

**Web Table C.** Simple sequence repeats in the barley *Mla* region

Sequence Name	Position		Length (bp)	Strand <sup>a</sup>	Repeat Name	Sequence environment	Repeat Type <sup>b</sup>
	Start	End					
Morex_Mla	4290	4365	76	+	(GGGGA)n	mid <i>711N16.15</i>	Simple_repeat
Morex_Mla	4572	4592	21	-	(GGAA)n	Intergenic	Simple_repeat
Morex_Mla	4715	4734	20	+	(TAG)n	Intergenic	Simple_repeat
Morex_Mla	10155	10246	92	-	(GAAAA)n	mid <i>711N16.14</i>	Simple_repeat
Morex_Mla	12816	12904	89	-	(TAAAA)n	Intergenic	Simple_repeat
Morex_Mla	13195	13223	29	-	AT_rich	Intergenic	Low_complexity
Morex_Mla	21422	21505	84	-	(CGG)n	5' <i>Bpm</i> (Intergenic)	Simple_repeat
Morex_Mla	21537	21567	31	+	(CAAAC)n	5' <i>Bpm</i> (Intergenic)	Simple_repeat
Morex_Mla	29149	29170	22	-	GC_rich	Intergenic	Low_complexity
Morex_Mla	35111	35203	93	+	(CGG)n	Intergenic	Simple_repeat
Morex_Mla	35838	35858	21	+	(CGA)n	Intergenic	Simple_repeat
Morex_Mla	41662	41755	94	-	(GAAAA)n	Intergenic	Simple_repeat
Morex_Mla	41765	41793	29	-	(TAAAAA)n	Intergenic	Simple_repeat
Morex_Mla	41839	42008	170	-	(TAAAAA)n	Intergenic	Simple_repeat
Morex_Mla	41935	42041	107	-	(GAAA)n	Intergenic	Simple_repeat
Morex_Mla	42601	42637	37	-	AT_rich	Intergenic	Low_complexity
Morex_Mla	43972	44040	69	-	(TAAA)n	Intergenic	Simple_repeat
Morex_Mla	45140	45309	170	-	(CGGGGG)n	Intergenic	Simple_repeat
Morex_Mla	47534	47560	27	-	(GA)n	<i>SoloBare-1.2</i>	Simple_repeat
Morex_Mla	50194	50240	47	-	(CA)n	mid <i>711N16.8</i>	Simple_repeat
Morex_Mla	53934	54111	178	-	(GAA)n	Intergenic	Simple_repeat
Morex_Mla	54382	54460	79	-	(GAA)n	Intergenic	Simple_repeat
Morex_Mla	54505	54650	146	+	(CGG)n	Intergenic	Simple_repeat
Morex_Mla	61081	61147	77	+	(GAGAA)n	Intergenic	Simple_repeat
Morex_Mla	66106	66126	21	-	(CGAGG)n	5' <i>RGH3b</i> (Intergenic)	Simple_repeat
Morex_Mla	66546	66619	74	-	AT_rich	Intergenic	Low_complexity
Morex_Mla	66661	66689	29	-	AT_rich	Intergenic	Low_complexity
Morex_Mla	66693	66759	67	-	(CGA)n	Intergenic	Simple_repeat
Morex_Mla	69826	69870	45	+	(GGA)n	<i>Sukkula-1a</i>	Simple_repeat
Morex_Mla	74065	74086	22	+	(CA)n	5' <i>80H14.15b</i> (Intergenic)	Simple_repeat

