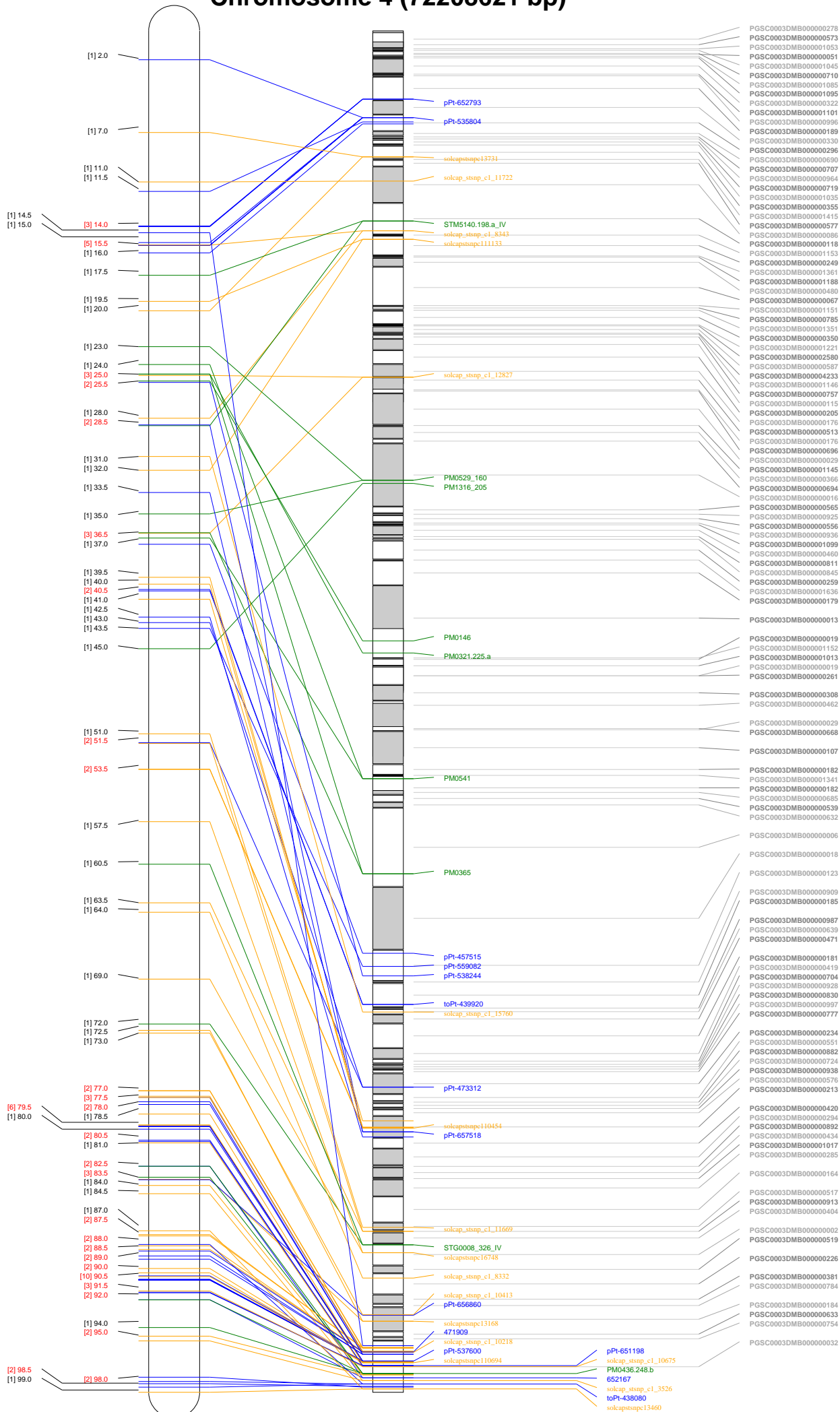
