Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Sat_137	*	A1	0.00	CC453692	31044522	(AT)16	GATGACGCCGCAGGTTTCTCC	GGTGCGGTTCCACAGTTTTTT	225
Satt684	*	A1	3.54	CC454037	31044867	(ATT)17	GGGCTTCATTTTAGATGGAGTC	TGGAGCTCATATTCGTCACAAAG	190
Sat_368		A1	14.37	CC453894	31044724	(AT)14	GCGATTTTAAGATAAACATATACTCCTGCTA	GCGTAGTTTTGGGTTGTTTTAATCAGCATTG	
Satt572		A1	14.65	BH126738	14970241	(ATT)14	GCGGAGCATGTAAATCCAGCCTATTGA	GCGGGCTAACTTATGTTACTAAACAAT	165
Satt276		A1	17.16	BH126472	14969975	(ATT)19	GCGGACGGTAAGGACTATTTATGATA	GCGTCAGATGAAAAAAAATAAGATAC	267
Sat_344		A1	19.38	CC453870	31044700	(AT)9	GCGGCTGGTCAAAAACTTCATAGTCAT	GCGCAATGTGTAACGAAATCTTATGTCTAAA	
Satt165		A1	23.00	BH126376	14969879	(ATT)18	CACGAATAACTTGACACATT	TAAAAACAAAGCAAACATAAA	277
Satt593		A1	25.56	BH126759	14970262	(ATT)15(TTG)10(TTC)4	GCGGGGTTGTTGATCTATAATGTAA	GCGGGTTTGGATTTTATAATGTGAT	190
Satt625	*	A1	26.16	CC453987	31044817	(AT)16(ATT)44	GCGCCTTATTTAACTACTTTTTTCACT	GCGCCCTCAATTTGGGTGGGAAAATAA	311
Satt382		A1	26.42	BH126567	14970070	(ATT)24	GCGACATTATTGTTTGGATAGTAAGATT	GCGCGATTCTTTTAAACAATTCAAACAC	259
Sat_371		A1	26.87	CC453897	31044727	(AT)21	GCGACACTTTTCGGGATTACTATTAGATTAT	GCGCTTTTTGAAATGTATTAGATGGTCAC	
Sat_369		A1	27.18	CC453895	31044725	(AT)28(GTAT)2	GCGAATGGGGATAAACAATAGAACAAGA	GCGCAGTGGCTTCACATTTAACTGA	
Satt042		A1	27.66	BH126311	14969814	(ATT)27	GACTTAATTGCTTGCTATGA	GTGGTGCACACTCACTT	172
Satt449		A1	27.78	CC453967	31044797	(ATT)21	GCGTGCTTCTTATATTAGGTGTTAGT	GCGCATTGGAGTTTTTGCTTTT	265
Satt471		A1	27.96	BH126643	14970146	(ATT)17	GCGCCCAAAACTATCTAGTAATTCTT	GGGCTATCAAATTGACTAAAGCCAAA	238
Satt526		A1	27.98	BH126696	14970199	(ATT)9	GCGGCAAATTCTAATGACTG	GTCGGAGTTCTCAGTCTACCTGTC	144
Satt454		A1	28.08	BH126628	14970131	(ATT)17	GCTTTTCTTAGAACACAAATTACAAG	CAACCATGATAAATGTGAGTGAG	254
Satt248		A1	28.29	BH126447	14969950	(ATT)12	GCGTGTTGCAATGATTAATTCTTTGA	GCAGAACTAGCCCAGACAGTTTGTAT	111
Satt364		A1	28.96	BH126552	14970055	(ATT)15	GCGGCATAAGTTTTCATCCCATC	ATCGGGTCATGACTTTTGAAGA	229
Sat_410		A1	29.63	CC453934	31044764	(AT)22	GCGATAACCAGGTAAAATTATTTTGGCTT	GCGTTAAATATCACTGATGAAAGTTCAAAGA	
Satt300		A1	30.93	BH126491	14969994	(ATT)19	GCGCCCACACAACCTTTAATCTT	GCGGCGACTGTTAACGTGTC	240
Sat_385		A1	31.07	CC453911	31044741	(AT)28	GCGAGTTATGATGAAATAAATCTAAGTCAAT	GCGTAGTTGCAAAGTTGTAGTAG	
Sat_384		A1	31.08	CC453910	31044740	(AT)32	GCGATTGCCAAGAGACACTAACA	GCGAATTCCATCTTTCATAATCTATCAC	
Satt591		A1	31.14	BH126757	14970260	(ATT)17	GCGCGACCTTAATGATA	GCGCCCAAAGCTTAAAATTTAATA	184
AZ536570		A1	31.39	AZ536570	11112855	(AT)12	GCGGCATGACAAGGAAATCT	GCGAATTAAAGGCAAAAGGAAAA	175
Satt155		A1	32.68	BH126367	14969870	(ATT)19	AGATCCAACACCTGGCCTAAT	GCTGCACAATTCATTCCATTT	157
Sat_265	*	A1	33.28	CC453800	31044630	(AT)14(CA)11	GCGTGAGTGCCACTTCTCCTG	GCGGCAGCATTAGAACCAAAAAGA	271
Satt073		A1	33.97	BH126321	14969824	(ATT)10	CATCCACCCAACAAAG	GCACAGTCTCACACGTC	213
Sat_356		A1	42.80	CC453882	31044712	(AT)26	GCGCCGGAAAAATGTGAGAAATCATAAAA	GCGTTGCATGACTATCATTCAATCAAAAAT	
Satt050		A1	46.45	BH126315	14969818	(ATT)13	GAACGTCCCAACAATG	GGCCTTGTAAACATATAGG	171
Satt717		A1	51.95	CC454062	31044892	(ATT)11	GCGTTTTGTGATTTGTTTTCCTCATTTACT	GCGGCTATCAAACATTTTTACATGATGGTTA	
Sat_407		A1	52.32	CC453931	31044761	(AT)29	GCGTCAAAGAACACAACTTAAATAATAAAT	GCGATGAATTACATTACATATGAAAAAGATA	
Sat_171		A1	57.79	CC453717	31044547	(AT)26	GCGCTCCTCTTTTTTTCACTTTC	GCGCGTGGGATTTTGGTATTTTT	216
Satt648		A1	59.18	CC454003	31044833	(ATT)12	ATGATTCGCACTAATGAATAGTTTT	GGCACAGTAACGAAGAGTAT	216
Satt385		A1	64.74	BH126570	14970073	(ATT)22	AATCGAGGATTCACTTGAT	CATTGGGCCACACAACAAC	310
SOYNOD26A		A1	66.80	M94764	170029	(AT)24	GAACAAAATGCCTGAGTT	CCATTCTCAATTCTTCTAGTT	119
Satt619	*	A1	69.21	CC453983	31044813	(ATT)11	GGCAGAACTAGTACGCTTCTGATT	GCGGTTAAGCATAATAGATCAGCCT	126
Satt545		A1	71.39	BH126713	14970216	(ATT)19	CAATGCCATTCCATATTTGTT	CAATTGCCCTAGTTTTGATAG	207
Sat_267	*	A1	78.45	CC453802	31044632	(AT)32	GCGATTGGATGATGGATTTATGAGTT	GCGCCCAACAAGGTGAGAAATCAAGA	261
Satt599		A1	85.58	BH126764	14970267	(ATT)10	GCGGTGTTTTTATTTGGTTTTTA	GCGCCCTGCAGCTCAAAAATTAACT	180

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt174		A1	88.58	BH126383	14969886	(ATT)10	TTTCATTTCTTTGCCTTCT	TTCGTAGTCCGTCTTTCAT	159
Satt200		A1	92.89	BH126407	14969910	(ATT)17	GCGATAAATGGTTAATGTAGATAA	GCGAAAGGACAGATAGAAAGAGA	240
Satt236		A1	93.23	BH126437	14969940	(ATT)19	GCGTGCTTCAAACCAACAAACAACTTA	GCGGTTTGCAGTACGTACCTAAAATAGA	224
Satt511		A1	94.20	BH126682	14970185	(ATT)19	GCGACTTTACTGAAAACCTGGAAA	GCTTCAAACCAACAAACAACTTA	263
Satt225		A1	95.16	BH126426	14969929	(ATT)13	AAAAATGTGTTAGAGCTTGTGTTGTTA	GCCACACTATTCCAGCCACTAC	112
Satt258		A1	95.54	BH126456	14969959	(ATT)9	CGAGGCGATTTGG	CCGAAAAGTGAAACAAGT	242
Sat_374		A1	95.68	CC453900	31044730	(AT)23	GCGTTGAAACCGTTATAAACCAACTCA	GCGCTTTATTGGCAATACTTTTAACTCACAT	
Satt211		A1	95.96	BH126417	14969920	(ATT)10	GAAAAAGCCCACATCCAA	CATGGGCATGCAGTAACA	118
Sat_271		A1	97.76	CC453805	31044635	(AT)17	GCGTCACTTTAATCATTACAATAAAACAACA	GCGACTTAGGCACACTCTAATATAACCA	226
Sat_217	*	A1	101.57	CC453757	31044587	(AT)21	GCGAAAAATTGTCAATGATATGATCAGTAAG	GCGGTCCTAGATGAAAAATGCTTTGTAA	293
Sat_383		A2	0.00	CC453909	31044739	(AT)12	GCGTTTCCCTCCCCTGTTTCCTACACCTC	GCGATTGAGCTATATTAAAAGAATGAACTAT	
Satt390		A2	9.14	BH126575	14970078	(ATT)17	AGTGGCTGATAAAAAAAATACTCA	ATAATCGCGGCACAATAATTC	223
Sct_067		A2	14.99	BH126776	14970279	(CT)19	CTCCCCATCTCTCTCTAAC	GGATTTTGTTATTTATTTATTTGA	
Sat_406		A2	25.90	CC453930	31044760	(AT)15	GCGCGTGTGGTGGTTACATTA	GCGTTTGCAGCCATTTCCATTTAC	
Satt207		A2	26.50	BH126413	14969916	(ATT)23	GCGTTTTTCTCATTTTGATTCCTAAAC	GCGATTGTGATTGTAGTCCCTAAA	235
Sat_319	*	A2	27.90	CC453850	31044680	(AT)14	GCGGGACCAAGTGGTCTTCCTCCCTAACATG	GCGTGGCATAGGCTACTAAAATACTCTAA	180
Satt480		A2	28.44	BH126652	14970155	(ATT)14	CGTCCCCACCATCACAAGCGATCA	GCGGTTAGCTTCGGTTATTAAT	177
Satt589		A2	33.96	BH126755	14970258	(ATT)19	GCGCAGACAATTTCAGTGGCAGATAGA	GCGAAAAAGTAATATAAGTAGAAAAAGG	185
Satt493		A2	35.02	BH126664	14970167	(ATT)11	GTTAACGGGAAAAAATTAAACCTA	GTGGCTGCCTAGTGCTGTTTTATA	251
Sat_409		A2	35.68	CC453933	31044763	(AT)22	GCGGAGGTTTGTGCATTTCTAGGTCTTC	GCGACGCGTATGTACATAAAATATGCTGTT	
BE820148		A2	35.93	BE820148	10252382	(AT)24	GCGTCCTGGTTTACTTTAACATTTACCT	GCGGCAACTTGAACCACCAACTA	194
Satt177		A2	36.77	BH126385	14969888	(ATT)16	CGTTTCATTCCCATGCCAATA	CCCGCATCTTTTTCAACCAC	112
Sat_181	*	A2	38.06	CC453724	31044554	(AT)28	CTGAATATGCCGCTGATAATCG	CATTGGCCTTACTTTTTAGCACATC	149
Satt315		A2	45.29	BH126506	14970009	(ATT)12	GCGCGACAACTCTAATGAAAATCT	GCGGAGTTTGATTTTTCAAAAGT	236
Sat_400		A2	49.39	CC453924	31044754	(AT)29	GCGTTGAGCCAATTAAAATTATATTTATGAT	GCGCAAATGCCATTCAATTAGTAGTCA	
Satt632		A2	51.51	BH126793	14970296	(ATT)17	GGGCTATGAAGGGAATGGAAAGGA	CCCATATTGAAGATTTGAAGTAAT	266
Sat_157		A2	51.57	BH126789	14970292	(AT)18	GCGGTTTTGCAAGATGTGATGAGT	GCGCGTACGCAAAATTTATATTCA	271
Sat_162	*	A2	51.86	BH126790	14970293	(AT)36	GCGTGGTTTTTCGCTGGATATA	GCGCATTTCGTAACATATTTTTCAC	175
Sat_215		A2	53.75	CC453755	31044585	(AT)25	GCGTAGCAACAAAGCAATCTACAG	GCGTCCCATTTTATTCCACACTATGTAAT	254
Satt187		A2	54.92	BH126394	14969897	(ATT)19	GCGTTTTAATTTATGATATAACCAA	GCGTTTTATCTCTTTTTCCACAAC	
Sat_212		A2	56.32	CC453752	31044582	(AT)24	GCGGACAATTTTTTATCAATAATTTATTT	GCGATGCTTACTTTTCCTATGATCACTT	303
GMENOD2B		A2	58.44	X16876	18578	(AT)17	TAGGCAAAAGACTAAAAGAGTA	GCATGTCATTTTGATTGA	169
Satt424		A2	60.59	BH126603	14970106	(ATT)52	CAACCTGTATTCCACAAAAAATCTCACC	GCGCCCCAATTTGACTATAAATAAAAGT	270
AW132402		A2	67.86	AW132402	6134073	(AT)17	GCGCCTCCCTCCTCTCCTTTCTT	GCGTTTCCCACATATTCTATCATTTGTT	153
Satt341		A2	77.70	BH126532	14970035	(ATT)17	GCGGAGCTTACCAACATAAAAAAACT	GCGGTCCAACATTGAGGCAAGAATAC	218
Sat_115		A2	81.02	BH126285	14969788	(AT)15	GGGGCTTCTACCTACTTACC	TCTCTCGATGTTACTTTTATTATTT	208
Sat_129		A2	84.08	BH126299	14969802	(ATT)28	GGGGACTCCCTCTCCAGAAGTAAT	GGGAGCAATTGATAAGTGTGAAAATAAT	
Sat_199		A2	84.09	CC453740	31044570	(AT)22	GCGCAATTTGACTATTTTTAGCTGTTG	GCGCGATATAAGATGATTTTTATTGAT	282
Sat_233	*	A2	86.42	CC453772	31044602	(AT)14	GCGGGGAGAACACTCAAAACTCTCTAAAGAA	GCGCCAGTCATTTTTTTTATGATATGTAGAT	336
Satt089		A2	87.57	BH126327	14969830	(ATT)27	AAAAATTAACGGTTGAGAAT	TTAAGGAAATAAAAGAAGAAAAG	154

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SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt377		A2	90.84	BH126564	14970067	(ATT)14	GCGATACACGTGACGAAGAGAATCATGC	GCGATAACATAATGGATTGACATAAAT	189
Satt119		A2	92.43	BH126335	14969838	(ATT)13	TGTGCCAGTGTTGATAGTTA	CTGATCCCCAATAAATCTG	
Satt525		A2	96.97	BH126695	14970198	(ATT)19	GCGCATAGCTTTCAGAGAAGTTT	CATTCACCAATCCTCATTAGA	305
Satt233		A2	100.09	BH126434	14969937	(ATT)16	AAGCATACTCGTCGTAAC	GCGGTGCAAAGATATTAGAAA	200
Sat_250		A2	105.18	CC453786	31044616	(AT)19	GCGGTTTTTGCTTTAGGACATTTTGATA	GCGTTGGGTACAACATATAATATTTTGGA	296
Sat_392		A2	106.29	CC453917	31044747	(AT)23	GCGTTCTATGATACCATGTTAAAAGAATGAA	GCGAAGGAAGAGGAAAGGTTTAAAAGAG	
Satt437		A2	107.05	BH126615	14970118	(ATT)25	ATCCCATTGTAGTGCATTTATAGTGACG	GCGGGTAACCTATTTTTTATGCTTCTGT	263
Satt508		A2	108.78	BH126679	14970182	(ATT)13	GCGGCCTCCTCAAAATAATAATAAT	GCGGTTAGGAATAGAAGATAGTTACATT	261
Satt327		A2	109.83	BH126518	14970021	(ATT)18	GCGCACCCAAAAGATAACAAA	GCGTCGTAGCAATGTCACCA	247
Satt329		A2	110.94	BH126520	14970023	(ATT)23	GCGGGACGCAAAATTGGATTTAGT	GCGCCGAATAAAACGTGAGAACTG	271
Sat_310	*	A2	111.46	CC453842	31044672	(AT)23	GCGGTTACTAAATTTCCTGAATCTGAA	GCGTCTAAACTTATTTGATATTTGATTGATA	255
Sat_232	*	A2	112.88	CC453771	31044601	(AT)16	GCGCGTCCTTTATTTAATTTAATATGAA	GCGTGGCTTTGCTAATAATGAATGAT	285
Sct_194		A2	113.57	CC454077	31044907	(CT)8(GT)2(CT)11(AT)1(	GCGTTGTGGTCACTCTTGATAATG	GCGAGTCACGAAATAATTTTGAATAAT	
Satt158		A2	115.25	BH126370	14969873	(ATT)40	GGGTAAATATTTTAAGAAAAGGGATAGTAA	GGGTTCTCCTGTCTTTTTATTTTTATTA	229
Satt421		A2	115.93	BH126600	14970103	(ATT)10	CAAAGCTTCTTCTTCTTCT	CACAGGTTGAGACAAAACAAA	236
Sat_382		A2	116.41	CC453908	31044738	(AT)25	GCGAAAGGTCGAGAAAATGAAATG	GCGTTTGCCTTGTTGGTGACTTG	
Sat_378		A2	116.62	CC453904	31044734	(AT)23	GCGGTGGGGACCGGAGGAGTATAATAAT	GCGTGAAGGCTAATAATATAGGCATGG	
Satt707		A2	116.62	CC454054	31044884	(ATT)9	GCGTGAGCAATACATTTTCTGTAAAAAAAAA	GCGATAGCATATTAAATGAATCTCTGACTTT	
Sat_377		A2	116.64	CC453903	31044733	(AT)20	GCGTTTACAGGACCAGGAACTTTTT	GCGGGCCAATGGAACTTAGTCTTTTTA	
Satt470		A2	116.73	BH126642	14970145	(ATT)15	GACCATTATGCTTTTTCTCTTT	CTTTATCCTCCTCCATTAGTTCTA	257
Sat_040		A2	118.64	CC453676	31044506	(AT)23(GA)24	GTTCTAGTTCTTCTTTTCACTTG	TTGTCATCAAATATCATCCATTT	261
Satt333		A2	119.59	BH126524	14970027	(ATT)21	GCGAATGGTTTTTGCTGGAAAGTA	GCGCAACGACATTTTCACGAAGTT	194
Sat_097		A2	122.05	BH126269	14969772	(AT)15	CGGCAACTGCGAAAAT	ACCCAACTTGTCAAACAGAC	
Sat_138	*	A2	123.26	CC453693	31044523	(AT)25	GCGGGACTTAGGAGTCTAGTATTA	GGGAACAGGGATTTAGGACGAGAA	190
Satt133		A2	125.38	BH126346	14969849	(ATT)10	GCAAATGAAGAAAAGATGGATT	TAAAGCGATGGTTGAAGAAAG	169
Satt209		A2	128.44	BH126415	14969918	(ATT)13	GCGGTGGATAAAAGCCATCTCTA	TCCATAGGCTTAATTCTTATGATGTT	166
Satt455		A2	129.86	BH126629	14970132	(ATT)19	CGGATTGTGTCCTTTGTTGTTATTAT	ACCTCGCACACAATTTGAGTC	256
Sat_294	*	A2	131.97	CC453827	31044657	(AT)23	GCGGAACCCTTTATTTGTATCCAACTTAG	GCGTGGTGGCACTTTGATTGTAGTA	191
Satt409		A2	145.57	BH126589	14970092	(ATT)27	CCTTAGACCATGAATGTCTCGAAGATA	CTTAAGGACACGTGGAAGATGACTAC	183
Satt228		A2	154.11	BH126429	14969932	(ATT)19	TCATAACGTAAGAGATGGTAAAACT	CATTATAAGAAAACGTGCTAAAGAG	250
Sat_347		A2	158.39	CC453873	31044703	(AT)22	GCGAAGCCAACACATATAACATTGAAG	GCGGGCAAGGGGACACTACAATAATAC	
Satt538		A2	159.63	BH126706	14970209	(ATT)12	GCAGGCTTATCTTAAGACAAGT	GGGGCGATAAACTAGAACAGGA	109
Satt429		A2	162.03	BH126608	14970111	(ATT)25	GCGACCATCATCTAATCACAATCTACTA	TCCCCATCATTTATCGAAAATAATAATT	265
Satt378		A2	165.73	BH126565	14970068	(ATT)11	TACAATGACGAGAGGAGAAGAGAC	TGAAACCACAAACAACAACAAC	166
BE806308		B1	0.00	BE806308	10237420	(AT)18	GCGATTTGACCCCGTTCATACAT	GCGGCAGAAATCCGCTCTCTTTA	210
Sat_272	*	B1	14.32	CC453806	31044636	(AT)19	GCGATGGCAATATGTTTTTGAGC	GCGGCCTTGTAATTTTCCTTGTTAATGTG	240
Sat_270	*	B1	21.99	CC453804	31044634	(AT)29	GCGAAAGCACTTGGATGACACATAA	GCGAGGGGTAGAGACTGGAGAGTA	231
Satt426		B1	28.33	BH126605	14970108	(ATT)16	GCGCCCATTATTATTTTCCTTGAATTGT	GCGAATGCCTAATGTGATGATAAAAAAATA	199
Sat_411		B1	30.87	CC453935	31044765	(AT)24	GCGAAATTACCCAATAAGTTGATGAGAAAGT	GCGGGTGAATCACTGATGTCTCTTGA	
Satt509		B1	32.51	BH126680	14970183	(ATT)30	GCGCTACCGTGTGGTGGTGTGCTACCT	GCGCAAGTGGCCAGCTCATCTATT	238

