

Supplementary Data

Genome sequence analysis of the oleaginous yeast, *Rhodotorula diobovata*, and comparison of the carotenogenic and oleaginous pathway genes and gene products with other oleaginous yeasts.

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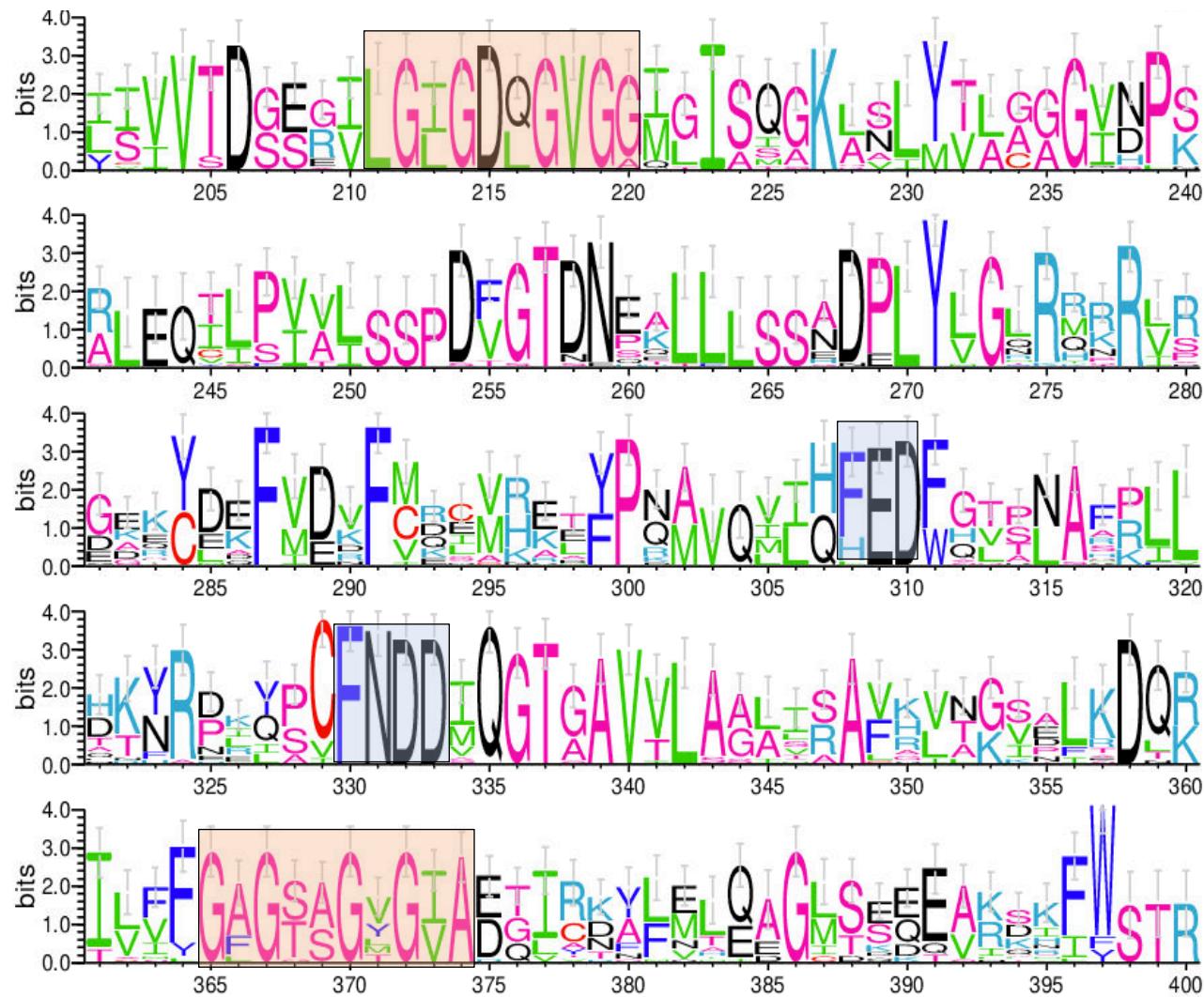


Figure S1. Weblogo plot of aligned sequences from *Rhodotorula diobovata*, *Lipomyces starkeyi*, *Rhodotorula toruloides NP11*, *Rhodotorula graminis WP1*, *Rhodotorula* sp. JG-1b, *Sporidiobolus salmonicolor*, *Phaffia rhodozyma*, *Yarrowia lipolytica*, and *Rhodotorula taiwanensis*. Plot shows relative frequency of each amino acid at each position. Red highlighted boxes show the dinucleotide binding sites while the blue boxes show the divalent ion binding sites.

