

Supplemental Material to:

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**Transcriptomic analysis of Ustilago maydis infecting
Arabidopsis reveals important aspects of the fungus
pathogenic mechanisms**

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Supplementary Table S1. *U. maydis* differentially expressed genes with the highest fold change during *A. thaliana* infection.

ID	Description	Fold change during <i>Arabidopsis thaliana</i> infection							
		Days post-infection with the haploid strain FB2				Days post-infection with the diploid strain Uid1			
		1	2	4	8	1	2	4	8
um04111	uncharacterized protein	230.3 up	198.3 up	-	-	-	-	-	-
um05812	Related to Cyclohexanone monooxygenase	17.4 up	66.4 up	174.0 up	84.6 up	2.8 up	2.2 up	7.8 up	9.3 up
um06085	related to ATO2 - putative transmembrane protein involved in export of ammonia	137.7 up	134.0 up	130.3 up	179.1 up	88.4 up	25.3 up	38.7 up	88.1 up
um02379	uncharacterized protein	80.9 up	124.5 up	28.3 up	43.5 up	2.0 up	2.0 up	6.1 up	3.0up
um05803	related to acid phosphatase	114.5 up	105.1 up	121.1 up	75.1 up	106.0 up	121.9 up	54.8 up	46.7 up
um11057	related to OPT1 - High-affinity glutathione transporter	90.2 up	116.0 up	89.7 up	89.3 up	5.6 up	4.2 up	41.5 up	5.0 up
um05968	related to peptide transporter Mtd1	111.1 up	80.4 up	11.4 up	2.1 up	35.0 up	6.7 up	12.8 up	25.4 up
um12015	uncharacterized protein	109.1 up	110.2 up	88.9 up	46.5 up	33.7 up	29.6 up	39.9 up	29.6 up
um06084	uncharacterized protein	79.2 up	72.3 up	68.9 up	104.9 up	38.2 up	12.7 up	24.0 up	47.2 up
um01528	uncharacterized protein	100.5 up	94.5 up	20.4 up	2.9 up	99.0 up	20.9 up	56.3 up	121.9 up
um01528	uncharacterized protein	100.5 up	94.5 up	20.4 up	2.9 up	99.0 up	20.9 up	56.3 up	121.9 up
um11002	uncharacterized protein	96.8 up	94.8 up	-	-	-	-	-	-
um05976	uncharacterized protein	17.4 up	29.9 up	94.0 up	50.0 up	8.4 up	8.4 up	13.6 up	11.2 up
um04309	probable Alpha-L-arabinofuranosidase precursor	8.1 up	13.9 up	91.8 up	53.2 up	3.3 up	8.1 up	18.2 up	32.9 up
um03310	related to ATO3 - plasma membrane protein with possible role in export of ammonia	52.9 up	57.3 up	63.3 up	57.8 up	72.9 up	79.0 up	81.8 up	91.5 up
um03664	uncharacterized protein	11.2 up	33.7 up	64.0 up	90.9 up	9.2 up	5.9 up	10.8 up	11.0 up
um05791	Related to Cytochrome P450	13.9 up	43.4 up	44.8 up	80.5 up	2.3 up	2.3 up	3.4 up	5.0 up
um10608	related to Quinate permease	10.3 up	39.8 up	42.0 up	80.3 up	8.6 up	13.6 up	20.2 up	25.8 up
um03049	related to neutral amino acid permease	45.8 up	72.7 up	56.1 up	71.5 up	46.0 up	46.6 up	78.9 up	64.5 up
um05122	related to carboxylic acid transport protein JEN1	43.6 up	57.3 up	64.4 up	78.6 up	20.5 up	17.9 up	21.2 up	22.3 up
um06253	probable DUR3 - Urea permease	76.5 up	77.1 up	16.3 up	6.5 up	60.5 up	21.1 up	48.7 up	59.1 up
um05046	uncharacterized protein	51.7 up	56.0 up	20.1 up	15.5 up	48.2 up	37.9 up	76.5 up	48.4 up
um01723	related to Cytochrome P450	64.1 up	72.9 up	59.2 up	75.4 up	17.1 up	18.2 up	23.4 up	28.8 up
um11773	uncharacterized protein	75.1 up	58.6 up	5.8 up	-	2.2 up	-	-	-
um05802	related to cell surface ferroxidase	74.4 up	67.2 up	61.3 up	29.6 up	41.4 up	53.5 up	31.0 up	23.3 up
um01136	uncharacterized protein	74.5 up	64.6 up	15.6 up	11.0 up	42.4 up	15.6 up	25.3 up	45.0 up
um03381	uncharacterized protein	73.8 up	48.2 up	33.6 up	16.5 up	36.6 up	34.6 up	23.9 up	13.8 up
um05068	Probable Arylsulfatase	70.6 up	60.3 up	8.2 up	-	-	2.4 down	-	-

um06335	uncharacterized protein	38.6 up	65.4 up	39.7 up	53.8 up	15.9 up	14.7 up	31.5 up	27.7 up
um10581	Related to Alcohol dehydrogenase class III chi chain	5.8 up	26.0 up	28.2 up	63.0 up	-	-	3.1 up	3.7 up
um11695	Related to 2-epi-5-epi-valiolone synthase	49.8 up	60.4 up	5.1 up	2.2 up	3.8 up	4.2 up	7.8 up	11.9 up
um01465	uncharacterized protein	56.4 up	66.4 up	-	-	-	-	-	-
um04347	probable isp4 - oligopeptide transporter	33.8 up	21.2 up	59.7 up	64.5 up	32.8 up	23.7 up	27.1 up	31.8 up
um11588	related to copper transport protein	32.7 up	21.6 up	57.0 up	24.5 up	38.6 up	23.9 up	18.1 up	12.9 up
um12316	uncharacterized protein	46.6 up	45.6 up	28.1 up	23.2 up	51.3 up	47.1 up	57.1 up	47.4 up
um04304	related to allantoinase	4.6 up	23.5 up	29.9 up	53.2 up	2.0 up	3.5 up	6.5 up	26.8 up
um06487	uncharacterized protein	12.5 up	11.3 up	51.2 up	50.3 up	3.9 up	3.7 up	4.3 up	7.1 up
um11604	related to Ferric reductase transmembrane component 1 precursor	30.7 up	18.9 up	51.4 up	28.8 up	45.0 up	30.8 up	27.7 up	22.0 up
um05704	uncharacterized protein	34.2 up	39.7 up	48.9 up	38.2 up	37.7 up	32.2 up	40.2 up	32.6 up
um06076	Related to quinate transport protein	44.1 up	48.0 up	13.9 up	7.3 up	6.2 up	4.5 up	11.2 up	4.1 up
um05967	Related to salicylate 1-monooxygenase	25.3 up	30.6 up	43.2 up	47.7 up	8.1 up	5.5 up	15.0 up	14.3 up
um06350	probable endo-1,4-beta-xylanase A precursor	2.8 up	2.9 up	10.3 up	3.2 up	30.2 up	47.0 up	33.4 up	31.8 up
