

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.

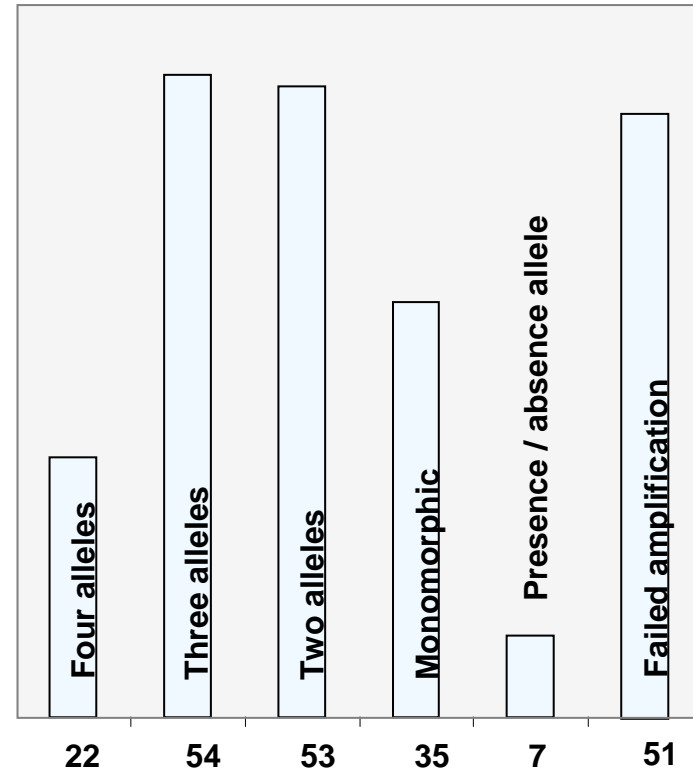
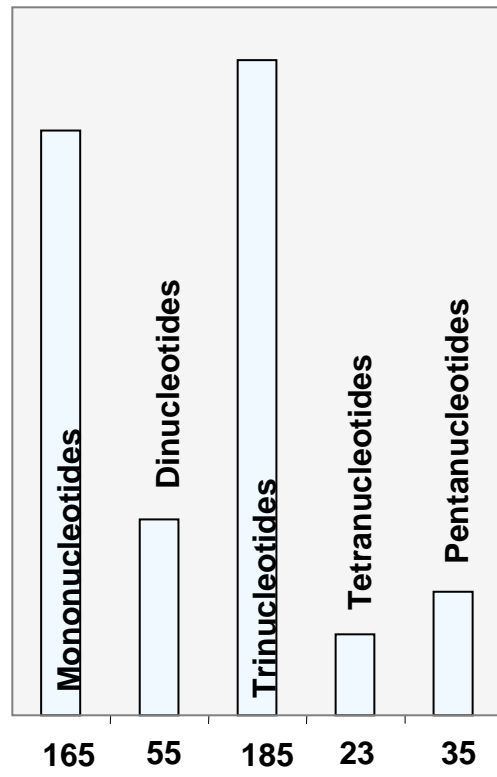
The frequency distribution of crossovers / chromosome is plotted for the *P. axillaris* x *P. inflata* (+) and for the *P. exserta* x *P. parodii* (x) populations. The last panel summarizes the average number of crossovers / chromosome.