	290	300	310	320	330	340	350
	gxxydxFvdxFxxxxxxxxPx--xih		FED	fxxxnaxxllxxkxxxxpc	FNDD	iQGTgAVvLaxxxxAxx	
ADI76993	.gr..k...d.vqcvkkl..r...vl.		.	glp..rr..dty.prla.	.	v.....t..alss.vr	
ODQ72042	.gr..k...d.vqcvkkl..r...vl.		.	glp..rr..dty.prla.	.	v.....t..alss.vr	
ADK56109	.gr..k...d.vqcvkkl..r...vl.		.	glp..rr..dty.prla.	.	v.....t..alss.vr	
AOW05618	.kq..d.i.n.vqsarrl..k...v..		.	gla..hki.d.y.pei..t..sita.lk	
XP_504112	.kq..d.i.n.vqsarrl..k...v..		.	gla..hki.d.y.pei..t..sita.lk	
BBE10583	.ae..k...r.celvree..q...ll..		.	gvs..aki.tty.nkqsv..	m...a....allsvk		
CDR37260	.ae..k...r.celvree..q...ll..		.	gvs..ski.tty.nkqsv..	m...a....allsvk		
PRQ74895	.ae..k...r.celvree..q...ll..		.	gvs..ski.tty.nkqsv..	m...a....allsvk		
KWU45829	.ka..e..ek.cdivred..q...ml..		.	gvs..ar..a.y.piqs..	m...a....alis.vk		
POY70860	.kq..e..ek.cdivred..q...ml..		.	gvs..ar..a.y.piqs..	m...a....alvs.vk		
KPV76802	.ek..q...k.cdivrea..q...ml..		.	avd..sr..q.f.pkqs..	s...a....alvs.vk		
TNY24152	.ek..q...k.cdivrqe..q...ml..	l..	.	ssa.smrfvd.y.hkqsi..	a...s....alas.vg		
CEQ39123	.ae..a...k.cdlvrem..q...ml..		.	gvs..gr..n.f.pkqs..	m...a....salvs.cr		
CED85069	.ki..e.i.k.iknckalf.d...l...		.	gls..qr..d.yadei..t.salma.vg		
ANJ02849	eekcle.m.v.mrcmhetf.nm..v.qh..		wqtpl.fp..h.n.dly..			gair.fh	
PRQ75739	eekcle.m.v.mrcmhetf.nmvqv.qh..		wqtpl.fp..h.n.dly..			gair.fh	
CDR45495	qekcle.mev.mrcmhetf.nm..v.qh..		wqtpl.fp..h.n.dly..			gair.fh	
EGU11086	eekcle.m.v.mrcmhetf.nm..v.qh..		wqtpl.fp..h.n.dly..			gair.fh	
GEM12284	edkcme.mev.mremhktf.nm..v.qh..		wqtpl.fp..hrn.dly..			gair.fh	
KWU43902	ddkcee..v.mkemhatf.nm..i.q..		httl.fp..q.n.dvy..			gair.fh	
POY76220	dedcek..ev.mkemhatf.nm..i.q..		httl.fp..hnn.eiy..			i..gair.fr	
KPV73817	ddkcee.mev.mremhkef.nm..i.q..		whttl.fp..h.n.diy..			gair.fa	
TNY17208	ddkcee.m.v.mremhkef.nm..i.q..		whttl.fp..h.n.diy..			gair.fa	
CEQ41698	detcea..v.mkamnkaf.nm..i.q..		httl.fp..e.h.ery..			gair.fq	

