

Fig. S1, electronic supplementary material. Frequency distribution and polymorphisms of the microsatellite markers.

On the left is shown the frequency of microsatellite motifs based on the number of nucleotides in the core unit. Among the pool of possible simple sequence repeats, trinucleotides (185 sequences, 40%) and mononucleotides (165 sequences, 36%) outnumbered dinucleotides (55 sequences, 12%), tetranucleotides (23 sequences, 5%) and pentanucleotides (35 sequences, 7%). On the right is summarized the number of amplified alleles of the microsatellite markers, after testing them on the four accessions *P. axillaris* subsp. *axillaris* N, *P. axillaris* subsp. *parodii* S7, *P. exserta* and *P. integrifolia* subsp. *inflata* S6. In total 136 primer pairs out of 222 tested (61%) were polymorphic in at least two species. Among these, 22 had the highest possible polymorphism information content, with different alleles for each of the four *Petunia* species tested, 54 had three different alleles, 53 had two alleles and 35 (16%) were monomorphic. In seven cases only a presence-absence allele could be detected. Fifty-one primer sets failed amplification, possibly due to an intron-exon boundary, or for errors or polymorphisms in the EST sequence.

Fig. S2, electronic supplementary material. Box plot with the length of orthologous genetic intervals in the two crosses.

The recombination rate in the two crosses is compared at 30 orthologous genetic intervals. A paired two tailed T-test indicates significantly ($p = 0.013$) higher recombination in the *P. axillaris* x *P. inflata* cross.

Fig. S3, electronic supplementary material. Distribution of the crossovers in the two mapping populations.

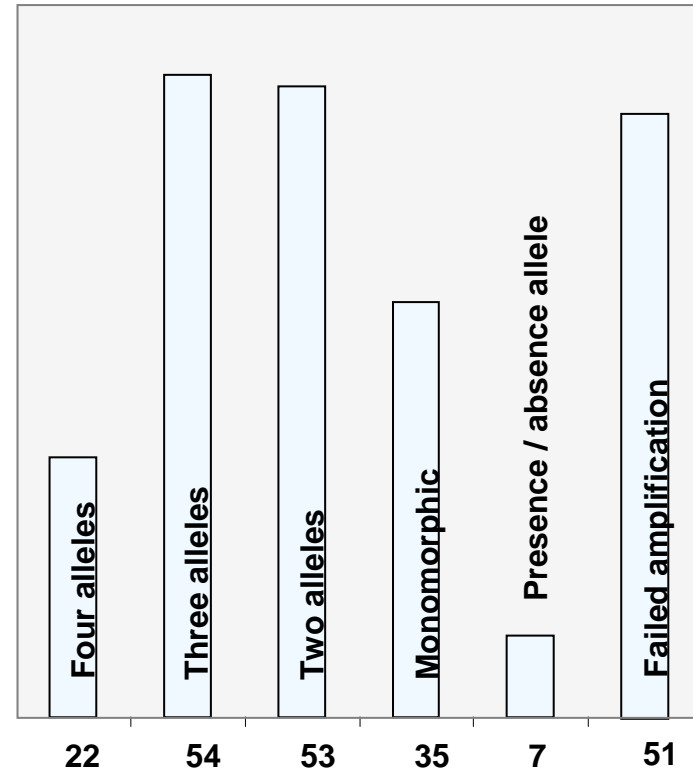
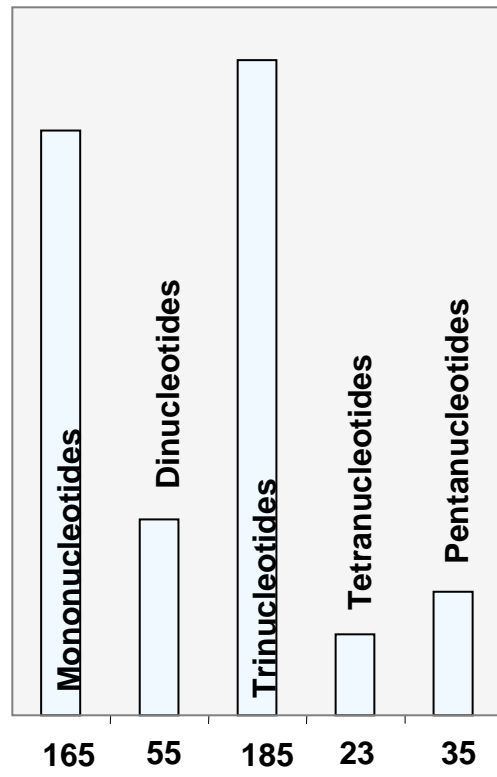
The frequency distribution of crossovers / chromosome is plotted for the *P. axillaris* x *P. inflata* (+) and for the *P. exserta* x *P. parodii* (x) populations. The last panel summarizes the average number of crossovers / chromosome.

