

茎用莴苣全基因组差异 SSR 鉴定及其在 QTL 定位中的应用

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Genome-wide Identification of Differential Simple Sequence

Repeats in Stalk Lettuce and Its Use for QTL Mapping

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附表 1 82 对有多态 SSR 标记的引物信息

Supplementary Table 1 Detailed information for polymorphic primer

编号 No.	标记 Marker	位置 Position	正向引物 Forward primer (5'-3')	反向引物 Reverse primer (5'-3')	退火温度 Tm (°C)	预测片段大小 Predicted product size (bp)
1	LS003	chr_1:22255132:22255145	TTGCAATGGTTGACCAAGAA	GCAGCACGTAGATGCCAGTA	60	231
2	LS004	chr_1:24192366:24192450	ACAATTTTGGCAGTTGGGTC	TGACTTTCGACATCCAAGTT	60	211
3	LS006	chr_1:40006840:40006875	AAGCAACCGTTCACGAACT	CTTTTCTGATTAGCCGCCAG	60	198
4	LS008	chr_1:53099316:53099325	CAATGGCAAGGGTAAAGCAT	CCAGGGACCACTTCTCTGAC	60	205
5	LS009	chr_1:61249342:61249351	AGTGACGACTTATCGTCGGG	ACAATTTGCCGAAAGAATGG	60	287
6	LS016	chr_1:140760340:140760355	TATTGACGTGGCATGGGATA	TCTTAGACCGCCTGATGTCC	60	285
7	LS022	chr_1:205413575:205413589	AGATCCGCTAACACCAAGGA	TTGGAGAAGCGAGCAATATG	60	300
8	LS029	chr_2:108243085:108243099	ACCACACAAACAGGGACCAT	GGCAGCATAGAGGATGGTGT	60	186
9	LS031	chr_2:124799707:124799721	ACGGATTTTGGCTTACAAC	AGCCGGTGGTTCAAGAACT	60	211
10	LS034	chr_2:167185504:167185518	TTTGGGCTAGTAATCGACCG	TAAACCGGCATGACTCTGTG	60	227
11	LS036	chr_2:202949611:202949628	GAGTGCCACCTCCATTTTGT	GAAAACCTTCTGAAATGCC	60	219
12	LS038	chr_3:5453266:5453305	GAGTCATGGGCAAACCCTAA	TGTCCAATGCTTCTCCTCAA	60	204
13	LS042	chr_3:52639540:52639549	CACGAGCATGTCCTTTTGAC	CGTTAAACCAAGTGCAGCAT	59	226
14	LS045	chr_3:87955540:87955554	CAGGTCAGGTCCAAACCCTA	TAGACCCTGGATCCACAAGC	60	244
15	LS051	chr_3:193076731:193076743	TCAAACATCTGTGCAAGAGTCC	TTCAAGGACTGCAGCAGCTA	59	285
16	LS053	chr_4:17635561:17635600	GGGAGAAGTGTAACAGGGA	CACAGTGGTGGTAGTGTCCG	60	275
17	LS054	chr_4:28226664:28226678	CATGCATGTATGCCTTGAG	TGCTCTGATACCAATTGTTGG	60	243
18	LS059	chr_4:76544126:76544145	AACTGGGATTAGCGATGTGG	AACTCGGTTTTGCCTTGTTG	60	187
19	LS064	chr_4:121851357:121851394	AACATCACTTTTCTGGGAGAT	TGAGATGCAAACAAAGTGGC	58	287
20	LS072	chr_4:264876867:264876878	TGACCAATTTGCCTGTGTGT	TGGCAACCAAAATCAAAAACA	60	234
21	LS073	chr_4:286570743:286570772	AACCGGCTCTTCGTTTTCTT	GCATTCGTCGAACAGGTTT	60	241
22	LS077	chr_4:313284518:313284531	TGAGTCTTGAGCGTTTGGTG	CCATGGAGACTACCCGACAT	60	300
23	LS078	chr_4:314577239:314577252	ATGCTTTAGTGGCCAGTTG	CAGATCGCCAATCATAGCAA	60	265
24	LS079	chr_4:317134947:317134996	TGTCGTTGTTACTGCCTCG	AACCCCGTACGTTTGTGTA	60	226
25	LS084	chr_4:329040927:329040956	TCCCGTAGATACGAAAGGA	CTCTGGTGACACTCAAGGCA	60	196
26	LS085	chr_4:331094617:331094649	TGCTACGCATAAGAAACGCT	TGCATGCTTTAATCCGACAA	59	227
27	LS086	chr_4:339436216:339436227	TCACAGAGGAGAACACGAAC	AAAGCTAACCTACGCGCAAA	59	264
28	LS091	chr_4:366642538:366642555	TCCTTACCATCTCCACCAGG	AACCGAGTCAGCAAAGGCTA	60	234
29	LS101	chr_5:154938646:154938675	TGTTCCCATGTTCTCCAAT	TAGAGCACAACACTACCCGC	60	253
30	LS103	chr_5:164313812:164313886	TGCCAAAAATCCCTAAGTTCT	GAAGCATGGGCAACCTTCTA	58	298
31	LS108	chr_5:182087214:182087229	TCGGCTTATTCGTGGCTACT	TGCACCAACCGTAATTTCAA	60	257
32	LS110	chr_5:211101389:211101406	CAATTGATTGACAAGCGGA	AGACCAACTTGAATGTGTGGG	60	284
33	LS115	chr_5:225640253:225640264	TTTCGGTCTAGCATTTGGCTT	CATATCCAATTGATGGTGGC	60	281
34	LS121	chr_5:249841412:249841439	CCAATGGCTCTAGGAGCAGTA	GGCTTACAAGCCAAGCACTC	59	292