um11514	probable High-affinity glucose transporter	25.8 up	46.7 up	24.5 up	38.9 up	7.1 up	11.0 up	20.8 up	30.7 up
um10055	Related to gamma-glutamyltransferase	44.7 up	45.5 up	12.7 up	5.4 up	14.7 up	7.4 up	11.4 up	10.3 up
um03149	Related to molybdenum cofactor sulfurase	7.0 up	3.5 up	31.1 up	44.7 up	-	-	-	-
um04481	Related to ADH2 - Alcohol dehydrogenase II	12.1 up	44.6 up	2.2 up	11.7 up	2.1 down	-	9.5 up	3.6 up
um03398	related to transesterase	29.8 up	29.5 up	42.8 up	39.4 up	27.8 up	23.2 up	36.9 up	32.2 up
um05247	Related to methylcrotonyl-CoA carboxylase beta chain, mitochondrial precursor	42.8 up	13.1 up	2.6 up	-	-	-	-	-
um03665	Probable aldehyde dehydrogenase family 7 member A1	3.6 up	22.0 up	32.8 up	42.2 up	3.4 up	2.5 up	9.2 up	9.3 up
um12104	Related to Cobalamin synthesis protein	2.7 up	9.9 up	41.9 up	10.6 up	5.7 up	5.4 up	7.1 up	5.1 up
um03585	uncharacterized protein	9.3 up	3.7 up	10.7 up	10.4 up	41.5 up	25.4 up	44.4 up	37.6 up
um10608	Related to Quinate permease	10.3 up	39.8 up	42.0 up	80.3 up	8.6 up	13.6 up	20.2 up	25.8 up
um03397	uncharacterized protein	8.0 up	10.4 up	41.5 up	29.8 up	19.4 up	16.7 up	24.3 up	13.6 up
um04247	related to Cholinesterase precursor	27.2 up	40.6 up	29.1 up	25.3 up	15.3 up	23.1 up	23.3 up	17.1 up
um03924	Rep1 - repellent protein 1 precursor	39.3 up	39.8 up	37.4 up	30.7 up	2.6 up	2.6 up	2.5 up	2.3 up
um12341	Related to Cytochrome P450	5.9 up	4.4 up	39.5 up	23.9 up	-	-	-	-
um00842	(probable aflatoxin efflux pump AFLT	9.6 up	8.6 up	12.1 up	10.9 up	39.2 up	32.3 up	32.8 up	30.2 up
um06433	Acu1 - K, P-type ATPase	14.3 up	3.9 up	-	2.6 down	14.7 up	24.6 up	36.9 up	30.0 up
um02215	Related to dibenzothiophene desulfurizing enzyme	31.5 up	35.7 up	11.1 up	5.7 up	2.2 up	-	2.1 up	2.4 up
um04971	probable OSM1 - fumarate reductase	15.9 up	30.8 up	34.0 up	37.0 up	9.9 up	12.1 up	21.5 up	25.7 up
um04971	Probable OSM1 - fumarate reductase	15.9 up	30.8 up	34.0 up	37.0 up	9.9 up	12.1 up	21.5 up	25.7 up
um02152	uncharacterized protein	3.5 up	3.2 up	5.8 up	8.5 up	16.4 up	19.7 up	30.4 up	34.8 up

um11922	Related to Chitin deacetylase precursor	25.3 up	34.0 up	31.6 up	28.7 up	11.2 up	10.0 up	15.7 up	12.9 up
um03619	Related to multidrug resistant protein	25.0 up	34.0 up	-	3.2 up	-	-	2.2 up	3.1 down
um05981	Related to TPO1 - Vacuolar polyamine-H+ antiporter	22.1 up	33.8 up	18.7 up	21.5 up	6.1 up	4.9 up	6.0 up	3.5 up
um00913	Glo2 - Glyoxaloxidase 2	18.8 up	33.7 up	4.4 up	3.7 up	15.5 up	10.5 up	26.8 up	16.1 up
um04841	uncharacterized protein	22.0 up	33.4 up	5.8 up	5.3 up	27.4 up	7.5 up	15.3 up	30.8 up
um06332	Egl1 - Endoglucanase 1 precursor (egl1)	19.0 up	33.2 up	30.3 up	9.3 up	-	-	4.4 up	3.5 up
um04987	uncharacterized protein	33.1 up	20.2 up	9.4 up	6.4 up	4.4 up	-	-	-
um02865	uncharacterized protein	27.6 up	32.4 up	17.6 up	25.6 up	15.4 up	13.3 up	17.2 up	16.1 up
um03148	Related to ATP-binding cassette protein (ABC) transporter	4.0 up	2.7 up	11.7 up	31.8 up	-	2.1 up	4.1 up	3.1 up
um01863	related to Cytochrome P450	7.3 up	12.3 up	7.8 up	21.9 up	25.0 up	20.6 up	31.7 up	31.3 up
um05254	uncharacterized protein	31.2 up	14.3 up	6.2 up	3.9 up	15.0 up	5.0 up	3.0 up	9.0 up
um04503	Related to Alpha-N-acetylgalactosaminidase precursor	14.6 up	16.2 up	31.0 up	20.9 up	4.4 up	2.0 up	3.2 up	2.0 up
um05819	uncharacterized protein	16.9 up	20.7 up	30.8 up	2.3 up	-	-	3.0 up	5.0 up
um00738	uncharacterized protein	30.5 up	15.1 up	15.4 up	13.6 up	14.5 up	18.9 up	13.5 up	12.1 up
um02008	related to TNA1 - high affinity nicotinic acid plasma membrane permease	9.3 up	23.6 up	20.1 up	30.1 up	7.6 up	10.3 up	12.8 up	18.7 up
um04027	uncharacterized protein	28.5 up	28.6 up	30.4 up	25.3 up	6.5 up	5.8 up	7.5 up	5.5 up
um02301	Related to C2H2-type zinc finger protein	26.5 up	26.6 up	27.1 up	30.4 up	5.4 up	4.7 up	5.6 up	7.5 up
um10544	related to BAS1 - Myb-related transcription factor	29.9 up	5.2 up	4.3 up	-	10.0 up	3.0 up	-	-
um01656	Probable sugar transporter	26.1 up	29.8 up	22.6 up	25.7 up	3.6 up	3.2 up	4.7 up	4.3 up
um01949	uncharacterized protein	28.9 up	6.6 up	7.6 up	4.1 up	21.1 up	29.4 up	11.8 up	6.9 up
um12300	Related to methylcrotonyl-coa carboxylase alpha chain, mitochondrial precursor	28.8 up	3.1 up	3.4 up	-	-	-	-	-
um04305	Probable AMS1 - alpha-mannosidase	4.0 up	14.2 up	16.3 up	28.1 up	2.7 up	4.4 up	6.2 up	15.9 up
um03402	Related to ALD4 - aldehyde dehydrogenase, mitochondrial	6.7 up	17.0 up	14.9 up	26.6 up	-	-	2.9 up	3.9 up
um05809	Related to KRE6 - glucan synthase subunit	19.0 up	26.4 up	7.6 up	9.4 up	4.0 up	4.3 up	7.5 up	5.2 up
um12315	uncharacterized protein	-	-	2.2 up	-	19.8 up	20.6 up	19.13up	26.2 up
um06470	related to BAS1 - Myb-related transcription factor	7.4 up	5.5 up	26.0 up	9.181 up	-	-	-	-
um06439	uncharacterized protein	-	-	3.3 up	3.5 up	3.6 up	11.4 up	17.7 up	25.7 up