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

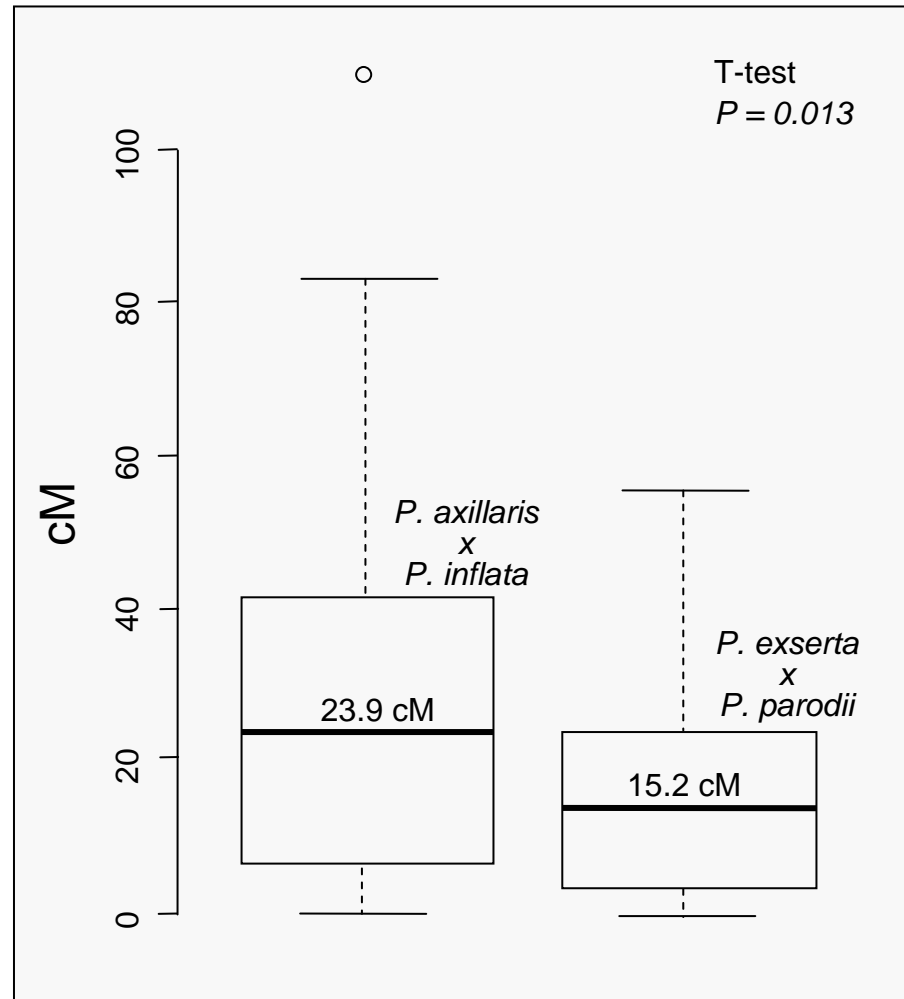
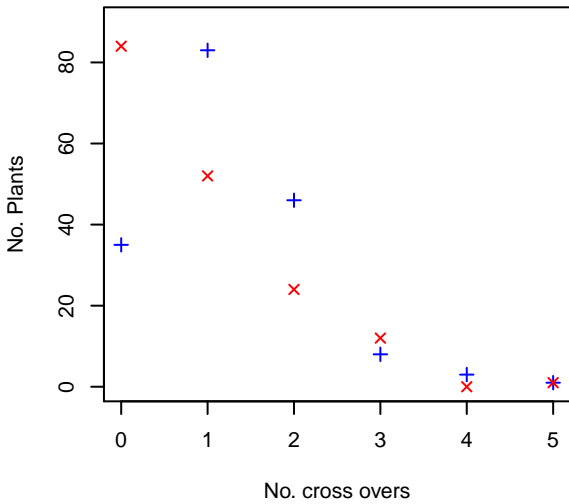
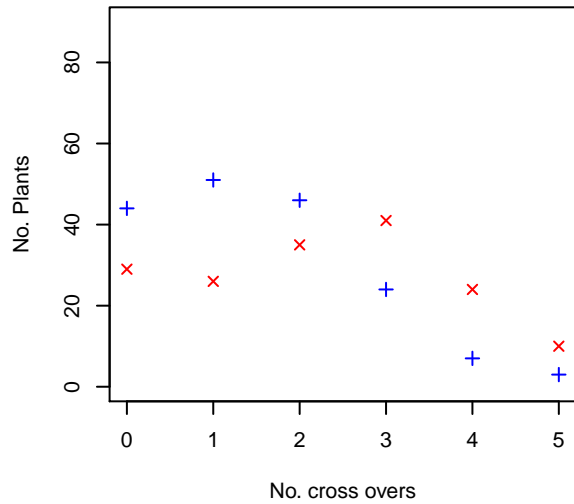
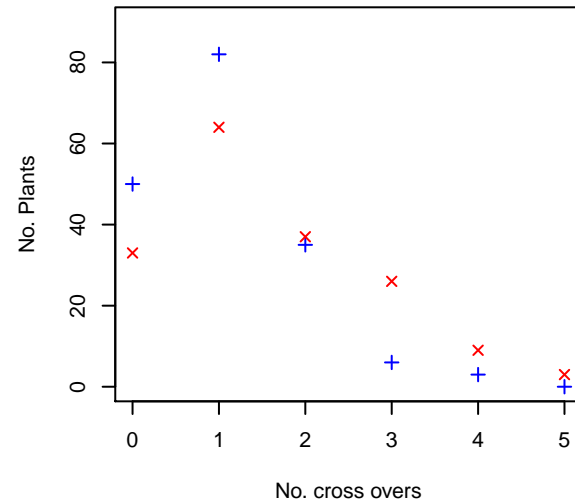
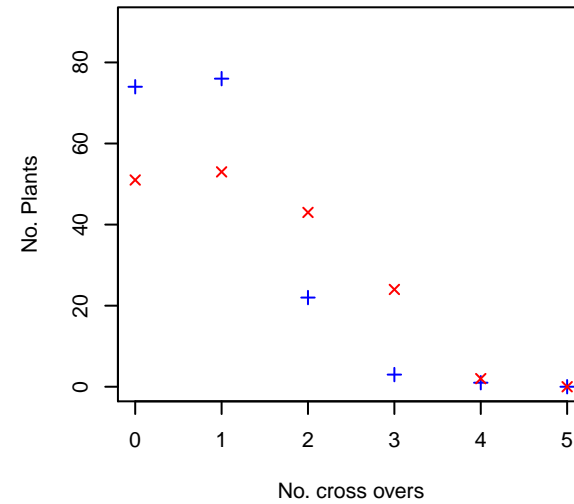
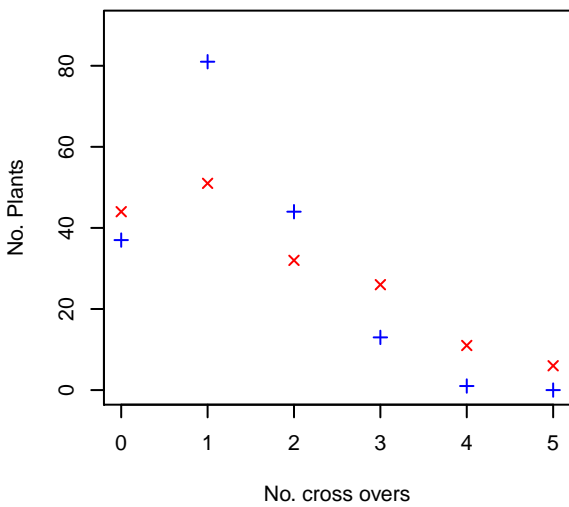
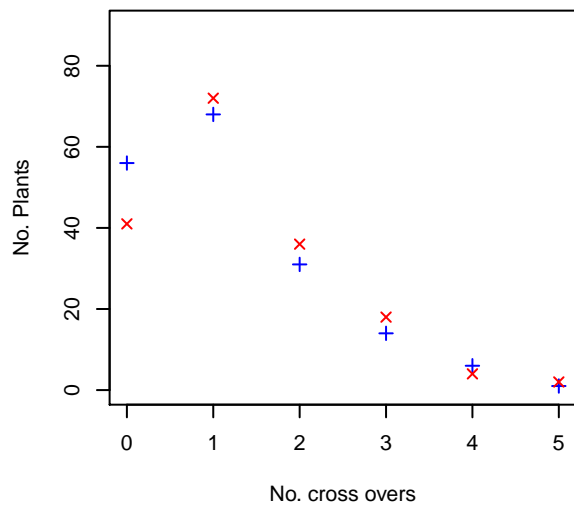
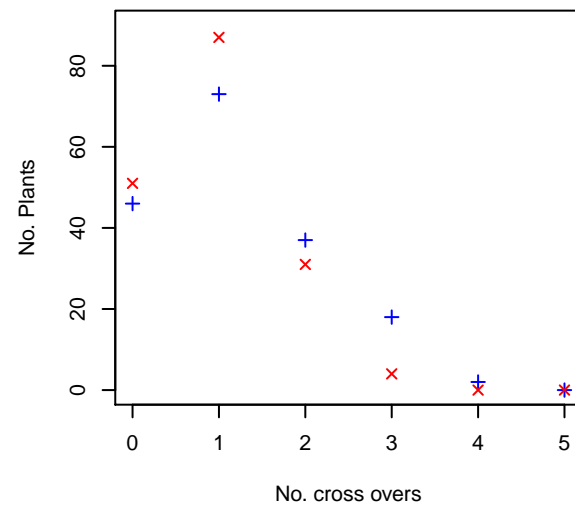
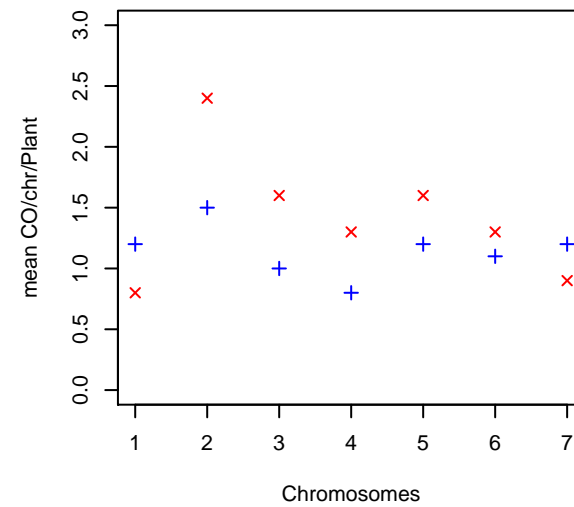
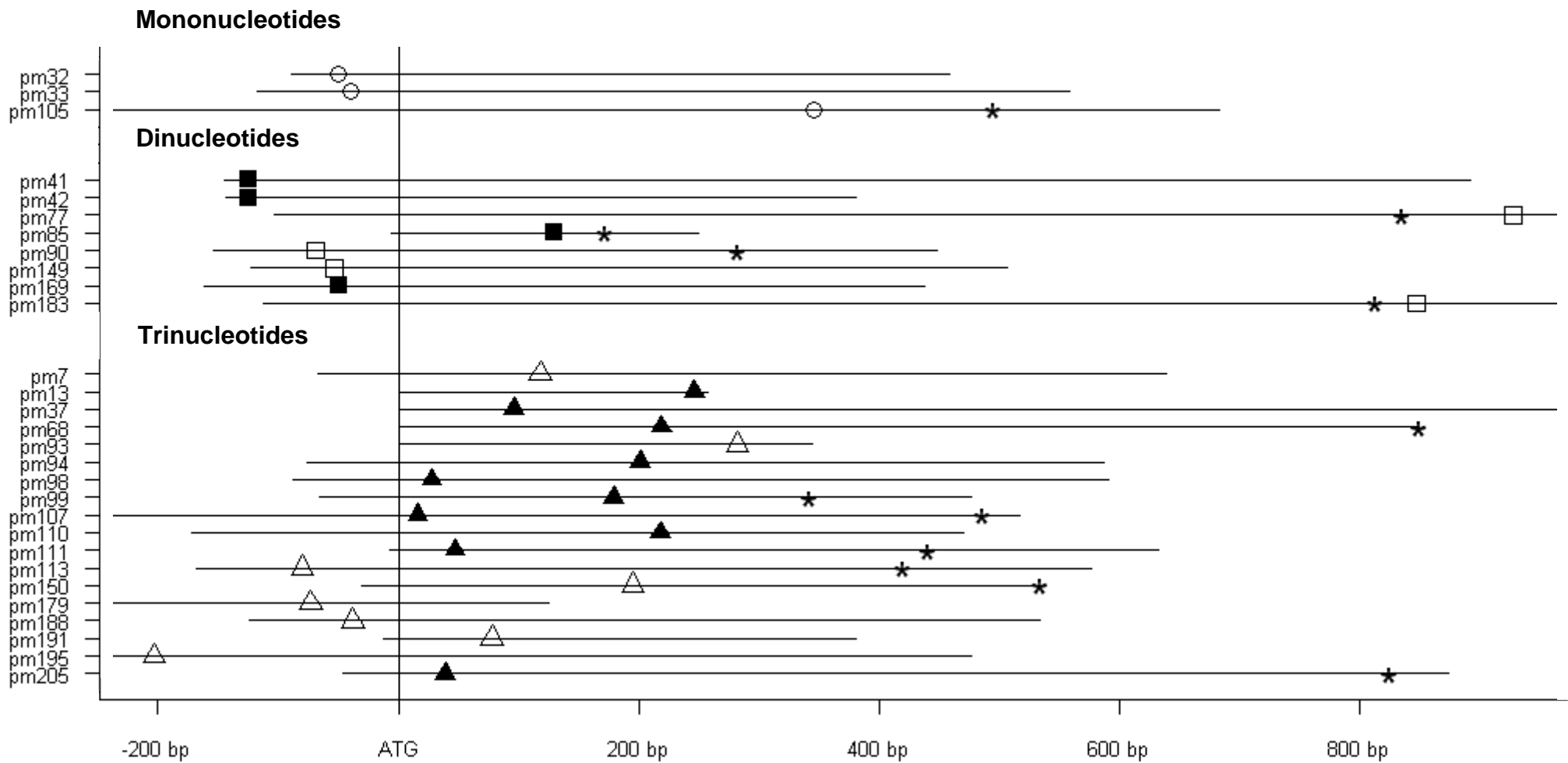


Fig. S2

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
13a14	EXPA	chr	2 cm	57					SL2.10ch01	85.97	563	77	2	1	561	79520416	79519854	8.00E-132	474
3kat	EXPA	chr	6 cm	8.7					SL2.10ch09	85.39	438	60	4	404	837	56063292	56062855	1.00E-87	329
adh1	EXPA	chr	4 cm	38.8					SL2.10ch04	93.81	97	6	0	150	246	54959423	54959519	1.00E-32	145
adh2	EXPA	chr	3 cm	86.4	AXIN	chr	3 cm	51	SL2.10ch06	89.77	352	35	1	52	402	33989619	33989970	1.00E-110	404
aldh1	EXPA	chr	3 cm	66.5					SL2.10ch03	94.27	157	9	0	9	165	58041780	58041936	5.00E-61	240
aldh2b	EXPA	chr	3 cm	63.5					SL2.10ch03	85.39	178	25	1	193	369	58040271	58040448	7.00E-41	171
an1	EXPA	chr	6 cm	7.2					SL2.10ch09	90.61	245	23	0	323	567	58552537	58552781	7.00E-80	303
an11	EXPA	chr	3 cm	84.1					SL2.10ch03	84.8	204	31	0	337	540	52934186	52934389	5.00E-37	159
an2	EXPA	chr	6 cm	3.2	AXIN	chr	6 cm	0.6	SL2.10ch10	88.55	131	15	0	130	260	64333512	64333382	2.00E-31	141
