

Additional file 1. Discordances between optical map and IRGSP sequence data**

Type of Discordances	Ch.	Start	End	Note
False_cut_on_optical_map	1	7649	7649	
False_cut_on_optical_map	1	20441464	20441464	
False_cut_on_optical_map	1	33025086	33025086	
False_cut_on_optical_map	1	29037434	29037434	
False_cut_on_optical_map	2	30044649	30044649	
False_cut_on_optical_map	3	12750657	12750657	
False_cut_on_optical_map	3	23522890	23522890	
False_cut_on_optical_map	3	33298465	33298465	
False_cut_on_optical_map	3	33826497	33826497	
False_cut_on_optical_map	4	4889434	4889434	
False_cut_on_optical_map	4	7086257	7086257	
False_cut_on_optical_map	4	27282914	27282914	
False_cut_on_optical_map	4	33183113	33183113	
False_cut_on_optical_map	4	33838933	33838933	
False_cut_on_optical_map	5	3529018	3529018	
False_cut_on_optical_map	5	9061417	9061417	
False_cut_on_optical_map	5	12240898	12240898	
False_cut_on_optical_map	5	15370306	15370306	
False_cut_on_optical_map	6	31922257	31922257	
False_cut_on_optical_map	6	17220206	17220206	
False_cut_on_optical_map	6	19317748	19317748	
False_cut_on_optical_map	6	12115279	12115279	
False_cut_on_optical_map	6	599847	599847	
False_cut_on_optical_map	7	4977698	4977698	
False_cut_on_optical_map	7	22673514	22673514	
False_cut_on_optical_map	7	23069905	23069905	
False_cut_on_optical_map	7	24515294	24515294	
False_cut_on_optical_map	9	4557176	4557176	
False_cut_on_optical_map	9	8295949	8295949	
False_cut_on_optical_map	9	9304258	9304258	
False_cut_on_optical_map	9	17874388	17874388	
False_cut_on_optical_map	9	19388949	19388949	
False_cut_on_optical_map	10	2875048	2875048	
False_cut_on_optical_map	10	6145612	6145612	
False_cut_on_optical_map	10	14105517	14105517	
False_cut_on_optical_map	10	16852166	16852166	
False_cut_on_optical_map	11	4982368	4982368	
False_cut_on_optical_map	11	10104787	10104787	
False_cut_on_optical_map	11	10128808	10128808	
False_cut_on_optical_map	11	11233356	11233356	
False_cut_on_optical_map	11	11710627	11710627	
False_cut_on_optical_map	11	21026963	21026963	
False_cut_on_optical_map	11	25079852	25079852	
False_cut_on_optical_map	11	29913977	29913977	
False_cut_on_optical_map	12	3786230	3786230	
False_cut_on_optical_map	12	18101121	18101121	
Gap_calling	1	36685440	36685440	16.21 kb insertion
Gap_calling	1	42925901	42925901	7.69 kb insertion validated
Gap_calling	1	19091351	19091351	op16.44kb_seq11.20kb
Gap_calling	1	33565707	33579930	Seq14.22kb_op18.16kb
Gap_calling	1	31506087	31533122	Seq_27.04kb_op34.30kb
Gap_calling	2	19238457	19270565	op37.65kb_seq32.11 kb
Gap_calling	2	11919828	11943528	Seq_23.70kb_op30.03kb
Gap_calling	3	14336730	14336730	3_fragments_inserted_7.17+22.79+20.15kb
Gap_calling	3	14808219	14816154	Seq7.94kb_op9.64kb**
Gap_calling	3	17596955	17645390	seq48.44kb_op56.36kb
Gap_calling	3	27180113	27191258	seq11.14kb_op15.56kb
Gap_calling	3	29608354	29623455	seq15.10kb_op18.79kb