um12175	related to BAS1 - Myb-related transcription factor	4.4 up	16.0 up	18.3 up	25.5 up	-	-	2.5 up	3.1 up
um05411	Probable quinate permease	4.4 up	11.7 up	15.9 up	25.3 up	6.7 up	7.3 up	7.4 up	7.8 up
um06138	Probable PTR2 - Di- and tripeptide permease	25.1 up	18.6 up	10.4 up	19.0 up	4.2 up	2.7 up	5.4 up	8.2 up
um05074	Probable Cytochrome P450 monooxygenase/Phenylacetate hydroxylase	24.9 up	10.5 up	4.9 up	3.7 up	6.2 up	3.7 up	4.8 up	-
um10529	uncharacterized protein	18.3 up	16.4 up	20.5 up	24.8 up	3.3 up	2.5 up	4.3 up	5.2 up
um04248	uncharacterized protein	14.9 up	15.5 up	17.9 up	14.9 up	24.7 up	20.8 up	22.7 up	13.1 up
um01424	Probable Cytochrome P450 monooxygenase/Phenylacetate hydroxylase	3.8 up	11.4 up	13.0 up	24.2 up	-	2.0 up	3.5 up	3.6 up

um11117	uncharacterized protein	-	2.6 up	12.6 up	24.2 up	7.2 up	8.7 up	2.3 up	4.2 up
um01984	Probable ADH1 - alcohol dehydrogenase I	20.9 up	23.4 up	24.0 up	23.4 up	12.4 up	11.5 up	15.5 up	12.7 up
um11051	uncharacterized protein	2.2 up	5.0 up	5.8 up	5.4 up	8.0 up	10.6 up	15.4 up	24.0 up
um10545	uncharacterized protein	23.8 up	8.0 up	3.7 up	3.9 up	8.3 up	4.2 up	5.9 up	5.7 up
um12178	Related to 5-carboxyvanillate decarboxylase	9.5 up	16.2 up	22.4 up	23.7 up	4.0 up	4.4 up	3.8 up	3.3 up
um01823	uncharacterized protein	15.7 up	23.3 up	8.3 up	5.2 up	9.4 up	5.5 up	15.1 up	6.3 up
um01425	Probable homogentisate 1,2-dioxygenase	4.9 up	7.9 up	10.7 up	23.3 up	3.2 up	3.2 up	5.1 up	5.8 up
um01888	Probable SERINE-TYPE CARBOXYPEPTIDASE F PRECURSOR	23.1 up	15.8 up	18.2 up	15.9 up	-	-	-	-
um00205	Related to HSP12 - heat shock protein	23.1 up	14.3 up	-	2.1 up	2.1 up	-	-	-
um11430	related to CSR1 - phosphatidylinositol transfer protein	15.8 up	22.9 up	22.5 up	21.8 up	12.3 up	8.9 up	16.3 up	11.7 up
um10070	related to Benzoate 4-monooxygenase	5.2 up	9.3 up	15.2 up	16.6 up	13.3 up	12.1 up	18.1 up	22.7 up
um03995	Related to JLP1 - Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase	22.6 up	20.8 up	12.2 up	6.1 up	2.4 up	-	-	-
um04353	Related to glycosyl transferase, group 2 family protein	22.3 up	22.4 up	15.9 up	6.1 up	13.3 up	10.3 up	14.9 up	14.0 up
um01868	Related to GIT1 - Glycerophosphoinositol transporter also able to mediate low-affinity phosphate transport	15.6 up	20.5 up	22.4 up	19.8 up	12.2 up	11.5 up	18.9 up	16.5 up
um10474	uncharacterized protein	16.3 up	22.2 up	17.5 up	16.3 up	5.6 up	6.3 up	8.4 up	8.6 up
um02157	uncharacterized protein	4.1 up	11.4 up	5.7 up	3.9 up	13.3 up	6.5 up	21.8 up	17.5 up
um10881	Probable ribonuclease T1	14.5 up	6.5 up	21.7 up	5.7 up	-	-	-	-
um03415	Related to putative monooxygenase	3.9 up	14.8 up	21.3 up	14.4 up	4.6 up	5.5 up	9.2 up	11.0 up
um04680	Related to Monocarboxylate transporter	8.8 up	13.8 up	16.9 up	21.1 up	6.0 up	4.9 up	8.0 up	8.1 up
um00116	Related to nicotinamide mononucleotide permease	9.8 up	20.9 up	12.7 up	20.2 up	3.0 up	4.0 up	9.9 up	6.8 up
um03076	uncharacterized protein	20.7 up	15.3 up	18.3 up	10.3 up	8.7 up	6.8 up	8.6 up	6.6 up
um02162	uncharacterized protein	-	-	-	-	17.4 up	21.1 up	20.7 up	18.8 up
um03023	Related to Ribonuclease Trv	20.5 up	14.0 up	18.3 up	10.3 up	11.1 up	14.6 up	13.7 up	8.5 up
um10946	Related to TNA1 - High affinity nicotinic acid plasma membrane permease	20.4 up	20.5 up	6.0 up	3.5 up	14.3 up	6.0 up	10.7 up	20.1 up
um03932	uncharacterized protein	3.7 up	13.8 up	13.3 up	19.4 up	3.1 up	6.2 up	20.3 up	8.8 up
um03474	related to TNA1 - high affinity nicotinic acid plasma membrane permease	2.3 up	7.3 up	15.7 up	20.2 up	-	-	3.5 up	6.8 up
um05301	uncharacterized protein	8.0 up	6.5 up	11.0 up	8.675 up	17.7 up	20.1 up	16.2 up	15.2 up
um12068	Related to N-acetylglucosaminyltransferase (C-terminal fragment)	20.0 up	13.1 up	12.0 up	11.0 up	4.3 up	5.0 up	3.4 up	7.1 up
um05528	uncharacterized protein	12.8 up	-	4.0 up	-	20.0 up	24.8 up	5.8 up	4.4 up
um11080	uncharacterized protein	10.1 down	17.8 down	18.0 down	20.6 down	6.4 down	6.6 down	4.7 down	3.2 down
um11815	uncharacterized protein	11.8 down	12.2 down	10.9 down	17.8 down	18.7 down	21.7 down	21.5 down	20.7 down
um00388	uncharacterized protein	19.1 down	23.2 down	20.7 down	18.8 down	-	-	-	-
um00204	related to Ca ²⁺ -transporting ATPase	4.3 down	14.5 down	9.1 down	14.8 down	23.5 down	18.7 down	5.8 down	4.2 down

um11244	related to FRE4 - Ferric reductase	12.4 down	11.3 down	9.1 down	12.3 down	23.7 down	21.0 down	13.5 down	12.9 down
um03116	Acyltransferase involved in MEL production	2.2 up	-	7.3 up	-	2.1 down	9.2 down	24.2 down	18.9 down
um03776	uncharacterized protein	2.9 down	8.4 down	12.7 down	17.6 down	18.5 down	13.1 down	23.4 down	24.6 down
um05782	Capsule-associated protein-like protein	7.3 down	14.3 down	6.2 down	11.7 down	8.9 down	9.3 down	24.8 down	18.6 down
um04118	uncharacterized protein	19.8 down	20.4 down	25.5 down	15.0 down	5.9 down	6.0 down	6.4 down	8.0 down
