Genome sequence of the oyster mushroom *Pleurotus ostreatus* strain PC9

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24 Abstract

25 The oyster mushroom *Pleurotus ostreatus* is a basidiomycete commonly found in the rotten wood and it is one of the most
 26 cultivated edible mushrooms globally. *P. ostreatus* is also a carnivorous fungus, which can paralyze and kill nematodes
 27 within minutes. However, the molecular mechanisms of the predator-prey interactions between *P. ostreatus* and nematodes
 28 remain unclear. PC9 and PC15 are two model strains of *P. ostreatus* and the genomes of both strains have been sequenced
 29 and deposited at the Joint Genome Institute (JGI). These two monokaryotic strains exhibit dramatic differences in growth,
 30 but because PC9 grows more robustly in laboratory conditions, it has become the strain of choice for many studies. Despite
 31 the fact that PC9 is the common strain for investigation, its genome is fragmentary and incomplete relative to that of PC15.
 32 To overcome this problem, we used PacBio long reads and Illumina sequencing to assemble and polish a more integrated
 33 genome for PC9. Our PC9 genome assembly, distributed across 17 scaffolds, is highly contiguous and includes six
 34 telomere-to-telomere scaffolds, dramatically improving the genome quality. We believe that our PC9 genome resource will
 35 be useful to the fungal research community investigating various aspects of *P. ostreatus* biology.

36
 37 Keywords: oyster mushroom, *Pleurotus ostreatus*, whole-genome sequencing

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39 Introduction

40 *Pleurotus ostreatus* is a common edible basidiomycete that ranks second for global mushroom consumption (Cohen et al.
41 2002; Sánchez 2010). In the wild, this fungus prefers temperate habitats, such as subtropical forest (Hilber 1997), where it
42 extracts nutrients from dead or dying trees (Karim et al. 2016). In order to degrade the wood, *P. ostreatus* releases several
43 enzymes such as lignin, cellulose, and hemicellulose (Sánchez 2009). Nematicidal toxins produced by *P. ostreatus* under
44 starvation conditions, such as, trans-2-decenedioic, can paralyze and kill their nematode-prey (Barron and Thorn 1987;
45 Kwok et al. 1992). Another potential toxin, linoleic acid, reduces nematodes head size (Satou et al. 2008). When nematodes
46 contact the mycelium of *P. ostreatus*, fungal toxins enter the prey through their sensory cilia, leading to hypercontraction
47 and calcium influx of pharyngeal and body wall muscles, ultimately causing necrosis process of the neuromuscular system
48 (Lee et al. 2020). However, the identity of the toxins and how exactly *P. ostreatus* induces rapid cell necrosis remain unclear.

49 The *P. ostreatus* dikaryotic strain N001 that produces fruiting bodies is a common commercial strain (Larraya et al.
50 1999a; Peñas et al. 1998). In Larraya et al. (1999b), differentiated two monokaryotic strains (PC9 and PC15) from N001
51 in order to study reproduction and cloning in this mushroom. These two monokaryotic strains of *P. ostreatus* exhibit
52 differences in growth pattern, with PC9 exhibiting faster growth relative to PC15. Although the genomes of these two
53 monokaryotic strains have already been sequenced (Riley et al. 2014; Alfaro et al. 2016; Castanera et al. 2016), the quality
54 of PC9 genome is poor for current standards. Whereas the latest version of the PC15 genome comprises only 12 scaffolds,
55 the currently available PC9 genome (hereafter denoted PC9_JGI) is still distributed across 572 scaffolds, and most of which
56 size are smaller than 1-kb (Alfaro et al. 2016; Castanera et al. 2016). Despite PC15 having a more complete genome than
57 PC9, PC9 is often the preferred strain for research due to its robust growth in the laboratory. For instance, PC9 has been
58 used to study ligninolytic activity (Nakazawa et al. 2017b; Nakazawa et al. 2017a; Nakazawa et al. 2019), gene
59 modification (Yoav et al. 2018), and transformation (Nakazawa et al. 2016). Genetic manipulation has proven to
60 significantly increase the production of primary and secondary metabolites in several filamentous fungi that are important
61 in industry (Banerjee et al. 2003; Kück and Hoff 2010). Therefore, a high-quality PC9 genome is needed to enable scientists
62 to conduct advanced genomic studies and to facilitate functional analyses of *P. ostreatus* genes.