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Sat_261	*	B1	32.95	CC453796	31044626	(AT)25	GCGGATAATTTTGCGTCATTATTAATTCAAT	GCGGCAGGGAGTTGTTTTCATTCCAGT	266
Sat_156	*	B1	35.00	CC453707	31044537	(AT)17	GCGGTGTGGATCCAAAAACTCAAACTT	GCGTGCTAGTTCGATCAGCTTAGTTTC	214
Satt251		B1	36.48	BH126449	14969952	(ATT)15	CCTCCACCCCCTTCCCACCCAAAA	GGTGATATCGCGCTAAAATTA	212
Satt638		B1	37.80	CC453997	31044827	(ATT)13	GCGGATCCTATGAGCCTATCTGTATTT	GCGGCAAGCATTATACTATTTATACGG	173
Satt197		B1	46.39	BH126404	14969907	(ATT)20	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	173
Sat_247		B1	49.73	CC453785	31044615	(AT)21	GCGGGGCAGGATATGATATTGTT	GCGTATTCGCCAAGCACTACTTTTT	260
Sat_128		B1	53.41	BH126298	14969801	(ATT)31	GGGGTTTTGTTAATCATTGTCCTTAGAT	GGGAGAAAATTTTTAATGCCAGTAGTTA	
Sat_149	*	B1	54.01	CC453701	31044531	(AT)21	GCGGAGCAACCACTTGTGTCTTCCTGT	GCGCGTAGTTGAATTAATTAAATTACT	208
Satt519		B1	57.91	BH126689	14970192	(ATT)14	GGATTTCAAAGAATGAACACAGA	CCGCAAGGTTACGAACTGCTCGAA	246
Satt298		B1	64.91	BH126490	14969993	(ATT)25	GCGGGTAATATGGGGCTGTAAATAGA	GCGGGATCCCCCATTATAATGAGT	202
Sat_348		B1	71.97	CC453874	31044704	(AT)34	GCGAAGCCGCACACTAAGATGAAGAT	GCGTGAATAACCAAATGGAAAGAGATT	
Satt597		B1	73.77	BH126762	14970265	(ATT)13	GCTGCAGCGTGTCTGTAGTAT	CGAGGCACAACCATCACCAC	155
Sct_026		B1	78.13	BH126772	14970275	(CT)14	CGAAACGCAAAATCTC	AAAACGTATCTGAAGTAGTGG	119
Sat_360		B1	80.19	CC453886	31044716	(AT)15	GCGCTTACGTTAACAACGTATGTTTTCGTTA	GCGTGGTTGGGTTACTGTATAACTCATAACT	
Satt332		B1	80.89	BH126523	14970026	(ATT)13	GCGCATCCAGGGCTTGCAACAAAG	GCGGTCCTTATATATGGAAGATCA	247
Sat_095		B1	81.31	BH126267	14969770	(AT)48	TGGACACGTTGAAAAGAGTAAAAAGTT	CAGGCCCAAAGTAAATCTGAAAAA	
Satt430		B1	81.92	BH126609	14970112	(ATT)11	GCGAAAACGGATATATAATAAGTTGAA	GCGCCCATGTAAAAGATAAATAAT	232
Satt415		B1	82.89	BH126594	14970097	(ATT)18	GCGTCTCCCTTAATCTTCAAGC	GCGTGTGACGGTTCAAAATGATAGTT	297
Satt583		B1	84.19	BH126749	14970252	(ATT)15	CCGAGCTAACAAAGGCGACCAAAT	GGGGCACAAGCCACACTT	116
Sat_364		B1	84.25	CC453890	31044720	(AT)11	GCGATCTTGTTAAAAAATAAACTTAACCATA	GCGCAGGTTCGGCCTTGGACCTTGTCTTAAG	
Satt444		B1	85.92	BH146217	15243083	(ATT)15	TGCAAAAATACGGGTTCATAAT	AGAGGAAGCGAGACTAATAGAAG	162
Satt665		B1	96.36	CC454020	31044850	(ATT)18	GCGTTGAATTCGCTGGTTTAATCCTA	GCGCATGACTTAATTTTACACCCTTTATTT	261
Sat_123		B1	100.88	BH126293	14969796	(AT)30	GGGGCCTACTAAGGTGAAAAGAAATAAT	GGGAAGCGATAAAAATTGTTTAATAAGA	
Satt359		B1	102.56	BH126548	14970051	(ATT)15	GCGAGAAAATAATCCTGCTCAAG	GCGTTTAAGTCCAATAACAAAGATAAC	179
Satt484		B1	118.53	BH126656	14970159	(ATT)12	GCGTTTAATAAAACTAATTTAATTGTACT	GCGTTCCCTTTCTCTCCTTTCTTTCTT	302
Satt453		B1	123.96	BH126627	14970130	(ATT)13	GCGGAAAAAAAACAATAAACAACA	TAGTGGGGAAGGGAAGTTACC	235
Sat_331	*	B1	125.74	CC453858	31044688	(AT)23	GCGGTGAATATCCATCAGCCATGAAATTATA	GCGTGCCCATTATTTGTTGGATATTTGTTTG	271
BE801538		B1	126.51	BE801538	10232650	(AT)16	GCGTAGCTTTCTATTGTCTAAT	GCGAACTCCACCACTCTG	230
AQ851479		B1	128.66	AQ851479	6063174	(CT)12	GCGCTGCAAAAATTAGTT	GCGTTCCAGGACCCAATA	184
Satt577		B2	6.05	BH126743	14970246	(ATT)12	CAAGCTTAAGTCTTGGTCTTCTCT	GGCCTGACCCAAAACTAAGGGAAGTG	119
Sat_177		B2	7.84	CC453722	31044552	(AT)13(AC)5	AGCCACGATACACAAAAACC	GGAGGGTACAAAAGTAGCAAAGATT	236
Sat_264	*	B2	12.56	CC453799	31044629	(AT)27	GCGAACGACTATTATAAATTTAAGTGATTGA	GCGGTATTGCGAGTGAGAATGACTAAATAAA	222
Satt467		B2	17.77	BH126639	14970142	(ATT)16	GCGAAGAGCTACATCTAACACAATTCAA	GCGTTAAGCACGGTCATATTTTCTCATA	169
Sat_342		B2	20.31	CC453868	31044698	(AT)11	GCGACTCTGGGGAAAATTAGTTTAG	GCGGAGTCGGGGAGCACTACTTGTC	
Satt126		B2	27.63	BH126340	14969843	(ATT)18	GCTTGGTAGCTGTAGGAA	ATAAAACAAATTCGCTGATAT	148
Sat_287		B2	31.88	CC453820	31044650	(AT)28	GCGCATTCCCTATTTTTTAGAATGAGTAAAT	GCGCCATAATCAGCATGCACACCTTATATGG	270
Sct_034		B2	51.45	BH126774	14970277	(CT)13	AATTCTCACTCTCACAACTTC	CCATGGAATAGTTGGGT	142
Satt083		B2	51.49			(ATT)	CAACACCCTAGCATAGTCA	AGCAGGTATGAAATGAAATT	
Satt168		B2	55.20	BH126379	14969882	(ATT)16	CGCTTGCCCAAAAATTAATAGTA	CCATTCTCCAACCTCAATCTTATAT	
Satt416		B2	56.96	BH126595	14970098	(ATT)30	TATAGCCCAGCAAAAAAAAACAGAGAT	ATCAAAACCGACCAATGAACAAAAAAA	348

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt304		B2	65.56	BH126495	14969998	(ATT)29	GGGTAGTGACGTATTTCATGGTC	GCGTAAAAACATTCGTTGACTACATAA	230
Sat_355		B2	66.24	CC453881	31044711	(AT)27	GCGATAACACTAAATGACCAGCAGGATT	GCGGAGCCAAGTATCAAACCAAAACAAC	
Satt601		B2	67.73	BH126766	14970269	(ATT)13	CCTACGCAAGTAACATTGGTTGTCAT	GCGGCTAAAACGTATTAAATTAAGA	168
Sat_182	*	B2	68.64	CC453725	31044555	(AT)26	GCGATATTACCAGGATTGTCTGTGTC	GCGTAGGCACACTTCGTTGTTTACT	202
Sat_083		B2	68.98	BH126261	14969764	(AT)24	ACCATTGGAATGTTCTACA	TTGAAGTTATAAAAAAGTTTACATC	255
Satt318		B2	70.12	BH126509	14970012	(ATT)16	GCGCACGTTGATTTTTTTATAGTAA	GCGATATTTATATGGCCGCTAAG	265
Sct_094		B2	70.56	BH126777	14970280	(CT)20	GGGTGAAGTGAGAGTAACA	CCCGGATCTCTTCATT	
Satt272		B2	71.68	BH126468	14969971	(ATT)14	ATGACAAGGAAAAATCAATCAAC	GCTGCTGTTAAGAGTGTTTG	223
Sat_230		B2	72.08	CC453769	31044599	(AT)26	GCGGTGGGACATTGGTTTAAGTTATTTT	GCGGGATATCTTCAGCGATGGATTTTA	283
Satt020		B2	72.13	BH146214	15243080	(ATT)16	GAGAAAGAAATGTGTTAGTGTAA	CTTTTCCTTCTTATTGTTTGA	117
Satt122		B2	72.46	BH126336	14969839	(ATT)8	AACCAACTTGGGAATAGAC	GCTCTCTATCATTCACTAATCA	126
Satt070		B2	72.81	BH126318	14969821	(ATT)24	TAAAAATTAAAATACTAGAAGACAAC	TGGCATTAGAAAATGATATG	177
Sat_189		B2	72.92	CC453730	31044560	(AT)10	GCGCACCTAGTTGACTCTTG	ACTACCCCACATACTTCCTTTTAT	117
Satt556		B2	73.21	BH126723	14970226	(ATT)14	GCGATAAAACCCGATAAATAA	GCGTTGTGCACCTTGTTTTCT	167
Satt474		B2	75.35	BH126646	14970149	(ATT)13	GCGAAATTTGGAAATGACATCTTAGAA	GCGACGGGAGAAATTGGATGTGAAGAA	261
Sat_009		B2	78.66	CC453672	31044502	(AT)14	CACACGTATTGTCTTACCAC	CTCCGAGAAGCACGTA	
Satt066		B2	78.84			(ATT)28	GGGAAGCTTAATAATGAAAATGACAC	TTGATCACTTCTGTAACATTC	
Satt534		B2	87.59	BH126703	14970206	(ATT)25	CTCCTCCTGCGCAACAACAATA	GGGGGATCTAGGCCATGAC	188
Sct_064		B2	89.31	BH126775	14970278	(CT)22	CCACAATTCCCAAAATAC	ATAAAAATGGCTGAATAATAGAC	146
AW620774		B2	90.30	AW620774	7326976	(CTT)9	GCGATTTCCCCTCTTACTC	GCGAAAAACCAAGTTC	152
Satt063		B2	93.49	BH126317	14969820	(ATT)20	AAATGATTAACAATGTTTATGAT	ACTTGCATCAGTTAATAACAA	145
Satt560		B2	97.92	BH126727	14970230	(ATT)12	GCGATCGTGCAAGAAAATA	GCGGTGGACTTCGCCTCAAATAAT	285
Sat_424		B2	100.10	CC453948	31044778	(AT)25	GCGAATAGAACAAAACAACACTCAT	GCGATGCTGATGCCATTTTCAGAAT	
Satt726		B2	100.55	CC454068	31044898	(ATT)20	GCGTTTTTAGTATGGATAATGTTTT	GCGAAGGGACAAGAGTGAT	
Satt687	*	B2	113.61	CC454040	31044870	(ATT)9	ACCGCAACTCACTCACCTT	GCGCCCAATTAACAGAAAC	166
Satt565		C1	0.00	BH126731	14970234	(ATT)19	GCGCCCGGAACTTGTAATAACCTAAT	GCGCTCTCTTATGATGTTCATAATAA	186
Satt690	*	C1	5.36	CC454042	31044872	(ATT)13	GCGCCCTTACACAATAATTCTAATGAGATG	GCGTTAGCATATATTTAAAAGAGCAAAACAT	223
Sct_186		C1	9.02	BH126780	14970283	(CT)15	AAAACCTAATAAAATGAAAA	CTGCCCAACCTAAAC	
SOYGPATR		C1	10.34	L23833	438898	(CTT)6(CTT)4	GGAAGAAAGTATTGGTCTGT	AGGAGAGAGTGGAGAGATTA	110
Satt396		C1	24.11	BH126579	14970082	(ATT)9	GCGAAAAGGGATAAGTTTAAAAAT	GCGGGCCTGTAAAGGGATTCC	177
Satt194		C1	26.35	BH126401	14969904	(ATT)23	GGGCCCAACTGATATTTAATTGTAA	GCGCTTTGTGTTCCGATTTTGAT	246
Sat_367		C1	28.04	CC453893	31044723	(AT)25	GCGTTTCTGTCCAAAATTTATGATATTAGTT	GCGGAACGCCCCATTTTACCTTATCATCCTT	
Sat_337		C1	32.10	CC453863	31044693	(AT)27	GCGCATGTTTTACAAATTTTGAAGCCTTAG	GCGATCAATCCATTTATGAGGTTAGTTTCTT	
Sat_140	*	C1	41.43	CC453695	31044525	(AT)13	GCGCCATGAAATTATTTGGCAAGTATT	GCGGTTGAAGAATGGAAACTAAAAATG	206
Satt578		C1	65.08	BH126744	14970247	(ATT)11	CCCACGTCATATCCACTGCTCCTTA	ACAGCATCGATACCATGATCTAT	152
Satt607	*	C1	67.03	CC453974	31044804	(ATT)15	GCGGTTTCATCTGCAGTGTATTATTAT	GCGCCACTTAATTATTTCAGATTAATT	225
Satt646		C1	70.52	CC454002	31044832	(ATT)11	GCGGGGTATGAATTAATTAATGTAGAAT	GCGCCTTCAAAAACTAATGACATATCAT	201
Satt190		C1	73.32	BH126397	14969900	(ATT)15	GGGAGTGTGAACTTACATTGTCT	GGGCCTTGAATTTTGTGCTAT	183
Satt161		C1	73.39	CC453953	31044783	(ATT)11	GGGTATATCAACATATCTTCACCTTTTT	GGGCTGCTTGTTAATGTTTTGTAGA	
Satt718		C1	73.79	CC454063	31044893	(ATC)15(ATT)15	GCGTGCAACACCTCAAGTTTCAAATAC	GCGTAGCTCTTTCCAAAGTTTTCATC	

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Sat_404		C1	73.85	CC453928	31044758	(GT)5(AT)25	GCGGATGCGCTTAGCCAGAAGATGAGT	GCGTTCTCCCCCAATGTACATACTTCTACCA	
Satt661	*	C1	74.36	CC454016	31044846	(ATT)12	TGATATGAGCAATGTAGTTCCTCT	TCCATGAAAAAGAAGTTAGAATAGC	236
Satt139		C1	74.46	BH126352	14969855	(ATT)12(TTTA)7	TATTATAAAAATCAATGCGAAAGG	CTTTTTAATAAGCCCAAATAATTACAT	182
AW277661		C1	74.79	AW277661	6666202	(ATT)23	GCGCATGGAGCATCATCTTCATA	GCGAGAAAACCCAATCTTTATATCAATA	247
Satt136		C1	75.11	BH126349	14969852	(ATT)11	CCCCATATATTCAACATATCTTCA	AACTAAGCCAAATCTTTTCCTACTA	283
Satt361		C1	75.52	BH126549	14970052	(ATT)17	GCGCGGTCAATGAATCGGGAGACAC	GCGGTTTTCAGCGTTATTAAGTTTTG	172
Sat_077		C1	76.00	CC453682	31044512	(AT)33	GACACTTGTGGAATTACTCA	GGGTTGAAGACTTAAATTTGAAATCTCT	
Satt399		C1	76.23	BH126582	14970085	(ATT)14	AAGCCAACCTTATAATTCTTTCAT	ATATGGGCTTACTTACCCATCATAGA	171
Sat_416		C1	76.42	CC453940	31044770	(AT)24	GCGTTAGTTTTTATTTTTAAGTTGA	GCGACATTGTGTGAGGGTAA	
Sat_357		C1	76.43	CC453883	31044713	(AT)17	GCGAGGGTTTAAGGTGTAGGTTGT	GCGCACCGCTTTTGTTTCTTTTTG	
Sat_085		C1	76.91	CC453684	31044514	(AT)23	GGTTTTAGATCCTTAAATTTGT	GGGGAAGCAAGTAGCT	206
Satt294		C1	78.65	BH126487	14969990	(ATT)23	GCGGGTCAAATGCAAATTATTTTT	GCGCTCAGTGTGAAAGTTGTTTCTAT	283
Sat_322		C1	79.27	CC453853	31044683	(AT)17(CA)3	GCGTAATTCCATCATAAATAATCCAGTCAC	GCGCCTCGAAGTAAATTTTATTTGTTCTTTC	248
Satt476		C1	80.62	BH126648	14970151	(ATT)20	TTTGCTGATTAAAAAAACAAAAACTG	TTGTTAGAATGGGGACTACTTCACTA	212
Sat_042		C1	82.51	BH126255	14969758	(AT)30	GCGCCACGTATTAGGGAATGATATGAAATT	GCGAACGGATACAAGTAAACTTGAATTTTA	139
Satt195		C1	84.81	BH126402	14969905	(ATT)11	GTGTAAACGAAAGATGGGATATTCTC	GAAGTGCGACACAAATTTATGAGTA	193
Satt670	*	C1	85.37	CC454023	31044853	(ATT)18	TCTAACCTCGTTTGTTTGTGAT	TTCTGCATAAGAGATTTTCAGTTTA	235
Sat_207	*	C1	87.31	CC453747	31044577	(AT)13	CGCTCCTTAAGAATTACTACTTTTT	CCGGATCTGAACATATTGCT	236
Satt713		C1	88.95	CC454059	31044889	(ATT)7(AAC)(ATT)2	GCGAAACGTATTAATTATGTGTCTTTCTTTA	GCGGTTTGCAGTGTGATATTACAATG	
Sat_311	*	C1	90.11	CC453843	31044673	(AT)21	GCGAACACAGAATGACCCTGATTGTAAT	GCGTGACTCCCACGTTAAAATCTCAAAA	243
Sct_191		C1	92.99	CC454074	31044904	(GA)16	GCGTGAAATGCTTGAGAAGTAA	GCGGCGCAGTTGAAACTATAACAC	
Sat_235	*	C1	94.62	CC453774	31044604	(AT)26	GCGTTGGGATGGGTGTAAAACATT	GCGGAAGGCAAGTCAAGTTGATGAG	281
Satt524		C1	120.12	BH126694	14970197	(ATT)14	GCGAATTATCCAAAGATACACTTAGTC	GCGGGTCTTACGAACGTGTCACATTAT	168
AI794821		C1	122.63	AI794821	5342537	(ATT)9	GCGTTCGGCTCAAATAATAT	GCGAAAAACTAGGAGAGAATGAA	166
Satt338		C1	123.79	BH126529	14970032	(ATT)16	GCGCCCAAGTATTATGAGATATTTGAT	GCGATAATTTTAAAACTGGACCA	250
Satt682	*	C1	127.06	CC454035	31044865	(ATT)29	GCGTTTAAACTATTTTGTAATTTATTGTGAA	GCGGGGGAAATATTAGAAAAGTGATACATAA	307
Satt180		C1	127.77	BH126388	14969891	(ATT)16	TCGCGTTTGTCAGC	TTGATTGAAACCCAACTA	242
Satt164		C1	132.46	BH126375	14969878	(ATT)16	CACCAATGGCTAAAGGTACATAT	AGGAGAAGAAAAAATCACATAAAATATC	231
Satt681	*	C2	3.15	CC454034	31044864	(ATT)20	GCGGTGCACTTGTCAATCTGTT	GCGGTGAGGCATATGTCAGTC	241
AW734043		C2	4.22	AW734043	7639726	(AT)18	GCGCCACTTGTACCTAGATTGATATA	GCGTTTTCAGATTAATTAGTACCTAGAT	111
Sat_130		C2	11.39	BH126300	14969803	(AT)30	GCGTAAATCCAGAAATCTAAGATGATATG	GCGTAGAGGAAAGAAAAGACACAATATCA	309
Satt227		C2	26.65	BH126428	14969931	(ATT)9	GCTCTGCCAAATAGTGTT	CACCCTGGCACATAGA	145
Satt640	*	C2	30.47	CC453998	31044828	(ATT)24	AGATACCTACGGAGTGTTTTTT	GGTTCCCCGGTGGCTACACAAC	234
Sat_062		C2	30.80	BH126257	14969760	(AT)27	GGGGAGTGTGTTAAAAGGAGTGATG	GGGAACGGTCTATTATTTTTATTCTTGA	
Satt432		C2	38.05	BH126610	14970113	(ATT)15	GCCAGGTTGTGTTCTTGAGATA	TTCACCGAATATTCTTTTAGGTC	275
Satt281		C2	40.30	BH126476	14969979	(ATT)19	AAGCTCCACATGCAGTTCAAAAC	TGCATGGCACGAGAAAGAAGTA	184
Satt520		C2	42.37	BH126690	14970193	(ATT)12	GCGGTGTGCAAGAGTGACA	GCGCATTTGGACTTTCTA	271
Satt422		C2	44.66	BH126601	14970104	(ATT)16	ATTAGGGGAGGGGAGGTAAAAAGT	TGAAGGCCCGATATCCAAATAAA	250
Satt291		C2	45.76	BH126484	14969987	(ATT)14	GCGATCCTTGAGTTTCAATTACAG	GCGGAAAAGAAGGAGATATGGTTA	214
Sat_336		C2	51.84	CC453862	31044692	(AT)19	GCGTTCCAAAGTCTTCTACATCATTT	GCGGACCAGCTTCAAGTTACTGTTC	