35	LS122	chr_5:256910514:256910525	GGTGGTGGTGGTTACGATTC	CACCACCGTGAGGTGATAGA	60	295
36	LS125	chr_5:282652846:282652875	GGCACTCATGGTGAAAGTGA	ACTTCGTGAGGATTCGGTTG	60	250
37	LS130	chr_5:333693628:333693672	TTACCTTCAATCGCCCATTC	AGCTAGGGTTTGGTCCACCT	60	216
38	LS135	chr_6:31559783:31559893	TTGAAATTTTAAGCACAAGGA CTG	TCAGTTCACGCAATAAAGGTT TT	60	234
39	LS138	chr_6:83697495:83697515	GAGCTTGTTTGCATTCCGAT	CGAAATGTCTCATGCAACG	60	211
40	LS142	chr_6:128770744:128770761	TCCTGAGTCTCCACCATTTC	CTCAAGAGGCCGATGGTCTA	60	286
41	LS143	chr_6:129850119:129850129	CACAAACGGGGATCGTACTT	GTGCATGGGGAAGAAAGAAA	60	256
42	LS147	chr_7:13314963:13314976	CAGAAGATGATCGGACAGCA	GAATCCGGGCTGTTACACAC	60	255
43	LS148	chr_7:16936346:16936581	CAAGTCCCAAACAATTGCTAA	AGGCTGCAATACTACTCTAT TGAC	58	300
44	LS150	chr_7:32334403:32334418	CGACAAACCAAACACCATCA	GCCGAACGAAGTAGAGGAAA	60	288
45	LS161	chr_7:179887947:179887972	AAATCCATATGGGGTGGGTT	CAGCGCAAAGGTTTTTGTAGT	60	163
46	LS168	chr_8:42295606:42295620	TGTCTCCAGGAAATTGGAA	GCCCGTGTCCAGTCTTTA	60	282
47	LS169	chr_8:52263247:52263276	CATGGTGGTGTGGATCAAG	GCCTTCTCCTACCGACTTC	60	211
48	LS173	chr_8:71916563:71916577	CGAAGGATGGATCTTCTTGC	GCACCTCAAATCAAGTTGGC	60	169
49	LS176	chr_8:99951927:99951942	CCAGGAAAGCCTGAAAACCTG	TTTCTGGGTTTCCATGTTT	60	199
50	LS184	chr_8:164948298:164948315	GGAATGGAATGGGTGAGAGA	CCCATCTACAAAACCAACAA	60	202
51	LS193	chr_8:285073369:285073386	ACCTCTCGATCATTGTTGCC	CTAATGAGGGAAACGTCGGA	60	267
52	LS197	chr_9:9392270:9392287	AAGGAGGAGGAGGTGATCGT	TTTGGCAGTAGGGGATGTTT	60	191
53	LS199	chr_9:13540598:13540633	AGAGCGTTTTACGCTTCGAG	CAACTCATCATCAAGGCC	60	294
54	LS205	chr_9:33912105:33912129	GGAGCCAACATTGGATGAAT	TCAGTCTCAGTCCAGTCCA	60	232
55	LS222	chr_9:202059042:202059085	TAAATTAGCCACCACGAGCC	GTGGTCGTGTTGATTTGTGG	60	205
56	LS225	chr_1:10068328:10068390	TCACGCTTAGATCATTGCGGA	ATAATTGAACCGTCAACCCA	59	216
57	LS228	chr_1:31605526:31605563	TGATTGATGCTCCCTTCTCC	TCGTAACCCTAAATCCCCCT	60	245
58	LS229	chr_1:40765859:40765923	TCCCTTGAAATGTGTGTTGG	TTTCATATCCAAACACCCCC	59	215