**Web Table C.** Simple sequence repeats in the barley *Mla* region

Sequence Name	Position		Length (bp)	Strand <sup>a</sup>	Repeat Name	Sequence environment	Repeat Type <sup>b</sup>
	Start	End					
Morex_Mla	75492	75516	25	-	(GA)n	5' <i>80H14.14b</i> (Intergenic)	Simple_repeat
Morex_Mla	76707	76782	76	+	(GGA)n	mid <i>80H14.14b</i>	Simple_repeat
Morex_Mla	86793	86833	41	-	(AGGGGG)n	mid <i>80H14.11b</i>	Simple_repeat
Morex_Mla	86894	87075	182	+	(CCCCG)n	mid <i>80H14.11b</i>	Simple_repeat
Morex_Mla	94902	94924	23	-	GC_rich	<i>HORGY-1</i>	Low_complexity
Morex_Mla	97560	97639	80	-	(GA)n	<i>HORMU-1</i>	Simple_repeat
Morex_Mla	98305	98366	62	-	(TA)n	<i>HORMU-1</i>	Simple_repeat
Morex_Mla	100796	100862	67	+	(GAGAA)n	<i>HORMU-1</i> (intergenic)	Simple_repeat
Morex_Mla	105821	105841	21	-	(CGAGG)n	5' <i>RGH3a</i> (intergenic)	Simple_repeat
Morex_Mla	106261	106334	74	-	AT_rich	intergenic	Low_complexity
Morex_Mla	106376	106404	29	-	AT_rich	intergenic	Low_complexity
Morex_Mla	106408	106474	67	-	(CGA)n	intergenic	Simple_repeat
Morex_Mla	109541	109585	45	+	(GGA)n	<i>Sukkula-1b</i>	Simple_repeat
Morex_Mla	113780	113801	22	+	(CA)n	5' <i>80H14.15a</i> (intergenic)	Simple_repeat
Morex_Mla	115205	115229	25	-	(GA)n	5' <i>80H14.14a</i> (intergenic)	Simple_repeat
Morex_Mla	116420	116495	76	+	(GGA)n	mid <i>80H14.14a</i>	Simple_repeat
Morex_Mla	126506	126546	41	-	(AGGGGG)n	mid <i>80H14.11a</i>	Simple_repeat
Morex_Mla	126607	126788	182	+	(CCCCG)n	mid <i>80H14.11a</i>	Simple_repeat
Morex_Mla	134615	134637	23	-	GC_rich	<i>HORMU-1</i>	Low_complexity
Morex_Mla	137274	137353	80	-	(GA)n	<i>HORMU-1</i>	Simple_repeat
Morex_Mla	138019	138074	56	-	(TA)n	<i>HORMU-1</i>	Simple_repeat
Morex_Mla	154282	154401	120	+	(CGG)n	<i>HORGY-1</i>	Simple_repeat
Morex_Mla	155559	155585	27	+	(G)n	<i>HORGY-1</i>	Simple_repeat
Morex_Mla	156478	156596	119	+	(CGGGGG)n	<i>HORGY-1</i>	Simple_repeat
Morex_Mla	156662	156846	185	+	(CGGGGG)n	<i>HORGY-1</i>	Simple_repeat
Morex_Mla	156748	156925	178	-	(CACCC)n	<i>HORGY-1</i>	Simple_repeat
Morex_Mla	156893	157076	184	+	(CGGGGG)n	<i>HORGY-1</i>	Simple_repeat
Morex_Mla	157499	157524	26	-	AT_rich	<i>HORGY-1</i>	Low_complexity
Morex_Mla	157955	158014	60	+	(CAGAG)n	<i>HORGY-1</i>	Simple_repeat
Morex_Mla	181488	181584	97	-	(CGA)n	<i>HORPIA-2</i>	Simple_repeat

**Web Table C.** Simple sequence repeats in the barley *Mla* region

Sequence Name	Position		Length (bp)	Strand <sup>a</sup>	Repeat Name	Sequence environment	Repeat Type <sup>b</sup>
	Start	End					
Morex_Mla	188509	188572	64	+	(GAGAA)n	mid <i>RGH1bcd</i>	Simple_repeat
Morex_Mla	192124	192155	32	-	AT_rich	<i>Alexandra</i>	Low_complexity
Morex_Mla	193878	193898	21	-	(G)n	<i>Alexandra</i>	Simple_repeat
Morex_Mla	195753	195782	30	-	AT_rich	mid <i>80H14.8</i>	Low_complexity
Morex_Mla	199811	199834	24	-	AT_rich	intergenic	Low_complexity
Morex_Mla	200835	200872	38	-	AT_rich	intergenic	Low_complexity
Morex_Mla	201097	201125	29	-	AT_rich	intergenic	Low_complexity
Morex_Mla	202516	202567	52	-	AT_rich	intergenic	Low_complexity
Morex_Mla	203458	203514	57	-	AT_rich	intergenic	Low_complexity
Morex_Mla	203559	203586	28	-	AT_rich	intergenic	Low_complexity
Morex_Mla	203712	203748	37	-	AT_rich	intergenic	Low_complexity
Morex_Mla	219736	219780	45	-	AT_rich	intergenic	Low_complexity
Morex_Mla	221418	221448	31	-	AT_rich	intergenic	Low_complexity
Morex_Mla	222677	222729	53	-	AT_rich	intergenic	Low_complexity
Morex_Mla	230915	230972	58	-	(GAGAA)n	<i>BARE-1c</i>	Simple_repeat
Morex_Mla	230933	230973	41	-	(GAAAA)n	<i>BARE-1c</i>	Simple_repeat
Morex_Mla	242584	242611	28	-	AT_rich	<i>BARE-1b</i>	Low_complexity

<sup>a</sup> + plus strand, - minus strand.

<sup>b</sup> Among the 77 events, 20 are AT rich, 3 are GC rich, and 54 are SSR. Nineteen of the SSRs are associated with transposable elements (TE), including fourteen in LTR retroelements, and five in the *Mutator* transposon, while 35 SSRs are in the non-TE region. These non-TE SSRs include ten in gene coding regions and 25 in the intergenic regions. Twenty-two SSRs are present in the 40-kb duplication (six of these are associated with genes).