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

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SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt457		C2	56.51	BH126630	14970133	(ATT)19	GTCCGTGTATTTTGTTTTGC	TTATCCATTTTCCCTTTAGTCC	264
Sat_153	*	C2	61.98	CC453704	31044534	(AT)17	GCGGGGAGTGAATAGTTAAGTGTAA	TGGCCTTTGCTAGGTTTGTAGTTA	191
Satt305		C2	69.67	BH126496	14969999	(ATT)17	TTCCCAACAACAGACAACAC	TTAATTCTCCTTTATCATCATCAC	210
Satt170		C2	70.56	BH126380	14969883	(ATT)10	GGGAAATCTAAATAAAATGATGGATAT	GGGGTAGTTAAAATTCATCCTTAAAA	123
GMAC7L	#	C2	75.43	X17120	18527	(CT)16	CCCTATCCCTCTTTTCTCGTG	AATTGGAATTGAGGTTGGGAC	112
Satt322		C2	82.23	BH126513	14970016	(ATT)10	GGGACCCATCATTAAGAA	GTTTTGCCGGACACCACA	214
Satt450		C2	89.31	BH126624	14970127	(ATT)11	GGATGTTTGAGACGTGACATCTTGAT	GGATTAATAAAATGTCATGCCTTAGT	303
Sat_213	*	C2	90.93	CC453753	31044583	(AT)17	GCGATCCCTAATTGTTATCTAATAA	GCGCAATATACTCCCCCATACCTTCGCA	195
Sat_246	*	C2	91.81	CC453784	31044614	(AT)22(GT)10	GCGCATGGTTTACAGATTACTTTATTTTCTA	GCGGCAATCATTTAAATTTATAATGATATAT	239
Satt643	*	C2	94.65	CC454000	31044830	(ATT)12	CGGGATAAATAGAAGTGGAACA	TTGGCAAATGTGAAATGTATA	261
Satt376		C2	97.83	BH126563	14970066	(ATT)14	GCTACGCATTTGGTTTGTTA	ACATGCAATACTTTTTTTTCAT	238
Satt363		C2	98.07	BH126551	14970054	(ATT)19	TAGAGGGATCCAATTAGAATCCAAGAAA	TCTTCGATCTTCATATTCATTTTTGTAA	271
Sat_076		C2	99.18	BH126259	14969762	(AT)40	GCGTAATTAACACCAATATATGACATG	GCGGGGTTAAAAATTCAAAATGT	162
Satt286		C2	101.75	BH126480	14969983	(ATT)17	GCGGCGTTAATTTATGCCGGAAA	GCGTTTGGTCTAGAATAGTTCTCA	217
Sat_402		C2	103.33	CC453926	31044756	(AT)25	GCGACACGTTGCCTTCTTTACTCACAT	GCGAGCGGAGGATACGAACACTCTAT	
Satt277		C2	107.59	BH126473	14969976	(ATT)40	GGTGGTGGCGGGTTACTATTACT	CCACGCTTCAGTTGATTCTTACA	243
Satt365		C2	111.68	BH126553	14970056	(ATT)26	TGCTCCCCTCTGCCTTTTTTTCTATTTT	AAGGATGAGTTTGATAAACATGAATGAAGAA	302
Satt557		C2	112.19	BH126724	14970227	(ATT)17(GAT)4	GCGGGATCCACCATGTAATATGTG	GCGCACTAACCCTTTATTGAA	213
Satt289		C2	112.35	BH126482	14969985	(ATT)16	GCGCCCAGGTTTAAAAGT	CTGCCCCATCACTAGCCCTTCTT	240
Satt134		C2	112.84	BH126347	14969850	(ATT)11	TTTCTTGTGATTAAATTTATATGAAATATC	TGCAGATCTAAAAATAAAAGTATG	294
Sat_312	*	C2	112.85	CC453844	31044674	(AT)22	GCGCCTCCCATTACTTCGGATTAGTTA	GCGAACGCAACAAATAATCAAACATC	273
Satt489		C2	113.39	BH126660	14970163	(ATT)23(GTT)8(ATT)8	GCGTGTGCTTGCTTCTCTTAGACTGACT	GCGTACTACTTACCCTGTTTGTCTAAAA	264
Satt319		C2	113.42	BH126510	14970013	(ATT)16	CAACTCAGTAGGGGTCAATAACAA	TGAAATAGGGAAAATAAGGGAACA	167
Satt658	*	C2	113.62	CC454013	31044843	(ATT)11	GCGTTGAGTGGTAAAATTTATAATTAAA	ACTTGGCCCGCGAAGTGCTCAATTG	227
Satt100		C2	113.96	BH126330	14969833	(ATT)33	ACCTCATTTTGGCATAAA	TTGGAAAACAAGTAATAATAACA	168
Sat_251	*	C2	114.20	CC453787	31044617	(AT)19	GCGTAGTTGCGCATTTTACATTTATGTAATT	GCGCTTGGTGGTCTTAGATCTTATTCTTA	309
Sat_142	*	C2	115.10	CC453696	31044526	(AT)11	GCGGTTCTTCTTAGAACTTCATATCAA	CTTGTGGTCCTCTTGCATCTTAGTAT	103
Satt708		C2	115.49	CC454055	31044885	(ATT)27(GT)4	GCGCAATTTTAAGAGATTTTCGGGATAA	GCGACTCGGTTGATTTTTTTTTCAATTTTTT	
Sat_238	*	C2	117.46	CC453776	31044606	(AT)28	GCGCTGAGACGTTTGTGATTGTTTGTAA	GCGGTGCATGCAATTCTAGTTAGATATT	287
Satt460		C2	117.77	BH126633	14970136	(ATT)26	GCGCGATGGGCTGTTGGTTTTTAT	GCGCATACGATTTGGCATTTTTCTATTG	156
Satt079		C2	117.87	BH126324	14969827	(ATT)13	AGTCGAAGATACACAATTAGAT	CTTTTAGACACAAATTTATCACT	148
Sat_263	*	C2	118.78	CC453798	31044628	(AT)17(TC)6	GCGGTCGATCGTTTCAATTAGTATG	GCGCTGGCAGCCCTTTATTATC	134
Staga001		C2	119.85			(CT)3(ATCT)18	GCGGAGGGGAGTTTGCAGATTA	GCGGCAAGGGCAACTGAAAAAT	
Satt307		C2	121.27	BH126498	14970001	(ATT)12	GCGCTGGCCTTTAGAAC	GCGTTGTAGGAAATTTGAGTAGTAAG	162
Sct_028		C2	122.02	BH146219	15243085	(CT)18	TCGCCGGTACAAAAG	CGAATGAACAAACAAACA	131
Satt202		C2	126.24	BH126409	14969912	(ATT)15	GGAATGCATGAGTATTAACCTCTTAT	GGGCTAACGAACATGTAACTTATCAAC	310
Sat_252	*	C2	127.00	CC453788	31044618	(AT)25	GCGTTTTTCTGTCATGTCTTTGAATTTT	GCGGCAGGTCTCATACAAGTCATCATCT	192
Satt316		C2	127.67	BH126507	14970010	(ATT)12	GTGAGAAACTAGCCAAGAATAGA	CAATTGTTTCCAAATGACACT	162
Satt433		C2	128.23	BH126611	14970114	(ATT)16	ATCAGCTGCATAAGTAAAGATACA	ACATGCTTGCAGAGGTGAATA	233
Satt371		C2	145.48	BH126558	14970061	(ATT)11	TGCAAACTAACTGGATTCACTCA	GAGATCCCGAAATTTTAGTGTAACA	248

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

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SSR locus	LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt357	C2	151.91	BH126546	14970049	(ATT)12	CCTGAGCAATTCATACTCC	TAACCGATCCGATCCTTGACA	212
Sat_332 *	D1a	5.25	CC453859	31044689	(AT)27	GCGTAAAAACCTTTAGAAAGAACAATAAGAA	GCGAGCAATCAATTCAAAAGAATAATGAAAA	250
Sat_413	D1a	5.93	CC453937	31044767	(AT)35	GCGCTCCCTTCTTTTCCACTGAATTGA	GCGTTTTCTCTCGGTTTCTCTCTTCTTATTA	
Satt184	D1a	17.52	BH126391	14969894	(ATT)13	GCGCTATGTAGATTATCCAAATTACGC	GCCACTTACTGTTACTCAT	168
Sat_353	D1a	36.23	CC453879	31044709	(AT)22	GCGGTCACTCGGCTAAGTAATTGTGTAGAAA	GCGGGTAATGCTAGGTTTTGGAAAATGATT	
Satt531	D1a	40.87	BH126700	14970203	(ATT)14	GCATGCAACTGAGGGAGCAGAT	GCCACAAATTATGCAGAATATA	240
Satt368	D1a	43.84	BH126555	14970058	(ATT)26	GCGAGTGCAAGAAAAAGGGAGAAAATA	GCGCTTTTCTTTCCTTTTTTTTCTCTT	268
Satt482	D1a	45.75	BH126654	14970157	(ATT)15	GCGCGTTAGTTTAACGTAAAAGGAAAT	GCGTCACCTCAATGGATATTTATTTTA	279
Satt320	D1a	46.80	BH126511	14970014	(ATT)13	GCGGTTACGTAAGAACTAATCAAACC	GCGATATGGAAGATAAAGGAAATGAGA	251
Satt221	D1a	47.04	BH126424	14969927	(ATT)23	GCGATTGTACCACTAAAAACCATAG	GCGGCAAACCATTATCTTCATT	210
Satt605	D1a	47.73	BH126770	14970273	(ATT)22	GGTAGTACCATCATATCTTTGATTTG	TGGGCGATAGTTTTCTAGATTAGGC	268
Satt342	D1a	48.14	BH126533	14970036	(ATT)21	GGTGCAAGGGAAAATGGAAATAA	GATACAACGTCGTGCTACTATCCAAATA	222
Satt032	D1a	48.63	BH126309	14969812	(ATT)7	GATCTTTAGCTCCATGTGT	CTTTTAGTAGTTTGTATGACCC	
Satt532	D1a	49.07	BH126701	14970204	(ATT)15	GCGCCAATATTATCATGCTTTATGT	GCGTGTAAAAATCTTTGAATCTTGA	167
Satt502	D1a	49.84	BH126673	14970176	(ATT)16	GCGCAACTCCCCTTCTAGTGTAATTGT	GCGACTCAACTCCCCTATAATGTATAT	262
Sat_159 *	D1a	50.08	CC453709	31044539	(AT)22	GCGCCTAGAAGTAATTAACTCTCT	GCATTCCCGTGCCCCACATATGCT	173
Satt321	D1a	50.16	BH126512	14970015	(ATT)14	CACCGTCGTAAAAACTGTGTCGT	GCGTGTCAAAGAGTTTTAGACATC	236
Satt169	D1a	50.55	CC453954	31044784	(ATT)15	GGCAAGTTTATGAAAGTTTTAAATTTACTA	GATTGCTTTTACAAAGTCTAGAGAACTATA	
Satt548	D1a	51.07	BH126715	14970218	(ATT)21	GCGGGTTAAGTCTCCTTTTGAACA	GCGCCAATTAAATCCATCATTAAATCAG	216
Sat_346	D1a	53.67	CC453872	31044702	(AT)25	GCGGTACGGCATCTGCAATGACTTT	GCGGAGCCAACCACCTCAGTATC	
Satt603	D1a	54.50	BH126768	14970271	(ATT)23	GCGTAGCAAATTGGTTTTC	GCGGGCAAGTCTTACTATATTGAGAT	238
Satt295	D1a	55.22	BH126488	14969991	(ATT)19	ACACTAAACTAATCCGATGAAAAACA	GTACGTACCATTGGACAACTCTG	212
Satt515	D1a	55.68	BH126685	14970188	(ATT)14	GCCCGTACAGATTGAAACACAGAC	GGACAGTCAAGGAGTTACTTCAAA	230
Sat_201	D1a	56.08	CC453742	31044572	(AT)20	GCGATCGTTAACTCCTTACAC	GCGGCCCAGAAGTAGTCAAAG	279
Satt179	D1a	56.20	BH126387	14969890	(ATT)25	GGGATTAGGTTTATGGAAGTTTATTAT	GGGTCATTAAAACGATCAGTAAGA	180
Satt254	D1a	56.43	BH126452	14969955	(ATT)25	GGGCATGCATAATCTCTCTGCAAC	GCGGGGATATTTATTGATTTAGT	258
Satt383	D1a	56.57	BH126568	14970071	(ATT)12	CGATCTAACACGCATATTTCCTCTG	CTTCCCTAATATTGGCAACCTCTATG	211
Satt267	D1a	57.34	BH126463	14969966	(ATT)16	CCGGTCTGACCTATTCTCAT	CACGGCGTATTTTTATTTTG	246
Satt402	D1a	57.75	BH126584	14970087	(ATT)22	GCGCAAAGGGAAGACTCGTTG	AATGGCTAATCATGTAAAAAT	342
AZ302047	D1a	57.76	AZ302047	10038587	(AT)15	GCGTGGAGCGAAAATCAACTCTT	GCGATGACCCCGTAATGGTGA	234
Satt203	D1a	59.00	BH126410	14969913	(ATT)20	GCGTGTCTTCCCAATCCATCTAATCT	GCGACTCTGCATTTCTGAATAAATTCAC	220
Satt283	D1a	60.97	BH126478	14969981	(ATT)20	CGACAATGGAGATACACAA	AGAGTGCAAGAATGAAGTAAA	265
Satt370	D1a	60.99	BH126557	14970060	(ATT)13	GCGGTTAAGGGAATTTGTAACTTGAA	GCGATCATGCATTTATTTGAGATA	247
Satt580	D1a	62.37	BH126746	14970249	(ATT)12	CCTGCCATCCTAGATTAAAA	GGGAATCAAGTCCACTGCCACTC	113
Sat_110	D1a	62.52	BH126280	14969783	(AT)13	AACATTTTTCATCGCTTTTCTTAG	TCTTCTCAGGAACTTGAATTACTCA	178
Sat_343	D1a	62.56	CC453869	31044699	(AT)19	GCGCAACCATAGCCTCTAAAGTAATAAGTT	GCGGGCTTCTTTATGTTCTGCTGATA	
Satt507	D1a	64.52	BH126678	14970181	(ATT)22	GCGCTCAGCCTTGTTAAATCACTT	GCGCTACTCTCGTGTCGTTAGTTA	217
Sat_345	D1a	65.63	CC453871	31044701	(AT)20	GCGGTAGGTACGATCATATCGTGTGACTATT	GCGAAGTGGGAAATCAATTCTCACGAGATTG	
Sat_106	D1a	66.39	BH126278	14969781	(AT)25	TGAGGTGAAGGAGAAGAGAG	CCCATTAAGTTGAAAGATTTATTAT	242
AW781285	D1a	67.78	AW781285	7795888	(CGA)8	GCGTCTTTTGCACGATGAA	GCGAATGGTGGGAGAAA	138

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus	LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt198	D1a	68.62	BH126405	14969908	(ATT)11	GAGCCAACCAATTAGAGCCAAGTTA	GGCGGTTTGTTTTTTATCTATTCA	233
Satt468	D1a	69.91	BH126640	14970143	(ATT)13	GCGTCTCTTATTTTGACCTTTTTAACTT	GCGTTTTGTATTTGGTCTATCTGCTTAG	218
Satt436	D1a	70.69	BH126614	14970117	(ATT)28	GCGTATAAAGAAAAACGAGCATATCAT	GCGCTTATAAAGGCTTGTGAAAGACACT	244
Satt439	D1a	72.27	BH126616	14970119	(ATT)10	GCGAAAATGATTAAATTGTTTTCTCAAG	GCGGCACGTTGCCATATAAGATAAAGG	281
Sat_036	D1a	75.25	CC453674	31044504	(AT)19	GCGACTCCAAGTTTTTTTTGTTT	GCGGGAGTTAGAGGAAGAGAACA	142
Satt077	D1a	77.49	BH126323	14969826	(ATT)12	GATCTAAAGTCTGATATTTTTAACTA	AAAAGGAGAAGGAATGC	118
Sat_414	D1a	85.48	CC453938	31044768	(AT)30	GCGTTGTGCTTAGGGAAAATAAAA	GCGAAAAACACTGTCTGAAATACT	
Sat_305 *	D1a	91.26	CC453837	31044667	(AT)28	GCGACAATGCAAAACACATTTGTATTACTT	GCGCTATGCCCATGTGTTTAGTGATTAG	337
Satt407	D1a	99.59	BH126587	14970090	(ATT)13	GCGTAACAAGCGTTTCTACTTTAA	GCGAATGAGCAAGATAAAAACTTT	305
Satt071	D1a	100.39	BH126319	14969822	(ATT)19	CTTGAAGTAGTTTTATTCTCTCA	CAGAGCTAAGCATCTATAATG	227
Sat_160 *	D1a	104.28	CC453710	31044540	(AT)25	GCGCATGATAACCTATAATGAGAT	CCAGCAAGCAATGCTCGGTCTACT	204
Satt408	D1a	106.69	BH126588	14970091	(ATT)19	GCGGTCCGTGCTGTTAATTCTATA	GCGTGATTTATTCATGATATATTTTTG	176
Satt147	D1a	108.89	BH126359	14969862	(ATT)14	CCATCCCTTCCTCCAAATAGAT	CTTCCACACCCTAGTTTAGTGACAA	174
Satt129	D1a	109.67	BH126343	14969846	(ATT)26	TTCAGTACAAGTCGGGTGAATAATAATA	TCACATGTTCGGGACTTAAGGTAT	146
Sat_096	D1b	0.00	BH126268	14969771	(AT)21	ATTATAGGGAGTAACCACAAAGAAAAA	GCTAGCTACCTGCCAGTGATTAT	
Sat_279 *	D1b	3.79	CC453812	31044642	(AT)28	GCGTTGCGTTGTTACGTGAAAGCACAGAAAC	GCGACTGGTTAATCTAGTCAGACTTAACAGA	276
Satt216	D1b	9.80	BH126420	14969923	(ATT)19	TACCCTTAATCACCGGACAA	AGGGAACTAACACATTTAATCATCA	197
Sat_227 *	D1b	11.14	CC453766	31044596	(AT)18	GCGCAAAATGATTTGGGAAAATAACTTACAA	GCGTTATATACTTTTGGCGAGTTATCC	246
Sat_351	D1b	20.61	CC453877	31044707	(AT)21	GCGCCACCCAAGGGCATCTTTCG	GCGGGCCGCAACTATGAAAAGAC	
Satt095	D1b	25.60	BH126329	14969832	(ATT)17	TATTTGTTATTGGTGAATTAAGA	ATTCCTGTAGAAATTGATCTG	
BE021153	D1b	30.23	BE021153	8283594	(GT)10	GCGAAACTGCTTGTATTTTA	GCGCTCCAATTGAAAGTG	153
BE475343	D1b	30.74	BE475343	9565834	(GT)11	GCGTCTCCCTGTCTCTC	GCGAGCTTAAAACAATCATC	181
Sat_373	D1b	35.75	CC453899	31044729	(AT)22	GCGCCGTAAATTCTAACATGTGTATGTGACT	GCGGGAAAAAAACAAAAAATTATGACTTCAA	
Satt157	D1b	37.07	BH126369	14969872	(ATT)31	GGGCTCACTCTCGATAGTAGGTATAAAG	GGGATACCAAAAGGAATAATTGTCTT	257
Sat_211	D1b	38.04	CC453751	31044581	(AT)35	GCGATCACCGGACTTAGAGAGTTA	GCGGAGCTAATTAAAAAGTCATTCCAATA	275
Satt698	D1b	38.04	CC454047	31044877	(ATT)17	GCGCAAATTTCGTTCTTATTA	GCGCAATCGCTTCTTTAGAT	288
Sat_173 *	D1b	38.63	CC453719	31044549	(AT)18	GGGATGGCCTTTTATTCTAC	TGTCTCCATTGCTACGACTAAG	252
Satt701	D1b	40.04	CC454050	31044880	(ATT)13	CTCAGCGGAAAGCCTTCTCA	ATGTCGCACCTACACCCAAAAA	236
Satt558	D1b	43.91	BH126725	14970228	(ATT)16	CTCACACCCTTTCATTATCTA	AAATCGCGCATCTAAATTTAC	230
Satt634 *	D1b	46.62	CC453993	31044823	(ATT)13	GCGCATACTGTTTATGCTAGACACCTA	GCGGGGTTGTTTTATTTACAAGAACAG	139
Sat_254 *	D1b	46.92	CC453790	31044620	(AT)9	GCGTGATTAACGGATAATATGTTATTGAA	GCGACACAAGCGGAATAATTAGAGATA	313
BF070293	D1b	47.28	BF070293	10847646	(CT)14	GCGCCACACCAGAAAGA	GCGAGCAGAAGAGCCCAATG	186
AI856415	D1b	50.11	AI856415	5509857	(AT)17	GCGAAGTCAGTAAAAACATTGGATA	GCGGGCGTGAATAAGAGAAGAA	224
Satt296	D1b	52.61	BH126489	14969992	(ATT)20	GCCCCACAACCAGAAACAC	GAAATTTGGCGACTAAAAACTGC	185
Satt542	D1b	53.02	BH126710	14970213	(ATT)19	CACCAGCACAGAACAATCATTT	CACGGTCTAACCTTTCCTTCTA	205
Satt266	D1b	59.61	BH126462	14969965	(ATT)22	GCGAAACTCTACGGGTCAGTAGTTAT	GCGTAAGATGGCCTAGAAAGAGGATG	174
Sat_423	D1b	67.63	CC453947	31044777	(AT)9	GCGTATACACAATGATAGG	GCGACCAACCACCACTTC	
Sat_135	D1b	70.65	BH126305	14969808	(AT)28	GCGCCTCGCCTATATTAAATTACAAAA	GCCTCCGCCTCCGAAATACACTTA	200
Satt412	D1b	72.57	BH126592	14970095	(ATT)17	TCGGGACAGGTGAAATCTGAAATA	TTCCTTTTAATTCTAACATTGAG	302
Satt141	D1b	72.89	BH126353	14969856	(ATT)26	CGGTGGTGGTGTGCATAATAA	CCGTCATAAAAAGTCCCTCAGAAT	205