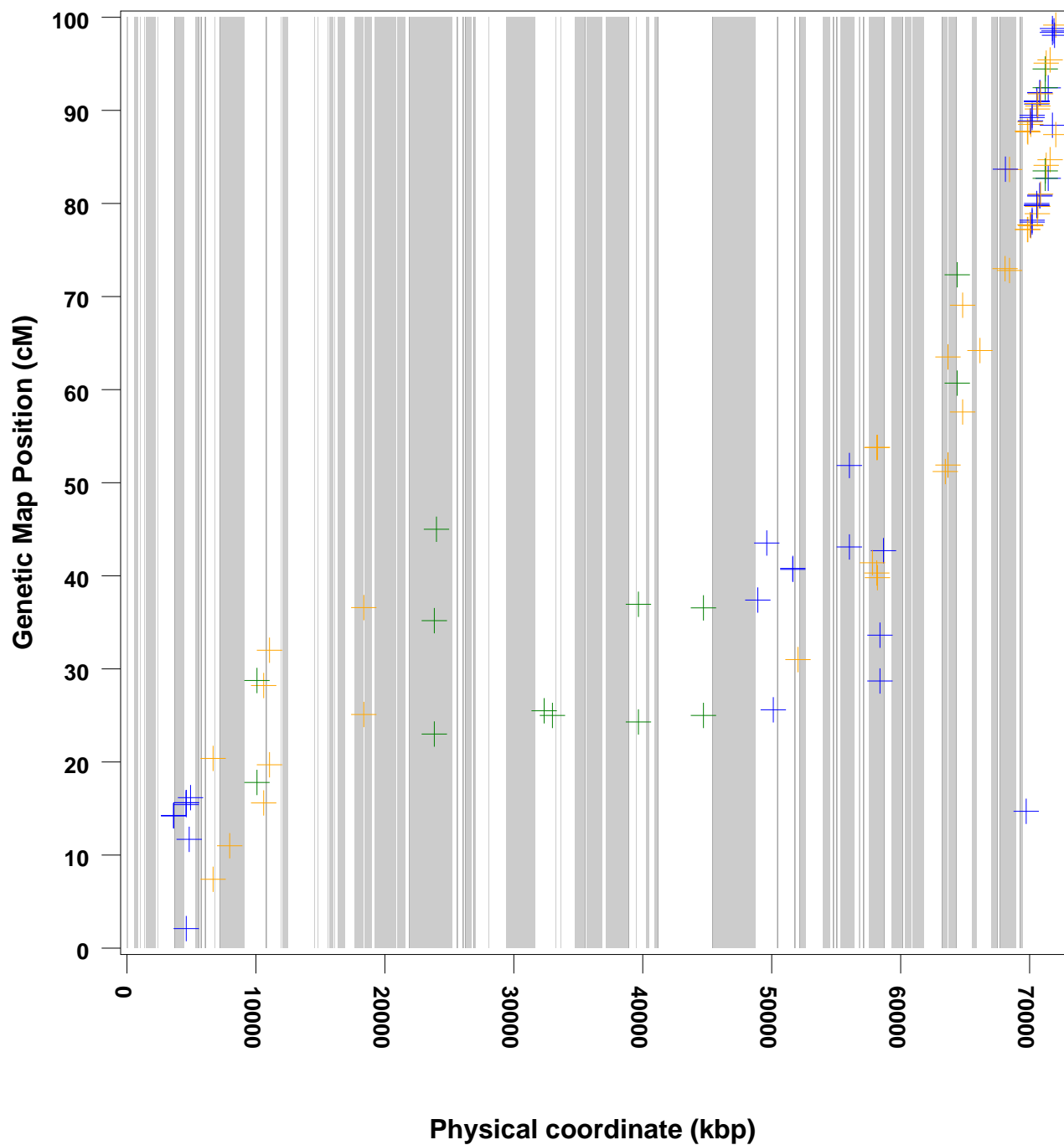