Fig. S4, electronic supplementary material. Annotation of the SSR position on the EST sequences of *Petunia*.

Mononucleotide-SSRs are represented with circles, dinucleotides with squares and trinucleotides with triangles. Empty symbols indicate that the microsatellite motif is present only in *Petunia*, whereas full symbols are used when the SSR was detected at the same place in the corresponding tomato unigene assembly, even if only as proto-microsatellite consisting of a few repeats. Stop codons were in general less well conserved than the first ATG, and when present they are annotated with an asterisk.

Table S1, electronic supplementary material. BLAST search of the *Petunia* marker sequences in the tomato genome.

Tabular BLASTN search of the *petunia* marker sequences in the tomato genome database with a hit e-value threshold of 1e-5.



electronic supplementary Fig. S1

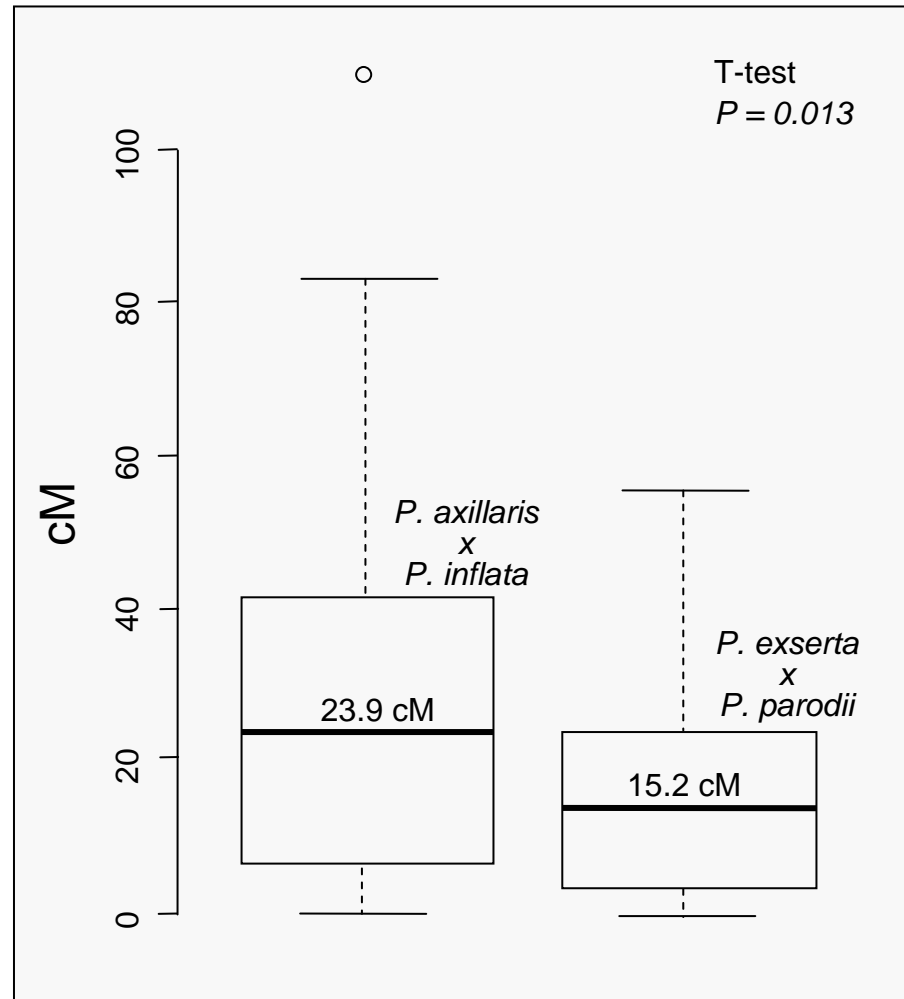
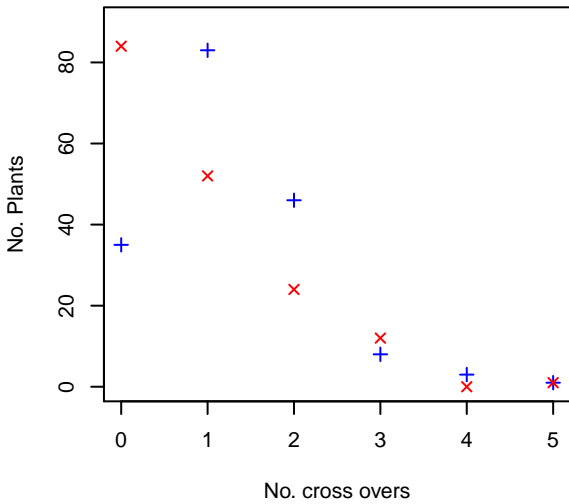