um11372	ENA2 - Plasma membrane P-type ATPase (N-terminal fragment - extended on um_contig_1.67 as um12056)	2.6 down	3.9 down	18.2 down	7.4 down	25.8 down	24.2 down	17.2 down	27.0 down
um12056	- probable ENA2 -	-	2.3 down	6.0 down	7.4 down	26.2 down	18.6 down	15.9 down	29.0 down
um01048	Odc - ornithine decarboxylase	2.5 down	2.6 down	2.9 down	2.5 down	27.0 down	27.9 down	21.6 down	27.1 down
um01983	uncharacterized protein	28.1 down	3.5 down	5.4 down	7.0 down	3.0 down	2.5 down	3.7 down	2.8 down
um05787	uncharacterized protein	13.8 down	28.3 down	15.8 down	31.6 down	4.1 down	4.5 down	19.4 down	15.2 down
um02497	uncharacterized protein	36.4 down	27.6 down	18.2 down	16.1 down	9.2 down	11.1 down	5.2 down	7.9 down
um02763	uncharacterized protein	16.2 down	37.4 down	3.4 down	5.9 down	14.6 down	16.8 down	8.9 down	5.8 down
um01434	Fer3 - Siderophore peptide synthetase involved in ferrichromeA biosynthesis	14.0 down	11.4 down	7.7 down	20.6 down	37.076 down	40.296 down	18.912 down	24.335 down
um00082	uncharacterized protein	41.6 down	36.9 down	20.1 down	23.0 down	10.4 down	8.5 down	8.6 down	3.9 down
um04791	related to G1/S-specific cyclin	-	-	-	-	24.6 down	18.2 down	38.4 down	26.2 down
um01439	Fer9 - related to FRE3 - Ferric reductase, reduces siderophore-bound iron prior to uptake	9.3 down	10.8 down	5.0 down	15.4 down	41.0 down	45.8 down	23.0 down	21.1 down
um11339	Fer7 - related to Siderophore iron transporter 3	3.0 down	2.7 down	-	2.7 down	47.3 down	24.3 down	3.0 down	7.2 down
um01432	Fer5 - related to N6-hydroxylysine acetyl transferase	3.4 down	6.8 down	5.3 down	11.9 down	47.4 down	36.9 down	12.1 down	18.2 down
um00309	uncharacterized protein	9.1 down	27.3 down	18.6 down	39.1 down	47.5 down	44.1 down	38.1 down	39.0 down
um01947	Related to cytochrome-c peroxidase precursor	2.6 down	16.5 down	14.8 down	48.2 down	-	-	3.0 down	3.6 down
um10221	uncharacterized protein	-	5.9 down	8.1 down	13.5 down	20.7 down	13.5 down	50.2 down	40.9 down
um05785	Acyl transferase-like protein	5.9 down	15.3 down	9.0 down	18.8 down	8.2 down	4.8 down	58.5 down	29.8 down
um01433	Fer4 - related to Enoyl-CoA hydratase	13.5 down	20.1 down	8.6 down	36.0 down	61.4 down	56.7 down	45.1 down	49.1 down
um03642	uncharacterized protein	2.0 down	2.7 down	-	-	37.0 down	37.6 down	76.8 down	38.5 down
um03524	related to peroxisomal amine oxidase (copper-containing)	3.6 down	2.9 down	2.9 down	-	80.5 down	79.1 down	63.2 down	73.8 down
um10186	uncharacterized protein	7.6 down	15.0 down	21.8 down	42.7 down	11.0 down	13.6 down	119.2 down	102.1 down

um10070		5.6 up	9.6 up	15.9 up	17.7 up	13.2 up	12.1 up	18.1 up	21.8 up	12.8 up
um02196		1.4 down	-	-	-	2.6 up	2.7 up	2.2 up	2.6 up	90.3 up
um02197		1.9 up	2.5 up	2.9 up	2.9 up	3.1 up	3.0 up	4.3 up	4.0 up	
um02472	5B(non pathogenic)	2.2 down	-	-	-	3.1 down	2.2 down	-	-	5.2 down
um02476		-	-	-	-	2.2 down	2.3 down	-	-	1.7 down
um11414	6A (virulence reduced)	3.5 up	2.9 up	3.4 up	3.0 up	5.5 up	6.4 up	5.1 up	5.4 up	
um02533		-	-	-	-	-	-	-	3.1 up	65.1 up
um11415		2.1 up	3.2 up	-	-	2.4 down	-	-	2.3 up	
um11416		-	2.3 down	-	-	-	-	-	-	32 up
um02537		-	-	-	-	2.4 up	2.0 up	-	-	41.8 up
um02538		-	-	-	-	-	-	-	-	
um11417		2.2 down	2.7 down	2.0 down	2.4 down	-	2.3 up	-	2.9 up	
um02540		2.1 down	2.4 down	-	-	4.9 up	4.2 up	3.3 up	4.2 up	2.9 up
um02541		2.6 down	3.6 down	2.7 down	3.1 down	2.0 up	-	2.1 up	2.5 up	
um02542		-	-	-	-	5.2 up	5.4 up	5.7 up	5.3 up	2.5 down
um03200	8A (virulence unaffected)	-	-	-	-	2.2 down	2.4 down	2.3 down	-	
um10403		-	2.3 up	-	-	-	-	-	-	315 up
um03315	9A (virulence unaffected)	3.0 up	2.5 up	2.7 up	2.4 up	-	2.0 down	-	-	
um03316		3.2 up	2.3 up	2.4 up	-	2.3 up	2.6 up	1.7 up	2.1 up	1.8 down
um03316		3.5 up	2.1 up	2.5 up	-	-	-	1.0	-	
um03743	10A (virulence reduced)	2.2 down	2.5 down	2.4 down	2.0 down	-	-	-	-	2.5 down
um03744		2.4 down	2.2 down	2.2 down	2.3 down	-	-	-	-	35.1 up
um03750		-	-	3.6 up	2.8 up	-	-	-	-	
um03751		-	2.4 down	-	-	2.4	-	2.5	-	18.9 up

						down		down		
um03753		5.7 up	4.9 up	5.0 up	4.7 up	3.7 up	3.9 up	2.4 up	3.6 up	1.6 up
um03754		-	2.4 up	-	-	-	-	-	-	
um10660	19A (virulence dramatically Reduced)	2.4 up	-	-	-	3.1 up	3.3 up	2.6 up	2.4 up	2 up
um05293		3.5 up	3.8 up	3.6 up	3.6 up	2.4 up	2.2 up	2.5 up	2.3 up	2.1 down
um05296		-	-	-	-	-	2.1 up	2.2 up	2.6 up	11.3 up
um05308		-	-	-	-	-	1.2 up	2.2 down	-	4.3 up
um05310		2.4 down	3.1 down	2.2 down	2.7 down	2.5 down	2.6 down	6.4 down	4.7 down	28.2 up
um10557		-	-	-	-	-	2.0 up	-	-	
um05319		-	-	-	-	2.0 up	3.0 up	-	-	2.6 up
um11233		22A (virulence unaffected)	2.0 down	1.2 down	1.2 down	-	-	-	-	-
um06221	2.6 down		2.2 down	3.3 down	2.6 down	-	-	2.1 down	-	
um06224	2.2 down		-	2.3 down	-	2.7 down	2.4 down	2.1 down	2.3 down	3.1 down

supplementary Table S3. Genes coding for transcription factors differentially regulated in *U. maydis* during *A. thaliana* infection.