59	LS231	chr_1:87701174:87701284	GTGATTAAACATTGCGCCCT	CAAAAACAATTTGGTGGTTGT T	60	202
60	LS246	chr_3:5022661:5022751	AACAGCTTGGTGTTCACGGC	TCCCAATCAAGCTGATGATG	60	288
61	LS249	chr_3:110646990:110647019	CCGCATAGATACGAGAGGGA	AGGCATGCTTTCGTATTCGT	60	285
62	LS253	chr_3:184651018:184651057	ATAGCCCAATCAAGTTTGACA	GGTTTATCGCTTGAGGTTGC	57	154
63	LS256	chr_4:3760204:3760300	TTGCAACCATAACCATTCCA	TAAAGTGGCCGAAATTTGAA	58	280
64	LS260	chr_4:97057879:97057964	CCACACAAACAGAACAAACA AAA	TCGGTCTATTTGCTTCACTCA	60	299
65	LS270	chr_4:344216816:344216977	CCTGAAGGACCATTTTATGAT GA	GCCTCCTTTGCCTCTTGAGT	60	297
66	LS275	chr_5:211456320:211456397	TCAATTCACAAATAAGGTGCT TTC	CAGTTTGTGTTTCATTTCCGA	59	200
67	LS277	chr_5:256201044:256201107	TGTGTGCATTTAAACACGGG	AAACCAAAAATTCAATGGCCT	60	289
68	LS281	chr_5:336360090:336360144	GACGGCAGTATCGGGTAGAA	GGCCGTAAACTCCTCTTCTT	60	277
69	LS282	chr_6:3974676:3974755	TGTCAAACATCAAATTAAGGC G	TCCAATGTAGGATATATGCAA AAAG	60	273
70	LS284	chr_6:56557818:56557864	TGGATGCAAAGTTCTTCACG	TCAATCATGGTATGAGTTAC AAA	60	296
71	LS291	chr_7:22964308:22964400	ATGTCAGCCACCTATCGGAC	TCGTTTATGCAAAAATCCGTA	60	184
72	LS298	chr_7:194364992:194365107	TTGTAGCTTGATATAGTTGTG CTTCA	CGACATTTAGAACAACTTGC C	59	259
73	LS306	chr_8:99952114:99952234	GAAACCCAGGAAAGTTGGAA	TCCCCAAAGTCAGGATAGA	59	298
74	LS309	chr_8:241290175:241290199	TAGGGAGCTTGAAGATGGGA	TTTCGTCTTCTTCCCCAC	60	300
75	LS310	chr_8:261651737:261651760	TTTCCAAAACCTCATCAATGC	CAACACAATGGTCCAATGA	60	291
76	LS320	chr_9:164739034:164739084	CAACAAATCCCTTCCATGCT	ATTGCCCTCATTCTGAAAAA	60	242
77	LS321	chr_9:191894857:191894946	TCGAGTCACGACAACACTGA	ATAATGCAAACAGTTGCGG	59	274
78	Ig501	chr_5:213110283:213110297	TGTGGTTTCAAATTTGGGGT	TGTTGGCAGGGAACCTTCTT	60	164
79	Ig525	chr_5:215551174:215551244	CAAGATGAAGATCTCGCACG	AATTCTCCCCTACCACCACC	60	274
80	WJ24	chr_4:90598556:90598650	TCGAATGTCCAAAATCACCA	TGCCATCATCTTAGGTTGTCA	60	234
81	WJ58	chr_8:91429827:91429916	CCAGTGGCAAACAAAAATG	TAGCTTGTCCCCTCATTCA	60	222
82	WJ81	chr_3:130865764:130865781	TTTTCTTTGATTTTCGCCA	GCTTGAATGGATGAAGGAT	61	176