63 Consequently, we decided to sequence and annotate an updated genome for PC9. In this study, we used long PacBio
64 reads and Illumina reads to assemble the genome of *Pleurotus ostreatus* strain PC9 and functionally annotated its predicted

proteins. The final assembly, obtained by merging draft assemblies built with CANU (Koren et al.) and FALCON (Chin et al.), was distributed across 17 scaffolds, including six telomere-to-telomere scaffolds. In addition, the N50 of our assembly is ~3.5 Mb, which ranks it among the best for currently available *Pleurotus* genomes. In summary, here we present a new high-quality PC9 genome that will help the fungal research community to study this important mushroom.

Materials and Methods

Fungal strain and DNA extraction

Pleurotus ostreatus strain PC9 was cultured on yeast extract, malt extract and glucose medium (YMG) at 25 °C for 7 days. Mycelia were collected from original plates (5-cm) and added to a 100 mL YMG liquid medium shaken at 200 r.p.m. at 25 °C for 3 days. After 3 days, the culture was transferred to yeast nitrogen base without amino acids liquid medium (YNB), and it was shaken at 200 r.p.m. for 2 additional days. DNA was extracted by using cetyltrimethylammonium bromide (CTAB) and purified with chloroform, isopropanol, and phenol-chloroform.

Genome sequencing and assembly

PacBio long reads were sequenced from the *Pleurotus ostreatus* PC9 genome using the Pacbio RSII platform, and a PacBio SMRTBell Template Prep Kit 1.0 SPv3 was used for library preparation. This approach resulted in a total of ~0.3 M reads with a mean length of 14,742 base pairs (bp), representing 161X genome coverage for PC9. The Pacbio reads were used to construct two draft assemblies. The first assembly was built with Canu (v1.7) (Koren et al. 2017) using the parameters genomeSize=36m, useGrid=false, and maxThreads=8. The second assembly was built with Falcon (pbalgn v0.02) (Chin et al. 2016). For this latter assembly, the configuration file was downloaded from: <https://pbalgn.readthedocs.io/en/latest/parameters.html>, and the parameter Genome_size was set to 36 Mb since published *P. ostreatus* published genome sizes range from 34.3 to 35.6 Mb (Riley et al. 2014; Alfaro et al. 2016; Castanera et al. 2016). Next, we used Quiver (genomicconsensus v2.3.2) (Chin et al. 2013) to polish both these PacBio assemblies. Information on the raw polished draft assemblies is presented in Table S1.

The Canu assembly contained more telomeric regions, whereas the Falcon assembly was more contiguous. We merged both assemblies using Quickmerge (v0.3) (Chakraborty et al. 2016), with Canu as reference and Falcon as donor (Canu-Falcon) or *vice versa* (Falcon-Canu). The Falcon-Canu assembly showed better contiguity, having only 29 scaffolds (Table

S2), so we selected it as the basis for our final assembly. Redundant contigs were detected using nucmer (Mummer4) (Marçais et al. 2018), which were subsequently filtered out of the assembly. Nucmer was also used to detect large overlapping regions within the scaffolds. When an overlapping region exceeded 10-kb, presented high identity (>99%), and lay at the end or beginning of the scaffolds, we manually merged the two scaffolds at the overlapping region (Table S3). In total, 10 scaffolds were merged in this way, yielding five larger and more complete scaffolds (scaffolds 2, 4, 6, 7, and 13 of the final assembly) (Table S3). Finally, the cleaned assembly consisting of 17 scaffolds was further polished using Illumina reads and Pilon (Walker et al. 2014). A total of 100 M Illumina sequence pair-end reads of 151 bp were used for Pilon polishing.

Genome annotation

To annotate the assembled PC9 genome, we used *funannotate* (v1.5.2) (Jon Love et al. 2019) with the pipeline described in <https://funannotate.readthedocs.io/en/latest/tutorials.html>. We used the following commands: *funannotate* mask, to softmask the genome, *funannotate* training and *funannotate* predict to generate preliminary gene models and consensus gene models [using: AUGUSTUS (Stanke and Waack 2003), GeneMark (Borodovsky and McIninch 1993), and EVidenceModeler (Haas et al. 2008)], and *funannotate* annotate to add functional annotation.