Figure S2. MAFFT alignment of malic enzymes showing the divalent ion binding sites [Borsch and Westhoff, 1990]. Identical amino acid residues in all the enzymes are signified by a dot (.). ADI76993, *Lipomyces starkeyi*; ODQ72042, *Lipomyces starkeyi* NRRL Y-11557; ADK56109, *Lipomyces starkeyi*; AOW05618, *Yarrowia lipolytica* CLIB89(W29); XP_504112, *Yarrowia lipolytica* CLIB122; BBE10583, *Rhodotorula toruloides* NBRC10032; CDR37260, *Rhodotorula toruloides* CECT1137; PRQ74895, *Rhodotorula toruloides* NBRC0880; KWU45829, *Rhodotorula* sp. JG-1b; POY70860, *Rhodotorula taiwanensis*; KPV76802, *Rhodotorula graminis* WP1; TNY24152, *Rhodotorula diobovata*; CEQ39123, *Sporidiobolus salmonicolor*; CED85069, *Xanthophyllomyces dendrorhous*; ANJ02849, *Rhodotorula toruloides* IFO0880; PRQ75739, *Rhodotorula toruloides* NBRC0880; CDR45495, *Rhodotorula toruloides* CECT1137; EGU11086, *Rhodotorula toruloides* ATCC 204091; GEM12284, *Rhodotorula toruloides* NBRC10032; KWU43902, *Rhodotorula* sp. JG-1b; POY76220, *Rhodotorula taiwanensis*; KPV73817, *Rhodotorula graminis* WP1; TNY17208, *Rhodotorula diobovata*; CEQ41698, *Sporidiobolus salmonicolor*.