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt290		D1b	73.35	BH126483	14969986	(ATT)16	GCGGATTTATAAAACATTAAAAATCA	GCGCGCACGGCTGAAACACTCTCTCA	236
Satt611	*	D1b	74.02	CC453976	31044806	(ATT)13	GCGGGGAATAATAAGAATATGGAC	GCGCTTTCACTATGTGACCTGAATTA	211
Satt604		D1b	74.21	BH126769	14970272	(ATT)11	GTGGCTCACAATCAACGTGAGCATCAGA	CTGTGCCACTTATGATTTGGTAA	149
Satt506		D1b	74.79	BH126677	14970180	(ATT)14	GCGAATTGGCATACATAGTACC	GCGTGAATTCGCCTAAGTTTAT	280
Satt005		D1b	75.29	BH146210	15243076	(ATT)19	TATCCTAGAGAAGAACTAAAAAA	GTCGATTAGGCTTGAAATA	141
Satt600		D1b	75.41	BH126765	14970268	(CAA)18(TAA)15	GCGCAGGAAAAAAAAACGCTTTTATT	GCGCAATCCACTAGGTGTTAAT	195
Satt537		D1b	75.67	BH126705	14970208	(ATT)33	GCGTGTACATCAAAATGGTGTATTC	GCGGGAGGAACTTTGTCTCAGTAAT	160
Satt579		D1b	75.94	BH126745	14970248	(ATT)20	GCGATTGGTTATTCTGATTAAAT	GCGGTTACGAAAATCGTAAATTGATG	215
Satt282		D1b	76.10	BH126477	14969980	(ATT)23	TGCGGGACAATTTTAGATTTAT	AGATGGATGAAAGTTGGAGAAAG	222
Sat_089		D1b	76.28	BH126264	14969767	(AT)26	AATTTTTTCTGTTGTCAGTGT	TGGAAATGTTAAATGTATGG	145
Satt189		D1b	76.32	BH126396	14969899	(ATT)15	CCATACGCAGCATTAGAG	GCTATTTGCATGTTGAGAA	239
Satt350		D1b	76.60	BH126540	14970043	(ATT)17	GCGGGAGTTTAAAATATGCTTTTG	GGCTTAGGCTTTGTGTCTGGAAGT	248
Satt428		D1b	77.35	BH126607	14970110	(ATT)20	GCGTTGTGCTTAACTGGTTGATTT	GCGGACCAGCTAGTTTTTAATGTG	250
Sat_169	*	D1b	78.44	CC453715	31044545	(AT)17	ATTCGTTAAATACTCCACATCAATA	TTATGCTTTGTTGTTTTTCAGTT	162
Satt644	*	D1b	79.42	CC454001	31044831	(ATT)13	TATGCCTCAAACCACAAA	CAGGCCACCATTTTTCTT	204
Satt041		D1b	84.04	BH126310	14969813	(ATT)17	TGTTGTGTGGCTTTATTATT	TTAAGGTGGGATATGGTC	173
Satt546		D1b	87.20	BH126714	14970217	(ATT)20	TGAGCGATCAAGAAGCACTTA	TTTGGATCGCATAACACTTTA	240
Sat_139	*	D1b	93.35	CC453694	31044524	(AT)15	CATGTTGAATCACTAATTCAATTT	GGGTCGTTCCTGCTACAGGCATGAAG	193
Satt703		D1b	98.75	CC454052	31044882	(ATT)29	GCGATGGGTGGATTCTAGAT	GCGGTGCTTGTAGGCTTTCCAAAAT	233
Satt172		D1b	100.89	BH126381	14969884	(ATT)9	AGCCTCCGGTATCACAG	CCTCCTTTCTCCCATTTT	222
Sat_069		D1b	102.60	CC453679	31044509	(AT)29	CGACCAGCTGAAGAAA	CTGAATACCCATCATTACTTAA	158
Sat_183	*	D1b	112.63	CC453726	31044556	(AT)28	GCGTCCAGCCTGACCATTTTA	GCGTTCCAATGTCTGATTATTT	282
Satt274		D1b	116.35	BH126470	14969973	(ATT)18	GCGGGGTCAATTAGTTTTCGTCAGTT	GCGCACGGTATATAATCGAACCTAT	188
Satt459		D1b	118.62	BH126632	14970135	(ATT)13	TCGTGTTAGATTTTTACTGTCACATT	AACTGCATACCCTTTGTTTGAA	204
Sat_202		D1b	118.86	CC453743	31044573	(AT)17	GCGGGCCAAGTGAATAACAAGTTTATAAATT	GCGTCCTGCCACACCATTTTTATACTTTTAA	349
Sat_198		D1b	118.95	CC453739	31044569	(AT)23	GCGTGATGATTTGTTGATATGACATTTA	GCGCCATTGAAACATACAGAGACTACAG	306
Staga002		D1b	126.45			(TAGA)9	GCGATGGCTTCGGATCTTAGCA	GCGGCACGACGCTACTGAGAA	
Sat_415		D1b	130.48	CC453939	31044769	(AT)34	GCGATTGTAAAGTAATAAGGGTATATTG	GCGTTTTGTACTCCATATACTACCTTCATC	
Sat_289	*	D1b	131.92	CC453822	31044652	(AT)24	GCGAATTCCAGCTTTTATCACTTTATGAC	GCGATTGGAAAGTGCCTTTTATGTT	276
Sat_192	*	D1b	135.26	CC453733	31044563	(AT)13	GCGGAATGGCAATAGTTGATGAGTA	GCGGGATGGGATATGAGAGTAAG	173
Sat_283		D1b	136.66	CC453816	31044646	(AT)26	GCGTGGTGCACGATCATATAGAG	GCGTCTCCTTCGCTATCTCAAAC	195
Satt271		D1b	137.06	BH126467	14969970	(ATT)11	GTTGCAGTTGTGCGTGGGAGAGAG	GCGACATAGCTAATTAAGTAAGTT	122
Satg001		D1b	137.97	CC453949	31044779	(ATG)15	GCGGCACCTCGTATTCTACCT	GCGTACGCCAAGCTTGTCCAG	
Sctt008		D2	3.16	BH126784	14970287	(CTT)9	ACGCAGAGATAGAGAAAGAGA	CCCCCAGACACAACATA	
Sat_333	*	D2	5.83	CC453860	31044690	(AT)30	GCGTCACAGCTAGGTATTCACGAAAGAGAAA	GCGGCCACCTTATTACACACCTCAAAACA	153
Sat_296	*	D2	6.42	CC453829	31044659	(AT)32	GCGAGACCCATTTAATTCTCAATATCAGACA	GCGCCCGTGAATGAGTCAAACAAGTA	233
Sct_192		D2	11.77	CC454075	31044905	(TC)19	GCGTTTGGCCTTGACATTTAGT	GCGAGCCCTATTTTTGTTCTTAT	
Satt328		D2	16.76	BH126519	14970022	(ATT)11	TGACCACCATGAGTTCATT	GGGGGTGGCTTTTAGATTC	237
Satt458		D2	24.52	BH126631	14970134	(ATT)31	TTGGGTTGACCGTGAGAGGGAGAA	GCGAACCACAAACAACAATCTTCA	177
Satt135		D2	26.05	BH126348	14969851	(ATT)19	CACGGATTTTAAATCATTATTACAT	TTCCAATACCTCCCAACTAAC	200

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

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SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Sat_277	*	D2	28.79	CC453811	31044641	(AT)31	GCGTGGGTTATTTATGTTTGTTTGAC	GCGTTTCGATAATTAAAATAACCTAGTGTAG	327
Satt014		D2	29.56	BH126306	14969809	(ATT)9	TCTGGTAAACATTCAACTTTTTATTT	TCCAAATATGACATCATAAACTTCTA	181
Sat_284	*	D2	30.80	CC453817	31044647	(AT)26	GCGCTCACCTAAAAGTGCTCTCACATA	GCGGGAGCATCAGTCTTTAGGAACATC	264
Satt498		D2	32.14	BH126669	14970172	(ATT)19	CAACCCCGAAATACAACTAATGTT	TGGTGAGGCTCATTTTCATAAGA	240
Satt486		D2	34.09	BH126657	14970160	(ATT)13	GCGCATGCATTACCATAGGCTATAATA	GGGGTCATGCATAATAGAGATAGAACCA	246
Satt372		D2	39.35	BH126559	14970062	(ATT)21	CAGAAAAGGAATAATAACAACATCAC	GCGAAAACATAATTCACACAAAAGACAG	259
Satt002		D2	47.73	BH146209	15243075	(ATT)25	TGTGGGTAAAATAGATAAAAAT	TCATTTTGAATCGTTGAA	127
Satt443		D2	51.41	BH126619	14970122	(ATT)10	GCGACTTAGGGTCCTAGATCCATA	AACTCCTCATACCTCTCTCTCTC	235
Satt582		D2	53.85	BH126748	14970251	(ATT)16	CCGGTGATACTCCATACCAATAAC	CAACGCCGATTTTCTATTTGTCTG	110
Satt154		D2	57.07	BH126366	14969869	(ATT)20	AGATACTAACAAGAGGCATAAAACT	AAAGAAACGGAACTAATACTACATT	269
Sat_092		D2	57.51	CC453687	31044517	(AT)31	AATTGAGTGAAACTTATAAGAATTAGTC	AAATAAGTAGGATGCTTGACAAA	244
Satt447		D2	66.27	BH126622	14970125	(ATT)10	CGAAACTACGGTTGATTAT	TCCAAACACTGTCCTTCTT	270
Satt669		D2	67.71	CC454022	31044852	(ATT)19	GCGCTTATGAACCAACAGAAAACAAG	GCGATGCCAAACCCAATGAGATA	154
Satt208		D2	67.91	BH126414	14969917	(ATT)9	GCGATCGTATTGGGTCT	CCCGTTATTTTCGTATGA	196
Satt397		D2	69.30	BH126580	14970083	(ATT)10	TCTCGGGATCCTTGTTAGAT	GCGAAGAAGAAGAGAACATGTGAA	173
Sat_292	*	D2	75.29	CC453825	31044655	(AT)33	GCGGCCCCCAATTATTATATGTTC	GCGAAGGGTTTAGCTTTGCTTATG	251
Sat_222	*	D2	76.69	CC453762	31044592	(AT)21	GCGGTCATGTGTCCCATTTAATTTAATCAA	GCGATGTGCCTCAAAAACTAACATCAATAA	168
Satt389		D2	79.23	BH126574	14970077	(ATT)22	GCGGCTGGTGTATGGTGAAATCA	GCGCCAAAACCAAAAGTTATATC	232
Satt461		D2	80.19	BH126634	14970137	(ATT)10	AAATACAAGCTTTAATAAAGTGCAGA	CTTACGTTTCCATAGATTTCTCG	157
Sat_114		D2	84.18	BH126284	14969787	(AT)29	AACTCAAATCCAAACTCACT	ACTCAGTAAATAACAAAAGTCATT	286
Satt311		D2	84.62	BH126502	14970005	(ATT)13	GGGGGAACCACAAAAATCTTAATC	GTTGAAGCTCAGGCTGTGATGAAT	174
Satt226		D2	85.15	BH126427	14969930	(ATT)18	GCGAAACAACTCACTTAAGCAATACAT	GCGTCCTCCTACCTTTCTTATC	325
Sat_209		D2	85.64	CC453749	31044579	(AT)25	GCGGTAAAATCCCACACCTGTCTCT	GCGTTGGAAGAATGATAACTTAAAACA	324
Satt514		D2	85.69	BH126684	14970187	(ATT)27	GCGCCAACAAATCAAGTCAAGTAGAAAT	GCGGTCATCTAATTAATCCCTTTTTGAA	236
Satt528		D2	86.34	BH126698	14970201	(ATT)22	GCGGGTGCAGGGTTTACTGTGTAAT	GCGGCTGGTTCTTGAAAAAA	243
Sat_362		D2	86.69	CC453888	31044565	(AT)23	GCGCAAACAAGTTATACCTTTATATTGGTGA	GCGAAGGGAACCTAACGTATGTCTTTTA	
Sat_194		D2	86.69	CC453735	31044718	(AT)32	GCGTTGGGCGTTTTTGAGAAGGTGACAA	GCGCCTTTTGTAATATTGTTAAATGTAA	227
Sat_338		D2	87.16	CC453864	31044694	(AT)15(CA)8	GCGGGGCATTAATAAACCTCCTCTAACT	GCGCCATTTTGGTCATTCCTAACAACT	
Satt082		D2	87.25	BH126326	14969829	(ATT)13	AATTCATTTAGGGAGTTGAT	CTAGCCAATGTCATATGACT	111
Sat_365		D2	87.39	CC453891	31044721	(AT)23	GCGCAAACAGTTATACCTTTATATTGGTGAA	GCGCAAACAAGTGTATATAAGGGAACCTAA	
Sat_300	*	D2	87.56	CC453833	31044663	(AT)23	GCGCGCATTCGCATGTGTGGTAACTA	GCGACAATCCCATGCAACTACATGATTAAGA	108
Satt574		D2	87.67	BH126740	14970243	(ATT)12	GCGCCTCTCATATGGTAT	GCGGGGGGGAAATGTAGA	161
Satt662		D2	87.88	CC454017	31044847	(ATT)19	TTGAAGGAAAGGGTAAACCTATAT	TCTTATCGTTCCGTGCTCCAGAT	154
Satt543		D2	88.02	BH126711	14970214	(ATT)19	GCGGATCTAAGGATAATTCATTAA	GGGAGCGGATCATTCGGTGAAA	173
Satt488		D2	89.20	BH126659	14970162	(ATT)16	CGGTGCTGTATTCCGTTTCAATGTTT	GGTTAACTGCCTCTGCAAAGAATAGT	232
Satt464		D2	89.75	BH126637	14970140	(ATT)16	GGGTTGGGAGAATTTAGGTT	TTTTGCATTAAAGGCTAATATGAA	216
Satt615	*	D2	91.21	CC453980	31044810	(ATT)24	GCGCCTGCTAACTAGTGTGCAAATTAT	GCGGGTGATGTCAAATTTTCTGTC	293
Sat_001		D2	92.12	BH126252	14969755	(AT)17	GCGGATACGACCAAAAATTGTT	GCGAACTGCGAAGATACTACCC	255
Sat_354		D2	93.71	CC453880	14969995	(AT)39	GCGGCGTCTACCAATTTATAAATGCCACT	GCGCATGCTTCGAATAAAAACATATTAGCCT	
Satt301		D2	93.71	BH126492	31044710	(ATT)24	GCGAAACACTCCTAGTTGATTACAAA	GCGATATAATGCACAAAGAAATTAAAGA	250

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
GMHSP179	#	D2	99.04	X07159	18651	(AT)9	ATACCAGTTGATCTGCATATT	AAAACATCGTCTACTTAAGTC	92
Satt186		D2	105.45	BH126393	14969896	(ATT)19	GGGAAGTTATAAGCAGAT	GGGAATCCATTCCTGATGAGT	234
Satt310		D2	107.49	BH126501	14970004	(ATT)14	GCGAGTTTTTATCTCATGACTTTT	GCGGGGGTATGGGACCTAAAGAAAC	240
Sat_326	*	D2	112.85	CC453856	31044686	(AT)27	GCGTATCGATGCACAGCCAAGTGCTCATCTA	GCGGAAGCTGATTGTAAATTTAAAAACAACG	192
Satt413		D2	113.61	BH126593	14970096	(ATT)18	CCTTGCCGTTCCTATTCCACAAGT	GCGTCAATTTTTTAGAGGATAAAA	308
Satt672		D2	114.97	CC454025	31044855	(ATT)20	GCGAAAGAACCTATTTTGTAATTGTAACATC	GCGCTCTTTCACTTTCAATCAAACATT	265
Satt031		D2	115.70	BH126308	14969811	(ATT)12	TTCCACTTTGTATCACTTTC	TGACTGTAAAAGAACAGATAAA	122
Sat_086		D2	118.66	BH126262	14969765	(AT)28	CAAAATCTATATGAATTGATTACA	GGAAATATCTGTAGAATTTTTTAA	
Sat_022		D2	120.30	BH126254	14969757	(AT)27	GCGGCCTTTTCTGACTGTTAA	GCGCAGTGACTAAAACTTACTAT	231
Satt256		D2	124.31	BH126454	14969957	(ATT)10	GCGATGCATAAATTAGACACAT	CCACTGCTTCATCACATTCACAC	238
Satt386		D2	125.00	BH126571	14970074	(ATT)15	GCGGATGATTTTTATAGAATAGATAAT	CTTCGTTGATACCTCAGTAGAGTACAAA	199
Sat_220	*	D2	128.73	CC453760	31044590	(AT)21	GCGCACGCCTCACTATATTATTTTTGAA	GCGATGGAAATTAAACGCTATCATGCTA	282
Sct_137		D2	128.95	BH126778	14970281	(CT)16	TGCTCTTGGGAATCTG	CTCAATAATTCATCATCACTTC	
Satt575		E	3.30	BH126741	14970244	(ATT)11	GCGGCTAATTTTGTTTATAGGAAT	CCGCTACCATCTCGGAGGACT	218
Satt213		E	3.72	BH126419	14969922	(ATT)15	CCGCTTATTTCTGTCATC	AGCCAAAACCCACAA	212
Sat_112		E	8.67	BH126282	14969785	(AT)8(GA)18	TGTGACAGTATACCGACATAATA	CTACAAATAACATGAAATATAAGAAATA	352
Satt411		E	12.92	BH126591	14970094	(ATT)10	TGGCCATGTCAAACCATAACAACA	GCGTTGAAGCCGCCTACAAATATAAT	97
Sat_124		E	15.86	BH126294	14969797	(AT)34	GGGTCCATTCCACTTTTTGTACAATAT	GGGAGTTCAAACATCCATTAGTGGTATA	
Satt384		E	19.30	BH126569	14970072	(ATT)15	TGGGGGTCAATTTTAATTTGTGC	ATTTCCCTTTCACCCACCTCTGTTT	147
Satt691	*	E	19.70	CC454043	31044873	(ATT)17	GCGAAAGATAAAAAGTAGATTGAAA	GCGCTCCTAAATCCAAATGAATC	
Satt720		E	20.80	CC454064	31044894	(ATT)19	GCGCATATACGAAACATATTGTCAAGTTACA	GCGTCATGAGTGGTTTGTTCTATACTTCTAT	
Satt651	*	E	32.10	CC454006	31044836	(ATT)10	GCGTGCTGTCTTTATACGAAGTACACTA	GCGTGGCAATAAATATTCTCACTGAA	171
Satt212		E	32.27	BH126418	14969921	(ATT)10	CCAATCCAAACAAATCCACT	CAGCAATGATGATAATGAATGA	149
Satt598		E	34.20	BH126763	14970266	(ATT)10	CGATTTGAATATACTTACCGTCTATA	CACAATACCTGTGGCTGTTATACTAT	168
Satt573		E	35.79	BH126739	14970242	(ATT)10	GCGGATTTCGATTTGAATATACTTAC	CCTGTGGCTGTTATACTATGCATATA	167
Sat_136		E	39.16	CC453691	31044521	(AT)19	ATCATGCTTCAACACTCTTT	TCCTATTTTTGCCCTTGTATTT	170
Satt606	*	E	39.77	CC453973	31044803	(ATT)26(AT)8	GCGTTCTAAATTAAGCAATTCTT	GCGTGGGTAATAATATTGGTTCAG	293
Satt699		E	41.24	CC454048	31044878	(ATT)9	GCGGATATTTTTGTCCTCAATAAT	GCGTACCGTATGTGGAGTTT	181
Satt602		E	41.68	BH126767	14970270	(ATT)11	GCGGCGTTAGTGGAATAGAACTA	GCGGGTATACCAAATGAGATAAT	175
Sat_172	*	E	42.74	CC453718	31044548	(AT)18	GCGTTCTAATTTCCTGACACTGTT	GCGGGACGTAAACGGATAATAAGGT	208
Sat_107		E	43.05	BH126279	14969782	(AT)31	TTTGGAAGTATAAAATTATGAATGACT	GGAGGAATTATTTGGGTTGTAC	178
Satt204		E	43.14	BH126411	14969914	(ATT)15	GCCATCTTGTTACAATGCAGGTA	CCTTACTCACTCCATTGGCATAATA	223
Sat_380		E	43.29	CC453906	31044736	(AT)39	GCGGCCACAGCCTTTTATGAATTAGAT	GCGATCCCCAACCCTAATGATAACG	
Satt706		E	43.36	CC454053	31044883	(ATT)23	GCGTTTTTTTCCCAACAATTAATTAGTATAT	GCGAAATGGTTATTATTGTTAAAAAATAATG	
Satt491		E	43.64	BH126662	14970165	(ATT)14	CCTAAATTGATGAAAGGATACAAG	GCCCCACAAATATTCAGAAGGTAA	203
Satt268		E	44.27	BH126464	14969967	(ATT)17	TCAGGGGTGGACCTATATAAAATA	CAGTGGTGGCAGATGTAGAA	236
Satt185		E	44.76	BH126392	14969895	(ATT)29	GCGCATATGAATAGGTAAGTTGCACTAA	GCGTTTTCCTACAATAATATTTCAT	250
Satt151		E	44.93	BH126363	14969866	(ATT)12	ATTGCCTAATTTCTGTTTGTTGTAA	CCAAAATTCAAGGCAGTGAC	
Satt403		E	44.93	BH126585	14970088	(ATT)10	GCGGGTTTTATTTTATTATAAATT	GCGGATGCCTGGGAGAATATTTCC	355
Satt483		E	44.98	BH126655	14970158	(ATT)13	GCGGACACGAAATTTTAATTATT	GTCTCAACTCTCCGACACCTACTT	271

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt452		E	45.10	BH126626	14970129	(ATT)12	GCGGTCGCTGCGTTCAATAT	GCGCCCAATTATCATGGTAGA	206
Satt355		E	45.15	BH126544	14970047	(ATT)14	GCGTCCCAGGACATCATCATCATC	GCGTAGCGTGTTATTTTGTGTTTG	242
Satt263		E	45.40	BH126460	14969963	(ATT)19	CACCCAATCATGATAGCATTTTAT	CTCATGGAATTGTCTTTCAGTTTC	222
Satt716		E	45.63	CC454061	31044891	(ATT)10	GCGTTTGCAGTTTGGATGATGTTGAT	GCGAACCCTTGAGTTGGACATGTTGA	
Satt117		E	45.78	BH126334	14969837	(ATT)11	AAAAATTGTATTTGTAAGAGAGAG	AATTGCATCTTGTACTTAACTG	144
Satt724		E	45.88	CC454066	31044896	(ATT)3(CAA)(ATT)4	GCGCCCTAACATGCATAATTTTGACT	GCGGAGAATACATTGAGTATAATTGAGAAGC	
Satt045		E	46.65	BH126312	14969815	(ATT)18	TGGTTTCTACTTTCTATAATTATTT	ATGCCTCTCCCTCCT	140
Sat_273	*	E	47.50	CC453807	31044637	(AT)27	GCGTTTCCTAGGGTAAGCACAGTGTATT	GCGGGGTGGAGAGAAAAAGAAAGAACA	253
Satt369		E	56.27	BH126556	14970059	(ATT)17	AACATCCAAAGAAATGTGTTCACAA	GCGAGTTCGAATTTCTTTTCAAGT	249
Satt685	*	E	56.70	CC454038	31044868	(ATT)14	ATCGTGGCATGTCTCACTAC	GAGGCGGAAGGAAATCTAAT	213
Sat_381		E	64.18	CC453907	31044737	(AT)25	GCGGGTTGTGTTCCTTTTAGAGAATCAG	GCGGCAGCATATATTATTGTCAAGTCAG	
BE347343		E	65.66	BE347343	9259196	(GA)18	GCGCAAGCACTGAATGTCA	GCGTCACTAACACCTATAACA	244
Satt553		E	67.92	BH126720	14970223	(ATT)32	GCGCCTTCTGTTCCATCACAGAT	GCGGCTTGTGAAACTGGCTGATTAT	182
Sat_376		E	69.23	CC453902	31044732	(AT)27	GCGTCCTACGTACGTTTATTCTTTTCT	GCGCAATTAAATAATACTTACCACATCTTGT	
Satt231		E	70.23	BH126432	14969935	(ATT)32	GCGTGTGCAAAATGTTCATCATCT	GGCACGAATCAACATCAAAACTTC	237
Satt230		E	71.31	BH126431	14969934	(ATT)15	CCGTCACCGTTAATAAAATAGCAT	CTCCCCCAAATTTAACCTTAAAGA	200
GMRUBP		F	0.00	V00458	18741	A20	CTGGCGTGCTAAAAGTA	GGACAGATTTGATCAATAATT	131
Sat_390		F	1.79	CC453915	31044745	(AT)7(CATA)3(AT)10	GCGTAGATGCTTATAATCGACCCTAACAATT	GCGCGAGGATCCCATAAAAAAAGTAAAATAG	
Satt146		F	1.92	BH126358	14969861	(ATT)17	AAGGGATCCCTCAACTGACTG	GTGGTGGTGGTGAAAACTATTAGAA	290
Satt325		F	2.23	BH126516	14970019	(ATT)19	GCGGGGTATTAAGGGAAAACAAAA	GCGTAAACGAACAATCACTTCATA	250
Satt343		F	3.04	BH126534	14970037	(ATT)13	CATGGCGGAAAGCGAAACA	TCCCAATTCACCTCTTCA	130
Sat_387		F	3.11	CC453912	31044742	(AT)35	GCGGAATTTACCAGTTTATAATATTGCTGA	GCGTACTAAATATTCAAAGACTCAAAGAGAA	
Satt569		F	3.35	BH126735	14970238	(ATT)14	GCGCAAATTGCTTCACGCATCCAAAT	GCGGCCTACTATAGTGAAGGGTATA	177
Satt193		F	3.42	BH126400	14969903	(ATT)23	GCGTTTCGATAAAAATGTTACACCTC	TGTTCGCATTATTGATCAAAAAT	239
Satt586		F	3.63	BH126752	14970255	(ATT)19	GCGGCCTCCAAACTCCAAGTAT	GCGCCCAAATGATTAATCACTCA	212
Satt030		F	3.95	BH126307	14969810	(ATT)21	AAAAAGTGAACCAAGCC	TCTTAAATCTTATGTTGATGC	164
Satt649		F	5.36	CC454004	31044834	(ATT)17	TTACTGGCCGTGTTTACCCGTGTAA	GCGGACGTTATAAGATTTTTTTATCATG	231
Sat_262	*	F	9.69	CC453797	31044627	(AT)27	GCGTTTGCATTAGGGATTATCTAGTTTATGA	GCGGGTTAGAACATTCTTAGTTAGCTCCAG	170
Satt145		F	10.65	BH126357	14969860	(ATT)12	AGCATATGGGATACAAGTGATTAG	CGGTGTTGGTGTGGTATGT	150
Satt269		F	11.37	BH126465	14969968	(ATT)11	GCGTGCCAGGTAGAAAAATATTAG	GCGGTTTTTCACTTTTCAAAATTC	213
Satt348		F	15.29	BH126538	14970041	(ATT)19	GCGCTTAGTAATGGTTCCCACAGATAA	GCGGTGATATCTAGCAACACAA	211
Satt252		F	16.08	BH126450	14969953	(ATT)23	GCGAATTTGGATTAATTAAATTTATG	GCGCTCGGTCCTCTCAAATAAGGTCTC	225
Satt149		F	18.13	BH126361	14969864	(ATT)17	TTGCACATTCTTTTTGGTAAACAGTCATAA	GTTGGAGGCCATAGTCACATTAATCTTAGA	275
Satt423		F	20.56	BH126602	14970105	(ATT)19	TTCGCTTGGGTTCAGTTACTT	GTTGGGGAATTAAAAAAATG	254
AW186493		F	21.04	AW186493	6455810	(CTT)13	GCGGTGATCCGTGAGATG	GCGGAAAGTAGCACCAAGAG	219
BE806387		F	22.97	BE806387	10237499	(CTT)14	GCGACCCCTTTTGTCTTCTT	GCGGAGGCCAGAGATGAA	205
Sat_240	*	F	25.58	CC453778	31044608	(AT)15	GCGGGCAGAAGTCTAATGAATGTGAAATGA	GCGGTTGTGACCGAAATAGATGTTATTTAAT	232
Satt659	*	F	26.71	CC454014	31044844	(ATT)	GCGGCTCAACTTCGTGTAACAAG	GCGCATCGGTAACTATCTAATATTCGTA	166
Satt206		F	26.98	BH126412	14969915	(ATT)12	GCGCATGTGAAAAGAATGAGATTATGTA	GCGTCCAAACTCATCCTTAAGGTATT	246
Sat_039		F	27.87	BH146207	15243073	(AT)17	CAAGAATAATCTAAAGGTACACTT	AGTTAAAAAACCCACACAAC	114