Genome analysis and comparison

General assembly statistics for example length and N50 of the scaffolds/contigs were calculated from the assembly fasta file using Perl scripts `count_fasta_residues.pl` (https://github.com/SchwarzEM/ems_perl/blob/master/fasta/count_fasta_residues.pl). BUSCO completeness was computed using BUSCO 3.0.1 (Simão et al. 2015; Waterhouse et al. 2018) against the Basidiomycota dataset basidiomycata_odb9 (Simão et al. 2015; Waterhouse et al. 2018). Repetitive elements were identified using a custom-made repeat library created according to a pipeline described previously (Coghlan et al. 2018). The repeat library was used as input for RepeatMasker (Smit 2013-2015), and the results were further analyzed using the `one_code_to_find_them` all script (Bailly-Bechet et al. 2014). The presence of telomeres in the scaffolds was established by searching for the telomeric repeats (TTAGGG)_n (Pérez et al. 2009). Finally, we used Circos (v0.69.0) (Krzywinski et al. 2009) and D-genies (minimap v2) (Cabanettes and Klopp 2018) to illustrate the different genomic features of our assembly and to compare it to the previously published PC9_JGI genome (Alfaro et al. 2016; Castanera et al. 2016).

Data availability

The final assembled and newly annotated genomes of *P. ostreatus* PC9 (denoted PC9_AS) has been uploaded to NCBI and is available with accession code: JACETU000000000.

Results and Discussion

A new genome assembly of the *Pleurotus ostreatus* PC9 strain

Long PacBio and Illumina reads were used to sequence *P. ostreatus* strain PC9 to improve genome quality. The size of our *P. ostreatus* PC9_AS genome assembly is ~35.0 Mb (Table 1), which concurs with the sizes of the currently available *P. ostreatus* genomes: PC9_JGI (35.6 Mb) and PC15 (34.3 Mb) (Riley et al. 2014; Alfaro et al. 2016; Castanera et al. 2016). A comparison with other *Pleurotus* species revealed that our *P. ostreatus* genome is smaller than that of *P. eryngii* strain 183 (43.8 Mb) (Yang et al. 2016), *P. tuoliensis* strain JKBL130LB (48.2 Mb) (Zhang et al. 2018), and *P. platypus* strain MG11 (40.0 Mb) (Li et al. 2018). PC9_AS is distributed across 17 scaffolds, with the maximum and minimum scaffold sizes being 4.86 Mb and 9.1 kb, respectively. The N50 value of our assembly data is 3.5 Mb, which ranks it highest among the available *Pleurotus* genomes, including for PC9_JGI (N50 = 2.09 Mb) (Alfaro et al. 2016; Castanera et al. 2016), PC15 (N50 = 3.27 Mb) (Riley et al. 2014; Alfaro et al. 2016; Castanera et al. 2016), CCMSSC03989 (N50 = 2.85 Mb) (Wang et al. 2018), *P. tuoliensis* strain JKBL130LB (N50 = 1.17 Mb) (Zhang et al. 2018), and *P. eryngii* strain 183 (N50 = 509 kb) (Yang et al. 2016). The total annotated gene number in PC9_AS is 11,875, which is slightly fewer than for PC9_JGI (12,206 genes). The completeness of our PC9 genome assembly was assessed with BUSCO (Simão et al. 2015; Waterhouse et al. 2018) using a Basidiomycota dataset. We obtained a 97.2% BUSCO completeness, with 1289 complete BUSCOs, 1284 complete and single copy BUSCOs (99.6%), 14 complete and duplicate BUSCOs (1.1%), 9 fragmented BUSCOs (0.7%), and 28 missing BUSCOs genes (2.2%). Overall, our statistical analysis suggests that our PC9_AS assembly is more completed and integrated than that of PC9_JGI (Alfaro et al. 2016; Castanera et al. 2016).

Table 1. Genomic features of the three *P. ostreatus* genome assemblies. nt, nucleotides.