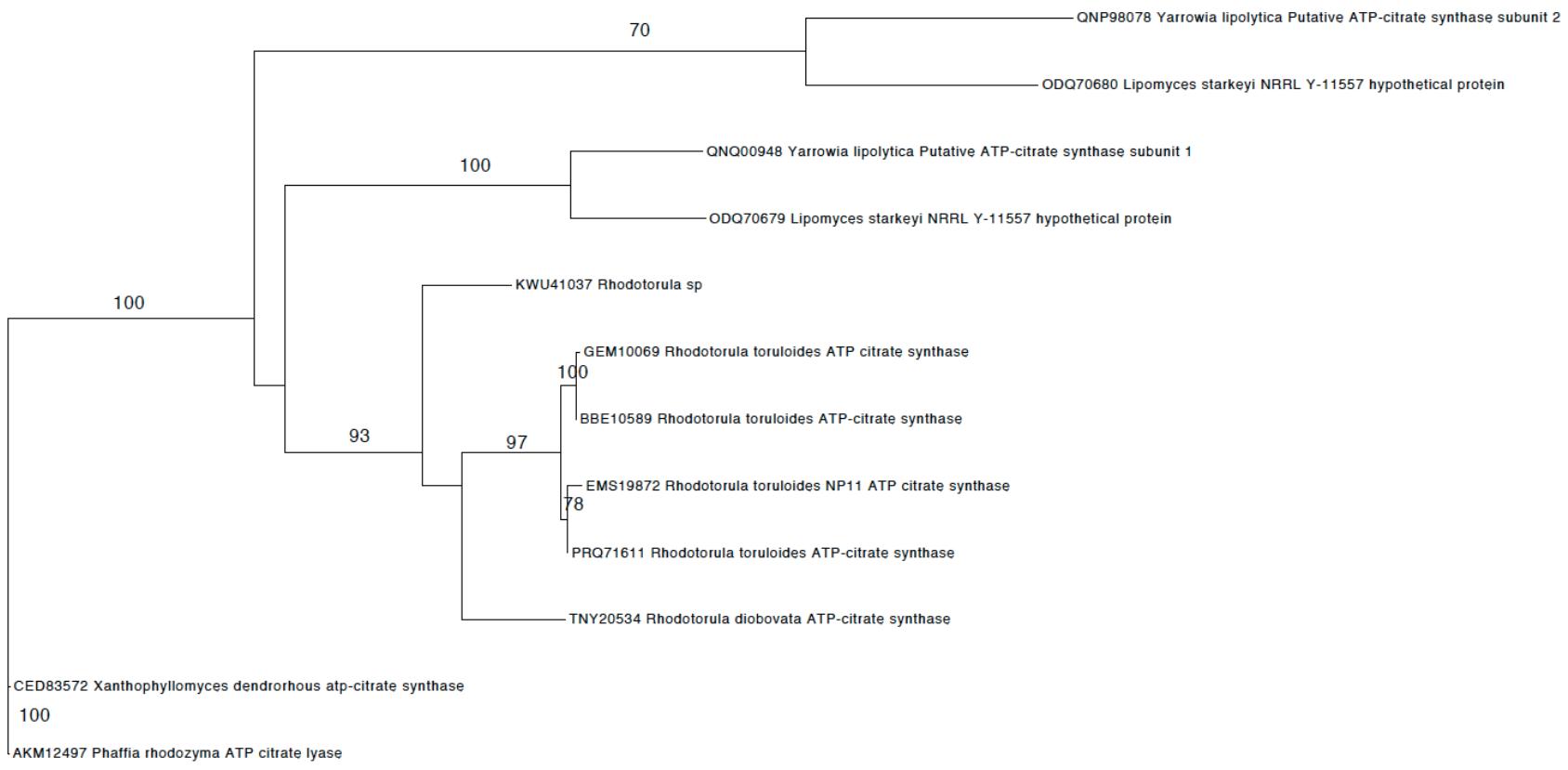


Figure S3. PROML phylogenetic tree constructed from an alignment of ATP:Citrate lyase sequences from *Rhodotorula* sp., *Yarrowia*, *Lipomyces*, and *Xanthophyllomyces*. Analysis shows the relationship between the two ACL subunits of *Y. lipolytica* and *L. starkeyi*. The significant nodes on the tree with bootstrap support values > 70% are highlighted.

