.gsf.de/genre/proj/ustilago/>), regions with similarities to these genes are denoted with _*. In no case do the DNA elements resemble functional transposable elements.

Genome positions of experimentally verified ARS elements from pCM plasmids (Tsukuda, T., Carleton, S., Fotheringham, S. & Holloman, W. K. Isolation and characterization of an autonomously replicating sequence from *Ustilago maydis*. Mol Cell Biol 8, 3703-9, 1988; highlighted in grey) were determined by sequencing the borders and alignment to the genome sequence. A graphic visualization of the distribution is given in Supplementary Fig. S2.