General features	PC9_AS	PC9_JGI	PC15
Total nt	35,032,978	35,630,309	34,342,730
Number of scaffolds	17	572	12
N50 scaffold size, nt	3,500,734	2,086,289	3,270,165
N90 scaffold size, nt	2,134,864	159,002	1,880,400
Scaffold max. nt	4,859,873	4,430,591	4,830,258
Scaffold min. nt	9,086	2,001	280,724
Number of contigs	17	3272	13
N50 contig size, nt	3,500,734	99,058	3,270,165
N90 contig size, nt	2,134,864	13,737	1,571,664
GC content, %	50.79	50.94	50.95
Genes	11,875	12,206	12,330
BUSCO completeness, %	97.2	97.2	97.6

The genome architecture of *Pleurotus ostreatus* strain PC9 is shown in Figure 1A. We used the highly conserved sequence (TTAGGG)_n to determine telomere locations (Moyzis et al. 1988), which represent the ends of the chromosomes in fungi (Farman and Leong 1995; Schechtman 1990). Out of 17 scaffolds, six possess telomeric repeats at both ends, indicating that these scaffolds represent complete chromosomes (Figure 1A). In contrast, three scaffolds have a telomere at only one end, and the remaining scaffolds lack any apparent telomeric repeats. Interestingly, the small scaffolds 13 (93,126 bp) and 14 (62,249 bp) have telomeric repeats, so they may constitute the ends of other scaffolds lacking telomeres. Larraya et al. (1999b) used pulsed-field gel electrophoresis to determine how many chromosomes of PC9 and PC15 have and reported a total of eleven chromosomes in *P. ostreatus*, thus suggesting that our assembly is close to the chromosome level.

The average coverage depth of PC9_AS is 135.3 reads per 10-kb (Figure 1A). Regions of high coverage depth are apparent at the ends of most scaffolds, perhaps due to the presence of telomeric repeats. Interestingly, regions of low coverage depth are found in some of the smallest scaffolds, such as 16 (45,074 bp) and 17 (9,086 bp). However, other small scaffolds show high coverage depth, such as 12 (135,750 bp), 14 (62,249 bp), and 15 (54,081 bp). The regions of higher coverage depth in these smaller scaffolds may correspond to the presence of repeats whereas, because of low repeat numbers in centromeric regions, the regions of lower coverage depth might represent misplaced centromeres. The gene density of PC9_AS in sliding windows of 100-kb is also illustrated in Figure 1A. Gene density is consistent among the different scaffolds, with an average of ~33 genes per 100 kb, suggesting that aneuploidy does not occur in the PC9 genome. Moreover, regions of low gene density mostly align with stretches of telomeric repeats and with clusters of transposable elements (TEs). Telomeres consist of several tandemly arrayed (TTAGGG)_n repeats, which hinder gene translation at these sites. Similarly,

low expression of genes proximal to TEs has been reported previously (Castanera et al. 2016), potentially explaining low gene density in their vicinity. Although TEs are located near centromeres in certain fungi (Klein and O'Neill 2018), density of TEs in PC9_AS is highly diverse among most scaffolds (Figure 1A). A similar phenomenon has been reported for the previously published PC9_JGI and PC15 genomes (Castanera et al. 2016), wherein regions of low gene density aligned with zones harboring many TEs. We identified a total of 253 TE families in our PC9_AS genome, i.e., more than the 80 TE families reported previously for PC9_JGI and PC15 (Castanera et al. 2016). These TE families account for 7.12% of the total PC9_AS genome, greater than the 6.2% and 2.5% cited previously for the PC15 and PC9_JGI genomes, respectively (Castanera et al. 2016). This striking difference between PC9_AS and PC9_JGI may be due to the fragmented nature of the latter, a scenario that often hinders TEs identification. In Table 2, we summarize the transposable elements identified in PC9_AS, and it reveals that Class I transposons account for 89% of the all TEs, with LTR-retrotransposons being the most abundant family of Class I elements (Table S4). This outcome corroborates findings for the PC15 genome (Castanera et al. 2016). More detailed information on the TEs identified in PC9_AS genome—including size, number of fragments and repeats, and total bp—is presented in Table S4.

Table 2. Classification of transposable elements identified from out *P. ostreatus* strain PC9_AS genome assembly.

