

Web Table A. Predicted genes in the 261-kb sequence contig spanning the Morex *Mla* locus.

Predicted gene product	Position ^a	Strand	BLASTX Search			Best EST BLASTN Match		
			Best homolog GenBank ID	E-value	Predicted function ^b	GenBank ID (Species) ^c	E-value	Longest match (bp)
711N16.16	<476 ... 2898	-	AAC17615	5e-38	unknown, similar to <i>Arabidopsis</i> hypothetical protein			
711N16.15	4045 ... 4466	+	CAA84230	6e-12	extensin-like protein [<i>Zea mays</i>]			
711N16.14	9073 ... 12450	-			unknown			
BPM	15373 ... 21468	-	AAK73144	1e-137	putative pumilio/Mpt5 RNA-binding protein [<i>Oryza sativa</i>]	AW982507	0	734
						BG414539	0	857
BMTa	<22721 ... >22903	-	AAF164398	1e-15	maturase [<i>Bromus inermis</i>]			
BMTb	<25299 ... >25490	-	AAF164384	7e-11	maturase [<i>Brachelytrum erectum</i>]			
BDI	<29965 ... >30140		AJ250665 (DNA only)	2e-38	induced in barley by chemicals that activate disease resistance	BF260884	6e-42	176
						BE420733	1e-41	158
711N16.9	37785 ... 39765	+			unknown			

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711N16.8 ^d	49502 ... 53442	-	BAB64724	1e-65	hypothetical protein [<i>Oryza sativa</i>]	BF617740	0	434
RGH3b	62862 ... 65673	-	AF149112	9e-45	stripe rust resistance protein Yr10 [<i>Triticum aestivum</i>]	BF200008 [<i>Triticum monococcum</i>]	1e-12	57
80H14.15b	74225 ... 74797	+			unknown			
80H14.14b	75570 ... 76794	+	T45059	8e-5	hypothetical protein [<i>Caenorhabditis elegans</i>]	BE196535	2e-28	107
RGH2b	77666 ... 81459	+	AAK92576	5e-91	putative disease resistance protein [<i>Oryza sativa</i>]			
RGH1f	81517 ... 85549	+	CAC29241	0.0	MLA6 protein	AV835011 [<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>]	e-132	496
			AAG37354	0.0	MLA1 protein [<i>Hordeum vulgare</i>]			
80H14.11b	86562 ... 87614	+	T05774	2e-5	putative protein [<i>Arabidopsis thaliana</i>]	BE419259 [<i>Triticum aestivum</i>]	3e-8	57
80H14.10b	89999 ... 93163				unknown			

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RGH3a	102577 ... 105388	-	AF149112	9e-45	stripe rust resistance protein Yr10 [<i>Triticum aestivum</i>]	BF200008 [<i>Triticum monococcum</i>]	1e-12	57
80H14.15a	113940 ... 114509	+			unknown			
80H14.14a	115283 ... 116507	+	T45059	8e-5	hypothetical protein [<i>Caenorhabditis elegans</i>]	BE196535	2e-28	107
RGH2a	117379 ... 121172	+	AAK92576	5e-91	putative disease resistance protein [<i>Oryza sativa</i>]			
RGH1e	121230 ... 125262	+	CAC29241 AAG37354	0.0 0.0	MLA6 protein MLA1 protein [<i>Hordeum vulgare</i>]	AV835011 [<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>]	e-132	496
80H14.11a	126275 ... 127327	+	T05774	2e-5	putative protein [<i>Arabidopsis thaliana</i>]	BE419259 [<i>Triticum aestivum</i>]	3e-8	57
80H14.10a	129712 ... 132873	+			unknown			

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RGH1bcd	184898 ...	-	CAC29241	0.0	MLA6 protein	AV835011 [<i>Hordeum</i>	0.0	514
	190492		AAG37354	0.0	MLA1 protein [<i>Hordeum vulgare</i>]	<i>vulgare</i> subsp. <i>spontaneum</i>]		
80H14.8	194760 ... 197571	+			unknown	BG344356	5e-89	341
CI2f	204440 ...	+	CAA40350	6e-39	chymotrypsin inhibitor 2 [<i>Hordeum vulgare</i>]	BE601601	1e-141	255
	204694					BG366350	1e-141	255
CI2e	206954 ...	+	CAB71340	2e-21	putative proteinase inhibitor [<i>Hordeum vulgare</i>]	BE425944 [<i>Triticum</i>	7e-73	196
	207172					<i>aestivum</i>]		

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RGH1a	207917 ...	+	CAC29241	0.0	MLA6 protein	BE587232 [<i>Secale</i>	2e-86	373
	212228		AAG37354	0.0	MLA1 protein	<i>cereale</i>]		
						[<i>Hordeum vulgare</i>]	BG606866 [<i>Triticum monococcum</i>]	7e-80
						AV835011 [<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>]	2e-77	442
CI2d	217540 ...	-	CAB71340	6e-26	putative proteinase	BG300496	1e-123	225
	217764				inhibitor	BE231068	1e-123	225
						[<i>Hordeum vulgare</i>]	BF257305	1e-123
CI2c	220610 ...	-	CAB71340	5e-35	putative proteinase	BF255218	1e-123	225
	220834				inhibitor	BF629382	1e-123	225
						[<i>Hordeum vulgare</i>]	BF253985	1e-123
CI2b	223775 ...	-	CAB71340	3e-24	putative proteinase	BG300496	1e-80	201
	224008				inhibitor	BF257305	1e-80	201
						[<i>Hordeum vulgare</i>]	BE231068	1e-80

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CI2a	224982 ...	-	CAB71340	2e-11	putative proteinase	BF258541	1e-42	109
	225149				inhibitor	BG300496	1e-42	109
					[<i>Hordeum vulgare</i>]			

^aThe carrots < > show the approximate sequence range.

^bIf the functional match is different from the best homolog, its GenBank accession number is given here.

^cAll GenBank EST matches originate from *Hordeum vulgare*, unless designated otherwise.

^dThe detection of ESTs for 711N16.8 only among monocots, but not in any dicot, may indicate that this is a grass-specific gene.