Gap_calling	3	37139366	37176175	seq36.81kb_op40.66kb**
Gap_calling	3	36572189	36572189	3.06kb_fragment_inserted**
Gap_calling	4	3384294	3384294	7.45kb_fragment_inserted
Gap_calling	4	15637045	15637045	3.69+11.60+43.86+35.15+8.13+9.01+15.25+4.55kb_fragment_inserted
Gap_calling	4	18478261	18478261	3.36kb_fragment_inserted**
Gap_calling	4	2342468	2351402	seq8.93kb_con9.46+9.77kb
Gap_calling	4	2646375	2647883	seq1.51kb_op1.69+4.25+4.89kb

Gap_calling	4	10478305	10533480	seq55.18kb_op62.23kb
Gap_calling	4	13677812	13721222	seq43.41kb_op47.90kb
Gap_calling	4	26072053	26078916	seq6.86kb_op9.62kb
Gap_calling	4	33299872	33319223	seq19.35kb_op27.73kb
Gap_calling	4	929540	933858	seq4.32kb_op4.70+25.46+8.14+3.71+13.22+7.59+0.52+9.45+6.89+3.40+4.04kb
Gap_calling	4	4838256	4838256	4.83+2.18kb_fragment_inserted
Gap_calling	4	8737584	8737584	4.52kb_fragment_inserted
Gap_calling	4	9395101	9395101	7.08+12.17+0.29+17.55kb_fragment_inserted
Gap_calling	4	11016759	11074066	seq1.56+2.88+35.72+17.15kb_op4.11+46.66+7.77+6.89+22.63kb
Gap_calling	4	20917354	20966747	seq49.39kb_op45.52+16.11kb
Gap_calling	5	2914305	2936456	seq22.15kb_op25.21kb
Gap_calling	5	11601005	11601005	7.33kb_fragment_inserted
Gap_calling	5	13188137	13188137	8.98kb_fragment_inserted
Gap_calling	5	15375747	15375747	10.10kb_fragment_inserted
Gap_calling	5	16612766	16616318	seq3.55kb_op7.69kb
Gap_calling	5	27559457	27559457	7.05kb_fragment_inserted
Gap_calling	5	27861245	27861245	14.42kb_fragment_inserted
Gap_calling	5	29901391	29939724	seq38.33kb_op44.16kb
Gap_calling	6	8435728	8435728	5.76kb_fragment_inserted
Gap_calling	6	19305114	19321367	seq16.25kb_op10.78+3.09+8.08kb
Gap_calling	6	24890394	24922274	Seq31.88kb_op37.65kb
Gap_calling	7	3045274	3045274	possible duplication including 5 restriction fragments(in total 42.94 kb) missing in seq but present in op
Gap_calling	7	16083298	16125030	Seq41.73kb_op47.64kb
Gap_calling	7	29139150	29148566	seq9.42kb_op15.72kb
Gap_calling	7	5480556	5546997	seq66.44kb_op44.51+34.66kb
Gap_calling	7	9467901	9467901	7.45kb_fragment_inserted
Gap_calling	7	12268150	12306610	seq38.46kb_op35.76+7.12kb
Gap_calling	7	18647429	18647429	23.33+10.36+24.37kb_fragments_inserted
Gap_calling	7	28008318	28008318	7.32kb_fragment_inserted
Gap_calling	8	726519	738868	seq12.35kb_op16.81kb
Gap_calling	8	14579410	14594515	seq15.11kb_op23.88kb
Gap_calling	8	3241575	3241575	0.41+30.07kb inserted
Gap_calling	8	16332574	16332574	15.28+6.15+5.93+3.85+9.04+9.03kb inserted
Gap_calling	8	17379172	17379172	5.82kb_fragment_inserted
Gap_calling	8	24694946	24694946	4.07+1.50kb_inserted
Gap_calling	9	19166999	19209916	seq1.50+41.41kb_op49.88kb
Gap_calling	9	19858814	19868417	seq9.60kb_op6.29+6.65kb
Gap_calling	9	11255290	11256432	seq1.14kb_op6.29kb
Gap_calling	10	2898200	2944438	seq46.24kb_op62.71kb
Gap_calling	10	19025141	19073074	seq47.93kb_op66.94kb