an4					AXIN	chr	7 cm	19.1	SL2.10ch10	88.49	139	16	0	386	524	64333519	64333381	1.00E-33	149
bsmt1	EXPA	chr	5 cm	0					SL2.10ch09	86.59	164	22	0	1389	1552	66152809	66152972	4.00E-34	151
bsmt2	EXPA	chr	5 cm	0					SL2.10ch09	86.59	164	22	0	689	852	66152809	66152972	2.00E-34	151
c4h1	EXPA	chr	3 cm	129.6					SL2.10ch06	93.18	88	6	0	592	679	44616951	44617038	2.00E-27	127
c4h1b	EXPA	chr	6 cm	0					SL2.10ch06	87.38	103	13	0	9	111	44617042	44616940	2.00E-19	101
ccl	EXPA	chr	1 cm	47.3	AXIN	chr	1 cm	120.9	SL2.10ch06	82.63	501	84	1	31	528	38947682	38947182	4.00E-79	299
chia	EXPA	chr	5 cm	42.7	AXIN	chr	5 cm	63.6	SL2.10ch05	85.24	210	31	0	264	473	4460299	4460508	2.00E-40	170
chs	EXPA	chr	5 cm	55.9					SL2.10ch06	83.21	280	47	0	286	565	26045622	26045343	4.00E-44	182
crc	EXPA	chr	1 cm	1.2	AXIN	chr	1 cm	34.1	SL2.10ch05	86.36	110	15	0	73	182	5271662	5271553	4.00E-19	99.6
egs	EXPA	chr	4 cm	38.8					SL2.10ch04	88.44	147	17	0	4	150	62267869	62268015	4.00E-36	157
epf1	EXPA	chr	3 cm	93.4	AXIN	chr	3 cm	124.5	SL2.10ch06	92.22	90	5	2	440	527	42719664	42719575	2.00E-21	107
f3h	EXPA	chr	4 cm	38.8					SL2.10ch02	91.8	61	5	0	2	62	41694040	41693980	1.00E-13	81.8
fls	EXPA	chr	2 cm	15	AXIN	chr	2 cm	43.3	SL2.10ch11	89.25	279	30	0	1521	1799	5965607	5965885	2.00E-83	315
gt	EXPA	chr	5 cm	42.7	AXIN	chr	5 cm	64.2	SL2.10ch12	85.4	322	41	2	1	316	64333485	64333806	1.00E-56	224
hf1	EXPA	chr	1 cm	16	AXIN	chr	1 cm	70.6	SL2.10ch11	84.73	609	93	0	3722	4330	49391581	49392189	9.00E-130	470