ID	Description	Name or Domain	Reference	Fold change during <i>Arabidopsis thaliana</i> infection								
				Days post-infection with the haploid strain FB2				Days post-infection with the diploid strain Uid1				
				1	2	4	8	1	2	4	8	16
um00174	Related to transcriptional regulator protein SPT6	SPT6	UniProt	2.4 down	-	-	-	2.6 down	2.8 down	2.4 down	2.4 down	2.4 down
um00195	Putative protein	gal4, Zn clus	UniProt	4.8 down	3.6 down	3.9 down	2.5 down	4.9 down	4.8 down	2.6 down	2.6 down	2.6 down
um00300	Conserved hypothetical protein	FSTF, GAL4	UniProt	5.5 down	4.4 down	4.9 down	3.7 down	6.2 down	4.9 down	4.8 down	4.8 down	4.8 down
um00316	Conserved hypothetical protein	gal4, Zn clus	UniProt	2.8 down	-	2.9 down	-	2.0 down	3.2 down	2.4 down	2.4 down	2.4 down
um00332	related to transcription factor TFIIC subunit	TFIIC	MIPS <i>Ustilago maydis</i> DataBase	-	-	-	2.0 up	-	-	-	-	-
um00377	Conserved hypothetical protein	FSTF	Pfam, MIPS <i>Ustilago maydis</i> DataBase, UniProt	-	-	-	2.1 up	-	-	-	-	-
um00467	Conserved hypothetical protein	gal4, Zn clus	UniProt	-	-	2.1 down	-	-	-	-	-	-
um00483	Putative protein	bZIP	PF00170, UniProt	4.0 down	3.6 down	2.7 down	2.4 down	2.4 down	2.3 down	-	-	-
um00489	um11825	Conserved hypothetical protein	Homeodomain	PF05920, UniProt	2.2 down	-	-	-	2.4 down	2.5 down	-	-
um00491	Related to BRF1 - TFIIB subunit, 70 kD	TFIIB	UniProt	2.0 down	2.1 down	-	-	-	-	-	-	-
um00523	Related to CDC36 - transcription factor	CDC36	MIPS <i>Ustilago maydis</i> DataBase	2.7 down	2.5 down	2.6 down	2.0 down	2.3 down	2.1 down	-	-	-
um00528	Conserved hypothetical protein	FSTF, GAL4	UniProt	2.5 up	2.1 up	3.9 up	3.4 up	-	-	2.8 up	2.8 up	2.8 up
um00533	Related to PPR1 - transcription factor regulating pyrimidine pathway	PPR1 FSTF "GAL4"	UniProt	-	-	-	-	2.1 down	2.4 down	-	-	-
um00577	um12052	bE1 - b mating type locus, bE1 allele	bE1	PF05920, PF05722, PF05062, UniProt	-	-	-	-	2.0 up	2.6 up	2.6 up	2.6 up
um00578		bW1 - b mating type locus, bW1 allele	bW1	PF00046, UniProt	-	-	-	-	-	2.6 up	5.3 up	5.3 up
um00669	Related to TFB3 - TFIIF subunit (transcription/repair factor)	MAT1, TFB3 - TFIIF	KEGG	2.2 down	2.1 down	2.2 down	2.4 down	-	-	-	-	-
um00750	Putative protein	gal4, Zn clus	UniProt	3.3 down	3.8 down	-	-	3.1 down	2.6 down	2.5 down	2.5 down	2.5 down
um00767	Hypothetical protein	bZIP	UniProt	-	-	-	-	2.2 down	2.4 down	-	-	-
um00808	Conserved hypothetical protein	Homeodomain, HMG	PF00505	2.5 down	-	-	-	2.7 down	2.9 down	2.6 down	2.6 down	2.6 down
um00841	Conserved hypothetical protein	gal4 Zn clus	UniProt	5.2 up	5.5 up	7.4 up	7.2 up	9.0 up	8.1 up	8.5 up	8.5 up	8.5 up
um00895	Conserved hypothetical protein	Znf GATA	UniProt	2.1 down	-	-	-	2.3 down	-	-	-	-
um00922	Related to TFIIF basal transcription factor complex p34 subunit	TFIIF	KEGG	-	-	-	-	-	2.0 up	2.1 up	2.1 up	2.1 up
um00946	Uncharacterized protein	Zinc finger, C2H2-like	MIPS <i>Ustilago maydis</i> DataBase	5.0 up	5.2 up	4.3 up	5.9 up	-	-	2.4 up	2.4 up	2.4 up
um01016	Conserved hypothetical protein	efg1	Zavrel, et al. ⁸³	2.4 down	2.4 down	2.6 down	-	-	2.0 up	-	-	-
um01025	Conserved hypothetical protein	gal4 Zn clus	UniProt	2.1 down	2.4 down	2.4 down	2.2 down	-	-	2.0 up	2.0 up	2.0 up
um01042	Putative protein	Fork head	SUPERFAMILY, UniProt	-	-	-	-	2.1 down	-	-	-	-
um01050	Urbs1 - Siderophore biosynthesis regulatory protein URBS1	Urbs1	UniProt	6.1 down	6.0 down	4.3 down	2.8 down	2.2 down	2.7 down	-	-	-
um01104	Conserved hypothetical protein	TFIIE2-beta	KEGG, UniProt	2.3 up	-	-	-	5.9 up	5.0 up	2.7 up	2.7 up	2.7 up
um01371	um01371.2	Related to RRN3 - RNA polymerase I specific transcription factor	RRN3	MIPS <i>Ustilago maydis</i> DataBase	2.3 down	-	-	-	2.0 down	-	-	-
um01390	Conserved hypothetical protein	HMG	PF00505	2.6 down	-	-	-	3.8 down	3.5 down	2.3 down	2.3 down	2.3 down
um01457	um11658	Hmg3 - HMG-box protein Hmg3	Hmg3	PF00505, UniProt	-	-	-	-	-	2.1 up	2.7 up	2.7 up
um01482	Hypothetical protein	gal4 Zn clus	UniProt	-	-	-	-	2.7 down	3.1 down	2.0 down	2.0 down	2.0 down
um01523	Conserved hypothetical protein	Fox1, Fork head	SUPERFAMILY, UniProt	2.0 down	-	-	2.1 down	-	-	2.2 up	2.2 up	2.2 up
