Chromosome	Protein ID	Start position	End position	N^{o} of aligned codons	N^{o} of codons in predicted protein	N^{o} exons	EST support in *M. graminicola*	Nonsyn. mutations	Syn. mutations	Nei-Gojobori Ka/Ks[1]	Nei-Gojobori Ka	Nei-Gojobori Ks	Nei-Gojobori Z-test
1	88648	345834	347144	178	178	2	-	29	1	8.4660	0.0701	0.0083	4.1163
5	80707	657996	658613	125	125	1	+	24	1	6.9278	0.0825	0.0119	3.5281
9	105739	1229120	1229686	106	106	1	+	29	2	4.5537	0.1198	0.0263	3.3637
8	105480	1228554	1229995	77	78	1	+	14	1	4.5507	0.0803	0.0176	2.3198
8	105585	1882466	1882964	67	67	1	+	8	0	4.5357	0.0536	0.0118	1.7116
14	106599	671189	671736	106	119	1	+	19	1	3.9890	0.0801	0.0201	2.5227
17	97831	366251	366577	108	109	1	-	12	1	3.7622	0.0486	0.0129	1.9019
7	105176	983411	984541	140	140	1	+	11	1	3.6357	0.0348	0.0096	1.7974
18	97878	208583	209645	121	255	3	-	13	1	3.5967	0.0457	0.0127	1.8658
4	104171	1509984	1510593	53	53	1	+	19	1	3.5180	0.1585	0.0450	2.3882
6	93764	887981	888401	118	121	2	-	11	1	3.4401	0.0408	0.0119	1.7168
9	105694	727490	728225	159	161	2	+	18	2	3.1043	0.0508	0.0163	2.1043
1	33513	5083051	5083254	66	68	1	+	16	2	2.9746	0.1109	0.0373	2.0017
1	90306	5988847	5989320	88	158	1	+	22	2	2.8947	0.1053	0.0364	2.0891
6	104710	179204	179771	76	88	2	+	27	3	2.7990	0.1574	0.0563	2.4156
5	104488	1196254	1197312	155	156	2	+	25	3	2.7381	0.0714	0.0261	2.2381
20	98031	173524	175257	139	259	5	-	27	3	2.5223	0.0871	0.0345	2.1813
2	103264	1992714	1993521	109	111	2	+	37	4	2.5060	0.1499	0.0598	2.5660
20	98060	362354	362878	132	152	2	-	23	3	2.4759	0.0768	0.0310	1.9565
7	100838[2]	1785582	1786221	115	115	2	+	21	3	2.4706	0.0824	0.0333	1.9163
1	90212	5612533	5613441	82	120	2	+	25	3	2.3849	0.1376	0.0577	2.0384
21	98101	253102	253948	70	120	2	-	19	2	2.3111	0.1204	0.0521	1.6650
9	105817	2092225	2092890	87	120	1	+	19	3	2.2047	0.1043	0.0473	1.7115
17	97821	302722	303180	116	119	2	-	20	3	2.1770	0.0762	0.0350	1.7010
1	83337	534698	534961	88	88	1	+	18	3	2.0135	0.0911	0.0452	1.4015
12	106257	176773	177370	96	98	1	+	28	5	1.7696	0.1323	0.0748	1.6746
20	98059	360675	361856	200	394	1	-	55	10	1.6948	0.1199	0.0708	1.8643
20	98027	152654	153616	293	321	1	-	45	7	1.6931	0.0663	0.0392	1.7099
1	88614	211916	212437	95	174	1	-	33	6	1.6150	0.1544	0.0956	1.3584
11	96691	938961	939374	138	138	1	-	55	10	1.6075	0.1753	0.1091	1.7475
14	106598	668801	670705	440	445	3	+	84	16	1.6044	0.0842	0.0525	2.0817
1	102326	2430482	2430800	71	74	1	+	3	0	-	0.0176	0.0000	1.7475
1	102715	4102944	4103468	59	62	1	+	3	0	-	0.0227	0.0000	1.7521
1	90122	5331411	5332291	107	108	3	-	4	0	-	0.0161	0.0000	2.0163
2	108330	3382976	3384058	40	64	3	-	10	0	-	0.1075	0.0000	3.3474
3	79746	55468	55976	47	76	2	+	3	0	-	0.0285	0.0000	1.7573
3	103617	907856	908908	92	92	1	+	8	0	-	0.0380	0.0000	2.8837
4	104217	1865219	1865677	76	76	1	+	9	0	-	0.0520	0.0000	3.0812
9	82188	1590928	1591453	52	52	1	+	16	0	-	0.1341	0.0000	4.2985
9	82188	1590928	1591453	49	52	1	+	4	0	-	0.0353	0.0000	2.0363
11	106231	1469937	1470567	75	75	1	+	3	0	-	0.0171	0.0000	1.7471
12	106324	564439	564970	57	57	1	+	10	0	-	0.0759	0.0000	3.2897
20	98001	35726	36951	13	254	4	-	4	0	-	0.1290	0.0000	2.1430

[1] Not calculated for synonymous muations = 0

[2] Signal peptide