Gap_calling	10	4863257	4863257	10.63kb_fragment_inserted
Gap_calling	10	5084346	5084346	4.99kb_fragment_inserted
Gap_calling	10	19186384	19218804	seq32.42kb_op35.66kb
Gap_calling	10	5818572	5818572	16.10kb_fragment_inserted
Gap_calling	10	10393768	10393768	8.66kb_fragment_inserted
Gap_calling	11	963784	988924	Seq25.14_op20.36+6.91+13.82_gapCalling
Gap_calling	11	10167049	10224531	seq18.63+38.86_op22.30+5.37+19.82+5.65+13.63
Gap_calling	11	22151860	22151860	11.15+6.44+7.26kb_fragment insertions
Gap_calling	11	28075555	28075555	6.99 kb_fragment_inserted
Gap_calling	11	24093333	24108967	Seq15.63kb_op18.44kb**
Gap_calling	11	24291509	24310926	Seq19.42kb_op25.10kb
Gap_calling	11	4189081	4189081	5.58 kb_fragment_inserted
Gap_calling	11	20175534	20175534	17.95 kb_fragment_inserted
Gap_calling+Misassembly	11	18316880	18365879	seq8.61+19.85+10.88+1.15+8.52=49.01_op3.29+10.49+19.80+8.65+11.65+11.81+11.98+12.04+12.12=101.83
Gap_calling	12	8240838	8240838	6.35+7.28+5.27kb_fragment_inserted
Gap_calling	12	15759281	15771071	Seq11.79kb_op15.14kb
Gap_calling	12	15893133	15893133	8.02+8.15 kb_fragments_inserted
Gap_calling	12	20686342	20686342	missing Sequence186.58kb:17.26+13.98+9.35+30.40+17.12+78.34+1.66+7.25+18.55
Gap_calling	12	21539949	21539949	8.07 kb_fragment_inserted
Gap_calling	12	23944506	23944506	22.08 kb_fragment_inserted
Gap_calling	12	16326278	16342254	op20.83 kb_seq15.98kb
Gap_calling	12	16762798	16783428	21.29+21.02+20.94kb_possible 3 copies of repeats_inserted
Gap_calling	12	6111361	6123109	op14.84_seq11.75
Gap_filling	1	10043781	10107330	seq63.55_op13.10+12.22kb_gap overestimated
Gap_filling	1	11518254	11673361	seq155.11_op34.91+13.73+24.42kb_gap overestimated
Gap_filling	1	15125350	15231698	seq106.35_op34.17kb_gap overestimated
Gap_filling	1	27126177	27238645	seq112.47_op15.46kb_gap overestimated

Gap_filling	1	42045301	42101211	seq55.91_op24.23kb	gap overestimated
Gap_filling	2	5933788	6009450	Seq75.66kb_op36.15+22.32kb	gap overestimated
Gap_filling	2	19566739	19662205	seq94.96 kb_op10.41+12.30 Kb	gap overestimated
Gap_filling	2	25635840	25721619	seq 85.78_op36.72+19.59kb	gap overestimated
Gap_filling	3	16891589	17027979	seq136.39kb_op30.48+12.25+9.28+2.83+4.90+37.33+3.33+37.31kb	
Gap_filling	3	31859635	31978001	seq118.37kb_op36.77+8.95+6.94+13.98+4.90+11.84+22.94+12.40kb	
Gap_filling	3	4812950	4902471	seq89.52kb_op34.92+16.72+22.32	gap overestimated
Gap_filling	3	13511891	14027950	seq508.58+2.56+1.55+3.37kb_op40	fragments totalling 258.35kb, gap overestimated
Gap_filling	4	3384294	3384294	7.45kb_fragment_inserted	gap underestimated
Gap_filling	4	11987580	12060534	seq4.87+8.62+8.91+6.03+5.69+4.87+6.04+2.60+25.33kb_op28.27+8.88+2.56+6.40+6.06+9.09+6.23kb	
Gap_filling	4	20184503	20242252	seq1.40+13.07+16.37+11.11+6.04+2.24+7.52kb_op2.55+8.25+2.49+19.91+14.57+11.11+1.79+9.06kb	