um01529	Related to TAF10 - TFIID and SAGA subunit	TAF10 - TFIID	KEGG	-	2.1 down	2.8 down	2.2 down	-	-	-	-	-
um01556	Related to transcriptional activator Mut3p	FSTF, GAL4	PF04082, UniProt	2.0 down	-	-	-	-	-	-	-	-
um01597	Hypothetical protein	hap2	Mendoza-Mendoza et al. ⁶⁸	5.2 down	2.8 down	2.6 down	-	2.9 down	2.2 down	-	-	-
um01908	Related to CCAAT-binding transcription factor subunit aab-1	aab-1	MIPS <i>Ustilago maydis</i> DataBase	11.2 down	4.1 down	5.9 down	3.5 down	6.5 down	5.4 down	2.3 down	2.3 down	2.3 down
um01925	um10450	Related to transcriptional regulator rds2	ERT1 gluconeogenic	UniProt	-	-	2.3 up	-	-	-	-	-
um01961	Hypothetical protein	FSTF, GAL4	UniProt	-	-	2.2 up	-	-	-	-	-	-
um01975	um11379	Putative protein	gal4, Zn clus	UniProt	4.8 up	2.9 up	3.9 up	2.8 up	-	-	-	-
um02061	um11462	Putative protein	gal4, Zn clus	UniProt	-	-	4.8 up	2.8 up	-	-	2.5 up	2.5 up
um02191	UM02191.2	Conserved hypothetical protein	yap1, B-ZIP	PF10297, PF00170	7.9 down	5.0 down	2.5 down	2.9 down	5.8 down	4.6 down	2.1 down	2.1 down
um02257	um15078	Hypothetical protein	gal4, Zn clus	UniProt	3.3 down	2.6 down	2.1 down	-	2.4 down	2.3 down	-	-
um02280	Putative protein	Homeodomain, Heat-shock	SUPERFAMILY, UniProt	-	-	-	-	-	2.6 down	-	-	-
um02301	Related to C2H2-type zinc finger protein	Zf	PF13465, MIPS <i>Ustilago maydis</i> DataBase	26.5 up	26.6 up	27.1 up	30.4 up	5.4 up	4.7 up	5.6 up	5.6 up	5.6 up

um02328	um11705	Hypothetical protein	TFIID	UniProt	5.5 down	5.5 down	3.0 down	2.5 down	2.1 down	-	-	
um02364	um10132	Probable NHP6B - nonhistone chromosomal protein	NHP6, FACT	UniProt	2.0 down	-	-	-	-	-	-	2.9 down
um02394	um10143	Probable TATA-box-binding factor TBP	TBP, TFIID	PF00352, KEGG, UniProt	2.3 up	2.2 up	2.8 up	2.9 up	2.5 up	2.6 up	3.7 up	
um02510	um02510.2	Probable PGU1 - Endo-polygalacturonase	pg2	MIPS <i>Ustilago maydis</i> DataBase	2.6 up	2.1 up	2.1 up		2.8 up	2.4 up		
um02582		Rum1 - regulator <i>Ustilago maydis</i> 1 protein (Rum1)	Rum1, JmjC, TF	MIPS <i>Ustilago maydis</i> DataBase	-	-	-	-	3.1 down	2.8 down	2.2 down	
um02447	um10159	Related to transcription activator amyR	FSTF, GAL4	UniProt	2.0 down	-	-	-	2.3 down	-	-	
um02602	um10282	Putative protein	FSTF, GAL4	UniProt	4.0 down	2.3 down	2.6 down	2.3 down	-	2.4 down	-	
um02664		Related to zinc finger protein white collar 2 (wc-2)	zf wc-2	UniProt	-	2.3 up	2.6 up	3.5 up	-	-	2.8 up	
um02775		Hypothetical protein	p53-like TF DNA-bd	UniProt	2.3 down	2.1 down	-	-	-	-	-	
um02827		Conserved hypothetical protein	FSTF, GAL4	PF04082, UniProt	2.6 down	2.1 down	2.1 down	-	2.3 down	2.1 down	2.1 down	
um02835		Conserved hypothetical protein	TEA	UniProt	-	3.9 up	3.8 up	-	4.6 up	3.1 up	5.2 up	
um02857		Conserved hypothetical protein	Znf C2H2	UniProt	-	-	-	-	2.1 down	2.1 down	-	
um02896		Putative protein	bZIP	UniProt	2.6 down	-	-	-	2.4 down	2.6 down	-	
um02989		Related to IME4 - positive transcription factor for IME2	IME4	Shah et al. ⁸⁴	-	-	-	-	2.7 up	2.2 up	-	
um03040		Hypothetical protein	gal4, Zn clus	UniProt	4.2 up	6.9 up	7.2 up	12.2 up	3.6 up	3.8 up	7.5 up	
um03053	um10368	Related to Heat shock factor protein	HSFDOMAIN, Heat-shock	SUPERFAMILY, UniProt	6.7 down	4.9 down	7.1 down	4.4 down	7.4 down	5.8 down	4.1 down	4.1
um03079		Related to TAF5 - TFIID and SAGA subunit	TAF5 - TFIID	KEGG	2.2 down	-	2.3 down	2.1 down	4.1 down	3.5 down	3.3 down	3.3
um03130	um10379	Related to CCR4 - transcriptional regulator involved in carbon catabolite repression (C-terminal fragment)	CCR4, Glucose-repressible, ADH2	UniProt	-	-	-	-	2.1 down	-	-	
um03172		Related to Zinc finger protein	Zf rbf1	PF13465	-	-	-	-	-	-	-	
um03296		Hypothetical protein	bZIP	PF00170, UniProt	5.6 up	15.3 up	8.5 up	13.7 up	-	2.5 up	8.7 up	
um03346	um03346.2	related to SKN7 - transcription factor (C-terminal fragment)	SKN7	MIPS <i>Ustilago maydis</i> DataBase	-	-	2.1 up	3.1 up	-	-	-	
um03328	um10654	Related to TFB5 - component of general transcription and DNA repair factor TFIIF	TFB5 TTDA TFIIF	PF06331, KEGG, UniProt	2.0 up	-	-	-	3.5 up	3.6 up	-	
um03396		Hypothetical protein	gal4 Zn clus	UniProt	-	-	2.0 up	-	-	-	2.1 up	
um03403	um03403.2	Conserved hypothetical protein	Znf C2H2	UniProt	-	-	2.6 up	2.2 up	-	-	-	