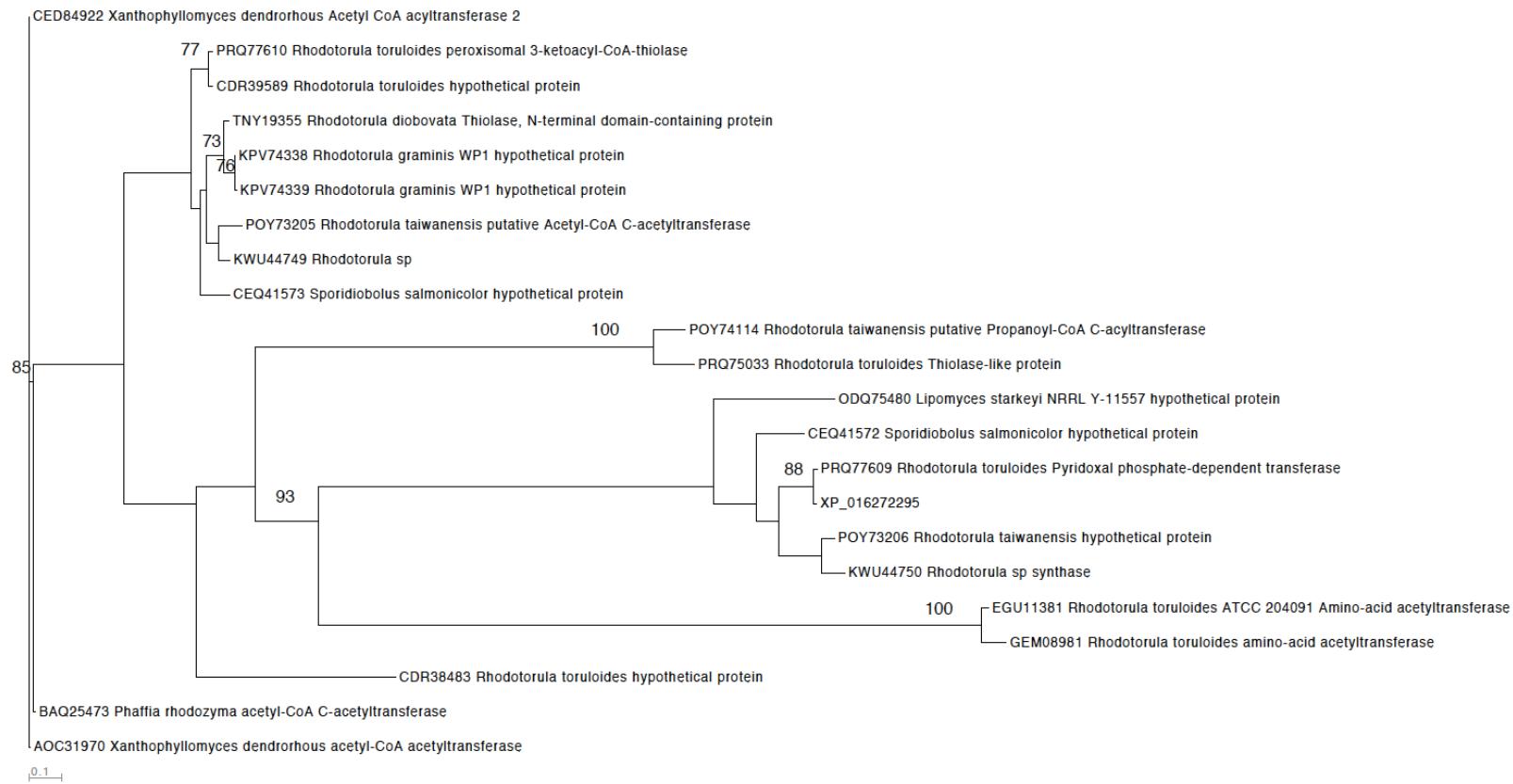


Figure S4. PROML phylogenetic tree constructed from a MAFFT alignment of Acetyl-CoA C-acetyltransferase sequences from *Rhodotorula* species, *Yarrowia*, *Lipomyces*, *Sporidiobolus* and *Xanthophyllomyces*. The significant nodes on the tree with bootstrap support values > 70% are highlighted.