igs	EXPA	chr	2 cm	13.2					SL2.10ch06	89.58	48	5	0	341	388	37871197	37871244	8.00E-06	56
myb109	EXPA	chr	3 cm	45.7					SL2.10ch03	85.07	134	17	1	173	306	62150686	62150556	4.00E-20	103
myb111	EXPA	chr	3 cm	84.8					SL2.10ch06	88.24	102	12	0	431	532	43404680	43404579	3.00E-21	107
myb14	EXPA	chr	2 cm	31.7	AXIN	chr	2 cm	43.9	SL2.10ch05	91.18	136	12	0	364	499	58682315	58682180	4.00E-42	176
myb58	EXPA	chr	2 cm	13.6					SL2.10ch10	90.24	82	8	0	228	309	455798	455717	6.00E-19	99.6
myb60	EXPA	chr	4 cm	61.7					SL2.10ch02	85.81	155	19	1	288	439	44755778	44755932	5.00E-28	129
myb75	EXPA	chr	3 cm	85.6					SL2.10ch05	83.74	123	17	1	336	455	61978917	61979039	9.00E-14	81.8
mybb	EXPA	chr	7 cm	56.6	AXIN	chr	7 cm	19.1	SL2.10ch10	88.04	92	11	0	81	172	64355483	64355574	2.00E-17	95.6
mybph3prot1	EXPA	chr	4 cm	59.7					SL2.10ch02	93.38	136	9	0	139	274	44911145	44911280	1.00E-48	198
mybph3prot2	EXPA	chr	5 cm	31.7					SL2.10ch09	88.39	155	15	1	5	159	65032694	65032845	1.00E-37	161
mybph3prot3	EXPA	chr	2 cm	44.7					SL2.10ch12	88.14	59	7	0	479	537	530139	530081	9.00E-08	61.9
odo1	EXPA	chr	7 cm	59.5	AXIN	chr	7 cm	133.9	SL2.10ch08	87.44	223	28	0	513	735	60106519	60106741	4.00E-55	220
paas2	EXPA	chr	2 cm	64.8					SL2.10ch03	85.93	405	57	0	109	513	15183423	15183019	4.00E-82	309
pal1	EXPA	chr	2 cm	39.9					SL2.10ch05	90.59	85	7	1	490	573	64726545	64726629	2.00E-18	97.6
pal2	EXPA	chr	7 cm	56.6					SL2.10ch09	91.14	429	37	1	1701	2128	1416695	1416267	1.00E-151	541