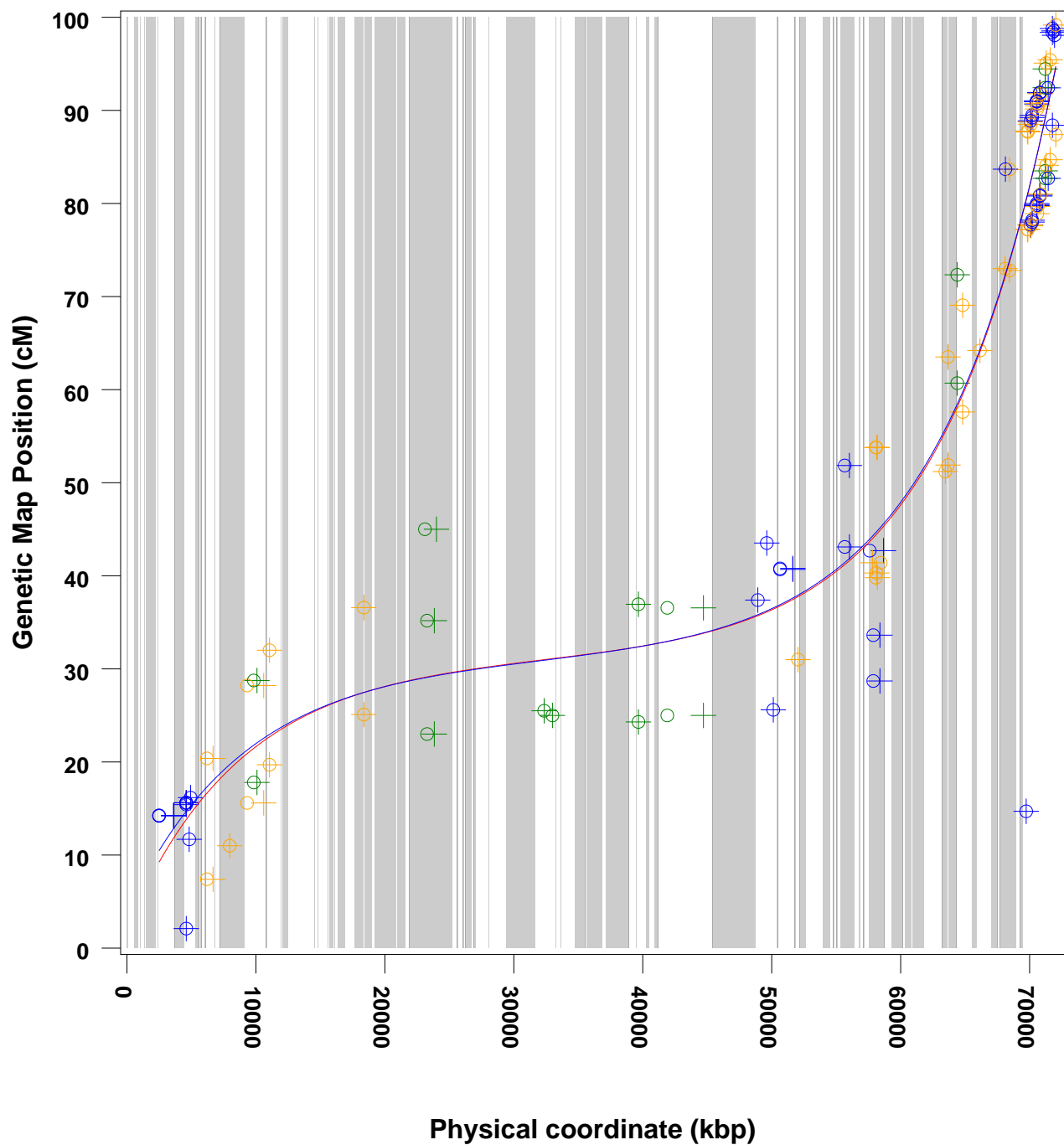
## Chromosome 4 (72208621 bp)