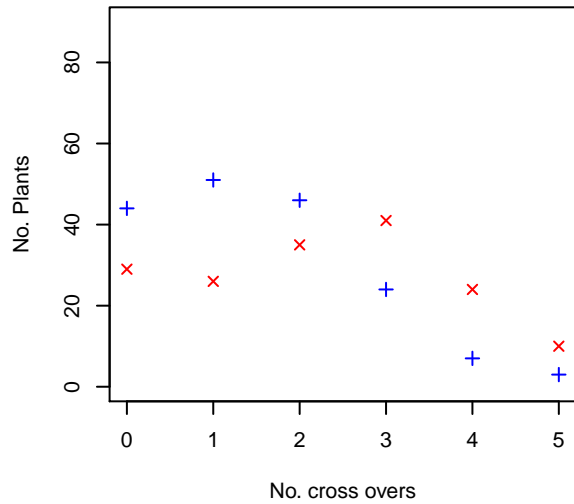
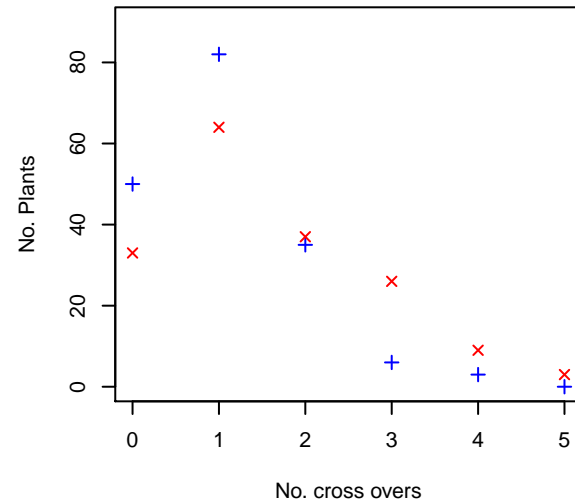
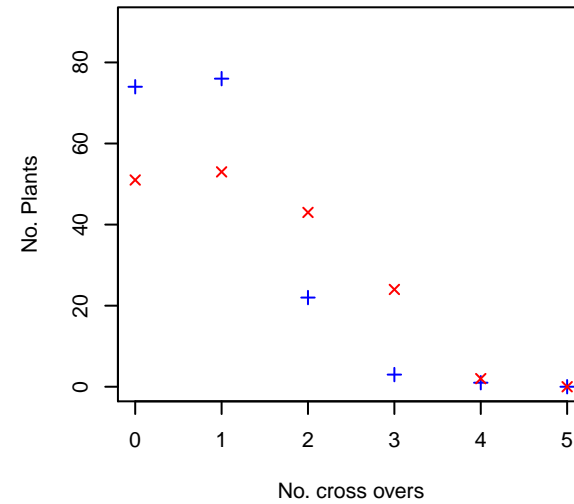
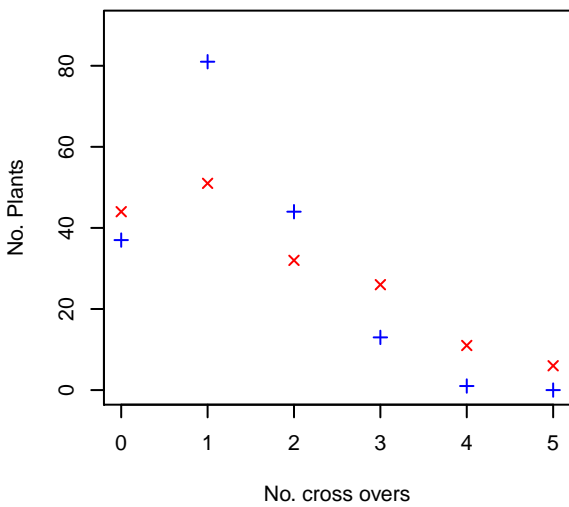
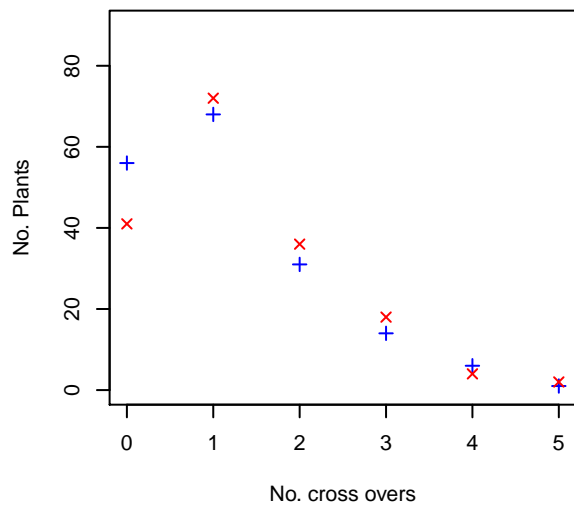
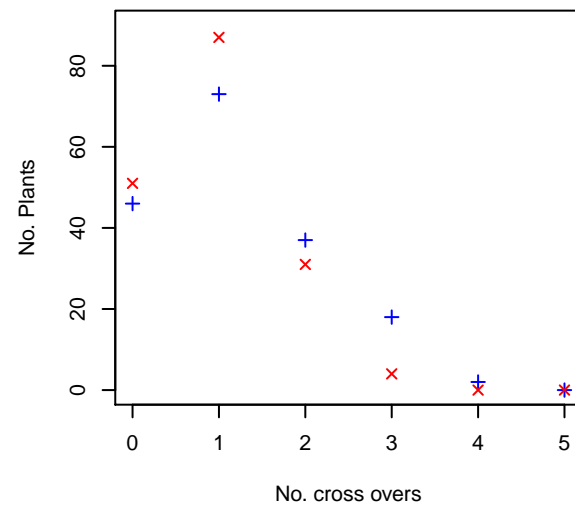
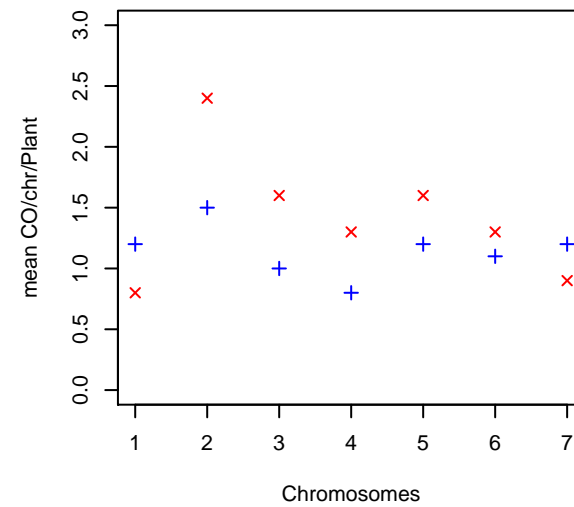
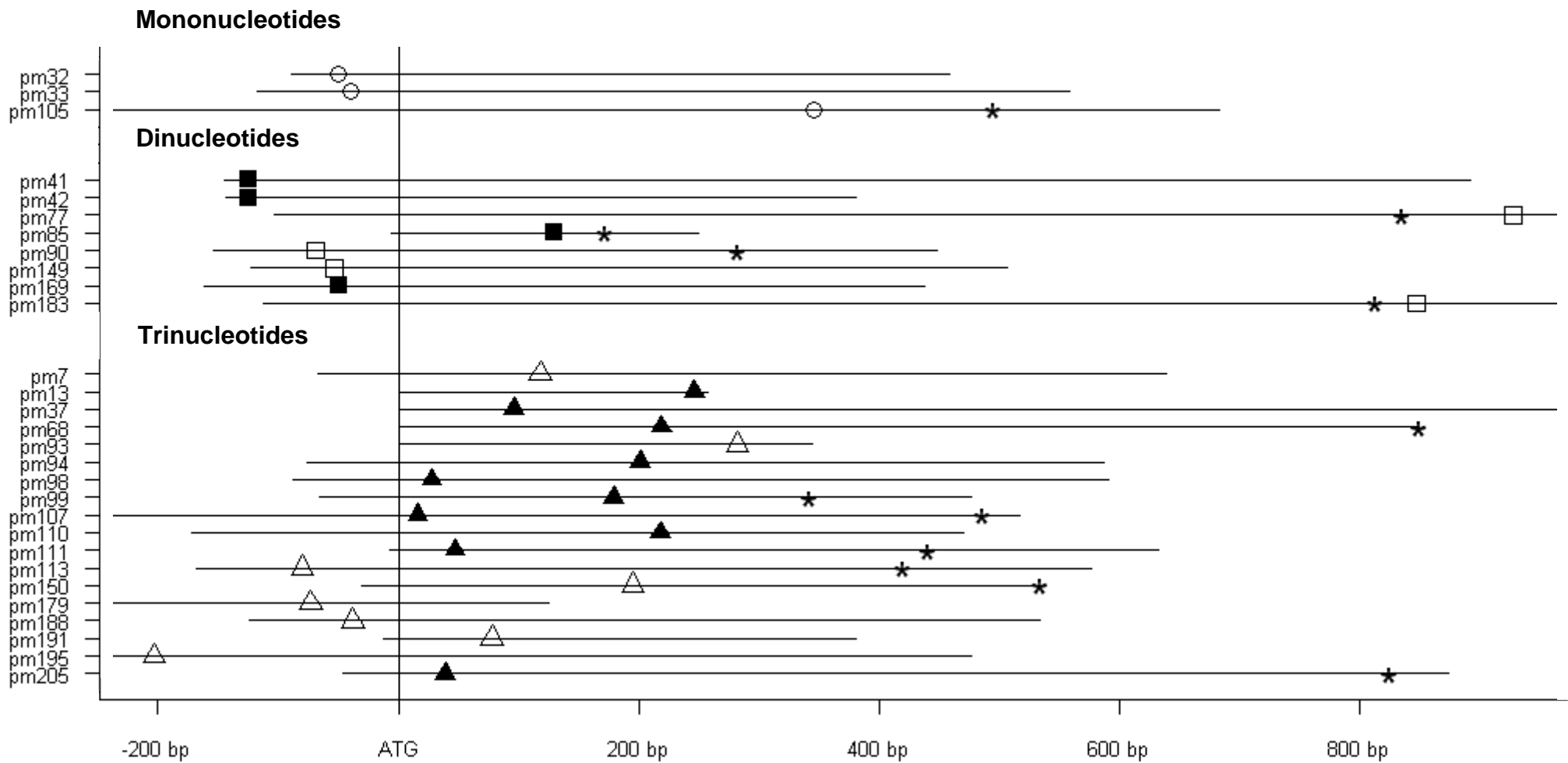