pm101	EXPA	chr	1 cm	15					SL2.10ch04	89.93	149	13	2	170	317	57691001	57691148	3.00E-37	161
pm103	EXPA	chr	7 cm	63.4					SL2.10ch10	87.32	205	25	1	272	475	60418095	60417891	4.00E-47	192
pm105	EXPA	chr	6 cm	89.5	AXIN	chr	6 cm	113.3	SL2.10ch01	85	240	36	0	308	547	89108595	89108834	3.00E-46	190
pm106	EXPA	chr	6 cm	59.9	AXIN	chr	6 cm	33.8	SL2.10ch01	86.01	143	20	0	176	318	89050714	89050572	8.00E-27	125
pm107					AXIN	chr	4 cm	82.7	SL2.10ch04	85.93	263	37	0	580	842	62428564	62428826	1.00E-57	228
pm110	EXPA	chr	5 cm	8.3	AXIN	chr	5 cm	50.8	SL2.10ch09	88.49	252	29	0	142	393	65879764	65880015	2.00E-70	270
pm111					AXIN	chr	2 cm	34.1	SL2.10ch07	87.39	119	15	0	276	394	61926939	61927057	2.00E-24	117
pm113	EXPA	chr	2 cm	13.4					SL2.10ch05	87.38	103	13	0	144	246	62972085	62972187	1.00E-19	101
pm114					AXIN	chr	5 cm	65.5	SL2.10ch07	87.5	64	8	0	331	394	164728	164791	3.00E-08	63.9

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	
pm117	EXPA	chr	6 cm	73.4	AXIN	chr	6 cm	73.1	SL2.10ch01	82.78	209	30	1	289	491	89858699	89858491	1.00E-28	131
pm119	EXPA	chr	2 cm	107					SL2.10ch08	80.3	335	66	0	293	627	84346	84012	1.00E-31	141
pm12	EXPA	chr	3 cm	89.7					SL2.10ch04	88.75	80	9	0	1	80	40995336	40995415	2.00E-15	87.7
pm124	EXPA	chr	2 cm	14.6					SL2.10ch02	95.45	44	2	0	40	83	32364516	32364559	1.00E-10	71.9
pm13					AXIN	chr	2 cm	31.2	SL2.10ch07	87.39	119	15	0	246	364	61927057	61926939	2.00E-24	117