Chromosome 4 correlation plot



Chromosome 4 correlation plot



## Report for Chromosome 4

	Mean Square Error	Mean Error	a	b	c	d
Initial Fit	4.496e+03	6.070e+01	3.100e+01	1.535e+00	4.494e-01	8.065e+00
Optimal Fit	4.496e+03	6.070e+01	3.088e+01	1.600e+00	4.441e-01	7.911e+00

Scaffold	Start	Length	Markers	Strand	Mean Square Error	Mean Error
PGSC0003DMB000000278 _0	1	48001	0	-	-	-
PGSC0003DMB000000051 _0	98002	433607	0	-	-	-
PGSC0003DMB0000000573 _0	581609	299337	0	-	-	-
PGSC0003DMB0000001053 _0	930946	34673	0	-	-	-
PGSC0003DMB0000001045 _0	1015619	35869	0	-	-	-
PGSC0003DMB0000000710 _0	1101488	183259	0	-	-	-
PGSC0003DMB0000001085 _0	1334747	30427	0	-	-	-
PGSC0003DMB0000001095 _0	1415174	29436	0	-	-	-
PGSC0003DMB0000000322 _0	1494610	734594	0	-	-	-
PGSC0003DMB0000001101 _0	2279204	28907	0	-	-	-
PGSC0003DMB0000000996 _0	2358111	44861	0	-	-	-
PGSC0003DMB0000000189 _0	2452972	1202211	3	forward	1.399e+02	1.183e+01
		inverted		reverse	1.096e+02	1.047e+01
PGSC0003DMB0000000330 _0	3705183	706898	0	-	-	-
PGSC0003DMB0000000296 _0	4462081	827814	8	forward	1.947e+02	1.395e+01
PGSC0003DMB0000000690 _0	5339895	198409	0	-	-	-
PGSC0003DMB0000000707 _0	5588304	63669	0	-	-	-
PGSC0003DMB0000000964 _0	5701973	50770	0	-	-	-
PGSC0003DMB0000000719 _0	5802743	178835	0	-	-	-
PGSC0003DMB0000001035 _0	6031578	37370	0	-	-	-
PGSC0003DMB0000000355 _0	6118948	640809	2	forward	3.027e+02	1.740e+01
		inverted		reverse	2.997e+02	1.731e+01
PGSC0003DMB0000001415 _0	6809757	11656	0	-	-	-
PGSC0003DMB0000000577 _0	6871413	295252	0	-	-	-
PGSC0003DMB0000000086 _0	7216665	1881773	1	forward	3.699e+02	1.923e+01
PGSC0003DMB0000000118 _0	9148438	1621203	4	forward	4.840e+02	2.200e+01
		inverted		reverse	4.640e+02	2.154e+01
PGSC0003DMB0000001153 _0	10819641	23846	0	-	-	-
PGSC0003DMB0000000249 _0	10893487	983285	2	forward	5.153e+02	2.270e+01
PGSC0003DMB0000001361 _0	11926772	13537	0	-	-	-
PGSC0003DMB0000001188 _0	11990309	22044	0	-	-	-
PGSC0003DMB0000000480 _0	12062353	419894	0	-	-	-
PGSC0003DMB0000000067 _0	12532247	1974816	0	-	-	-
PGSC0003DMB0000001151 _0	14557063	24084	0	-	-	-