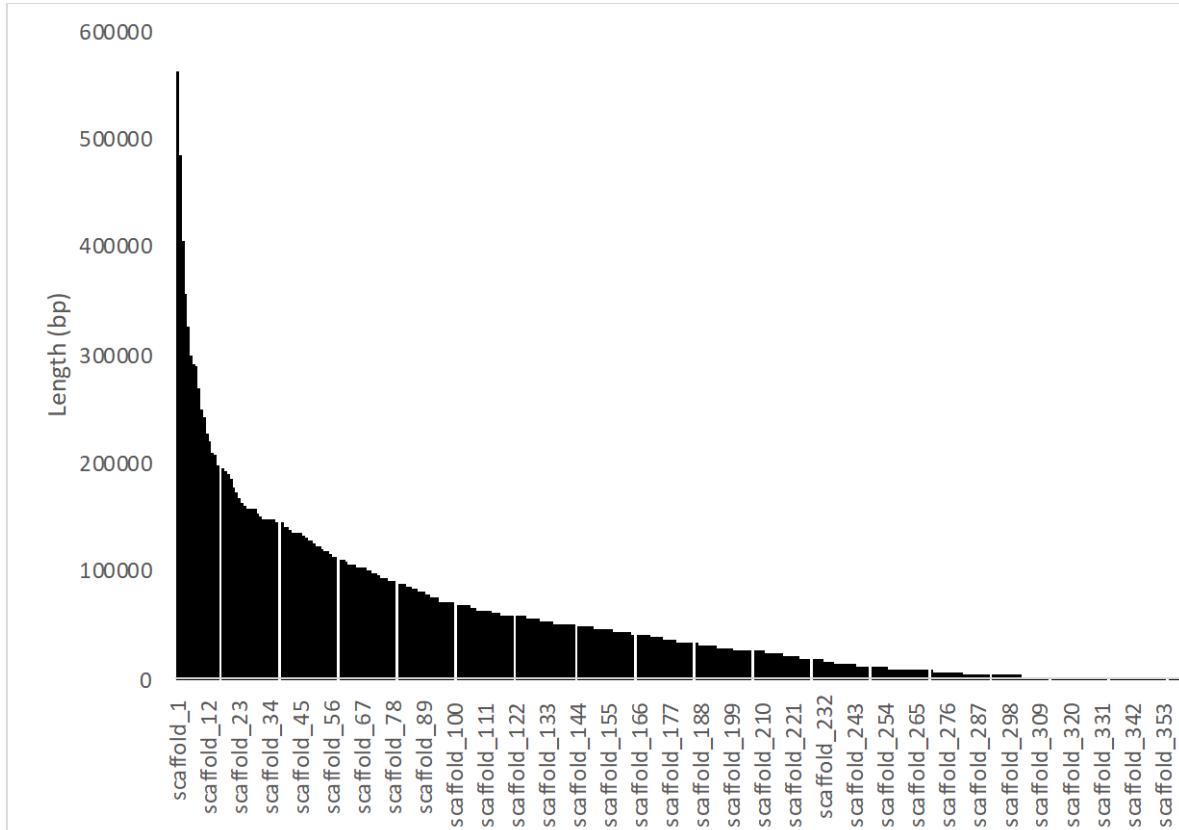


Figure S5. Scaffold length distribution of all 361 scaffolds from the *de novo* assembly of *Rhodotorula diobovata* 08-225.

Table S1. Scaffold length distribution for the 361 scaffolds used to assemble the *Rhodotorula diobovata* genome.

Scaffold	Length	Scaffold	Length	Scaffold	Length	Scaffold	Length	Scaffold	Length	Scaffold	Length	Scaffold	Length	Scaffold	Length
scaffold_16	56371	scaffold_51	12403	scaffold_101	70207	scaffold_151	47520	scaffold_201	27893	scaffold_251	12278	scaffold_301	3813	scaffold_351	1315
scaffold_28	48599	scaffold_52	12268	scaffold_102	69632	scaffold_152	47110	scaffold_202	27855	scaffold_252	12155	scaffold_302	3579	scaffold_352	1288
scaffold_31	40750	scaffold_53	12207	scaffold_103	69347	scaffold_153	46676	scaffold_203	27588	scaffold_253	11161	scaffold_303	3478	scaffold_353	1262
scaffold_49	35655	scaffold_54	12003	scaffold_104	69211	scaffold_154	46507	scaffold_204	27584	scaffold_254	11093	scaffold_304	3335	scaffold_354	1196
scaffold_66	32810	scaffold_55	11864	scaffold_105	68795	scaffold_155	45997	scaffold_205	27231	scaffold_255	10956	scaffold_305	3331	scaffold_355	1182
scaffold_63	30036	scaffold_56	11562	scaffold_106	67249	scaffold_156	45708	scaffold_206	27201	scaffold_256	10836	scaffold_306	3278	scaffold_356	1148
scaffold_73	29350	scaffold_57	11446	scaffold_107	66952	scaffold_157	45575	scaffold_207	27151	scaffold_257	10701	scaffold_307	3271	scaffold_357	1139
scaffold_77	29071	scaffold_58	11289	scaffold_108	65288	scaffold_158	44317	scaffold_208	27066	scaffold_258	10544	scaffold_308	3211	scaffold_358	1128
scaffold_78	27138	scaffold_59	11171	scaffold_109	64973	scaffold_159	44249	scaffold_209	26740	scaffold_259	10276	scaffold_309	3102	scaffold_359	1120
scaffold_100	24985	scaffold_60	11081	scaffold_110	64231	scaffold_160	44153	scaffold_210	25954	scaffold_260	10268	scaffold_310	3078	scaffold_360	1075
scaffold_119	24325	scaffold_61	10847	scaffold_111	64191	scaffold_161	44053	scaffold_211	25607	scaffold_261	10259	scaffold_311	3070	scaffold_361	1004
scaffold_129	22697	scaffold_62	10766	scaffold_112	63824	scaffold_162	43711	scaffold_212	25160	scaffold_262	10071	scaffold_312	3057		
scaffold_130	22107	scaffold_63	10634	scaffold_113	63298	scaffold_163	43639	scaffold_213	25044	scaffold_263	9990	scaffold_313	3033		
scaffold_141	21165	scaffold_64	10612	scaffold_114	62868	scaffold_164	42655	scaffold_214	24880	scaffold_264	9730	scaffold_314	3006		
scaffold_150	20697	scaffold_65	10430	scaffold_115	62290	scaffold_165	42332	scaffold_215	24258	scaffold_265	9721	scaffold_315	2936		
scaffold_165	19904	scaffold_66	10353	scaffold_116	61395	scaffold_166	41672	scaffold_216	24237	scaffold_266	9686	scaffold_316	2918		
scaffold_177	19569	scaffold_67	10345	scaffold_117	60354	scaffold_167	41657	scaffold_217	23663	scaffold_267	9332	scaffold_317	2863		
scaffold_188	19338	scaffold_68	10287	scaffold_118	60277	scaffold_168	41460	scaffold_218	23278	scaffold_268	9308	scaffold_318	2831		
scaffold_199	19036	scaffold_69	10230	scaffold_119	59913	scaffold_169	41325	scaffold_219	23196	scaffold_269	9255	scaffold_319	2815		
scaffold_200	18552	scaffold_70	10041	scaffold_120	59639	scaffold_170	40336	scaffold_220	23024	scaffold_270	8581	scaffold_320	2791		
scaffold_211	17883	scaffold_71	10016	scaffold_121	59502	scaffold_171	40183	scaffold_221	22963	scaffold_271	8234	scaffold_321	2619		
scaffold_222	17349	scaffold_72	98624	scaffold_122	59183	scaffold_172	38870	scaffold_222	22185	scaffold_272	8062	scaffold_322	2561		