Fig. S2

Chrom 1**Chrom 2****Chrom 3****Chrom 4****Chrom 5****Chrom 6****Chrom 7****Average No. Cross Overs /Chrom /Plant**



electronic supplementary Fig. S4

Marker	<i>P. exserta</i> x <i>P. parodii</i> map				<i>P. axillaris</i> x <i>P. iinflata</i> map				Tomato chrom.	% Identity	Align. length	Mismatches	Gap openings	q. start	q. end	s. start	s. end	e-value	bit score
pm63	EXPA	chr	4 cm	38.8					SL2.10ch09	88.89	234	26	0	1133	1366	859670	859903	2.00E-66	258
pm66	EXPA	chr	6 cm	11.4					SL2.10ch01	85.37	82	12	0	571	652	82283678	82283597	2.00E-09	67.9
pm68					AXIN	chr	4 cm	81.5	SL2.10ch09	88.37	129	12	1	724	849	1893799	1893927	5.00E-29	133
pm7	EXPA	chr	4 cm	38.8					SL2.10ch04	93.22	177	12	0	429	605	59933337	59933161	4.00E-66	256
pm71	EXPA	chr	5 cm	23.2					SL2.10ch07	91.3	46	4	0	1	46	60627125	60627080	7.00E-08	61.9
pm77					AXIN	chr	4 cm	76.3	SL2.10ch04	91.23	114	10	0	756	869	56125718	56125831	4.00E-33	147
pm79	EXPA	chr	3 cm	88.7					SL2.10ch06	87.6	121	15	0	17	137	43488707	43488827	8.00E-26	121
pm8	EXPA	chr	4 cm	38.8					SL2.10ch04	94.33	141	8	0	133	273	60261066	60260926	3.00E-54	216
pm81					AXIN	chr	1 cm	91	SL2.10ch06	91.11	45	4	0	211	255	40664254	40664298	1.00E-06	58
pm83	EXPA	chr	1 cm	10.9					SL2.10ch02	93.18	88	6	0	7	94	36731762	36731849	2.00E-27	127
pm85	EXPA	chr	1 cm	6.8					SL2.10ch05	93.1	116	8	0	297	412	630494	630379	2.00E-39	167
pm9	EXPA	chr	6 cm	31.1	AXIN	chr	6 cm	16.7	SL2.10ch02	90.91	66	6	0	302	367	15676571	15676506	3.00E-14	83.8
pm90	EXPA	chr	6 cm	7.8					SL2.10ch09	83.93	112	18	0	182	293	64125266	64125155	4.00E-13	79.8
pm91	EXPA	chr	6 cm	10.9					SL2.10ch01	91.82	110	9	0	416	525	83416490	83416599	3.00E-33	147
pm94	EXPA	chr	2 cm	125.6					SL2.10ch01	84.4	218	31	1	43	257	81719741	81719524	6.00E-37	159
pm98	EXPA	chr	4 cm	95.9					SL2.10ch02	93.88	147	9	0	475	621	41818923	41819069	2.00E-55	220
pm99	EXPA	chr	3 cm	0					SL2.10ch07	88.62	167	16	1	66	229	60216662	60216496	1.00E-42	176
pt100					AXIN	chr	4 cm	27	SL2.10ch04	86.42	383	48	4	4	386	6963753	6963375	5.00E-84	315
pt102a					AXIN	chr	3 cm	115.5	SL2.10ch03	91.95	435	35	0	5	439	536535	536101	5.00E-165	585
pt102b					AXIN	chr	3 cm	102.2	SL2.10ch03	91.95	435	35	0	5	439	536535	536101	5.00E-165	585
pt104	EXPA	chr	5 cm	44.3					SL2.10ch08	85.71	399	54	2	12	410	39125260	39125655	1.00E-87	327
pt105					AXIN	chr	6 cm	119.1	SL2.10ch01	85.69	622	66	13	1	615	74143352	74143957	9.00E-123	444