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Sat_298	*	F	32.32	CC453831	31044661	(AT)28	GCGCGTCGAAGCAAAAATTAAA	GCGGCGAAACCCACAAAGCATA	282
Satt160		F	33.19	BH126372	14969875	(ATT)30	TCCCACACAGTTTTCATATAATATA	CATCAAAAGTTTATAACGTGTAGAT	252
Sat_309		F	41.47	CC453841	31044671	(AT)31	GCGAACGGATATATACCCATAAATTTTCATG	GCGTCATCCAATATAACAATTGTTAAAGTCA	298
Satt374		F	43.01	BH126561	14970064	(ATT)12	AACATTTGCCGAAAAAAATAACTATGATG	GCGTATCAATTAAGATCCATTAAGTG	205
Satt425		F	43.44	BH126604	14970107	(ATT)12	GCGCAATTAAGATCCACTAAGTGATT	GCGGCTTTTCACTCTTCTTTTATTATT	144
Satt516		F	44.42	BH126686	14970189	(ATT)19	GCGTTAGCACTATTTTTTTACAAGA	GCGCCGTTCCTCTTTACTTTAT	250
Satt595		F	50.24	BH126761	14970264	(ATT)9(GTT)5	GATGGGAAGCAAACAAGAAG	AACCCCCTCCCCTAAAT	209
Sat_133		F	50.78	BH126303	14969806	(AT)27	GCGCACATCTTAACTCAAATAATTGATAAAG	GCGTTCAATTGGATTTGATGAAATTTTAAAT	257
Satt663	*	F	56.17	CC454018	31044848	(ATT)28	GCGTCATGCAATGTTGTATAAT	GCGACTGCAGATAACTTGACTGGTAGT	256
Sat_103		F	57.77	BH126275	14969778	(AT)30	ACTGGGAATCCATTTCTTGTTA	AAAGAACTTTCAATCAAATGTTGTG	219
Sat_297	*	F	59.60	CC453830	31044660	(AT)23	GCGTGAAAATAAATACATAGACATCCACCAT	GCGTTTTAACACGCATCAACACTCTTC	173
Sat_229	*	F	62.79	CC453768	31044598	(AT)21	GCGTGTGCTACTTCACATCTTGAGAGAAAGA	GCGAGGGTTTAGAAAAAGATTCACCAAATAT	257
Satt114		F	63.69	BH126332	14969835	(ATT)17	GGGTTATCCTCCCCAATA	ATATGGGATGATAAGGTGAAA	109
Sat_234	*	F	66.55	CC453773	31044603	(AT)22	GCGATGCGTTTAATAAGTTTTGAAAAATGCC	GCGGAAACCATCCTTATATGTCAATTGCTCA	332
SOYHSP176		F	68.44	M11317	169984	(AT)15	TTTTTGTTTAAGTTACTGTACTGT	GCTAGTCTTCTACAACCTTCTA	116
Sat_154		F	68.91	CC453705	31044535	(AT)25	GCGTCAGGGTCAAGTCATCTAACA	GCGGACGCATTTCCTATTGATCAAG	138
Satt510		F	71.41	BH126681	14970184	(ATT)21	GCGAGTTTCGCCGTTACCACCTCAGCTT	CCCTCTTATTTCACCCTAAGACCTACAA	133
Sat_317	*	F	72.97	CC453848	31044678	(AT)24	GCGACAGTCCCAATACCATTAACAAGT	GCGTCCTTAGGTACCTAGAATAATTCTTCAC	222
Sct_033		F	74.13	BH126773	14970276	(CT)12(AT)9	CTTTTAAATTATAATAGCATGATCT	TGCTAATTTAGATTACGTTATGT	160
Sat_120		F	75.97	BH126290	14969793	(AT)31	CATATAAAAATGGTCCTCTCACATA	GCTTGAGCAACTTACAATTCACT	385
Satt335		F	77.70	BH126526	14970029	(ATT)12	CAAGCTCAAGCCTCACACAT	TGACCAGAGTCCAAAGTTCATC	162
Satt334		F	78.06	BH126525	14970028	(ATT)16	GCGTTAAGAATGCATTTATGTTTAGTC	GCGAGTTTTTGGTTGGATTGAGTTG	202
Satt362		F	82.83	BH126550	14970053	(ATT)14	GCGTTGTTGTTTCAAATGTATTTTAGTT	GCGGACGGATCATCAAACCAATCAAGAC	259
Sct_188		F	85.33	BH126782	14970285	(CT)13	TTCAACCATGTCATAAAAT	CTCACTCCTCCATAAAAAT	
Satt072		F	87.01	BH126320	14969823	(ATT)10	GGAAAGAATCAGCAAAAT	CCCCCACATAAATAATAAA	202
Sat_375		F	88.09	CC453901	31044731	(AT)12	GCGTGTTAATGATTGCATAAGGTTCG	GCGTGTCAAAAGAAACTCAATAAAGAAAAAT	
Sat_313	*	F	91.87	CC453845	31044675	(AT)18	GCGTATTCCCTTAACAAAATTAAAGTTTCAC	GCGCGTCAGCCTAACAAAAAGAATAAAAT	224
Satt490		F	97.97	BH126661	14970164	(ATT)18	GCGGCACGAGTCAACTTTCTGTTTCCT	GCGGAAGAAGATTTTCGTTTTTAT	295
Satt144		F	102.08	BH126356	14969859	(ATT)18	CGTCGCCATCACTATGAGAA	CCATCTTGAGCAGAGTTTGAAGTT	225
Sat_197	*	F	103.51	CC453738	31044568	(AT)33	GCGATTTTGGTTTTGTTTTATTAG	GCGGTTAACAGCCAAGTTCTTTC	194
Satt554		F	111.89	BH126721	14970224	(ATT)33	GCGATATGCTTTGTAAGAAAATTA	GCGCAAGCCCAAATATTACAAATT	261
Satt657		F	116.91	CC454012	31044842	(ATT)11	GCGCATTTGGACTTTTACTTC	GCGACGATGTTAATTGGTAGAATC	263
Satt218		F	117.65	BH126422	14969925	(ATT)17	TCAATCAACAAAAACATAATTCTTC	ATTTGTGTTTTGTTTTAGCTCTCTA	236
Satt522		F	119.19	BH126692	14970195	(ATT)16	GCGAAACTGCCTAGGTTAAAA	TTAGGCGAAATCAACAAT	262
AW756935		F	124.88	AW756935	7686224	(ATT)18	GCGGCTGGTGATTGTGTAAT	GCGTAATATAGTTTTGTATTGAAAT	232
Sat_090		F	130.64	BH126265	14969768	(AT)16	CTCGCTGCTACTGGTC	AAGAATGCGTTGGATTTA	162
Satt656	*	F	135.12	CC454011	31044841	(ATT)10	GCGTACTAAAAATGGCAATTATTTGTTG	GCGTGTTTCAGTATTTGGATAATAGAAT	155
Sat_417		F	135.95	CC453941	31044771	(AT)16	GCGAATATGGCGTTGAAAATAGTGAT	GCGACCCAGATTCTGTGCTAAGA	
Sat_074		F	142.35	CC453681	31044511	(AT)30	GGGTGAGAAATACATGCAACTTACA	GGGCATCAAAATTGATATTAAATGTCTAA	
Satt395		F	146.42	BH126578	14970081	(ATT)10	CGCGCTAGTTGAATGAATGT	GCGCATTGAGGAATTTTTTAT	275

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus	LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt163	G	0.00	BH126374	14969877	(ATT)16	AATAGCACGAGAAAAGGAGAGA	GTGTATGTGAAGGGGAAAAACTA	250
Satt038	G	1.84	CC453951	31044781	(ATT)17	GGGAATCTTTTTTTCTTTCTATTAAGTT	GGGCATTGAAATGGTTTTAGTCA	176
Satt275	G	2.20	BH126471	14969974	(ATT)11	GCGGGATAATTGGTTTTACGAAAATGC	GCGCCTAATCACCTAAAAAAACGTTTA	205
Sat_210	G	3.70	CC453750	31044580	(AT)35	GCGCCAGCAACAAAGTTCCTGACAAA	GCGCATGCAAATGAAATAATAA	255
Sat_168	G	3.90	BH126794	14970297	(AT)15	TGTGGATAAAAGAGCATTCAAAATG	GCGATCCTTGTTTATCTCAAAAAAGTGT	157
Satt309	G	4.53	BH126500	14970003	(ATT)13	GCGCCTTCAAATTGGCGTCTT	GCGCCTTAAATAAAACCCGAAACT	146
AZ254740	G	8.23	AZ254740	9292935	(AT)12	GCGAATTTTAATTTTTTTACTTCCTAAATA	GCGAATCTCTGTACCCGTGTGATGTATG	260
Sat_141	G	9.18	BH126788	14970291	(AT)24(GA)11	CGCAATCAAAGACCTGTT	GCCTTGGCTATTTCCTTA	177
Sat_163	G	10.06	BH126791	14970294	(AT)21	GCGGTATATATGTTTGCAAGACATATT	GCGGAATCTCGCCCAGGAGGAACTT	228
Satt610	G	10.92	BH126792	14970295	(ATT)12	CCCTCCGCAAGCAATAATTAATCT	GCGGAATGCTTCCATTTTAT	222
Satt356	G	12.18	BH126545	14970048	(ATT)13	CATGCCTGGTCCATTTTG	TCAAGCCACGATAACAGTA	246
Satt688	G	12.54	CC454041	31044871	(ATT)11	ATGCCTCCAAAGAGAAAT	CTGCCCATTGACCCATCT	175
Satt570	G	12.74	BH126736	14970239	(ATT)11	CTCATGTGGTCCTACCCAGACTCA	CGCTATCCCTTTGTATTTTCTTTTGC	105
AW734137	G	15.63	AW734137	7639823	(AT)24	GCGATTTTCATTGGTTCCCTTATTG	GCGGGGCTTTTAATTTTATTTTTCTGAT	198
Satt217	G	18.25	BH126421	14969924	(ATT)19	AATGATTTTGCGTATGTAAGATGA	GCGGATGACATTAATAGTTTTTAGA	249
Satt235	G	21.89	BH126436	14969939	(ATT)16	GCGGGCTTTGCCAAGAAGTTT	GCGGTGAGGCTGGCTATAAG	135
Satt130	G	23.10	BH126344	14969847	(ATT)14	TAAACGAAATTTAGTTTTAAGACT	TGAATGGCTAAAAACGTGATT	243
Sat_315 *	G	27.48	CC453846	31044676	(AT)17	GCGTCATGGCTTCCCTAAAACAAAAAATGTC	GCGTGATGGATACTTCATCCACAGAATTATA	203
Sat_290 *	G	29.03	CC453823	31044653	(AT)34	GCGATGCCAAACTAGCTGAAGAGAAAT	GCGTAGCCTGCTTGGATGGTAGATTC	265
Sat_131	G	31.33	BH126301	14969804	(AT)29	GGCTTGTGGTAAGGGGAAGACTTC	GCGGAATGAAGAATAGATGATTCT	239
Satt324	G	33.26	BH126515	14970018	(ATT)19	GTTCCCAGGTCCCACCATCTATG	GCGTTTCTTTTATACCTTCAAG	250
Sat_403	G	34.87	CC453927	31044757	(AT)34	GCGGCGTCATGTTAGTTGGAACC	GCGAGCCATTTTTCTCTTTTAGACAAT	
Sat_308 *	G	43.09	CC453840	31044670	(AT)19	GCGTTGGCAATTCAGGATATATTTAAGATTT	GCGGCTGCGTTTTTATTCAAACTTGTT	301
Satt394	G	43.38	BH126577	14970080	(ATT)31	GCGTTTTTTCAATTTAAAGAGAATTGAC	GCGTAACTTGCATGTGTATATCGAGATG	306
Satt115	G	43.78	BH126333	14969836	(ATT)18	GGTTCGTTTTTTATTGATG	ACGACGAAATTGATGATAA	153
Sat_358	G	45.49	CC453884	31044714	(AT)33	GCGCTACGTAAATAAATTAAAATCAACATCT	GCGCAGTAGTTCAAGGACATAGGACTT	
Sctt010	G	45.87	BH126786	14970289	(CTT)8	CGCATGTGCAAGTAAC	TAGTTGGGGAGAAACAG	
Satt501	G	47.27	BH126672	14970175	(ATT)11	GCGAATTAATTGGTGGTATTATAAAAACT	GCGAAGTATTGATGTGAAATGTAAACAAC	360
Satt340	G	48.54	BH126531	14970034	(ATT)12	TCCTCACGTCCATAACAAAATCC	GTCTGGCCGCCACAAAAT	222
Satt131	G	48.92	BH126345	14969848	(ATT)13	AATTTCCCATTATCATTTAGAA	GGCCTTCATTCCAAAAC	173
Satt566	G	49.91	BH126732	14970235	(ATT)16	GCGGCTTTTTCGTAATATAGGATGAT	GCCGTTAGGACATAAGAGGCATT	292
Satt352	G	50.53	BH126541	14970044	(ATT)18	GCGAATGTATTTTTGTTTCTCCATCAA	TGATAAGCCAAAAAATGGAAGCATAG	
Satt427	G	51.69	BH126606	14970109	(ATT)15	GCGAGTATCCACCCTTTTATAATAAT	TCTCCACGCCACCTTATTTCCTCTCC	181
Satt594	G	52.94	BH126760	14970263	(ATT)23	GCGGTAACTCCTCGAGTCCCTCTCAAT	GCGCCGCTAACAGACATCCAATA	144
Satt303	G	53.42	BH126494	14969997	(ATT)20	AAAAGCGACGACCTATG	TGAACGTTCTATCAACACA	253
Satt138	G	55.99	BH126351	14969854	(ATT)47	GACATTTTTCCACGGATATTGAAT	AACGGGCGATTTATGGCTAT	293
Sat_094	G	56.18	BH126266	14969769	(AT)23	CTTGAATAGGATGTATAAATTATTGTAG	AAAAATTTTAATATTGTGGAAGTCT	251
Satt533	G	56.52	BH126702	14970205	(ATT)15	GAACAGGTAGCAGTAAGTAATG	TCGTTTTGCTTTGTAGAACA	256
Satt564	G	57.32	BH126730	14970233	(ATT)22	GCGCTTCCACCACAATAACA	GCGGCAGAGGACTGACAGCTA	164
Sat_088	G	58.00	BH126263	14969766	(AT)17	TTCAATTGTACATAGTCATCAA	TAATGAGCGAGGAATCTAA	130

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt504		G	59.83	BH126675	14970178	(ATT)21(ATTT)9	GCGCATGTGCAACTTGAAAAACA	TCGTTGGTTGACCCAATGTCATC	210
Sat_185		G	60.37	CC453727	31044557	(AT)31	GCGGCTGGAGAAAACCTTTTATG	GCGAATAAAAACCGAGAATGATTT	230
Sat_260	*	G	61.42	CC453795	31044625	(AT)25	GCGCCGTTAGTTGTCGAGGTGTCAACC	GCGTCGGTGATTAAAAATAAGTATCAAAG	300
Sat_223	*	G	61.64	CC453763	31044593	(AT)24	GCGCGGTTTTAAGCTATAACACATC	GCGCAAGCACACTACTATTTATCATT	194
Sat_203		G	62.08	CC453744	31044574	(AT)25	GCGTGTGGCAAGTTATAGTTGAGTAGTTGAA	GCGGGCTATAATGTCCTTAATACTTATTTAT	275
Satt199		G	62.16	BH126406	14969909	(ATT)15	GCGGTAAATGGTGAAAATCATTTATGGTT	GCGTTTTCATACGGTGTTTTGCCTAT	198
Satt505		G	63.00	BH126676	14970179	(ATT)14	CGCATCGGTGGTTGTTAA	TGACCCAAAAGTAATTTGGAG	226
Satt400		G	63.28	BH126583	14970086	(ATT)11	TTGGTCATCAAACTGTTA	CATAAGGGGTCCCACTCTA	205
Satt012		G	66.55	BH146213	15243079	(ATT)19	GCAATTAGTTTTAAAATGTTTC	AGAATAGAGCCTACATATAATCATA	
Sat_164	*	G	68.67	CC453711	31044541	(AT)19(CT)22	GTGATCTTCGAAAGTTCAAT	GCTGTCCCTGAACAAGACTAT	
Satt503		G	68.77	BH126674	14970177	(ATT)18	GGGTGGCCATGGAATAAT	TTTCGGGTAGATGAGTGTAGG	256
Satt517		G	69.87	BH126687	14970190	(ATTT)9(ATT)25	CTTGTTGCCTTTAACACACTTCAT	TCAACTGAAAAAGGAAACTAGAATAATG	280
Sat_143	*	G	73.42	CC453697	31044527	(AT)13	GAAGATTGGGTAGATACTTCAACAC	GGATGGATGGTCCATTGATTCTTT	177
Satt288		G	76.77	BH126481	14969984	(ATT)17	GCGGGGTGATTTAGTGTTTGACACCT	GCGCTTATAATTAAGAGCAAAAGAAG	228
Satt612		G	80.38	CC453977	31044807	(ATT)10	GTCATACTGGGTGTTTCATTTATGAC	GCGCCTTTTAGTCTCTGAAAGTATTT	241
AF162283		G	87.94	AF162283	8886430	(CT)11	GCGAGTTCTGGATGTAGG	GCGTGGCGGCTTTGGTAG	221
Sct_199		G	94.40	CC454080	31044910	(CT)8(TC)17(AT)14	GCGACAATGGCTATTAGTAACAATCA	GCGATTTTCTATTTTCCTCACAGTG	
Satt472		G	94.84	BH126644	14970147	(ATT)37	GCGAATACATAAAACTCAAATTCAAATCATA	GCGTTCTATAAATTTCATTCATAGTTTCAAT	278
Satt191		G	96.57	BH126398	14969901	(ATT)18	CGCGATCATGTCTCTG	GGGAGTTGGTGTTTTCTTGTG	227
Sat_117		G	100.00	BH126287	14969790	(CT)6(CA)8'(AT)9	TTTGGCAGTTTCTTGTAG	GCTGGATCGCAGTTA	238
Sct_187		G	107.11	BH126781	14970284	(CT)10	CATGCTCCCATTCTCT	AACATTGGCTTTTTACTTAG	
Sat_372		G	107.75	CC453898	31044728	(AT)27	GCGTCTCGAGGTAATTATCTATTTATCTTTT	GCGAGTTTGGTAACATCGAGTATTGAT	
Sat_064		G	108.70	CC453678	31044508	(AT)34	TAGCTTTATAATGAGTGTGATAGAT	GTATGCAAGGGATTAATTAAG	146
Satt666		H	0.59	CC454021	31044851	(ATT)14	TGGCTTGTCATCTCTACTTTTATTAG	TCATGCATCTAATTTGTTTTATCTATCA	232
Sat_214		H	2.85	CC453754	31044584	(AT)31	GCGATGGGCAAGAAGAGA	GCGCAGCATCCCATTCAT	253
Sat_200		H	3.02	CC453741	31044571	(AT)25	TAGAGGAAAACAACAAGTAAGAAGA	TGGCTGGTATTCGTTATTAG	274
Satt635		H	4.88	CC453994	31044824	(ATT)7CAA(TAA)3	GCGGTGTATTAAAATTGTCCATGT	GCGCTGTCCTAATTTAAATGAGAAAAC	171
U08405		H	7.26	U08405	475603	(AT)10	GCGTGGTGAGTCTAT	GCGAAATAAGCGTTTTACAGATG	
Satt353		H	8.48	BH126542	14970045	(ATT)16	CATACACGCATTGCCTTTCCTGAA	GCGAATGGGAATGCCTTCTTATTCTA	172
Satt568		H	27.64	BH126734	14970237	(ATT)17	GCGGAATAATCCAATTCAATTTA	CGGACACCGGTCTACTAGGAAAGTAA	
Sat_127		H	28.80	BH126297	14969800	(AT)28(CA)15	GGGGTTTTGTGTCTAGTCTA	GGGATTAAAAATAACAATACT	277
Sctt009		H	38.89	BH126785	14970288	(CTT)10	TGGTAAAGGAGGAACTT	AGAATGTGCTGATGACA	
Satt192		H	44.04	BH126399	14969902	(ATT)32	CACCGCTGATTAAGATTTTT	CGCTGAGTTGTTTTCATC	252
Satt442		H	46.95	BH146216	15243082	(ATT)35	CCTGGACTTGTTTGCTCATCAA	GCGGTTCAAGGCTTCAAGTAGTCAC	265
Satt541		H	53.35	BH126709	14970212	(ATT)22	GCGAATCCATCACACATAAA	GCGGTACTCCCTCCAGAAAATAACC	174
Satt469		H	58.91	BH126641	14970144	(ATT)14	GCGGGGAAAGGAAGAATAAAC	GCGCAGACCTCCTTTCTTTATACAT	151
Sat_334	*	H	59.01	CC453861	31044691	(AT)21	GCGTAACGTAGCAAATTGACTATAAGA	GCGTGTGCAAAGACAATTTCAATGA	224
Sat_122		H	61.33	BH126292	14969795	(AT)23	GTGACAAATGGATGGACAATAG	AAGAAAAATAAAATAATGTAGAGTGGTGAT	206
Sat_118		H	61.86	BH126288	14969791	(AT)23	TAACTTTTTAAATAAATTTTAGTAACTC	TCATTATTAGCTAAAACCACATA	201
Satt052		H	64.10	BH126316	14969819	(ATT)16	GAATAAAATTAGGATAAGTGATAAG	ACAGAAAAAAGAAAATGTCA	237