Gap_filling	4	22066096	22247421	seq5frags_totalling_181.33kb_op14frags_totalling_190.05kb	
Gap_filling	4	8370251	8493801	seq123.55kb_op59.03+1.24+13.35+23.54kb	gap overestimated
Gap_filling	4	9157652	9241705	seq84.05kb_op113.54kb	gap underestimated
Gap_filling	4	20819816	20876371	seq56.55kb_op62.06kb	gap underestimated
Gap_filling	4	22350316	22682110	seq331.79kb_op36.43kb	gap overestimated
Gap_filling	5	17113786	17162579	seq48.79kb_op21.19kb	gap overestimated
Gap_filling	5	7320072	7376860	seq56.01+0.77kb_op22.45+2.36+9.87+0.44kb	gap overestimated
Gap_filling	5	21545269	21644475	seq99.21kb_op13.04+1.48+49.49kb	gap overestimated
Gap_filling	5	24918959	25027358	seq108.40kb_op12.81+13.54+4.53+63.25kb	gap overestimated
Gap_filling	5	27221681	27262023	seq40.34kb_op26.33+2.19+11.87+14.88+2.11+7.33kb	gap underestimated
Gap_filling	6	23725416	23779876	seq54.46kb_op36.91+4.95+4.88kb	gap overestimated
Gap_filling	6	10547383	10659317	seq111.93kb_op43.85kb	gap overestimated
Gap_filling	9	11978855	12031822	seq52.97kb_op13.66+3.83+12.72kb	gap overestimated
Gap_filling	9	14157645	14310115	seq111.18+41.29kb_op58.78+1.84+8.89+39.22kb	gap overestimated
Gap_filling	9	20931828	21248626	seq93.42+27.28+43.45+13.57+139.08kb_op4.16+6.82+2.49+26.79+42.22+13.61+45.83+22.19kb	gap overestimated
Gap_filling	9	19858814	19868417	seq9.60kb_op6.29+6.65kb	
Gap_filling	10	6824864	6913518	seq88.65kb_op9_fragments_totalling_50.58kb	
Gap_filling	10	10008505	10155829	seq147.32kb_op50.98+3.26+43.84+21.45kb	
Gap_filling	10	12449667	12561032	seq111.37kb_op15.59+10.34+9.29+4.48+2.18+21.09kb	
Gap_filling	10	3968375	4068843	seq100.47kb_op29_fragments_totalling_507.18kb	
Gap_filling	10	7462307	7557416	seq95.11kb_op35.78+8.81+9.83+7.49+3.03+7.42+31.68kb	gap underestimated
Gap_filling	11	15166134	15264194	seq74.89+23.17 op:8.46+8.15+4.96+6.82+10.34+4.35+8.66+9.34+20.39+22.33=103.08	
Gap_filling	11	8910659	8997466	Seq:86.53 op:27.59+9.60+8.66+8.32+22.46=76.63, Gap overestimated	
Gap_filling	11	7289804	7322407	Seq:32.60 Op:43.35, gap underestimated	
Gap_filling	11	21622456	21735641	seq:113.19 op:5.00+11.28+1.16+35.12, gap overestimated	
Misassembly	1	0	36306	telomere misassembly_seq1.43+34.88kb_op9.68+29.92kb	
Misassembly	1	21857134	21871082	seq9.78+2.23+1.95kb_op10.88+2.98kb	
Misassembly	1	31003925	31011100	two misscuts and one false cut	
Misassembly	2	2414507	2423458	extra cuts and fragments in sequence	
Misassembly	2	31774568	31777369	sequence is 0.45+0.88+1.47 optical_map is 2.02+0.75kb	
Misassembly	3	6773564	6908765	seq0.66+61.54+12.64+6.58+2.29+2.18+49.30kb_op50.78+2.12+2.50+6.87+0.36+12.30+36.39kb	
Misassembly	3	19606225	19613728	extra sequence_7.5kb	
Misassembly	3	21713465	21715657	extra sequence_seq1.73+0.46+4.03+3.06+1.30+1.85+0.85_op6.54+3.23kb	
Misassembly	3	37139366	37257346	telomere misassembly_seq36.81+81.17kb_op40.66+89.88kb	
Misassembly	4	3331488	3347275	extra sequence_2.92+3.69+9.18kb	