um03416		Crg1 - carbon source-regulated protein (putative arabinase)	Crg1	MIPS <i>Ustilago maydis</i> DataBase	5.4 up	4.5 up	9.9 up	6.6 up	-	-	-	
um03450		Related to FAP7 - involved in the oxidative stress response	FAP7, TAB9	KEGG	-	-	-	-	-	2.0 up	-	
um03509	um11782	Putative protein	bZIP	PF00170, UniProt	3.8 down	3.4 down	3.2 down	3.1 down	5.4 down	5.5 down	2.8 down	2.1
um03514		Putative protein	FSTF, GAL4	UniProt	2.2 down	-	-	-	2.4 down	2.1 down	-	
um03568		Related to regulatory protein alcR	gal4, Zn clus	UniProt	4.4 up	8.2 up	16.5 up	13.4 up	2.2 up	2.2 up	3.9 up	
um03613		Putative protein	FSTF, GAL4	UniProt	2.1 up	-	-	-	2.5 down	2.8 down	2.0 down	
um03672	um10482	Probable transcription initiation factor iia gamma chain	IIA subunit 2	KEGG, SUPERFAMILY, UniProt	-	-	-	-	3.8 up	3.9 up	2.1 up	
um03680		Related to TFA1 - TFIIE subunit (transcription initiation factor), 66 kD	TFA1 - TFIIE1	KEGG	8.1 down	8.6 down	6.0 down	5.3 down	3.2 down	3.0 down	2.2 down	
um03714		Related to lactose regulatory protein	FSTF, GAL4	PF04082, UniProt	-	-	2.0 up	2.2 up	-	-	-	
um03802		Related to TAF6 - Subunit (60 kDa) of TFIID and SAGA complexes	TAF6, TAF_TATA-bd	KEGG, UniProt	-	-	-	-	2.3 down	-	-	
um03843		Putative protein	gal4, Zn clus	UniProt	2.9 up	2.5 up	4.9 up	3.0 up	2.4 up	-	2.1 up	
um03907	um11970	Putative protein	Znf_gata Erythroid transcription factor GATA-1	SUPERFAMILY	3.9 down	3.6 down	4.2 down	4.0 down	7.8 down	6.8 down	5.4 down	5.1
um03981	um11973	Probable NIT2 - nitrilase	nit2	Horst et al. ²⁹	2.2 up	-	-	-	-	-	-	
um04007		Conserved hypothetical protein	HMG	PF00505	2.0 down	-	-	-	-	-	-	
um04024	um11055	Conserved hypothetical protein	HTH APSES	UniProt	-	-	-	-	3.0 down	2.6 down	-	
um04076		Conserved hypothetical protein	Znf GATA	SUPERFAMILY, UniProt	2.1 down	-	2.8 down	3.3 down	3.9 down	5.4 down	4.9 down	4.1
um04083		Conserved hypothetical protein	FSTF, GAL4	PF04082, UniProt	2.8 down	2.2 down	2.4 down	2.2 down	-	2.4 down	2.0 down	2.1
um04101		Related to BAS1 - transcription factor	BAS1	MIPS <i>Ustilago maydis</i> DataBase	-	-	-	-	3.2 up	-	2.8 up	
um04208		Conserved hypothetical protein	FSTF, GAL4	UniProt	9.0 down	16.0 down	7.1 down	6.6 down	11.1 down	9.0 down	6.0 down	2.1
um04235	um12255	Conserved hypothetical protein	FSTF, GAL4	Pfam, MIPS <i>Ustilago maydis</i> DataBase, UniProt	3.2 down	2.5 down	2.1 down	-	2.5 down	2.7 down	-	
um04242		Conserved hypothetical protein	FSTF, GAL4	PF04082, UniProt	3.5 down	2.3 down	2.0 down	2.2 down	-	-	-	
um04252	um10417	Related to transcription factor ScGATA-6	Znf_gata Erythroid transcription factor GATA-1	SUPERFAMILY, UniProt	-	-	-	-	2.7 down	2.7 down	2.2 down	
um04274	um10426	PacC - Transcription factor pacC	pacC	Arechiga et al. ⁸⁵	6.8 down	6.6 down	7.1 down	6.8 down	6.9 down	6.6 down	5.2 down	3.1
um04293		Conserved hypothetical protein	gal4, Zn clus	UniProt	-	2.4 up	3.2 up	4.1 up	-	-	-	

um04412	um10519	Putative protein	bZIP	PF00170, UniProt	2.3 up	2.9 up	3.7 up	4.2 up	-	-	2.8 up	2
um04416		Probable POB3 - protein that binds to DNA polymerase I	POB3, FACT	UniProt	-	-	-	-	2.0 up	2.3 up	2.9 up	2
um04421		Hypothetical protein	gal4, Zn clus	UniProt	2.5 up	-	-	-	2.7 up	2.9 up	-	2
um04465		Related to transcription regulator SPT7	SPT7, BromodomainTF	MIPS <i>Ustilago maydis</i> DataBase	-	-	-	-	2.1 down	2.1 down	-	2
um04688		Conserved hypothetical protein	gal4, Zn clus	UniProt	2.5 up	3.6 up	5.1 up	6.4 up	-	-	3.0 up	3
um04774	um12004	Conserved hypothetical protein	Zf_ace	PF13465	2.0 down	-	-	-	2.8 down	3.1 down	2.5 down	2
um04806		Conserved hypothetical protein	FSTF, GAL4	UniProt	-	-	2.0 up	2.1 up	-	-	-	3
um04875		Conserved hypothetical protein	Zf	PF13465	-	-	-	2.0 up	-	-	2.3 up	3
um04885		Conserved hypothetical protein	FSTF, GAL4	PF04082, UniProt	-	-	-	-	-	-	3.6 up	2
um04902		Cyclin-dependent ser/thr protein kinase	CDK7 kin28	KEGG	-	-	-	-	3.8 up	4.1 up	3.5 up	2
um04999		Related to RDS2 - Regulator of drug sensitivity	RDS2, gal4, Zn clus	UniProt	3.9 down	4.0 down	-	-	-	-	-	2
um05050		Hypothetical protein	gal4, Zn clus	UniProt	-	2.1 up	3.8 up	3.1 up	-	-	-	2
um05054		Conserved hypothetical protein	Fork head	SUPERFAMILY, UniProt	2.1 down	2.1 down	2.0 down	-	2.6 down	2.6 down	-	2