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Sat_401		H	66.21	CC453925	31044755	(AT)36	GCGGTAAACTCCTCGTTCAAGCACTT	GCGAAAGGATCAATTTTATATTTAAGCCTCA	
Satt253		H	67.17	BH126451	14969954	(ATT)18	GCGCCCTAATAAAGATAAGACAAG	GCGTGGCCTTTTCCCATTTA	154
Sat_206		H	67.79	CC453746	31044576	(AT)28	GCGAACATTTGATATCATTATGATAATTGG	GCGAATTGTAATTTTTCTTTGTATCTAAACC	271
Satt222		H	68.08	BH126425	14969928	(ATT)20	GCGTGTTTTGTGAAAATAATAATTAAAGATG	GCGCCACAAGTAACTAATGTAATAGGTGTT	
Sat_205		H	68.18	CC453745	31044575	(AT)26	GCGCCTTTTCGTCTGTTCTGTTC	GCGAGCTTTTAAAAATTTAGAAATCAAT	219
Satt279		H	68.50	BH126475	14969978	(ATT)28	GCGCAAAAGGACGCCCACCAATAG	GCGGTGATCGGATGTTATAGTTTCAG	192
Satt676		H	68.86	CC454029	31044859	(ATT)22	GCGCAAAAGCCCAATTGAAACAC	GCGGATTGGGAAAAAATAATTAGTTG	285
Satt314		H	69.12	BH126505	14970008	(ATT)13	GCGGAGATTGGAACCTACTCATTC	GCGGGGACCAAAAATTCAAAA	235
Satt629	*	H	72.18	CC453990	31044820	(ATT)12	GCGGGACTACACCATTTTTTTTAACAG	GCGGAGGCCTTGATTATTAGACAATAG	216
Sat_158	*	H	73.46	CC453708	31044538	(AT)29	GCGCCTATTCGAGCCAACAATATACAT	GCGGATTGAATGAATTTACTGAACCTT	183
Satt302		H	81.04	BH126493	14969996	(ATT)12	GCGAACTGTAGTTTACTAAAAATAAGTG	GCGGACTGAATTAATATTGGTGTTGAATT	254
Sat_175	*	H	83.19	CC453721	31044551	(AT)23	GCGTCATTGTTAAAACTTAGTGTCTAATAAA	GCGGTCAAAGTCAGTTAGTGAAAGAGA	288
Sat_216	*	H	85.27	CC453756	31044586	(AT)21	GCGACAAGATATTTGAATGTAGATGAGAC	GCGCCGATCCTCTCGTAAATATAAGGAA	338
Satt637	*	H	85.79	CC453996	31044826	(ATT)11(AT)18	GCGCCATAAGCGAAAGCGATGAAT	GCGGAGAAAAATAAGAACATCACCCA	202
Satt142		H	86.49	BH126354	14969857	(ATT)21	GGACAACAACAGCGTTTTTAC	TTTGCCACAAAGTTAATTAATGTC	155
Satt293		H	89.09	BH126486	14969989	(AT)13(ATT)16	GCGCAGAAGGTTTGCATAAAAAGAAT	GCGGGCTAAAAAGTTGATGTAATGTG	208
Satt317		H	89.52	BH126508	14970011	(ATT)20	GCGAACAAACTTTCTATACATGATAACA	GCGGGTATATTTTTGTACATAAGTTGGAA	250
Satt181		H	91.12	BH126389	14969892	(ATT)18	TGGCTAGCAGATTGACA	GGAGCATAGCTGTTAGGA	214
Sat_218		H	99.50	CC453758	31044588	(AT)26	GCGCACGTTAAATGAACTGGTATGATA	GCGGGCCAAAGAGGAAGATTGTAAT	290
Sat_180	*	H	104.37	CC453723	31044553	(AT)23	GATCTAGGGCAAACAAGGTT	CTCGCTCTTCGCAACATA	235
Satt434		H	105.74	BH126612	14970115	(ATT)32	GCGTTCCGATATACTATATAATCCTAAT	GCGGGGTTAGTCTTTTTATTTAACTTAA	340
Satt571		I	18.50	BH126737	14970240	(ATT)14	GGGTAGGGGTGGAATATAAG	GCGGGATCCGCGGATGGTCAAAG	153
Satt451		I	20.34	BH126625	14970128	(ATT)10	GCGCAATTAAAAGGATAACTTATATC	CCCCTCTTTGGCCCTCACACCTTCTC	318
Satt419		I	21.90	BH126598	14970101	(ATT)22	GCGCCATGACGCCAGCTTGCTTTTCC	GCGCCATTATATACAAATTACGATCAT	246
Satt562		I	22.84	CC453971	31044801	(ATT)18	GCGGATTGACTGAGATGTTTAT	GCGGCGGCAGGTTAAATGGATTGA	203
Satt367		I	27.98	BH126554	14970057	(ATT)21	GCGGATATGCCACTTCTCTCGTGAC	GCGGAATAGTTGCCAAACAATAATC	208
Satt587		I	31.49	BH126753	14970256	(ATT)15	GCGAATGGTTGCTCAAATAATC	GCGCAAACCGCACAAGTTTATGT	161
Satt614	*	I	31.94	CC453979	31044809	(ATT)37	CTCCCCTTTAACCTTTCCTTTATTAG	GCGCGGTAGGAATTAATTGTAGATAGGAT	318
Sctt012		I	33.98	BH126787	14970290	(CTT)11	CCATTATCGCACATCATT	GCTGCATTTTCCCTCTA	
Satt700		I	35.03	CC454049	31044879	(ATT)12	GCGGGGGTTAAGAGGAGGAAAAATA	GCGCACTTTGCAAATGAGAGAT	147
AB002807		I	35.16	AB002807	1944186	(AT)14	GCGATAACAACAACAACAACAAATGAATA	GCGACATTGTCCCCAAAAATAACA	226
Satt127		I	35.35	BH126341	14969844	(ATT)23	CGCTTGTGAACCCTGCTAAA	CCATCCTCTGAAACCGTTATCT	227
Sat_219	*	I	36.03	CC453759	31044589	(AT)26	GCGTCATGCCACGTGATATTTTAT	GCGTGTGTCCCAAATGTGATTCA	262
Satt496		I	36.40	BH126667	14970170	(ATT)13	GCGATCCCTTTATGTTGGTATTACATT	GCGGCACACAAGTAGTTGTGAAACTAA	330
Sat_174	*	I	36.59	CC453720	31044550	(AT)21	TACGAAATATTGCAAGAGATACATT	GCCTTAGATCAATTGTGATAAAAA	227
Satt239		I	36.94	BH126440	14969943	(ATT)22	GCGCCAAAAAATGAATCACAAT	GCGAACACAATCAACATCCTTGAAC	192
Satt354		I	46.22	BH126543	14970046	(ATT)14	GCGAAAATGGACACCAAAAGTAGTTA	GCGATGCACATCAATTAGAATATACAA	258
Sat_105		I	49.34	BH126277	14969780	(AT)30	TTCCATACAAGATATCAAGTGAATTG	GCTCCCCTACATTGGTAGTAAA	269
Satt270		I	50.11	BH126466	14969969	(ATT)16	TGTGATGCCCCTTTTCT	GCGCAGTGCATGGTTTTCTCA	222
Sat_268	*	I	55.10	CC453803	31044633	(AT)26(AC)6	GCGTGCAACATATGACACCATAAAT	GCGTGAGGAGGTTCAAAAATAACAT	254

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt049		I	58.82	BH126314	14969817	(ATT)16	GCGTCTATTCTTTTATGTGTTTATCTTAG	GCGTTATTTTTACAGAAACTCACCTA	145
Satt650	*	I	63.33	CC454005	31044835	(ATT)10	CAGTTGGCTGGTCAAATC	TCTGGGTTACTTTTATTGTCA	247
Sat_104		I	65.62	BH126276	14969779	(AT)22	CCCTTGACAACCTTTTTAC	ACGAGTTGCTACAAATGAAT	
Satt671	*	I	72.09	CC454024	31044854	(ATT)9	GCGTAAATCCAAAAGTAGAATAAAATAA	GCGAGAAATGAGATAAGTGGTGATA	201
Sat_418		I	74.26	CC453942	31044772	(AT)26	GCGTCATGTCGCTACTAA	GCGTGGCTACACAACTTTT	
Sat_170	*	I	75.00	CC453716	31044546	(AT)26	GCGGATTGATTTAATTAAGTGTGATTAA	GCGCCGATGATCATGAATTAGAATAACA	168
Satt330		I	77.84	BH126521	14970024	(ATT)18	GCGCCTCCATTCCACAACAAATA	GCGGCATCCGTTTCTAAGATAGTTA	152
Sat_421		I	81.40	CC453945	31044775	(AT)13	GCGTGAAGCCGCACCAATA	GCGAACTCCTACTATAATG	
Satt292		I	82.78	BH126485	14969988	(ATT)16	GCGGAATTAGAACTCCAGTAAAGA	GCGAGGCCAACATTGAAAAGT	236
Sat_324	*	I	84.48	CC453854	31044684	(AT)27	GCGCAATGTCCCTCTTTCTTCCAATGATAA	GCGTGCAGGGGAGATTAGCTAGAAATGTG	205
Satt162		I	86.74	BH126373	14969876	(ATT)16	GGGAAGAAGTATATGCTACATCAA	GGGTTAATTTTTATCTTCTAATAGTTT	145
Satt623	*	I	92.52	CC453985	31044815	(ATT)15	GCGGTGCAATGATTTTAATGATATGAT	GCGCGTGTAAAAGGTTATAACGTGTAA	238
GMGLPSI2		I	97.05	X01425	18607	A18	TTCGAAGCATTCAAGG	AAAAGACAAAAACATACTATAAAA	118
Sat_155	*	I	98.06	CC453706	31044536	(AT)19	GGGACAGCACCGTCAAGGAGGAGA	TGGGAAAGAAATTGTAGC	171
Sat_419		I	98.11	CC453943	31044773	(AT)22	GCGTTATTGGCATGATGTATTAGT	GCGTGCTATATCATCTTACAAACTT	
Sat_420		I	98.39	CC453944	31044774	(AT)19	GCGGATGGAGCCAACA	GCGTGTAGCCCTAGAAAGTT	
Sat_299	*	I	99.83	CC453832	31044662	(AT)23	GCGACAAGGCACTCACATCTCTTCTC	GCGCTACCCATAACAAAAAGTTCAAATC	292
Satt148		I	100.78	BH126360	14969863	(ATT)16	AATCCGGGACGCAAAATTATTATTAA	TGCAAATTCCCTAATTAACACCCTTTATAC	289
AQ851518		I	106.80	AQ851518	6063213	(AT)23	GCGTAGAGCTGGGTTAGAGTAGTTA	GCGTAGAGCTGGGTTAGAGTAGTTA	190
Satt440		I	112.70	BH126617	14970120	(ATT)14	TGAGAACGTTTGAAAAGAGAT	GAAGAGATTAAGCATAAAGAATACTT	185
Sct_189		I	113.77	BH126783	14970286	(CT)17	CTTTTCCTGGCAATGAT	AAAATCGCAAAACCTTAGT	
AW310961		J	5.19	AW310961	6726607	(ATT)16	GCGCAACTTTTTAGTAAATATTGCATAA	GCGCATACATCTTTTGGGATTTCT	177
Satt249		J	11.74	CC453958	31044788	(ATT)20	GCGGCAAATTGTTATTGTGAGAC	GGCCAGTGTTGAGGGATTTAGA	250
Satt405		J	12.41	CC453963	31044793	(ATT)9	GCGGAAATTGTGAAAAATGTCCTAGTAA	GCGTTTTAGTCGTTAAATTTATGAAATG	303
Satt287		J	15.69	CC453961	31044791	(ATT)18	GGGGTGAATGAATGTCAAGATGA	GCGCGAGGTATCAACACAATTACT	230
Satt674	*	J	15.95	CC454027	31044857	(ATT)17	GCGAATCCTCTAGCTTACCAAAGAA	GCGATTAGCCATCAAAACCTAT	247
Sat_228		J	23.91	CC453767	31044597	(AT)24	GCGTGACTACGGGAAGTTGGAAC	GCGTTGGCGGTAAGAGCACTATA	252
Sct_046		J	24.09	CC454071	31044901	(CT)11	AAAAAGGAAACTTCGTCA	AAACTAAACAGTGTCCATAAGA	157
Satt285		J	25.51	CC453960	31044790	(ATT)19	GCGACATATTGCATTAAAAACATACTT	GCGGACTAATTCTATTTTACACCAACAAC	236
Sat_339		J	27.97	CC453865	31044695	(AT)27	GCGAAAAAGGATTATGTAAACGGTATAAAAA	GCGGTCGAAAATTTAGGATGTAAGATGTTA	
Sct_065		J	32.10	CC454072	31044902	(CT)16	CCCTGTGTTTCCCTCT	GAAAAGTTTTATGTTCTGAGTG	
Satt693	*	J	33.88	CC454044	31044874	(ATT)20	GCGAGGCCACTCATGTCACTGTCATT	GCGCCAAGAATAAGTTATTTGAAATAAT	280
Satt414		J	37.04	CC453965	31044795	(ATT)23	GCGTATTCCTAGTCACATGCTATTTCA	GCGTCATAATAATGCCTAGAACATAAA	306
Sat_370		J	37.40	CC453896	31044726	(AT)39	GCGTAAACCATTGTTTTTAATTTTAAACAAA	GCGGGAGGGAGAATGATATGACATACCTACT	
Satt654		J	38.10	CC454009	31044839	(ATT)15	AGACGCGCACACAAGCATATA	GCTGGGACTCCTCATGTC	156
Satt406		J	38.19	CC453964	31044794	(ATT)31	GCGTGAGCATTTTTGTTT	TGACGGGTTTAATAGCAT	171
Satt280		J	38.70	CC453959	31044789	(ATT)14	GCGGAATCTGCTTATTCATTGTGTG	GCGCCATGCTGTAACACGTCAAT	228
Satt132		J	39.18	CC453952	31044782	(ATT)18	AAAACTGTACATATTACATCAAACT	GCAAGCATTGTAGAGAAATAC	250
Satt596		J	39.64	CC453972	31044802	(ATT)17	TCCCTTCGTCCACCAAAT	CCGTCGATTCCGTACAA	252
Scaa003		J	39.96			(CAA)	TTTGGAATATTTGGATACAA	GGAGACCCTAGGCTAAAT	145

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Sat_259	*	J	40.34	CC453794	31044624	(AT)22	GCGCGTTCCAACCCGGTTTATTATCTAA	GCGAATTATGACCCAAAATACGTGAGACATC	302
Satt686	*	J	40.50	CC454039	31044869	(ATT)14	ACGGAAAATAAATGAAACTAAGA	GCGCTATCAGATAGAGAAGCAGAAGAAT	286
Satt456		J	40.83	CC453968	31044798	(ATT)9	GGGCCTTCGTTTGAGTTCATAG	GGGATCATTGGTTAATTGTTGTAAGA	288
Sat_412		J	41.11	CC453936	31044766	(AT)27	GCGATGCTAACGGAGATAATAAATTGAGAAT	GCGTTGTTCAATCTGCAGGCTAGTAGA	
Sat_151	*	J	41.35	CC453703	31044533	(AT)13	GCTGCATCAGATCACCCATCCTTC	CATGCCATGTTGTATGTATGT	230
Sct_193		J	41.50	CC454076	31044906	(CT)19	GGCGGAGGTTCTAGTTTAGGCTTTCTCT	GGCGGATTCAAAATACATCGTTTC	
Satt529		J	41.90	CC453969	31044799	(ATT)13	GCGCATTAAGGCATAAAAAAGGATA	GCACAATGACAATCACATACA	210
Sat_165	*	J	42.20	CC453712	31044542	(AT)19	GCGGACAGGCAGCCACACATCTTA	GCGGATTAAATCAGTTTGTATCGA	
Satt622	*	J	42.25	CC453984	31044814	(ATT)27	GCGGTGTAGGTAATAATTTTAATTCTCAT	GCGGTGTAGGTTTCACACTTCATTCAC	236
Satt183		J	42.51	CC453955	31044785	(ATT)13	TAGGTCCCAGAATTTCATTG	CACCAACCAGCACAAAA	240
Satt380		J	43.01	CC453962	31044792	(ATT)15	GCGAGTAACGGTCTTCTAACAAGGAAAG	GCGTGCCCTTACTCTCAAAAAAAAA	137
Sat_255	*	J	43.85	CC453791	31044621	(AT)32	GCGGCATGTCATGGTATACGTAACTTTAGA	GCGCAACTGAAGCAAGAAAAGAAACCT	291
Satt215		J	44.08	CC453956	31044786	(ATT)11	GCGCCTTCTTCTGCTAAATCA	CCCATTCAATTGAGATCCAAAATTAC	132
Sat_361		J	44.49	CC453887	31044717	(AT)19	GCGTTAGATTTCCTTAGAATACATTGCTTCC	GCGTTGACACTCATGATGTTATCTTACACC	
Sct_001		J	44.68			(CT)13	TTAAGTTTCCCTCTCTCTCT	CTTGTTCCTTCGCTCAC	
Sat_093		J	46.09	CC453688	31044518	(AT)24	CAAGGACTAAATAAGATTAATCACTT	TATTCATAAGCTTTAATTACACTATAAGAA	207
Sat_366		J	52.84	CC453892	31044722	(AT)8	GCGGCACAAGAACAGAGGAAACTATT	GCGGACATGGTACATCTATATTACGAGTATT	
Satt621		J	53.68	AF237409	7621492	(ATT)11	GCGGGAGCATGCAGCAACCAATGTTTT	GCGGGATAATATATTTAGTGTT	230
Satt620		J	53.71	AF237408	7621491	(ATT)15	GCGGGACCGATTAAATCAATGAAGTCA	GCGCATTTAATAAGGTTTACAAATTAGT	311
Sat_350		J	55.73	CC453876	31044706	(AT)31	GCGTAAGAGCATCTCCAAACCATCAAACTCA	GCGATTTATTACATTTAACAATTGTTATTTA	
Sctt011		J	62.89	CC454081	31044911	(CTT)10	CTCCGTTGCTGAT	TAAGCTGAATTAGTAAAA	
Satt244		J	65.04	CC453957	31044787	(ATT)27	GCGCCCCATATGTTTAAATTATATGGAG	GCGATGGGGATATTTTCTTTATTATCAG	210
Satt547		J	67.79	CC453970	31044800	(ATT)18(ACT)3	GCGCTATCCGATCCATATGTG	TGATTTCGCTAGGTAAAATCA	209
Sat_396		J	69.30	CC453921	31044751	(AT)35	GCGCCCTAGGGAATGAAAGAAGGAAATAATA	GCGAGAACGCAAACAATCATAGCAGAAT	
Sat_224	*	J	75.13	CC453764	31044594	(AT)19	GCGGGGAACAGTTGTTAACTCAGTCAAAGT	GCGAATGGATCAAGAATCAGTGGTATAATCA	194
Satt431		J	78.57	CC453966	31044796	(ATT)21	GCGTGGCACCCTTGATAAATAA	GCGCACGAAAGTTTTTCTGTAACA	250
Sat_394		J	89.43	CC453919	31044749	(AT)36	GCGGACAGTGTGCTCCTCATATAATAG	GCGTGACTCGGACTTGAAGATAATAATG	
Sat_395		J	89.48	CC453920	31044750	(AT)31	GCGTCTTAGTCGTGCTGACACTACTC	GCGAGTTTGTTTAGCTCAATCTTTCACTCA	
Satt712		J	89.61	CC454058	31044888	(ATT)21	GCGAATATAGCCAAATTTAGGTTGAATGACA	GCGACCACCCATCACCTCCACCTCAAACAAC	
Sat_144		J	90.13	AF237389	7621472	(AT)24(GA)11	GCGCCCTCTTCATTTCCCTTGGTT	GCGCCCAATATCTTTGGGATAAAT	181
Sat_393		J	90.33	CC453918	31044748	(AT)14	GCGGTCCTGCATGTTAATGTTGATT	GCGGGTCCCTACAATGTGAGTGG	
Satt715		K	0.91	CC454060	31044890	(ATT)14	GCGAAAAAATTTCAATTTCTTGTTTATGTGA	GCGGGCTTATTTTTAATAACAAGTTAGATTC	
Satt539		K	1.80	BH126707	14970210	(ATT)11	GCGGTTGTAATTTAATGAACACATT	GCGGATTTTGGACTGGATTAAATAA	160
Sat_087		K	4.85	CC453685	31044515	(AT)19(GT)7	AAGATTATTTTTGGTGAGTTG	AAGCACTAGTTATGAATCAATG	
Satt242		K	14.35	BH126443	14969946	(ATT)26	GCGTTGATCAGGTCGATTTTTATTTGT	GCGAGTGCCAACTAACTACTTTTATGA	193
Sat_119		K	17.11	BH126289	14969792	(AT)25	TAGGCTTTCAATTTGCAGAACT	GTTAGGTGTCCCAAGCAACTTA	152
Satt102		K	30.28	BH126331	14969834	(ATT)11	CACCTTGCTTCAAAATTC	AATAAGTGAGAGCATAGAAAATAC	136
Satt055		K	32.96			(ATT)	AGTTAAGGAAGAATTTATTGTTAT	AACATTTTATTTGAGTATTTAGAAT	123
Satt137		K	36.99	BH126350	14969853	(ATT)13	TAACCAAAGAGTTCCCAATAAA	CCTCAAATTAACCTTGTCTCAC	225
Satt178		K	40.86	BH126386	14969889	(ATT)9	GGGAAAATTCTTTTCATATAGATG	GGGGTTGAGATATTTTGTTCATAC	165