Scaffold	Start	Length	Markers	Strand	Mean Square Error	Mean Error
PGSC0003DMB000000785 _0	14631147	125787	0	-	-	-
PGSC0003DMB0000001351 _0	14806934	13936	0	-	-	-
PGSC0003DMB0000000350 _0	14870870	653514	0	-	-	-
PGSC0003DMB0000001221 _0	15574384	20232	0	-	-	-
PGSC0003DMB0000002580 _0	15644616	1569	0	-	-	-
PGSC0003DMB0000000587 _0	15696185	284688	0	-	-	-
PGSC0003DMB0000004233 _0	16030873	848	0	-	-	-
PGSC0003DMB0000001146 _0	16081721	24563	0	-	-	-
PGSC0003DMB0000000757 _0	16156284	148404	0	-	-	-
PGSC0003DMB0000000115 _0	16354688	554200	0	-	-	-
PGSC0003DMB0000000205 _0	16958888	685448	0	-	-	-
PGSC0003DMB0000000176 _0	17694336	587707	2	forward	7.542e+02	2.746e+01
PGSC0003DMB0000000513 _0	18332043	16231	0	-	-	-
PGSC0003DMB0000000176 _1	18398274	556909	0	-	-	-
PGSC0003DMB0000000696 _0	19005183	193979	0	-	-	-
PGSC0003DMB0000000029 _0	19249162	1617400	0	-	-	-
PGSC0003DMB0000001145 _0	20916562	24615	0	-	-	-
PGSC0003DMB0000000366 _0	20991177	618486	0	-	-	-
PGSC0003DMB0000000694 _0	21659663	194925	0	-	-	-
PGSC0003DMB0000000016 _0	21904588	3297897	3	forward	8.587e+02	2.930e+01
		inverted		reverse	8.452e+02	2.907e+01
PGSC0003DMB0000000565 _0	25252485	302738	0	-	-	-
PGSC0003DMB0000000925 _0	25605223	58541	0	-	-	-
PGSC0003DMB0000000556 _0	25713764	311949	0	-	-	-
PGSC0003DMB0000000936 _0	26075713	56254	0	-	-	-
PGSC0003DMB0000001099 _0	26181967	29165	0	-	-	-
PGSC0003DMB0000000460 _0	26261132	453641	0	-	-	-
PGSC0003DMB0000000811 _0	26764773	107875	0	-	-	-
PGSC0003DMB0000000845 _0	26922648	86923	0	-	-	-
PGSC0003DMB0000000259 _0	27059571	953395	0	-	-	-
PGSC0003DMB0000001636 _0	28062966	5555	0	-	-	-
PGSC0003DMB0000000179 _0	28118521	1261821	0	-	-	-
PGSC0003DMB0000000013 _0	29430342	2222458	0	-	-	-
PGSC0003DMB0000000019 _0	31702800	1491765	2	forward	9.637e+02	3.104e+01
PGSC0003DMB0000001152 _0	33244565	23988	0	-	-	-
PGSC0003DMB0000000019 _1	33318553	282481	0	-	-	-
PGSC0003DMB0000001013 _0	33651034	41012	0	-	-	-
PGSC0003DMB0000000261 _0	33742046	927429	0	-	-	-

Scaffold	Start	Length	Markers	Strand	Mean Square Error	Mean Error
PGSC0003DMB000000308 _0	34719475	777274	0	-	-	-
PGSC0003DMB000000462 _0	35546749	70922	0	-	-	-
PGSC0003DMB000000029 _1	35667671	1181844	0	-	-	-
PGSC0003DMB000000668 _0	36899515	213131	0	-	-	-
PGSC0003DMB000000107 _0	37162646	1707067	0	-	-	-
PGSC0003DMB000000182 _0	38919713	509922	0	-	-	-
PGSC0003DMB0000001341 _0	39479635	14368	0	-	-	-
PGSC0003DMB000000182 _1	39544003	697895	2	forward	1.048e+03	3.238e+01
PGSC0003DMB000000685 _0	40291898	201548	0	-	-	-
PGSC0003DMB000000539 _0	40543446	337557	0	-	-	-
PGSC0003DMB000000632 _0	40931003	246125	0	-	-	-
PGSC0003DMB000000006 _0	41227128	4153083	2	forward	1.144e+03	3.382e+01
		inverted		reverse	1.086e+03	3.295e+01
PGSC0003DMB000000018 _0	45430211	3280928	0	-	-	-
PGSC0003DMB000000123 _0	48761139	1603874	3	forward	1.302e+03	3.608e+01
PGSC0003DMB000000909 _0	50415013	62784	0	-	-	-
PGSC0003DMB000000185 _0	50527797	1228324	2	forward	1.403e+03	3.745e+01
		inverted		reverse	1.361e+03	3.690e+01
PGSC0003DMB000000987 _0	51806121	46844	0	-	-	-
PGSC0003DMB000000639 _0	51902965	236815	1	forward	1.426e+03	3.776e+01
PGSC0003DMB000000471 _0	52189780	434327	0	-	-	-
PGSC0003DMB000000181 _0	52674107	1256539	0	-	-	-
PGSC0003DMB000000419 _0	53980646	520326	0	-	-	-
PGSC0003DMB000000704 _0	54550972	188311	0	-	-	-
PGSC0003DMB000000928 _0	54789283	57889	0	-	-	-
PGSC0003DMB000000830 _0	54897172	93880	0	-	-	-
PGSC0003DMB000000997 _0	55041052	44651	0	-	-	-
PGSC0003DMB000000777 _0	55135703	131888	0	-	-	-
PGSC0003DMB000000234 _0	55317591	1048121	2	forward	1.732e+03	4.162e+01
		inverted		reverse	1.716e+03	4.142e+01
PGSC0003DMB000000551 _0	56415712	317501	0	-	-	-
PGSC0003DMB000000882 _0	56783213	70569	0	-	-	-
PGSC0003DMB000000724 _0	56903782	173674	0	-	-	-
PGSC0003DMB000000938 _0	57127456	55901	0	-	-	-
PGSC0003DMB000000576 _0	57233357	295815	0	-	-	-
PGSC0003DMB000000213 _0	57579172	1107634	8	forward	1.993e+03	4.464e+01
		inverted		reverse	1.987e+03	4.457e+01
PGSC0003DMB000000420 _0	58736806	516866	0	-	-	-

