

Table 1 Newly designed SSR markers on LG16

Marker	Primer sequence F-R	Source contig	Contig position	Amplicon (bp) ^z	SSR ^z	Map position
LG16-769020-1	F- CATCAGATGATTATCCCTTG ACTAC	MDC013096.127	chr16:769020..8161 47	115	(AT) ₁₅	LG16
	R- TGATCGGAAACAGGACCACT					
LG16-769020-2	F- GGACGCGAACACATGCTTAT	MDC013096.127	chr16:769020..8161 47	297	(AT) ₁₂	LG16
	R- GTCCTTTTCATACCGCTGGA					
LG16-837763	F- TCAGGCCACAAAACAAACAAA	MDC013096.125	chr16:837763..8967 6	150	(AG) ₂₅	LG16
	R- TTCTCTGCCAAACCCCTTT					
LG16-1003247-1	F- CCTCAACTGCACAAAGCAAA	MDC006875.277	chr16:1003247..105 2856	149	(AC) ₁₈	LG16
	R- CGTCATCAACAGGATGCAGA					
LG16-1003247-2	F- TAGAGGCAAACCGACGGTAG	MDC006875.277	chr16:1003247..105 2856	142	(AG) ₁₄	not determined
	R- CCTTTCCTTTCCCTCCAAAG					
LG16-1140516	F- GCAGGAAACTTCAGCAAACA	MDC010932.700	chr16:1140516..115 6076	393	(AG) ₂₄	not determined
	R- GTGAAGATCACGCGGTTGAG					
LG16-1159074	F- TTCTCTGCCAAACCCCTTTT	MDC010932.632	chr16:1159074..116 3563	136	(CT) ₁₇	LG16
	R- ACATTCCGCCACACTACCTC					
LG16-1199876	F- GCGATCGGTTCCGTTCTA	MDC010344.263	chr16:1199876..124 3332	135	(TC) ₂₁	LG16
	R- GTGAGCCGGACTTTTGGTTA					
LG16-1352468	F- AGGGTGAGTGGGCAAAAAT A	MDC012995.82	chr16:1352468..136 6194	249	(TA) ₂₀	LG16
	R- GACTCCGACTGCCGTGTTAT					
LG16-1437845	F- GAATCGAACCCACATGCAG	MDC018421.263	chr16:1437845..145 6844	232	(CT) ₂₀	LG16
	R- TTGTGTGCTCGAAAACATGC					
LG16-LAR-SSR	F- TGGATACAGGGAACCAAAA CA	MDC015897.278	chr16:1526288..156 4541	238	(AT) ₁₅	LG16
	R- GCCCTTCCACTGCAAAATTA					
LG16-1526288	F- TGTTGCTTTCTGTTTGGTTCA	MDC015897.278	chr16:1526288..156 4541	168	(AG) ₂₃	LG16
	R- TTAATTGTGCTGCCTGCTTG					
LG16-1568112	F- GGCATCCTAATTCCTTGGT	MDC002276.243	chr16:1568112..158 2774	241	(AT) ₁₇	LG16
	R- CAGGACCTGCAATTGTTACA TC					
LG16-1636246	F- CCCCAAAACCAAACCCCTA	MDC001111.374	chr16:1636247..164 9334	231	(CT) ₁₅	not determined
	R- GGACTCCTCGGTGTTGATGT					
LG16-1661111	F- CGTCATTGTTGCAGGGTATG	MDC006784.248	chr16:1661111..168 3666	153	(AG) ₂₀	LG16
	R- GCTTTCCTGCCACCACTACT					
LG16-1728791	F- TTTGTCATGCTCGTTTCCTG	MDC014193.228	chr16:1728791..176 0724	247	(AG) ₁₃	LG16
	R- GCTTAATTCTCGTGCCTTCG					
LG16-1788357	F- GCACAGAGAGTCATGCCAGA	MDC018602.176	chr16:1788357..182 9914	222	(AT) ₂₂	LG16
	R- TGACAACACATCAGCCAAAA					
LG16-1860066	F- GCAGTCTATCATCCCAGGAC A	MDC027868.28	chr16:1860066..187 2585	243	(GA) ₁₄	LG16
	R- CAACCACAGGTCCACAACAC					

Note: ^z: Product size and SSR motif amplified from each primer pair were calculated from 'Golden Delicious' genome sequence