pm132					AXIN	chr	6 cm	0	SL2.10ch01	87.18	117	15	0	183	299	69609671	69609555	4.00E-23	113
pm134	EXPA	chr	2 cm	0					SL2.10ch05	89.41	510	54	0	711	1220	64643372	64643881	2.00E-164	583
pm142					AXIN	chr	2 cm	41	SL2.10ch07	97.5	40	1	0	526	565	10028249	10028210	1.00E-10	71.9
pm144	EXPA	chr	7 cm	56.6	AXIN	chr	7 cm	128.7	SL2.10ch08	87.88	99	12	0	369	467	42761712	42761810	1.00E-19	101
pm149	EXPA	chr	1 cm	7.5					SL2.10ch11	91.58	95	8	0	362	456	4925928	4925834	9.00E-27	125
pm15	EXPA	chr	1 cm	6.1					SL2.10ch09	90	70	7	0	64	133	49390219	49390150	2.00E-14	83.8
pm150	EXPA	chr	5 cm	56.5					SL2.10ch12	84.78	230	35	0	298	527	250859	250630	6.00E-43	178
pm155	EXPA	chr	4 cm	38.2					SL2.10ch04	92.11	114	9	0	290	403	59933573	59933460	7.00E-36	155
pm157	EXPA	chr	7 cm	56.6	AXIN	chr	7 cm	131.6	SL2.10ch08	94.48	290	16	0	304	593	59658369	59658658	5.00E-124	448
pm164					AXIN	chr	1 cm	145.7	SL2.10ch06	90.75	346	29	1	407	752	36392027	36392369	5.00E-118	428
pm165	EXPA	chr	2 cm	165.6					SL2.10ch08	84.81	362	55	0	476	837	2919317	2919678	9.00E-74	281
pm166					AXIN	chr	4 cm	82.1	SL2.10ch03	100	31	0	0	603	633	64444201	64444171	1.00E-07	61.9
pm167	EXPA	chr	5 cm	56.5					SL2.10ch12	89.74	117	12	0	505	621	47457651	47457767	3.00E-20	103
pm169	EXPA	chr	1 cm	19.5					SL2.10ch06	85.36	239	32	1	344	579	32238385	32238623	4.00E-47	192
pm17	EXPA	chr	6 cm	7.8					SL2.10ch09	87.3	126	13	2	301	426	59179010	59178888	4.00E-22	109