Scaffold	Start	Length	Markers	Strand	Mean Square Error	Mean Error
PGSC0003DMB000000294 _0	59303672	837082	0	-	-	-
PGSC0003DMB000000892 _0	60190754	68122	0	-	-	-
PGSC0003DMB000000434 _0	60308876	492488	0	-	-	-
PGSC0003DMB0000001017 _0	60851364	40536	0	-	-	-
PGSC0003DMB000000285 _0	60941900	852987	0	-	-	-
PGSC0003DMB000000164 _0	61844887	1333923	0	-	-	-
PGSC0003DMB000000517 _0	63228810	363216	1	forward	3.077e+03	5.548e+01
PGSC0003DMB000000913 _0	63642026	62299	2	forward	3.141e+03	5.605e+01
PGSC0003DMB000000404 _0	63754325	538315	0	-	-	-
PGSC0003DMB000000002 _0	64342640	1117982	4	forward	3.457e+03	5.880e+01
PGSC0003DMB000000519 _0	65510622	362340	0	-	-	-
PGSC0003DMB000000226 _0	65922962	1073400	1	forward	4.103e+03	6.405e+01
PGSC0003DMB000000381 _0	67046362	446652	0	-	-	-
PGSC0003DMB000000784 _0	67543014	126254	0	-	-	-
PGSC0003DMB000000184 _0	67719268	1231615	4	forward	5.319e+03	7.292e+01
PGSC0003DMB000000633 _0	69000883	245990	0	-	-	-
PGSC0003DMB000000754 _0	69296873	150518	0	-	-	-
PGSC0003DMB000000032 _0	69497391	2711231	58	forward	7.476e+03	8.638e+01

Molecule	Assembly order	Map order	Difference
PGSC0003DMB000000189 _	1	4	3
PGSC0003DMB000000296 _	2	2	-
PGSC0003DMB000000355 _	3	3	-
PGSC0003DMB000000086 _	4	1	-3
PGSC0003DMB000000118 _	5	5	-
PGSC0003DMB000000249 _	6	7	1
PGSC0003DMB000000176 _	8	9	1
PGSC0003DMB000000016 _	9	11	2
PGSC0003DMB000000019 _	11	6	-5
PGSC0003DMB000000006 _	12	8	-4
PGSC0003DMB000000123 _	13	12	-1
PGSC0003DMB000000185 _	14	13	-1
PGSC0003DMB000000639 _	15	10	-5
PGSC0003DMB000000234 _	16	15	-1
PGSC0003DMB000000213 _	17	14	-3
PGSC0003DMB000000517 _	18	16	-2