scaffold_23	169270	scaffold_73	96503	scaffold_123	59093	scaffold_173	38656	scaffold_223	21937	scaffold_273	7848	scaffold_323	2561
scaffold_24	163365	scaffold_74	95059	scaffold_124	59047	scaffold_174	38429	scaffold_224	19985	scaffold_274	7662	scaffold_324	2541
scaffold_25	161871	scaffold_75	94951	scaffold_125	58310	scaffold_175	38188	scaffold_225	19640	scaffold_275	7603	scaffold_325	2455
scaffold_26	159488	scaffold_76	94947	scaffold_126	57999	scaffold_176	37859	scaffold_226	19609	scaffold_276	7573	scaffold_326	2398
scaffold_27	159370	scaffold_77	92703	scaffold_127	57994	scaffold_177	37811	scaffold_227	19541	scaffold_277	7182	scaffold_327	2354
scaffold_28	159096	scaffold_78	92176	scaffold_128	57347	scaffold_178	37429	scaffold_228	19450	scaffold_278	7022	scaffold_328	2332
scaffold_29	158621	scaffold_79	91617	scaffold_129	56638	scaffold_179	36516	scaffold_229	19432	scaffold_279	6981	scaffold_329	2307
scaffold_30	153256	scaffold_80	88545	scaffold_130	56506	scaffold_180	35512	scaffold_230	18937	scaffold_280	6597	scaffold_330	2306
scaffold_31	150981	scaffold_81	88281	scaffold_131	55444	scaffold_181	35373	scaffold_231	18664	scaffold_281	6112	scaffold_331	2136
scaffold_32	148907	scaffold_82	88211	scaffold_132	55156	scaffold_182	35306	scaffold_232	18241	scaffold_282	6002	scaffold_332	2134
scaffold_33	148760	scaffold_83	87649	scaffold_133	55140	scaffold_183	35020	scaffold_233	17528	scaffold_283	5847	scaffold_333	2110
scaffold_34	148594	scaffold_84	86773	scaffold_134	54795	scaffold_184	34800	scaffold_234	16884	scaffold_284	5792	scaffold_334	2046
scaffold_35	148281	scaffold_85	83878	scaffold_135	54361	scaffold_185	34598	scaffold_235	16141	scaffold_285	5677	scaffold_335	2024
scaffold_36	148251	scaffold_86	83170	scaffold_136	52756	scaffold_186	34189	scaffold_236	15173	scaffold_286	5612	scaffold_336	2016
scaffold_37	145750	scaffold_87	82556	scaffold_137	52428	scaffold_187	32948	scaffold_237	14969	scaffold_287	5555	scaffold_337	1955
scaffold_38	145744	scaffold_88	82150	scaffold_138	52202	scaffold_188	32887	scaffold_238	14778	scaffold_288	5488	scaffold_338	1920
scaffold_39	142015	scaffold_89	82131	scaffold_139	52179	scaffold_189	32159	scaffold_239	14566	scaffold_289	5348	scaffold_339	1893
scaffold_40	140972	scaffold_90	78598	scaffold_140	52053	scaffold_190	32109	scaffold_240	14123	scaffold_290	5080	scaffold_340	1878
scaffold_41	138849	scaffold_91	78428	scaffold_141	52024	scaffold_191	31878	scaffold_241	14118	scaffold_291	4585	scaffold_341	1783
scaffold_42	136445	scaffold_92	76379	scaffold_142	50806	scaffold_192	31807	scaffold_242	13859	scaffold_292	4585	scaffold_342	1733
scaffold_43	135953	scaffold_93	76331	scaffold_143	50753	scaffold_193	31432	scaffold_243	13561	scaffold_293	4539	scaffold_343	1644
scaffold_44	135147	scaffold_94	75530	scaffold_144	50418	scaffold_194	30795	scaffold_244	13431	scaffold_294	4397	scaffold_344	1615
scaffold_45	135023	scaffold_95	72949	scaffold_145	50179	scaffold_195	30199	scaffold_245	13142	scaffold_295	4396	scaffold_345	1560
scaffold_46	133771	scaffold_96	71833	scaffold_146	50109	scaffold_196	29853	scaffold_246	13101	scaffold_296	4353	scaffold_346	1541