um05144	um10181	Conserved hypothetical protein	Ace2	MIPS <i>Ustilago maydis</i> DataBase	2.5 down	2.4 down	-	-	-	-	-	2
um05151		Related to Cyclin H	CCNH, Cyclin H	KEEG	-	-	2.1 down	-	-	-	-	2
um05182		Hypothetical protein	HSFDOMAIN, Heat-shock	SUPERFAMILY, UniProt	4.7 down	5.4 down	3.8 down	2.6 down	-	-	-	2
um05183		Related to TOA1 - transcription factor TFIIA-L	TOA1 "TFIIA-L" "TFIIA1	KEGG, SUPERFAMILY, UniProt	2.3 up	2.2 up	2.8 up	2.7 up	3.8 up	3.5 up	3.3 up	3
um05274		Related to Heat shock factor protein 4	HSFDOMAIN, Heat-shock	SUPERFAMILY, UniProt	3.0 up	3.2 up	3.7 up	4.3 up	-	-	-	2
um05281	um10551.2	Probable SSL1 - TFIIH subunit (transcription initiation factor), factor B	SSL1 - TFIIH2	KEGG	-	2.2 down	2.0 down	-	-	-	-	2
um05338		Related to transcription factor MBP1	MBP1	UniProt	-	-	-	-	3.7 down	3.9 down	4.2 down	3
um05401		Conserved hypothetical protein	FSTF, GAL4	UniProt	3.6 down	2.7 down	4.2 down	2.9 down	8.2 down	8.7 down	4.3 down	8
um05483	um12303	Hypothetical protein	gal4, Zn clus	UniProt	-	-	3.5 up	6.0 up	-	-	-	2
um05515		Hypothetical protein	gal4, Zn clus	UniProt	-	-	-	-	2.0 down	2.1 down	-	2
um05518		Hypothetical protein	Znf_GATA	UniProt	2.2 down	2.1 down	-	-	2.3 down	2.4 down	-	2
um05577		Conserved hypothetical protein	Znf_GATA	UniProt	-	-	-	-	2.0 down	-	-	2
um05578	um11176	Conserved hypothetical protein	bZIP	PF00170, UniProt	3.5 down	2.9 down	2.8 down	2.7 down	4.6 down	4.8 down	3.5 down	3
um05601		Hypothetical protein	FSTF, GAL4	PF04082, UniProt	2.3 down	2.0 down	2.5 down	2.5 down	-	-	-	2
um05694		Hypothetical protein	bZIP	PF00170, UniProt	3.2 up	2.5 up	-	-	2.0 up	2.1 up	2.2 up	2
um05723	um10941	Conserved hypothetical protein	gal4, Zn clus	UniProt	-	-	-	-	-	-	2.3 up	2
um05762	um12024	Putative protein	Homeodomain, hdp1	PF00046, UniProt	-	-	5.6 up	2.0 up	-	-	-	2
UM05770		Tsd2 - TSD2 protein, required for DNA replication	TSD2, CDC45	UniProt	-	-	-	-	-	-	-	2
um05773		Putative protein	Znf_GATA	UniProt	4.0 down	2.5 down	3.7 down	2.3 down	7.4 down	6.1 down	5.2 down	3
um05801		Related to C2H2 zinc finger protein	Znf_C2H2	UniProt	-	2.1 down	-	-	-	-	-	2
um05820		Hypothetical protein	gal4, Zn clus	UniProt	2.3 up	3.0 up	2.0 up	2.8 up	-	-	2.4 up	2
um05854		Conserved hypothetical protein	EAF1, Helicase, Homeodomain-like	UniProt	2.1 down	-	-	-	2.0 down	-	-	2
um05888		Related to transcription elongation factor TFIIIS	TFIIIS	PF08711	-	2.2 down	-	-	-	2.3 up	2.3 up	2
um05937		Putative Cys(2)His(2) zinc finger protein	Znf23	MIPS	2.7 up	2.7 up	4.4 up	2.6 up	-	-	-	2
um05966		Conserved hypothetical protein	FSTF, GAL4	UniProt	13.7 up	12.7 up	17.6 up	16.3 up	7.7 up	6.1 up	6.5 up	1
um06025	um12033	Rop1 - HMG-box transcription factor (C-terminal fragment)	rop1	Brefort et al. ⁸⁶	-	-	3.1 up	-	-	-	-	2
um06115	um11211	Conserved hypothetical protein	cut1	MIPS <i>Ustilago maydis</i> DataBase	-	2.3 down	2.0 down	-	-	-	-	2
um06160	um11298	Related to NHP6B - nonhistone chromosomal protein	HMG, NHP6B	PF00505	3.3 down	2.8 down	2.4 down	2.6 down	3.3 down	4.4 down	4.9 down	3
um06196	um11222	Related to MBP1 - transcription factor, subunit of the MBF factor	MBP1	MIPS <i>Ustilago maydis</i> DataBase, UniProt	-	-	-	-	2.5 down	-	-	2
um06231		Conserved hypothetical protein	Fork head	SUPERFAMILY, UniProt	-	-	-	-	-	-	-	2
um06256		Hypothetical protein	FSTF, GAL4	UniProt	-	-	-	-	2.5 down	2.5 down	2.3 down	2
um06257		Conserved hypothetical protein	FSTF, GAL4	UniProt	3.3 down	3.7 down	3.1 down	2.8 down	3.0 down	2.8 down	3.0 down	2
um06278		Conserved hypothetical protein	gal4, Zn clus	UniProt	-	-	-	2.8 up	-	-	-	2
um06280		Related to J kappa-recombination signal binding protein	J kappa-recombination	UniProt	2.1 down	-	-	-	-	2.4 down	-	2
um06283	um12332	Conserved hypothetical protein	Homeodomain	PF00046, UniProt	15.1 down	13.6 down	14.4 down	13.0 down	8.7 down	8.3 down	9.8 down	6
um06296		Probable TFB2 - TFIIH subunit (transcription/repair factor)	TFB2 - TFIIH4	KEGG	-	-	-	-	2.0 up	-	2.0 up	2
um06385		Conserved hypothetical protein	bZIP	PF00170, UniProt	2.3 down	2.5 down	2.2 down	2.2 down	-	-	-	2
um06493		Conserved hypothetical protein	FSTF, gal4 Zn_clus	Pfam, MIPS <i>Ustilago maydis</i> DataBase, UniProt	2.1 up	2.5 up	2.7 up	2.0 up	-	-	2.3 up	2