Molecule	Assembly order	Map order	Difference
PGSC0003DMB000000913 _	19	17	-2
PGSC0003DMB000000002 _	20	19	-1
PGSC0003DMB000000226 _	21	18	-3
PGSC0003DMB000000184 _	22	20	-2
PGSC0003DMB000000032 _	23	21	-2

Marker	sequence position	map position	calculated fit	error
pPt-539955	69734450bp	14.701	80.344	65.643
657518	58394528bp	28.7	44.871	16.171
PM1316_205	24001939bp	45.001	29.331	15.670
STG0008_326_IV	64387747bp	72.340	58.145	14.195
440837	4598950bp	2.1	13.820	11.720
pPt-656860	68123508bp	83.683	72.215	11.468
pPt-657518	58394528bp	33.623	44.871	11.248
pPt-538244	50122836bp	25.604	36.420	10.816
pPt-473312	56023947bp	51.850	41.623	10.227
solcap_stsnp_c1_3731	6679700bp	7.4	17.399	9.999
solcapstsnpc13168	68440006bp	83.651	73.699	9.952
solcapstsnpc16748	64806237bp	69.068	59.446	9.622
solcapstsnpc111133	11053592bp	32.005	22.701	9.304
solcapstsnpc110441	58148643bp	53.782	44.493	9.289
solcapstsnpc110454	58197792bp	53.795	44.567	9.228
solcapstsnpc112827	18365274bp	36.585	27.463	9.122
PM0365.144.a	44705440bp	25.0	33.825	8.825
solcap_stsnp_c1_1172 2	7966263bp	11.0	19.233	8.233
PM0541.188.a	39663159bp	24.3	32.379	8.079
652167	71441736bp	82.7	90.713	8.013
solcapstsnpc111679	63668823bp	63.511	56.048	7.463
pPt-559082	49617143bp	43.522	36.110	7.412
solcap_stsnp_c1_3460	72029679bp	87.4	94.766	7.366
STM5140_198_IV	10082273bp	28.753	21.734	7.019
solcap_stsnp_c1_3526	71589141bp	84.7	91.704	7.004
solcapstsnpc14111	69829741bp	87.775	80.872	6.903
solcap_stsnp_c1_1576 0	52037580bp	31.0	37.757	6.757
solcapstsnpc110207	70032061bp	88.764	82.012	6.752



Marker	sequence position	map position	calculated fit	error
pPt-471909	70066825bp	88.876	82.210	6.666
solcap_stsnp_c1_8343	10602553bp	15.6	22.265	6.665
solcapstsnpc14179	69865290bp	87.678	81.070	6.608
pPt-458171	70194882bp	89.472	82.948	6.524
PM0436.248.b	71213513bp	82.7	89.209	6.509
solcap_stsnp_c1_1071 0	70600460bp	78.9	85.356	6.456
PM0529.160.a	23834723bp	23.0	29.289	6.289
pPt-458391	70194882bp	89.235	82.948	6.287
solcapstsnpc110218	70090159bp	88.499	82.344	6.155
PM0321.225.a	32995595bp	25.0	31.098	6.098
solcapstsnpc18343	10602553bp	28.214	22.265	5.949
solcap_stsnp_c1_1069 4	70642405bp	79.7	85.612	5.912
pPt-456750	70555749bp	90.986	85.085	5.901
pPt-471670	70555749bp	90.985	85.085	5.900
pPt-457379	70555749bp	90.984	85.085	5.899
pPt-540321	70555749bp	90.982	85.085	5.897
pPt-539574	70555754bp	90.982	85.085	5.897
PM0529_160	23834723bp	35.183	29.289	5.894
solcap_stsnp_c1_1067 5	70849355bp	81.0	86.889	5.889
pPt-655705	70555749bp	90.954	85.085	5.869
pPt-537600	70555749bp	90.954	85.085	5.869
toPt-438080	71768395bp	98.792	92.932	5.860