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

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SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt349		K	42.39	BH126539	14970042	(ATT)10	GCGGGAACGAACGGGAAGAAGAAC	GCCATCCAATGTTTAGAAGAAC	182
Satt555		K	42.71	BH126722	14970225	(ATT)13	GCGGTTGGCTTTGATGATGT	TTACCGCATGTTCTTGGACTA	265
Sct_196		K	43.04	CC454079	31044909	(CT)24(AT)8	GCGGGTCGAAGGTAGGGATTTA	GCGGATGGATCTATGTTCAGAA	
Satt544		K	43.35	BH126712	14970215	(ATT)23	GCTATGGGAAAAGGATGTGTG	GAGCTACCCGAGATGATACTC	150
Satt247		K	43.96	BH126446	14969949	(ATT)21	GCGCCCATGTGGCTATTTCTTTATTT	GCGGATCAATAATAAACAAAGTGACAA	
Sat_399		K	44.66	CC453923	31044753	(CATA)12(AT)25	GCGTTCATCGAAATGCGTTTAGGATA	GCGACTGATATGCACCTCTAAGTCTCAA	
Satt381		K	44.99	BH126566	14970069	(ATT)10	TTTGAAGGGTCTACACTACTTGTG	AAGAATGAAGGCCTATGTTAGTTT	228
Sat_281	*	K	45.14	CC453814	31044644	(AT)17	GGCGGTCATATAAGCCTGATAGGTCGG	GGCGGCAGCCTGTATAGAAACTTCTCAAGC	284
Satt046		K	45.59	BH126313	14969816	(ATT)20	AAAATAACTAAAATGTCTTCTCA	TTGGTCAGATTATTATAAGATTG	222
Satt167		K	45.74	BH126378	14969881	(ATT)25	GATTTACGGGTACTTGGATTCAATA	AGCTACCCAATATGATACTCTACACAGT	
Satt375		K	45.81	BH126562	14970065	(ATT)14	GCGTTTTCGTTTCCAATTAAAAATTC	GCGGGATGCAATATTATGTAACATGA	250
Satt124		K	46.18	BH126338	14969841	(ATT)19	AACAACAACACCACAACA	TTTCATCCCGAAGATTT	138
Satt441		K	46.20	BH126618	14970099	(ATT)32	AAACCCACCCTCAAAAATAAAAA	AAATGCACCCATCAATCACA	285
Satt417		K	46.20	BH126596	14970121	(ATT)18	TCTTGCTAATTGCTTCATTTCAT	AATTGCTTGGGATTTTCATTT	340
Satt264		K	46.25	BH126461	14969964	(ATT)14	CCTTTTGACAATTATGGCATATA	GCATAGAAGGGCATCATTCAGAT	222
Satt552		K	46.44	BH126719	14970222	(ATT)14	CGAACCGGCAAAACCAAGAT	GATCCGCATTGGTTTCTTACTT	154
Satt518		K	46.63	BH126688	14970191	(ATT)19	GCGCATATCAAATTGCATATAAAAATACG	GCGGGAATATAAAATAAAAATGCTCACTT	255
Satt727		K	46.80	CC454069	31044899	(ATT)16	GCGTGTTGTTCTGCTTGACT	GCGAAGGAATAATGATACA	
SOYPRP1		K	46.94	J02746	170048	(ATT)20	CGTGCCAAATTACATCA	TGATGGGAACAAGTACATAA	143
Satt337		K	47.38	BH126528	14970031	(ATT)19	GCGTAAATCTGATATATGTTACCACTGA	GCGTAATACGCAAAACATAATTAGCCTA	208
Satt326		K	49.53	BH126517	14970020	(ATT)18	AGATTCTCCTTTGCTTCTTAGT	GTTAGTTCACCTTCCAGTATTTGA	216
Satt628	*	K	49.59	CC453989	31044819	(ATT)9	CTACCTTTAAGGTCGTTTTCAAGT	GCATGCTCCTTTTATGCTCCTTTT	214
Sat_349		K	50.31	CC453875	31044705	(AT)13	GCGTTTCCAAATCCTACCCATTGTTATC	GCGAAATCCTTTCTGTTTGTTACATCTC	
Satt001		K	50.56	BH146208	15243074	(ATT)25	AAAGTCTTTAAAAGTGTGTCTTA	TTAAAAGAAAAATGCAACAT	117
Sat_363		K	50.58	CC453889	31044719	(AT)33	GCGCGGTCCTTCTAAAACAACC	GCGTTGATTGATTAAAAAGTGTCACATAG	
Satt673	*	K	50.80	CC454026	31044856	(ATT)24	GCGCAAATTAAATTGACAGTATAGAAAT	GCGACAAAGCATTAAATTACAAAAC	313
Satt617	*	K	50.94	CC453981	31044811	(ATT)15	GCGCCTACAAAGCCAGGAGTCAGACTG	GCGAGGGTGAATTAAATTATATGAGAA	250
Satt710		K	51.00	CC454056	31044886	(ATT)24	GCGTTTATTCTAGATATGTAATTTGTTGATA	GCGATATTCATTAATACTAAACAATAGGAGT	
Satg002		K	51.45	CC453950	31044780	(CAT)8	GCGAGGCCAGGGCTTGAGGAT	GCGTAAAAGGCCCATGCTGAG	
Sat_116		K	52.28	BH126286	14969789	(AT)17(GA)20	CGTGAACCATAATTAAAATATAAAT	TTTTCTTATCTCTTTTAACCTATCA	216
Satt240		K	52.88	BH126441	14969944	(ATT)11	GCGCCCTTTGGATTTTATTGC	TTTCACCTTCCCTTCTTTTGA	239
Sat_325	*	K	54.01	CC453855	31044685	(AT)38	GCGATTCTCAATTAAGTCAGTTCAATGATGA	GCGTTGTCTCCTTATGTTTGTTCTCCC	290
Satt559		K	54.97	BH126726	14970229	(ATT)23	GCGATTCGAAATATTAGTCAAACAA	GCGCGAGCATATAGTCGGTAAAGTT	304
Sat_111		K	55.70	BH126281	14969784	(AT)16	TTTCTGATGTACCCTTTATGTC	GCATGTTCTTAGGTCAATGAA	173
Satt273		K	56.62	BH126469	14969972	(ATT)13	GCGCCTGATTACATTATCGCTTA	GCCTTTCGTTCTCAAACTGAGAGT	268
Satt725		K	56.85	CC454067	31044897	(ATT/ATT)25	GCGATAGAGCAACTGGCAAACTTGAT	GCGAATGGAGAAAATATGGACAAAA	
Sat_044		K	58.01	BH126256	14969759	(AT)21	AAAAAATATTTATAGGTTACATGTG	TTACCACTAAGAATTAGGTCTAA	165
Sat_043		K	61.67	CC453677	31044507		GCGGTCCGTCAATGAATATTAAATTAAAA	GCGAAAGCGGCAGAGAGAGAAAGGT	148
Satt499		K	71.01	BH126670	14970173	(ATT)25	GCGGCAGAGATAATTGTATTTTTG	GCGCTGCCCACTAGGGAACGAAAGATGA	318
Sct_190		K	77.37	CC454073	31044903	(CT)12	GCGAGCATTCCCTTTCATTTT	GCGGCCACACTAACAAGTAAC	

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SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt475		K	78.68	BH126647	14970150	(ATT)16	AAATGCAACTTACACAACTTTAT	TGCTTGCTTCAATTTGGATGAGTG	250
Satt260		K	80.12	BH126458	14969961	(ATT)22	GCGCCAAATGTATACTTTAAATTCTT	GCGGGTTTAGCTAAAATAGTTCGTGC	229
Sat_167		K	85.19	CC453714	31044544	(AT)23	AAGGCACTCTTCCATCAATACAA	TTGAGCCGAAAGTTCAATTCTA	206
Sat_243	*	K	86.78	CC453781	31044611	(AT)20	GCGATGTCGAATGATTATTAATCAAAATC	GCGGCAACCGCTTAAAAATAATTTAAGAT	303
Sat_352		K	93.64	CC453878	31044708	(AT)32	GCGTATTAGACTAGTGCTATTCGCGAGTTA	GCGTGTCATTTCATTAAAAACAAAAACATAA	
Sat_293	*	K	99.10	CC453826	31044656	(AT)26	GCGTTAGGCAAATGAGATGTCAA	GCGCAGGGCAGTCATCGGAGGTAT	278
Sat_020		K	103.60	CC453673	31044503	(AT)17	AAAGGAGTAGGATGTAAGAGA	CAAACCACCAGTGACC	
Satt196		K	104.79	BH126403	14969906	(ATT)12	TTGGGAAATAGTGATTGAGGTAAAA	AAATCCCCATTGAATGAGAATAAG	189
Sat_126		K	108.20	BH126296	14969799	(AT)17	GGGGGGATGCATATATTGTCTA	AGAAAAAGAGGGAGAATGA	383
Satt588		K	117.02	BH126754	14970257	(ATT)18(AT)10(CT)14	GCTGCATATCCACTCTCATTGACT	GAGCCAAAACCAAAGTGAAGAAC	169
Satt495		L	0.00	BH126666	14970169	(ATT)11	TGCCGCGAGATTAATATAATTTGT	GTGCGGCAAGAAGTTGAAATAAAG	245
Satt723		L	1.07	CC454065	31044895	(ATT)15	GCGGTTTCCCATTAATGTTACAGTTTT	GCGGAAGCAAAGCAGCAAATTAGATG	
Sat_408		L	1.31	CC453932	31044762	(AT)32	GCGGAGTTGGAATCAAGTAATCAAAGAGTG	GCGATTAGGGCAACTATACGACAAATGAA	
Satt232		L	10.35	BH126433	14969936	(ATT)28	GCGGCGTGAATAGTATACGTTGAGA	GCGGACATAAATGCAATCACTTAAAAAG	250
Sat_301	*	L	11.12	CC453834	31044664	(AT)21	GCGCACAGGACTTAGTGTTATCATTCAATGT	GCGGGGTTCCCATATTCTTGGTATGAAACTA	159
Satt446		L	11.47	BH126621	14970124	(ATT)21	CCGCATAAAAAACACAACAAATTA	GCGGGCAAATTTGACCTAACTCACAAC	299
Satt182		L	14.03	BH126390	14969893	(ATT)17	GGTCCACATGAAATGAAGGT	TCTCAGCCTGCAAAGAAAA	218
Satt238		L	19.93	BH126439	14969942	(ATT)12	GCGCCATTTTAATGATTTATTTA	GCGGAAAGAAGAGGAAGAAAG	177
Sat_071		L	20.78	CC453680	31044510	(AT)24	GAGTGCTGATCTATTTGTCA	TTTCTTTTACTGGAATTAACATAT	
Satt388		L	23.55	BH126573	14970076	(ATT)14	GCGTAACTGGTATTTTTAGAACAAAAGT	GCGTCTGGGACTGGATTTATTGTTTGAA	285
Satt523		L	27.92	BH126693	14970196	(ATT)15	GCGATTTCTTCCTTGAAGAATTTTCTG	GCGCTTTTTCGGCTGTTATTTTTAACT	168
Sat_134		L	28.27	BH126304	14969807	(AT)35	GCGATGAGGAAAGGTGATAGTGAACTTG	GCGCTCAGCTTGCATATATAAAATAATA	284
Sat_405		L	29.62	CC453929	31044759	(AT)33	GCGTAACCGTGGTAAGTGTGGTGTCGTA	GCGTTTCGTTTTAATTGCTCCTGAAAGT	
Satt143		L	30.19	BH126355	14969858	(ATT)18	GTGCCACAAATTTAAAATTACTCA	TCCCTCCCTTTTGATTTACAC	251
Satt398		L	30.58	BH126581	14970084	(ATT)29	GTAAGGGCGGGTATCAACAGTGCT	GGTAACCGCGGACTCAGTTAAAC	194
Satt694	*	L	30.80	CC454045	31044875	(ATT)24	GCGTGTTCTAAAAATAAGTGGATTTTTTAAT	GCGGGTTTGAATAATTAGACTAATTCAATAA	318
Sat_195	*	L	30.83	CC453736	31044566	(AT)29	GCGATTACCAACACAGGAACCTTATA	CGCGACTCTGATAACAACAATGTAT	220
Sat_388		L	30.86	CC453913	31044743	(AT)16	GCGGTTCAATATGAAGAGTTATGAGGAGATA	GCGGCATGAAAACTCATTAAGAAAAATC	
Satt652	*	L	30.88	CC454007	31044837	(ATT)18	GCGAACATTCCAAAATTAATGATAAAAA	GCGGGGTAATATGCACTCTCCAGTAT	217
Satt711		L	30.88	CC454057	31044887	(ATT)21	GCGCAATCCATAAATTCCATAAGACACA	GCGTCCACTTTTAATTTTGTTAACATCATAA	
Sat_187	*	L	30.89	CC453729	31044559	(AT)29	GCGTAACGGTGATACAAACAGATT	GCGGCGACTCTGATAACAACA	239
Satt418		L	30.93	BH126597	14970100	(ATT)27	GCGAAAGCACATATGGGTTTGAAT	GCGAGGGCATATATATGATGAGGTA	238
Satt278		L	31.22	BH126474	14969977	(ATT)26	GCGCTGGTGCATTGAGAAATCTAA	GCGGATTCCGTTATCGCCAGTAAT	249
Sat_397		L	31.25	CC453922	31044752	(CA)5(AAC)(AT)30	GCGTAACTTGCTTGAGACATACATGC	GCGTGGATACACATGTCACGTTGTTAGTGGA	
Sat_191	*	L	32.01	CC453732	31044562	(AT)24	GCGGCTGTTCAAAGTGAAAACGA	GCGGTGGCAAAAAATTTATAAAAAATA	227
Sat_320	*	L	32.36	CC453851	31044681	(AT)28	GCGTCCTGCTATCTGCTATTTCAT	GCGCACCGCTACAAGTTACACTCTTA	271
Satt497		L	33.71	BH126668	14970171	(ATT)22	GCGGTTTTGGATTGACTTTGTTGA	GGCTCAATTAGAGCATGCAACATC	267
Satt313		L	34.54	BH126504	14970007	(ATT)14	GCGGTAAGTCATGGCTTTTTAATCTT	GCGCGAGGTATGGAACCTAACTCACA	249
Satt613		L	36.05	CC453978	31044808	(GTT)8(ATT)3(GTT)3(AT	GCGGAATATGATCATTGGTAATGTAC	CGGCTTCAAACGGCAAATAATC	151
Satt284		L	38.16	BH126479	14969982	(ATT)15	TGGGCTAGGAGTGACCAC	GGTCACCACTCACCATCA	251

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SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
AW508247		L	38.83	AW508247	7146325	(CTT)10	GCGCCCAATCCCAATCTCAC	GCGAAGCCAATAAATGATAAAAATC	153
Satt462		L	41.00	BH126635	14970138	(ATT)20(AT)24	GCGGTCACGAATACAAGATAAATAATGC	GCGTGCATGTCAGAAAAAATCTCTATAA	253
Sat_150	*	L	53.67	CC453702	31044532	(AT)24	GCGCACATGCTCACCAAGCAAAGTAT	GCGGTAGAGCGGATTAAACTTGTC	212
Satt481		L	54.57	BH126653	14970156	(ATT)14	GGGTTAACCGTCCACACATCTATT	GACGGTTTTAAACGGTAAGAAAAT	148
Sat_340		L	55.51	CC453866	31044696	(AT)31	GCGATGGAGCCGTGCTTATTCAC	GCGGCTTTCCCCTTTTAACTCTGAG	
Satt156		L	56.14	BH126368	14969871	(ATT)17	CGCACCCCTCATCCTATGTA	CCAACTAATCCCAGGGACTTACTT	223
Sct_010		L	59.52	BH126771	14970274	(CT)10	TCCCAAAAGCATTGAG	TATGCACGGAAGAGGA	150
Satt076		L	61.35	BH126322	14969825	(ATT)10	TAATCGAGATTTAATAGAAAACA	TGGATGGACATTTTCAG	166
Satt448		L	64.66	BH126623	14970126	(ATT)15	GCGCTAAGGGCAATTTTATTCAA	GCGCAGCCTGTTCAGTTTTTCTTTTGTC	270
Satt166		L	66.51	BH126377	14969880	(ATT)19	TTGCACAGTTGATTTTTGTTT	GCATCGAATTTCTGGATTTAC	252
Sat_113		L	68.26	BH126283	14969786	(AT)24	GGAGCATACAGCCTTAAGAGAT	TGGGCATCAAAACTAAGAAAA	273
Satt678	*	L	70.20	CC454031	31044861	(ATT)10	CTAAGCGTGACAAACAGACCATTA	CGGCCATATCTACCAATCAGA	158
Satt527		L	70.36	BH126697	14970200	(ATT)17	GCGGTTACATCTTGCAAACTAAATTAAC	GCGGAATTTTGCACATAAATTAATAACT	195
Satt561		L	71.44	BH126728	14970231	(ATT)10	GCGGACGAATTTTCCAGA	GCGGGGCAACAATATTTGAATCTA	243
Sat_099		L	78.23	BH126271	14969774	(AT)25	GCGAAAATGGCAGAGATAA	AATGCTAAAAGAGGAATGAAATAA	260
Sat_286	*	L	87.42	CC453819	31044649	(AT)32	GCGTTGCTTGCTAAGTAGTGTTTTTAATCCT	GCGTCTCCCATCATGCAACTTCAATA	161
Satt006		L	92.00	BH146211	15243077	(ATT)12	CAATGTGATTAGTTTTGGAAA	GGGTTAATGTTGTTTTTTATA	118
Satt664	*	L	92.66	CC454019	31044849	(ATT)12	GCGTAGATGCTCAACATCAACACTAATCTG	GCGGACGATGAAGAAATATACTATTACGAA	238
Satt229		L	93.89	BH126430	14969933	(ATT)22	TGGCAGCACACCTGCTAAGGGAATAAA	GCGAGGTGGTCTAAAATTATTACCTAT	225
Satt513		L	106.37	BH126683	14970186	(ATT)14	GCGCATCACAAGTTTTATAGATGCTGA	GAGGTCTAGTGCTTTGGTAAGGTT	139
Satt373		L	107.24	BH126560	14970063	(ATT)21	TCCGCGAGATAAATTCGTAAAAT	GGCCAGATACCCAAGTTGTACTTGT	254
Sat_245	*	L	115.07	CC453783	31044613	(AT)27	GCGAGCCTACTTTTACTAGAACGTCAACAAG	GCGAAAAATTCAACTCCCCTTTAATAGATTC	176
Sat_389		M	0.00	CC453914	31044744	(AT)29	GCGGGTAGCCATATTCATATATTGCTG	GCGAAGGCTTATAAGGAGATACGATTTA	
Satt404		M	0.84	BH126586	14970089	(ATT)15	TCATCCGCCATTGATTTT	GCCCGGAACATACAAAAT	181
Sat_391		M	1.02	CC453916	31044746	(AT)37	GCGTAGGCATCGGTCAATATTTT	GCGTTAGCGAGTGGATCAAGATCA	
GMSC514		M	3.05	X56139	18745	(AT)13	TACCTTTCTTGTGAGTCGTA	TATTGAGATGGATATTGTAGATC	160
Satt636	*	M	5.00	CC453995	31044825	(ATT)22	GTCATGACTCATGAGTCACGTAAT	CCCAAGACCCCCATTTTTATGTCT	172
Satt590		M	7.84	BH126756	14970259	(ATT)26	GCGCGCATTTTTTAAGTTAATGTTCT	GCGCGAGTTAGCGAATTATTTGTC	318
Satt201		M	13.56	BH126408	14969911	(ATT)16	GCGTTGATACTTTCCTAAGACAAT	GGGAGAGAAGGCAATCTAA	282
Satt150		M	18.58	BH126362	14969865	(ATT)20	AAGCTTGAGGTTATTCGAAAATGAC	TGCCATCAGGTTGTGTAAGTGT	201
Sat_316	*	M	21.00	CC453847	31044677	(AT)16	GCGCAACGTCTAAAGCACAAGGATT	GCGCGACTACGTTACAGTTCCAA	298
Satt567		M	33.47	BH126733	14970236	(ATT)13	GGCTAACCCGCTCTATGT	GGGCCATGCACCTGCTACT	110
Satt540		M	35.85	BH126708	14970211	(ATT)12	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	152
Satt435		M	38.94	BH126613	14970116	(ATT)15	GCGGTGAAACGGCTCTCTTTGATAGTGA	GCGTTGGATTAATTAATTAAATTATTTT	286
Sat_244	*	M	48.86	CC453782	31044612	(AT)27	GCGTCAACCGGTGAAAAAACCTA	GCGTGGCTGGCAGTAGTCTATATCA	224
Satt463		M	50.10	BH126636	14970139	(ATT)19(CAA)17(ATT)13	TTGGATCTCATATTCAAACTTTCAAG	CTGCAAATTTGATGCACATGTGTCTA	226
Sat_253	*	M	51.60	CC453789	31044619	(AT)22	GCGATTGGTTGGGTGTTTAATTTTAAGAT	GCGTGTTGATGGTATAAAGATCGCTACTCT	275
Satt245		M	53.54	BH126445	14969948	(ATT)13(ATG)15	AACGGGAGTAGGACATTTTATT	GCGCCTCCTGAATTTCAAAGAATGAAGA	211
Satt220		M	56.29	BH126423	14969926	(ATT)18	GAGGAGGATCCCAAGGTAATAAT	GCGCATGGAGAAAAGAAGAG	245
Satt626	*	M	58.60	CC453988	31044818	(ATT)14	GCGGATGGAGACGGGGGGCACGGACGA	GCGCATAGCTAATTTTATATCAATTAT	238