	Family	Fragments	Copies	Total bp
Class I	LINE/I-Jockey	26	8	18516
	LINE/L1	9	3	5065
	LINE/Tad1	39	27	77409
	LINE/R2-NeSL	4	4	6740
	LINE/LOA	7	2	2406
	LINE/L1-Tx1	15	7	13873
	LTR/Copia	307	182	238979
	LTR/Gypsy	1468	825	1681184
	LTR/NGaro	51	31	38588
	LTR/ERVk	14	5	5240
	Other LINE	11	5	3390
	Total Class I repeat	1951 (82.4%)	1099 (80%)	2091390 (89%)
Class II	DNA/hAT-Charlie	11	11	5823
	DNA/hAT-Restless	5	2	3894
	DNA/TcMar-Fot1	4	4	4431
	DNA/TcMar-Tc1	31	26	18898
	DNA/hAT-Ac	1	1	546
	DNA/TcMar-Sagan	34	22	10141
	DNA/CMC-EnSpm	69	39	89604
	DNA/TcMar-Pogo	2	2	2140
	DNA/RC	68	49	55928
	DNA/TcMar-Ant1	5	5	2064
	DNA/PIF-Harbinger	144	99	38476
	Other DNA	44	16	25489
	Total Class II repeat	418 (17.6%)	276 (20%)	257434 (11%)
	Total Repeat	2369	1375	2348824

173 **Genome annotation**

174 A total of 11,875 genes were annotated from PC9_AS, which is close to the current gene numbers of *P. ostreatus* PC15 and
 175 PC9_JGI genomes (12,330 genes and 12,206 genes, respectively). We used the Clusters of Orthologous Groups of proteins
 176 database (COGs) (Tatusov et al. 2000) to catalog the functions of those genes (Figure 1B). A considerable number of the
 177 gene functions are unknown, but the second biggest cluster in PC9_AS, containing 595 genes, consists of genes coding for
 178 putative carbohydrate transport and metabolism, such as transporters, chitinase, and carbohydrate-active enzymes
 179 (CAZymes), among others. CAZymes are essential to saprotrophic fungi like *P. ostreatus* to decay materials that are
 180 subsequently used as carbon sources (Mikiashvili et al. 2006). These enzymes play important roles in cellulose and
 181 hemicellulose degradation (Alfaro et al. 2016), with over 130 families described to date (Cantarel et al. 2009; Davies and
 182 Williams 2016), including glycosyl hydrolases (GHs), carbohydrate esterases (CEs), polysaccharide lyases (PLs),
 183 carbohydrate-binding modules (CBMs), glycosyl transferases (GTs) and auxiliary activities (AAs). We further explored
 184 the number of CAZymes-related genes in PC9_AS using the CAZymes database (Cantarel et al. 2009) and identified 459
 185 such genes, an outcome consistent with our calculations for other *P. ostreatus* strains (Table S5; PC15=562; PC9_JGI=408).
 186 The EuKaryotic Orthologous Groups (KOG) database, which is a eukaryote-specific version of the COGs has been used
 187 previously to identify the orthologous and paralogous proteins from the PC15 and PC9_JGI genomes (Grigoriev et al.
 188 2012). Therefore, we used the KOG classification available from the JGI for those genomes to reveal how gene families
 189 are distributed in *P. ostreatus* and to compare with our PC9_AS COG classification. As shown in Table S5, the biggest
 190 gene class among PC15 and PC9_JGI (both with 662 genes) is signal transduction mechanisms. However, PC9_AS only
 191 contains 447 genes coding for signal transduction mechanisms. In the classes of extracellular structures and nuclear
 192 structures, PC15 and PC9_JGI both have ~100 genes associated with each class, whereas PC9_AS only harbors two
 193 extracellular structure genes and five nuclear structure genes. We acknowledge that these differences may reflect the use
 194 of different databases for gene function classification. Interestingly, PC9_AS also contained fewer PFAM domains (6770)
 195 compared to the other two *P. ostreatus* genomes (PC9_JGI=7914; PC15=7972).

196 **Genomic/genetic comparison of PC9 genomes**

197 We performed a comprehensive comparison of the PC9_JGI (Alfaro et al. 2016; Castanera et al. 2016) and PC9_AS
 198 genomes. First, we observed that the number of scaffolds and contigs of PC9_AS (17) is smaller than that of PC9_JGI