Misassembly	4	3361970	3366748	extra sequence_4.78kb	
Misassembly	4	4635007	4642772	extra sequence_7.77kb	
Misassembly	4	9577907	9605620	seq27.71kb_op24.06kb	
Misassembly	4	11649186	11729152	seq59.10+0.66+20.21kb_op53.25+0.41+16.52kb	
Misassembly	4	11897948	11941483	seq43.54kb_op39.02kb	
Misassembly	4	12428850	12585538	probable_inversion_14_fragments_totalling_157kb	
Misassembly	4	14430459	14487748	seq15.30+2.42+2.60+4.26+2.60+5.46+4.56+11.83+8.25kb_op12.63+8.83+5.45+2.40+4.43+2.58+4.90+7.60+4.77kb	
Misassembly	4	15161710	15321129	seq95.47+2.70+4.70+56.56kb_op89.21+41.61+4.66+2.74+16.35+7.11kb	
Misassembly	4	16748041	16813450	probable_inversion_4_fragments_totalling_65kb	
Misassembly	4	19425512	19431218	seq5.71kb_op0.89+15.36kb	
Misassembly	4	26046131	26058543	seq12.41kb_op9.84kb	
Misassembly	4	27079649	27216366	probable_inversion_4_fragments_totalling_137kb	
Misassembly	4	32888041	33012958	seq11.94+112.98kb_op23.86+101.13kb	
Misassembly	4	35808771	35925326	telomere_seq0.72+54.43kb_op91.01+9.88+3.72+4.79+7.79+34.40kb	
Misassembly	5	1316949	1345426	inversion_2_fragments_totalling_28kb	
Misassembly	5	1934326	1987260	seq52.93kb_op47.37kb	
Misassembly	5	4689388	4709887	extra sequence_seq20.50_op18.45kb	
Misassembly	5	9770658	9791799	seq8.90+1.86+10.38kb_op1.85+11.94+8.41kb	
Misassembly	5	12275478	12371237	seq83.04kb_op39.60+4.63+36.32kb	
Misassembly	5	29098829	29125165	probable_inversion_2_fragments_totalling_21kb	
Misassembly	5	29964586	30039015	telomere_misassembly_seq5frags_totalling_74.42kb_op5frags_totalling_309.28kb	

Misassembly	6	47968	89682	Extra sequence_seq41.71kb_op36.37kb
Misassembly	7	1353106	1386259	extra sequence_33.15kb
Misassembly	7	23445232	23464459	seq19.23kb_op16.82kb extra sequence
Misassembly	7	24434265	24439698	extra sequence_5.43kb
Misassembly	8	26752812	26790061	seq17.37+8.12+11.76kb_op8.31+12.98+17.22kb
Misassembly	9	23788435	23843361	seq13.67+35.31+5.94kb_op35.89+14.12+13.95+3.73+11.17kb
Misassembly	10	4773782	4782684	extra sequence_8.90kb
Misassembly	10	12981438	12985434	possible inversion_seq2.44+1.55kb_op1.80+2.25kb
Misassembly	10	14828584	14978980	seq78.53+33.53+3.89+34.45kb_op48.36kb
Misassembly	11	6740759	6779556	Seq2.48+13.8+11.47+7.18+3.86_op6.08+6.73+11.23+15.36kb
Misassembly	11	11111564	11129825	seq18.26kb_op16.05kb extra sequence**
Misassembly	11	11266629	11399303	seq:49.12+10.77+24.71+0.44+7.40+10.83+7.37+22.03 op:22.51+6.80+6.82+12.68+9.18+8.71+14.25+8.68+9.32+6.01+2.91+18.97
Misassembly	11	17024965	17040514	one missing cut and 2.97 kb deletion, seq:1.30+0.87+13.38 op:1.81+10.41
Misassembly	11	30174987	30485656	Misassembly_at_telomere_seq_frags_totalling_310.67kb
Misassembly	12	13784153	13802033	seq17.988kb_op15.29kb; 2.7 kb extra sequence
Misassembly	12	10313612	10318270	two missing cuts and one extra cu
Misassembly	12	15683128	15698718	seq15.59_op12.87kb