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt323		M	60.05	BH126514	14970017	(ATT)17	GCGGTCGTCCTATCTAATGAAGAG	TGTGCGTTTAAATTGCAGCTAAAT	156
Sat_258	*	M	60.47	CC453793	31044623	(AT)23	GCGCAATAGATAATCGAAAAACATACAAGA	GCGGGGAAAGTGAAAACAAGATCAAATA	193
Satt702		M	61.04	CC454051	31044881	(ATT)26	GCGGGGTTCTGTGGCTTCAAC	GCGCATTGGAATAACGTCAAA	
Satt536		M	62.14	BH126704	14970207	(ATT)20	GCGCCACAGAAATTCCTTTTTCTA	GCGCCATAAGGTGGTTACCAAAAGA	162
Sat_003		M	62.31	BH126253	14969756	(AT)21	TGATTTTTGGTGTAGAACTC	CAAATTGGTTAGCTTACTCCA	161
Sat_148	*	M	63.93	CC453700	31044530	(AT)28(GT)15	GCGGAGTTTCCCCTAATTAGAT	GCGCAAGCTAGCTTCACCCAAAACTA	162
Sat_226	*	M	65.79	CC453765	31044595	(AT)22	GCGGAAACCCACCTATATGTGATCAAATG	GCGCAATTCCAGATGAAACAGAAGAAGGAT	212
Satt175		M	66.99	BH126384	14969887	(ATT)16	GACCTCGCTCTCTGTTTCTCAT	GGTGACCACCCCTATTCCTTAT	163
Satt494		M	71.71	BH126665	14970168	(ATT)13	GGCCGGTTCTCATTACAGGTCTCT	GGATTTCCATCTTGAATTTTATTA	218
Sct_147		M	73.88	BH126779	14970282	(CT)10	TCTCGACTCACGACTCA	CCAAGGTCTCTCAGAGG	
Sat_256	*	M	74.53	CC453792	31044622	(AT)30	GCGCGGAAAATTATTTTACTTTTTCAAT	GCGCACGGATTGAGAGAAAGCAGAAAGA	253
Satt677		M	75.57	CC454030	31044860	(ATT)11	CAACGACCAACTGACGAGACCT	GGGAATTCAACATGTGATGGTTTT	157
Sat_288	*	M	76.41	CC453821	31044651	(AT)19	GCGACAGACTGCAAGAATTGATGTAAATCT	GCGGGAAGGTAGGTAAAGAAAATTCAAATGA	215
Satt655		M	76.41	CC454010	31044840	(ATT)12	GAAGACCAAAACTTATTTCAGATC	ATTTTAAGCACCAGCAAAGACT	287
Satt680		M	77.19	CC454033	31044863	(ATT)33	GCGGGATATCGTGAGCATAGTTTTAC	GCGGCCTGAATATTTTAGGTTTAGAGTT	304
AF186183		M	77.24	AF186183	6671123	(ATT)22	GCGTATTTTGGGGGATTTTGAACA	GCGTTTCTCTTCTTATTCTTTCTCT	204
BE823543		M	78.38	BE823543	10255728	(CT)10	GCGAAATGCCGAAAGAG	GCGGGGATAAGAAAAACAAT	156
Satt306		M	80.02	BH126497	14970000	(ATT)13	GCGCTTAAGGACACGGATGTAAC	GCGTCTCTTTCGATTGTTCTATTAG	212
Satt728		M	80.90	CC454070	31044900	(ATT)12	GCGTACCCCTATATGGATGTTTCTTCCT	GCGTATGCAGCAAACAAAAAATATATAAT	
Sat_422		M	80.97	CC453946	31044776	(AT)21	GCGTTTTCCTAATGAAGATTT	GCGTGTAATAGTGATGGATGTAA	
Satt697	*	M	85.35	CC454046	31044876	(ATT)11	GCGTGCTTTAAATGATTGATTGA	GCGTGCGAACATAACTAATACAT	302
Satt551		M	95.45	BH126718	14970221	(ATT)12	GAATATCACGCGAGAATTTTAC	TATATGCGAACCCTCTTACAAT	238
Sat_121		M	103.98	BH126291	14969794	(AT)30	GACAAATGTAAAAAGTGACAGATAGAATGT	GTGTGGTGGTGGTACAGTTTTATACTAA	189
Satt250		M	107.70	BH126448	14969951	(ATT)16	CGCCAGCTAGCTAGTCTCAT	AATTTGCTCCAGTGTTTTAAGTTT	202
Satt618	*	M	111.06	CC453982	31044812	(ATT)13	GCGGTGATATTACCCCAAAAAAATGAA	GCGCTAGTTTCTAGTGGAAAGATGAGT	117
Satt210		M	112.08	BH126416	14969919	(ATT)25	GCGAAAAACGTCAGGTCAATGACTGAAA	GCGGGGCTTAGATATAAAAAAAAAGATG	260
Satt346		M	112.79	BH126536	14970039	(ATT)17	GGAGGGAGGAAAGTGTTGTGG	GCGCATGCTTTTCATAAGTTT	208
Sat_147	*	M	122.37	CC453699	31044529	(AT)12	GTGCGACGTCATGCCTTACTCAAT	GCGCTCCGTACACTTAAAAAAGAA	265
Sat_276	*	M	128.48	CC453810	31044640	(AT)29	GCGGAAACCCATCTAGAATATGAAAAACA	GCGTTCTTCTCGAGGTGAGATACAATC	271
Satt308		M	130.76	BH126499	14970002	(ATT)21	GCGTTAAGGTTGGCAGGGTGGAAGTG	GCGCAGCTTTATACAAAAATCAACAA	170
Satt336		M	133.83	BH126527	14970030	(ATT)14	AATTGGAGTGGGTCACAC	TTCCCGGAAAGAAAGAAA	170
Sat_359		M	139.81	CC453885	31044715	(AT)21	GCGGGTCACGATTCTAGTCACTATAACTTCA	GCGCAACGTAAGAAATGTAAATACAATGGA	
Sat_330	*	M	140.69	CC453857	31044687	(AT)24	GCGTTAGGATTTAGGATGAGGATAGG	GCGCAAATCAGTTGAGCAATGACTTA	265
Sct_195		N	2.44	CC454078	31044908	(CT)11	GCGCTATGCAAGGTCTAACTACA	GCGAAACCGTCACACAGTCTCTG	
Sat_379		N	4.33	CC453905	31044735	(AT)10	GCGTTTTGGCTCATCTTTCTTTTA	GCGGCCCTAAGCACAACTGAACCTAT	
Satt152		N	22.67	BH126364	14969867	(ATT)14	GCGCTATTCCTATCACAACACA	TAGGGTTGTCACTGTTTTGTTCTTA	230
Satt631	*	N	26.14	CC453991	31044821	(ATT)21	GGTAGATCCAGGAGCTTGAGTCAG	GCGCATCTCACTGCACTTGATTTT	175
Satt159		N	27.13	BH126371	14969874	(ATT)13	GAAATGCCCAGAAAAACCTAATAAC	TGAAGCAACAAAATAGAGGAATAGAG	286
Satt009		N	28.52	BH146212	15243078	(ATT)14	CCAACTTGAAATTACTAGAGAAA	CTTACTAGCGTATTAACCCTT	163
Satt641		N	29.28	CC453999	31044829	(ATT)10	GCGGAACATCACGGTTATA	GCGGGAGGCTCTGTCTCTTAGA	318

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Sat_186	*	N	30.11	CC453728	31044558	(AT)25(CT)18	GCGACGCGCTAGTCTTATTT	GCGGATGGCTTTTACTTT	293
Satt530		N	32.85	BH126699	14970202	(ATT)12	CATGCATATTGACTTCATTATT	CCAAGCGGGTGAAGAGGTTTTT	220
Satt683	*	N	34.52	CC454036	31044866	(ATT)29	GCGGGTGTGGGTCCTCAATTAAATA	GCGGTTTTCCCTAAACTAACCTAAC	257
Satt675		N	34.65	CC454028	31044858	(ATT)14	GCGCTATTTCCGTCCTATTATCATTTTCGTC	GCGTCTAACACGTATTTATTATTGGTCAATT	155
Satt624	*	N	35.32	CC453986	31044816	(ATT)23	GCGATGGCTTGTGGGAACACTAAT	GCGGACGTGGGACCAACACACTAA	151
Sat_084		N	36.86	CC453683	31044513	(AT)14	AAAAAAGTATCCATGAAACAA	TTGGGACCTTAGAAGCTA	151
Satt393		N	37.44	BH126576	14970079	(ATT)15	CAAGCCCATAAACGAAATAA	GCTCGGCTTGGCTTGTTTACTA	296
Satt584		N	37.98	BH126750	14970253	(ATT)18(ATAATT)6	GCGCCCAAACCTATTAAGGTATGAACA	GCGGGTCAGAAGATGCTACCAAACTCT	189
Satt485		N	38.07	BH146218	15243084	(ATT)9	GCGAATACGCATAAAAAAATCAACAAGA	GCGAAAAGAAAATTTAAAAAAAAATATAT	262
Sat_166	*	N	38.59	CC453713	31044543	(AT)15	GCGCTAATTTATCGGGACCCAACATAT	GCGGAAATAGTGCATTGATGAAAAACA	
Sat_208		N	39.35	CC453748	31044578	(AT)30	GCGTATCAAATCATGTAGGACTATCATTG	GCGCCTGGTTTTGGTACTAAAGAACTGT	241
Satt125		N	40.63	BH126339	14969842	(ATT)22	CAAATAAAAACATATACCTCTTGT	TGCCTTACTCTACTCTGTTTC	191
Sat_275	*	N	40.81	CC453809	31044639	(AT)24	GCGCGCTGGCAATTATTCAAAACTTAACGAT	GCGAAGGCTACGGTGAATAGAAAGGAC	258
Sat_280	*	N	43.45	CC453813	31044643	(AT)10	GGCGGTGGATATGAAACTTCAATAACTACAA	GGCGGGCTTCAAATAATTACTATAAAACTACGG	297
Satt080		N	45.14	BH126325	14969828	(ATT)23	CCATAAAATAATAAAGGTCAAT	TAATCAGTGGAAAAAAAGTTAT	
Sat_266	*	N	47.28	CC453801	31044631	(AT)30	GCGCTCCCACTAAAGAAATATTTTGGA	GCGGCCATTTGTTTCAAACTTTGAGGTA	231
Satt387		N	53.25	BH126572	14970075	(ATT)10	GCGTTACGTTTCACTATTTATTTAACAT	GCGGCAGGCTAGCTACATCAAGAG	209
Sat_236	*	N	57.59	CC453775	31044605	(AT)9	GCGGGTGCCTATGGTTCTACGTAGTTAC	GCGTTTGGATTAGATCAATAAAAATCACATT	220
Sat_033		N	58.38	BH146206	15243072	(AT)16	GCGGCAGATATTTAATCCCCTCACC	GCGATCTCGGAGAGAAAGAAATCGC	199
Satt521		N	65.46	BH126691	14970194	(ATT)12	GCGCTTCACTCTGGTGTAGTGTAG	GCGTTAGATAACGACACATTATTA	242
Satt549		N	70.60	BH126716	14970219	(ATT)29	GCGGCAAAACTTTGGAGTATTGCAA	GCGCGCAACAATCACTAGTACG	238
Satt660	*	N	72.60	CC454015	31044845	(ATT)11	GCGCTTCAAGTTTTACTGTCATAGAGG	GCGACCAAACTTATAACAAGACTTCTGT	178
GMABAB		N	73.10	X53404	18522	(AT)25	CAAAACATAAAAAAGGTGAGA	AAGAACCACACTAATATTATT	162
Satt237		N	74.99	BH126438	14969941	(ATT)17	GCGTGATTTCAATCCTTTTTC	GCGGTTGTCCTGTTAGAACCT	250
Satt339		N	75.91	BH126530	14970033	(ATT)26	TAATATGCTTTAAGTGGTGTGGTTATG	GTTAAGCAGTTCCTCTCATCACG	236
Satt255		N	76.49	BH126453	14969956	(ATT)11	GCGCTTTTAGCGTCGTCTGGC	TACCCCTCTCTTATTCTTCTT	141
Sat_304		N	77.10	CC453836	31044666	(AT)31	GCGAAACATGGTTGGGTTAAATAATAA	GCGGTCACCGCTAACGAGTTCTTGAA	182
Sat_091		N	79.51	CC453686	31044516	(AT)25	CTTCTGGATAGTTGGGACTGATA	GGAACAGGTCGTGAAAAGTTAT	181
Satt312		N	79.86	BH126503	14970006	(ATT)11	GGGATCAGCCTACTGCCGGTGCCC	GCGGGTTTTATTAAATGATATATT	165
Sat_285	*	N	81.92	CC453818	31044648	(AT)34	GCGATCCCACAATATTTCTATTTCTTT	GCGGGCAAAATGCAGATGTATAAAC	289
Satt234		N	84.60	BH126435	14969938	(ATT)16	TGAGAGCAGGACATTTTT	TCTGCGAGTGTTTTCTG	216
Sat_239	*	N	87.35	CC453777	31044607	(AT)17	GCGTTGTGTCCCTTATCCATTCATTATTC	GCGTGAGTTTATGCTTTGAGGTATTACA	249
Sat_241	*	N	89.38	CC453779	31044609	(AT)21	GCGTATTTTCTAATTCCACTATAACTTCAAT	GCGGGTATAAGTATCCATCAAATGTCAG	301
Satt257		N	92.56	BH126455	14969958	(ATT)10	GCGACTTTCTTTTCAATTTCACTCC	GCGCAATTGTCACCAACACAT	252
Sat_306	*	N	93.11	CC453838	31044668	(AT)22(GT)8	GCGGTTCTGGGTTCTCTGTTTTCTTA	GCGTGATCCCACTATTTTAATTATACATTTT	283
Sat_295		N	95.00	CC453828	31044658	(AT)27	GCGGGCCATATATTTTATTTGTAGGTTCA	GCGCCAGGTCTAGTTTCTATTGATTTGG	287
Satt022		N	102.06	BH146215	15243081	(ATT)17	GGGGGATCTGATTGTATTTTACCT	CGGGTTTCAAAAAACCATCCTTAC	
Sat_125		N	103.34	BH126295	14969798	(AT)20	GGGACGAAACAAAGTCACAT	GGGATGCTGTTATCAAAATCA	
Sat_196	*	O	0.00	CC453737	31044567	(AT)28	GCGAAACGAGATACTAGGATTTTGACTT	GCGAGCCTTAGGAGTAGTTAATGATGAT	232
Satt358		O	5.44	BH126547	14970050	(ATT)18	GCGGCGCTTTATGTAACAATACGATTT	GCGAGTAAAAGCAGAGTGCGGAGTA	188

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

(Information can be downloaded at http://bldg6.arsusda.gov/~pooley/soy/cregan/soy map1.html)

SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Sat_132		O	8.75	BH126302	14969805	(AT)19	GCGGTTTTGGTTTTTAATAGTCTCTTA	GCGGGATTGTATGTTGACAAAAGATTT	244
Satt487		O	9.53	BH126658	14970161	(ATT)22	ATCACGGACCAGTTCATTTGA	TGAACCGCGTATTCTTTTAATCT	209
Satt500		O	14.17	BH126671	14970174	(ATT)21	GCGAACGACCATGATAATCACA	GCGCTCATTTGAAAGCATTGTTATA	322
Satt492		O	17.25	BH126663	14970166	(ATT)15	GTATCGTTCGCGTCTTGAGTC	GCAGCGGTGTAGTTCGTTCTTTCT	221
Sat_321	*	O	19.44	CC453852	31044682	(AT)17	GCGTTGGAATCATGCAAACTTAACTTCAGAC	GCGTTGGAGCATGTAAGTCAAAACAAAAGAC	240
Satt445		O	20.43	BH126620	14970123	(ATT)23	GCGCATTGCATCGAATTATTA	GCGTTGGAATTTGTGATTGACA	214
Sat_303	*	O	20.93	CC453835	31044665	(AT)13(GT)20	GCGCGAGCAAAATTCCTACAAGTA	GCGCTGGCCAAATATCATCTCACA	259
Sat_318	*	O	24.61	CC453849	31044679	(AT)28	GCGGAAAGCCAAATATCAGATGTTCAACTTA	GCGGGCATTATGGAGCAAAATACTTGTT	184
BF008905		O	28.95	BF008905	10709181	(GCA)9	GCGTCTGGCTCTTCA	GCGAGCAGTGATGTTGTT	144
Satt653		O	38.09	CC454008	31044838	(ATT)11	GCGAAACTCAAATTTGACACAACTG	GCGCAAGGTTAACTACTAACAAGACACA	230
Sat_145	*	O	39.25	CC453698	31044528	(AT)15	CCAATTTGGTTTAGATCATTAACTC	GCATTTAGGGATTACAATGACTCAA	240
Satt259		O	39.82	BH126457	14969960	(ATT)14	TGGGCCATTTGGGCAGCTCGACT	ATTCACACGCATCTGGAATAATA	207
Satt347		O	42.29	BH126537	14970040	(ATT)11	GCGCGCTTCCATTTTAAAGTA	GCGGTCACCGTTGTATACCTA	238
Satt420		O	49.71	BH126599	14970102	(ATT)16	GCGTATTCAGCAAAAAAATATCAA	TTATCGCACGTGTAAGGAGACAAAT	232
Sat_221	*	O	51.01	CC453761	31044591	(AT)19	GCGCCCTAAAATGGAGTAAAATGGAAGA	GCGAAAGGAGCTAACTCAGTTGATTGA	277
Sat_291		O	51.90	CC453824	31044654	(AT)34	GCGATGTGTGCAGGAATTAAATATATCAATA	GCGAAGCCACAAAAATTAAGAATATAAAGC	315
Satt473		O	52.12	BH126645	14970148	(ATT)18	ATCTCGACCTAGTTGTCCATGTTCAA	CGAGAGTTGCTAACTTTAGGATAGTG	258
Satt679		O	53.19	CC454032	31044862	(ATT)15	GCGAACAAAGGAAGAATAGAG	CAATTACCCCCAACAACTAAGT	262
Satt466		O	53.67	BH126638	14970141	(ATT)13	GGTGTGGTGGTCAACAACAATA	ACCACTGATTCAAGCCAACAAGAA	148
Satt479		O	54.20	BH126651	14970154	(ATT)16	GCGCTTTCAAAAAGTAACAATTAATGAAA	GCGGGAATTGGTTAATCTCATCGTGAC	116
Satt585		O	54.68	BH126751	14970254	(ATT)22	CCCAATGCCCTTGCGGGATAG	GGGGAGTGAAGGTAATGGTTT	126
Satt550		O	55.09	BH126717	14970220	(ATT)16	CGTCAATTAAGCAAAAATGTGA	GCGCGGATGAGCGTGCGTTTTTA	210
Satt188		O	55.58	BH126395	14969898	(ATT)30	GCGTTTTAATTTTAATTTATTATTTTC	GCGCTGTCTTAATTGGAGATAC	243
Satt576		O	55.81	BH126742	14970245	(ATT)19	GCGGGACACACACAAACACCTACA	GCGGGTTTGCGTTCTTATATTATC	297
Satt128		O	56.13	BH126342	14969845	(ATT)14	CCTTCTCCCTCTCATAC	CAAGTTTTATACCATTCATC	277
Satt608		O	56.28	CC453975	31044805	(ATT)18	GCGGGATCACATAATGATCTTTATAGA	GCGCTATCATCAATGCAATGGGATTTA	166
Satt094		O	56.58	BH126328	14969831	(ATT)18	CCAAGTGCCAATGAAG	ATCCATGGTTTTTTGATG	164
Satt633		O	56.93	CC453992	31044822	(ATT)12	GGGACACTATCGGCCTAGAAAGTT	GGGTGATAAAGTTCCCCCTCTAAG	131
Satt262		O	57.02	BH126459	14969962	(ATT)20	GCGCCCCATTAATGTTAACACA	GCGGAGTTCAACGCATTCACCTT	256
Satt173		O	58.40	BH126382	14969885	(ATT)18	TGCGCCATTTATTCTTCA	AAGCGAAATCACCTCCTCT	197
Satt345		O	59.43	BH126535	14970038	(ATT)27	CCCCTATTTCAAGAGAATAAGGAA	CCATGCTCTACATCTTCATCATC	254
Satt241		O	59.49	BH126442	14969945	(ATT)21	GCGCTTGGTCTAAGAAAACTTTTGGT	GGGGGTTTTATCTCTTAAATGTG	249
Sat_193	*	O	61.11	CC453734	31044564	(AT)21	GCGTTCCAATAATAGTTGTCATGTT	GCGGGTAAATTGCAAGAGGATAAAT	190
Sat_282	*	O	63.81	CC453815	31044645	(AT)21	GCGTCCCGATGATTCTTGGATCTA	GCGCGATTCTTGCCACTGTATTT	175
Sat_341		O	67.93	CC453867	31044697	(AT)30	GCGGTGTGGGTTTGTGAGATACGATTA	GCGCGTTGCAGATTAGTTGTTTTATTTTCTA	
Satt563		O	68.39	BH126729	14970232	(ATT)18	GATGACAACGTAGGCTAAAAA	GCGCCCACATGATTTTGTACTGAT	163
BE801128		O	68.97	BE801128	10232240	(CAA)13	GCGACAGTTCTCCACTCTTC	GCGCCCCTTATAGATTTGTAAC	172
Satt478		O	71.10	BH126650	14970153	(ATT)17	CAGCCAAGCAAAAGATAAATAATA	TCCCCCACAAGAGAACAAGAAGGT	190
Sat_242	*	O	74.05	CC453780	31044610	(AT)18	GCGGATCCACCACTTGTTCTAAGAATCTC	GCGTAGGGTCGGGTTTTAGTATGTCATT	265
Satt477		O	82.09	BH126649	14970152	(ATT)11	GTTGGGAAAAGGTTACTACCATATC	GGTCCGTATGCAATTCTTGACTAATA	160

Soybean SSR Loci, Linkage Group (LG), PCR Primer and Other Associated Information

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SSR locus		LG	cM Position in LG	GenBank accession	GenBank GI number	Repeat motif	Upper primer sequence (5'-->3')	Lower primer sequence (5-->3')	Allele Size in Williams
Satt123		O	86.86	BH126337	14969840	(ATT)10	TTCAACCATTCAAACATG	AATTGAAAAGATGTGAAACAT	110
Satt331		O	93.37	BH126522	14970025	(ATT)14	GCAGAGTCCCCCCTAAATATAG	CGGGAACAACCACACTCTCCATT	243
SOYLBC		O	95.00	V00452	18593	(AT)26	GTGGTTTCAGTGAGTGATC	AAGGTGGAGATGAACTCA	173
Satt592		O	100.38	BH126758	14970261	(ATT)12	GCGAAGATTGGTCTTTTATGTCAAATG	GCGGAGGAATACAAGTCTCTATTCAA	231
Satt581		O	106.03	BH126747	14970250	(ATT)11	CCAAAGCTGAGCAGCTGATAACT	CCCTCACTCCTAGATTATTTGTTGT	144
Sat_274		O	107.58	CC453808	31044638	(AT)19	GCGCCGATCTTTAGTGAGGTTACAAGT	GCGTTCAGCGAGTCCAGAAATAG	264
Sat_038		O	112.17	CC453675	31044505	(AT)20	GCGTCGCAACTTTTTCATTTTTCTTACT	GCGAGTTCTTTTAACAACACTCACTTTT	117
Satt153		O	118.14	BH126365	14969868	(ATT)12	GGGTTATATCAGTTTTTCTTTTTGTT	CCATCCTCGTTAGCATCTAT	211
Satt243		O	119.50	BH126444	14969947	(ATT)17	GCGCATTGCACATTAGGTTTTCTGTT	GCGGTAAGATCACGCCATTATTTAAGA	200
Sat_307	*	O	123.43	CC453839	31044669	(AT)34	GCGAATTGGACTAAAAGAATAAGCATCA	GCGTGTTTGGTATAGAAATGAGAAATAAAAT	213
Sat_109		O	127.50	CC453690	31044520	(AT)28	CAACTCTTCAAATATAGCATCATA	TAGGACAATGTCTTAAATTTCAGTA	182
Sat_231	*	O	128.44	CC453770	31044600	(AT)22	GCGGTATGTTTAGTGAATAAATGACTCG	GCGAGACTCATCCAACTATAATTTATCATAT	296
Sat_108		O	129.30	CC453689	31044519	(AT)16	AAAAATCTATTCACTTTGAGTCTA	TTGAAAGAGTCACGTCTATTCTAT	203
Sat_190	*	O	129.80	CC453731	31044561	(AT)9	GCGTGGAAAATATTTTAAAGATTAGGA	GCGTGTGTACATTTAGTCTACTTGAGAA	193
Scaa001		O	146.37			(CAA)	AGAATTAGAAAACCATAAATCTG	TATGGCGGGAGTTGA	115

*** SSR developed in cooperation with Monsanto Co.**

 # SSR from M.Morgante, A. Rafalski, P.Biddle, S. Tingey and A.M. Olivieri, Genome, 37 (1994) 763-769.