pt108					AXIN	chr	3 cm	118.4	SL2.10ch03	88.55	297	28	1	10	300	34492916	34493212	7.00E-86	321
pt11					AXIN	chr	7 cm	133.9	SL2.10ch08	93.45	168	11	0	361	528	60502294	60502127	3.00E-63	246
pt110					AXIN	chr	6 cm	119.1	SL2.10ch09	83.41	458	76	0	13	470	36523236	36522779	6.00E-81	305
pt111					AXIN	chr	1 cm	34.1	SL2.10ch05	87.96	457	52	3	11	467	42058382	42058835	3.00E-123	446
pt113	EXPA	chr	5 cm	37.2					SL2.10ch12	92.26	155	12	0	141	295	37979375	37979529	4.00E-53	212
pt114					AXIN	chr	5 cm	1.3	SL2.10ch11	96.22	556	8	13	1	554	43061911	43061367	0	833
pt115	EXPA	chr	2 cm	11.5					SL2.10ch07	90.11	182	18	0	149	330	54713618	54713799	8.00E-55	218
pt116					AXIN	chr	4 cm	27.9	SL2.10ch10	89.73	185	19	0	6	190	1724624	1724440	3.00E-54	216
pt13	EXPA	chr	7 cm	43.6					SL2.10ch08	94.35	124	6	1	182	305	61357581	61357459	6.00E-44	182
pt134					AXIN	chr	7 cm	10	SL2.10ch10	87.21	297	38	0	146	442	43454203	43453907	1.00E-75	287
pt140					AXIN	chr	5 cm	2.4	SL2.10ch12	86.1	410	46	5	5	406	2094620	2094214	2.00E-89	333
pt148					AXIN	chr	2 cm	98.4	SL2.10ch02	88.63	343	38	1	24	366	13660567	13660226	2.00E-98	363
pt149					AXIN	chr	6 cm	102.3	SL2.10ch09	85.96	178	25	0	196	373	59388225	59388402	1.00E-35	155
pt15	EXPA	chr	7 cm	6.3					SL2.10ch08	92.31	91	7	0	1	91	62857303	62857393	1.00E-26	125
pt21					AXIN	chr	1 cm	20.6	SL2.10ch05	86.89	267	28	5	260	523	5267368	5267630	4.00E-54	216
pt22	EXPA	chr	5 cm	25.7					SL2.10ch01	89.86	217	20	2	219	435	60774645	60774431	2.00E-61	240
pt25					AXIN	chr	6 cm	112.3	SL2.10ch03	86.17	282	32	5	1	278	47604652	47604374	5.00E-54	216
pt26					AXIN	chr	5 cm	9.2	SL2.10ch09	93.57	140	9	0	34	173	56990830	56990691	2.00E-51	206
pt27	EXPA	chr	4 cm	0					SL2.10ch09	84.1	390	60	2	9	398	64282472	64282859	5.00E-69	266
pt3					AXIN	chr	7 cm	131	SL2.10ch09	87.86	280	30	4	16	294	9630761	9630485	1.00E-65	254
pt30					AXIN	chr	7 cm	23.9	SL2.10ch08	92.31	130	9	1	382	511	50183439	50183311	2.00E-40	170
pt36					AXIN	chr	5 cm	0	SL2.10ch10	93.7	381	23	1	87	467	61488459	61488080	9.00E-157	557
pt37					AXIN	chr	5 cm	3.1	SL2.10ch11	90.62	224	19	2	78	299	35782935	35782712	5.00E-68	262
pt39a					AXIN	chr	7 cm	72.3	SL2.10ch03	89.63	463	46	2	3	465	56894312	56894772	4.00E-146	521
pt39b	EXPA	chr	3 cm	73.7					SL2.10ch03	89.63	463	46	2	3	465	56894312	56894772	4.00E-146	521
pt40					AXIN	chr	2 cm	182.3	SL2.10ch08	91.44	187	14	2	59	245	29511569	29511753	7.00E-58	228