scaffold_4 7	13014 3	scaffold_97	71784	scaffold_14 7	49962	scaffold_19 7	29742	scaffold 247	13100	scaffold_297	4278	scaffold_3 47	1538
scaffold_4 8	12869 7	scaffold_98	71720	scaffold_14 8	49783	scaffold_19 8	29437	scaffold 248	12984	scaffold_298	4261	scaffold_3 48	1494
scaffold_4 9	12853 2	scaffold_99	71082	scaffold_14 9	49600	scaffold_19 9	28908	scaffold 249	12429	scaffold_299	4090	scaffold_3 49	1457
scaffold_5 0	12560 6	scaffold_10 0	71010	scaffold_15 0	48167	scaffold_20 0	27926	scaffold 250	12336	scaffold_300	3987	scaffold_3 50	1397

Table S2. Genome coverage calculation for Illumina and Ion Torrent reads.

GENOME COVERAGE

	Illumina	IT
Desired coverage (50-fold)		
genome size G	21000000	21000000
avg. read size	144	305
probability of coverage P	0.99	0.99
fraction of genome per read f	6.86E-06	1.45E-05
desired coverage C	50	50
1-fold coverage $\ln(1-P)/\ln(1-f)$	671585.016	317074.9889
req. reads N = C[$\ln(1-P)/\ln(1-f)$]	33579250.8	15853749.45

Actual coverage

Illumina

file	format	type	num_seqs	sum_len	min_len	avg_len	max_len
DL300_S1_L001_R1_001.fastq.gz	FASTQ	DNA	4878013	713623894	30	146.3	151
DL300_S1_L001_R2_001.fastq.gz	FASTQ	DNA	4878013	703035995	30	144.1	151
DL400_S2_L001_R1_001.fastq.gz	FASTQ	DNA	4003821	580031498	30	144.9	151
DL400_S2_L001_R2_001.fastq.gz	FASTQ	DNA	4003821	568995556	30	142.1	151
DL700_S3_L001_R1_001.fastq.gz	FASTQ	DNA	2830249	412524162	30	145.8	151
DL700_S3_L001_R2_001.fastq.gz	FASTQ	DNA	2830249	401509203	30	141.9	151
total			23424166	3379720308			
Illumina coverage = total seqs/1-fold C			34.87892885				

Ion Torrent

file	format	type	num_seqs	sum_len	min_len	avg_len	max_len
Pollux-corrected IT reads	FASTQ	DNA	2965701	904538805	25	305	529
IT coverage = total seqs/1-fold C			9.353311058				
Total Illumina + IT coverage			44.23223991				