pm173	EXPA	chr	4 cm	36.3					SL2.10ch02	93.46	107	7	0	565	671	33978684	33978790	6.00E-36	157
pm177					AXIN	chr	5 cm	91.9	SL2.10ch12	90.43	94	9	0	454	547	1539159	1539066	8.00E-24	115
pm179	EXPA	chr	5 cm	52.6					SL2.10ch12	96	50	2	0	324	373	5294387	5294436	2.00E-14	83.8
pm183	EXPA	chr	3 cm	34.5	AXIN	chr	3 cm	0	SL2.10ch03	85.37	287	42	0	585	871	63393405	63393691	6.00E-60	236
pm186					AXIN	chr	2 cm	0	SL2.10ch08	87.9	281	34	0	942	1222	39856371	39856091	2.00E-75	287
pm187	EXPA	chr	4 cm	36.8					SL2.10ch09	90.14	71	7	0	511	581	4957706	4957636	9.00E-15	85.7
pm188	EXPA	chr	1 cm	26.1	AXIN	chr	1 cm	97.3	SL2.10ch06	92.44	119	9	0	121	239	40335388	40335270	1.00E-38	165
pm190	EXPA	chr	2 cm	34.6	AXIN	chr	2 cm	86.9	SL2.10ch07	86.78	174	23	0	227	400	23720300	23720127	5.00E-38	163
pm191	EXPA	chr	3 cm	87.4	AXIN	chr	3 cm	61.6	SL2.10ch03	94.44	36	2	0	312	347	7006283	7006318	4.00E-06	56
pm192	EXPA	chr	5 cm	112.5	AXIN	chr	5 cm	150.2	SL2.10ch04	89.33	225	24	0	92	316	56323088	56323312	4.00E-66	256
pm195	EXPA	chr	1 cm	3.4					SL2.10ch05	88.75	160	18	0	287	446	2887673	2887514	1.00E-41	174
pm197					AXIN	chr	3 cm	43.8	SL2.10ch03	84.98	273	41	0	22	294	46232287	46232015	3.00E-54	216
pm200					AXIN	chr	2 cm	24	SL2.10ch06	88.29	111	11	1	121	231	36512733	36512625	1.00E-22	111
pm202					AXIN	chr	2 cm	45.8	SL2.10ch10	86.78	227	30	0	638	864	76946	77172	7.00E-53	212