Marker	<i>P. exserta</i> x <i>P. parodii</i> map				<i>P. axillaris</i> x <i>P. inflata</i> map			Tomato chrom.	% Identity	Align. length	Mismatches	Gap openings	q. start	q. end	s. start	s. end	e-value	bit score	
Pt44	EXPA	chr	2 cm	88.5	AXIN	chr	2 cm	171.5	SL2.10ch08	93.75	208	13	0	77	284	6089377	6089584	4.00E-82	309
pt5					AXIN	chr	7 cm	124	SL2.10ch08	90.22	184	18	0	1	184	51489722	51489905	5.00E-56	222
pt50	EXPA	chr	2 cm	56.8	AXIN	chr	2 cm	141.5	SL2.10ch02	93.65	189	12	0	269	457	49781988	49782176	2.00E-73	280
pt52					AXIN	chr	2 cm	100.5	SL2.10ch02	89.16	332	32	2	199	527	21286103	21286433	1.00E-97	361
pt55					AXIN	chr	1 cm	13.6	SL2.10ch12	91.6	238	14	6	193	430	44185933	44186164	4.00E-69	266
pt57					AXIN	chr	2 cm	98.4	SL2.10ch04	89.8	245	24	1	153	397	5968314	5968557	3.00E-73	280
pt6					AXIN	chr	7 cm	15.7	SL2.10ch08	92.64	163	12	0	5	167	57487527	57487365	8.00E-58	228
pt7					AXIN	chr	7 cm	132.2	SL2.10ch08	86.13	274	34	3	1	271	57080463	57080191	2.00E-55	220
pt71					AXIN	chr	1 cm	12.4	SL2.10ch01	88.01	342	36	5	52	393	5777246	5777582	3.00E-85	319
pt72					AXIN	chr	2 cm	118.3	SL2.10ch10	88.44	294	30	4	3	296	14754289	14754000	2.00E-74	283
pt76					AXIN	chr	2 cm	99.3	SL2.10ch07	88.41	233	26	1	34	266	8649303	8649534	2.00E-61	240
pt8					AXIN	chr	7 cm	87.1	SL2.10ch03	94.25	174	8	1	4	175	59939732	59939559	3.00E-67	260
pt84					AXIN	chr	6 cm	119.1	SL2.10ch02	92.27	194	15	0	143	336	39895890	39896083	4.00E-69	266
pt85					AXIN	chr	2 cm	99.7	SL2.10ch06	89.8	255	26	0	4	258	876038	875784	3.00E-79	299
pt87					AXIN	chr	7 cm	71.6	SL2.10ch03	91.78	365	27	3	40	404	6663309	6663670	4.00E-128	462
pt93					AXIN	chr	1 cm	13	SL2.10ch12	91.6	238	14	6	193	430	44185933	44186164	4.00E-69	266
pt96					AXIN	chr	2 cm	98.4	SL2.10ch10	86.62	299	31	6	41	337	6708399	6708690	1.00E-59	234
pt97					AXIN	chr	4 cm	29.6	SL2.10ch04	93.96	331	20	0	10	340	59571225	59571555	6.00E-139	498
pt99					AXIN	chr	1 cm	12.4	SL2.10ch11	91.96	199	16	0	155	353	292267	292069	1.00E-69	268
rat	EXPA	chr	5 cm	86.9	AXIN	chr	5 cm	129.1	SL2.10ch12	87.07	526	68	0	110	635	62005921	62006446	9.00E-141	504
rt	EXPA	chr	6 cm	5.5					SL2.10ch09	85.19	1371	194	1	23	1393	49180822	49179461	0	1116
sams1	EXPA	chr	4 cm	40.9	AXIN	chr	4 cm	90.8	SL2.10ch09	92.67	696	51	0	56	751	1749238	1749933	0	975
sho	EXPA	chr	1 cm	0	AXIN	chr	1 cm	13.6	SL2.10ch05	91.94	62	5	0	890	951	3561351	3561412	5.00E-14	83.8