Misassembly	12	17297998	17330565	Seq:2.66+10.35+1.81+12.96+4.79;op:1.79+13.83+3.05+10.59
Misassembly	12	20951253	21079884	possible inversion plus extra sequence includec
Misassembly	12	21587567	21596438	possible inversion containec
Misassembly	12	25258350	25383803	seq:21.71+1.91+5.38+13.14+17.94+4.75+2.87+6.52+51.25 op:54.95+6.46+2.73+17.81+13.12 extra seq included and inversion:
Missing_cut_on_optical_map	1	1795138	1795138	
Missing_cut_on_optical_map	1	14263736	14263736	
Missing_cut_on_optical_map	1	14662689	14662689	
Missing_cut_on_optical_map	1	14692988	14692988	
Missing_cut_on_optical_map	1	15113929	15113929	
Missing_cut_on_optical_map	1	12100950	12100950	
Missing_cut_on_optical_map	1	12212121	12212121	
Missing_cut_on_optical_map	1	12217951	12217951	
Missing_cut_on_optical_map	1	12516225	12516225	
Missing_cut_on_optical_map	1	13373306	13373306	
Missing_cut_on_optical_map	1	18694396	18694396	
Missing_cut_on_optical_map	1	19578972	19578972	
Missing_cut_on_optical_map	1	11102232	11102232	
Missing_cut_on_optical_map	1	11408362	11408362	
Missing_cut_on_optical_map	1	11471609	11471609	
Missing_cut_on_optical_map	1	4610341	4610341	
Missing_cut_on_optical_map	1	5478015	5478015	
Missing_cut_on_optical_map	1	7600298	7600298	
Missing_cut_on_optical_map	1	20530374	20530374	
Missing_cut_on_optical_map	1	21478979	21478979	
Missing_cut_on_optical_map	1	22984003	22985003	
Missing_cut_on_optical_map	1	23722415	23722415	
Missing_cut_on_optical_map	1	23980805	23980805	
Missing_cut_on_optical_map	1	23986606	23986606	
Missing_cut_on_optical_map	1	23991644	23991644	
Missing_cut_on_optical_map	1	36110677	36110677	
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Missing_cut_on_optical_map	12	3603181	3603181
Missing_cut_on_optical_map	12	3698348	3698348
Missing_cut_on_optical_map	12	4821656	4821656
Missing_cut_on_optical_map	12	4824121	4824121
Missing_cut_on_optical_map	12	5501843	5501843
Missing_cut_on_optical_map	12	6251130	6251130
Missing_cut_on_optical_map	12	7591337	7591337
Missing_cut_on_optical_map	12	14465629	14465629
Missing_cut_on_optical_map	12	14524676	14524676
Missing_cut_on_optical_map	12	16232667	16232667
Missing_cut_on_optical_map	12	16234802	16234802
Missing_cut_on_optical_map	12	8196732	8196732
Missing_cut_on_optical_map	12	8500833	8500833
Missing_cut_on_optical_map	12	8677851	8677851
Missing_cut_on_optical_map	12	10592005	10592005
Missing_cut_on_optical_map	12	11443593	11443593
Missing_cut_on_optical_map	12	12811678	12811678
Missing_cut_on_optical_map	12	12876436	12876436
Missing_cut_on_optical_map	12	12902080	12902080
Missing_cut_on_optical_map	12	12946285	12946285
Missing_cut_on_optical_map	12	12957370	12957370
Missing_cut_on_optical_map	12	13440898	13440898

*Start=start position based sequence; End=end position based on sequence; seq=sequence; op=optical map; Ch=chromosome; **with less confidence