pm205	EXPA	chr	2 cm	13.2					SL2.10ch07	85.84	219	31	0	324	542	1885445	1885227	1.00E-45	188
pm206	EXPA	chr	4 cm	38.8					SL2.10ch02	88.17	93	11	0	315	407	32915390	32915298	1.00E-18	97.6
pm208	EXPA	chr	7 cm	56.6					SL2.10ch10	85.37	123	18	0	78	200	61404994	61404872	8.00E-20	101
pm21	EXPA	chr	2 cm	14.8					SL2.10ch02	90.54	148	14	0	268	415	32162218	32162365	4.00E-44	182
pm210	EXPA	chr	5 cm	37.2					SL2.10ch09	90.91	132	12	0	284	415	65560528	65560659	2.00E-39	167
pm218	EXPA	chr	4 cm	38.8					SL2.10ch10	83.25	197	33	0	182	378	62074719	62074915	1.00E-28	131
pm219	EXPA	chr	3 cm	90.9					SL2.10ch06	95.29	85	4	0	218	302	45031168	45031084	2.00E-30	137
pm32	EXPA	chr	2 cm	102	AXIN	chr	2 cm	177	SL2.10ch08	80.67	357	67	2	143	498	967024	966669	8.00E-33	145
pm33	EXPA	chr	7 cm	56.6					SL2.10ch12	86	100	14	0	569	668	3057159	3057060	2.00E-15	87.7
pm37	EXPA	chr	1 cm	16					SL2.10ch02	87.9	248	30	0	594	841	39747991	39748238	2.00E-65	254
pm40	EXPA	chr	4 cm	38.8					SL2.10ch09	91.76	85	7	0	541	625	2357778	2357862	4.00E-23	113
pm41					AXIN	chr	1 cm	86.5	SL2.10ch01	89.11	101	11	0	677	777	311352	311452	7.00E-23	113
pm44	EXPA	chr	5 cm	58.9	AXIN	chr	5 cm	64.2	SL2.10ch12	90.62	128	12	0	837	964	64855374	64855501	1.00E-36	159
pm54	EXPA	chr	7 cm	57.3					SL2.10ch08	91.38	58	5	0	185	242	55893322	55893265	3.00E-12	75.8

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 x P. parodii</i> map				<i>P. axillaris x 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