(572) (Table 1). In terms of size, both genomes are similar at ~35 Mb, but PC9_JGI is slightly larger than PC9_AS by ~600-kb. In terms of the N50 scaffold and N50 contig sizes, values for PC9_AS (N50 scaffold size = 3,500,734; N50 contig size = 3,500,734) are larger than those of PC9_JGI (N50 scaffold size = 2,086,289; N50 contig size = 99,058), which reflects greater contiguity in the former. PC9 and PC15 are protoclonal of N001 (Larrraya et al. 1999b), and the genome size of PC9 is slightly larger than that of PC15. The latest updated assembly of PC15 is distributed across 12 scaffolds, with a size of 34.3 Mb that is similar to PC9_AS. We used D-Genies (Cabanettes and Klopp 2018) to construct a dot-plot alignment of the genome between PC9_JGI and PC9_AS assemblies. The result, shown in Figure 2A, demonstrates that the PC9_JGI and PC9_AS genomes are highly similar, with small scaffolds of PC9_JGI corresponding to portions of the larger PC9_AS scaffolds, which indicates that our PC9_AS assembly is more complete. Moreover, when we aligned the two genomes in a circos plot (Figure 2B), we observed long regions of high similarity between the most relevant scaffolds of PC9_AS (scaffolds 1-11) (Table S6) and PC9_JGI (scaffolds 1-81) (Table S7). Figure 2B also reveals that, in general, more than five PC9_JGI scaffolds can be mapped to single PC9_AS scaffolds, with scaffolds 6 and 7 of PC9_AS incorporating 12 and 10 of the PC9_JGI scaffolds, respectively.

Conclusions

In this study, we used long PacBio and Illumina reads to assemble a new genome of *P. ostreatus* strain PC9. A combination of high read coverage and the latest bioinformatic tools resulted in a high-quality PC9_AS genome. Compared to the currently available PC9_JGI genome, our new assembly is more complete, comprising only 17 scaffolds that include six telomere-to-telomere scaffolds and the highest N50 values yet achieved for a *Pleurotus* genome. Genomic comparisons between PC9_AS and the current available assemblies of *P. ostreatus* evidence the high quality of our genome assembly. This new PC9 genome will enable the fungal research community to perform further genomic and genetic analyses of *P. ostreatus* and advance our understanding of this common edible mushroom.

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Figures and caption

Fig. 1. (A) Genome architecture of *P. ostreatus* strain PC9 based on our PC9_AS assembly. Tracks (outer to inner) represent the distribution of genomic features in our PC9_AS assembly: 1) sizes (in Mb) of PC9_AS scaffolds, with numbers prefixed by the letter “C” indicating the order of scaffold size; 2) gene density with 100-kb sliding windows, ranging between 0-50 genes; 3) distribution of transposable elements along the PC9_AS genome; 4) distribution of telomere repeats with 10-kb sliding windows, ranging between 10-30 repeats; and 5) depth of gene coverage with 10-kb sliding windows, ranging between 0-300 depth. (B) Predicted functions of genes identified from the PC9_AS genome, cataloged using Cluster of Orthologous Groups (COGs) database.

Fig. 2. Comparisons between the PC9_AS and PC9_JGI *P. ostreatus* PC9 genomes. (A) Dot-plot alignment of *P. ostreatus* PC9_AS (target) and PC9_JGI (query) generated by D-Genies minimap2. (B) Circos plot showing regions of similarity shared between PC9_AS (scaffolds 1-11) and PC9_JGI (scaffolds 1-81) (identity>95%, length>10-kb).

Supplemental information

Table S1. Features of the preliminary *P.ostreatus* PC9 assemblies obtained with Canu, Falcon, and Quiver (polishing). nt, nucleotides.

Features	Canu	Canu+Quiver	Falcon	Falcon+Quiver
Total nt	36,056,011	36,058,485	36,394,568	36,404,395
Scaffolds	32	32	47	47
ACGT nt	36,056,011	36,058,485	36,394,568	36,404,395
GC%	50.8	50.8	50.51	50.51
Scaffold N50 nt	2,884,572	2,884,610	2,946,748	2,947,601
Scaffold N90 nt	1,116,861	1,116,922	1,098,381	1,098,853
Scaffold max nt	4,834,601	4,834,751	4,859,598	4,860,115
Scaffold Min nt	1,971	1,971	9,168	9,168

Table S2. Features of the merged *P. ostreatus* PC9 assemblies constructed in Quickmerge, using the Canu assembly as reference and the Falcon assembly as donor (Canu-Falcon) or *vice versa* (Falcon-Canu). nt, nucleotides.

Features	Canu-Falcon	Falcon-Canu
Total nt	36,454,866	36,097,392
Scaffolds	40	29
ACGT nt	36,454,866	36,097,392
GC%	50.46	50.79
Scaffold N50 nt	3,310,143	2,947,616
Scaffold N90 nt	1,369,931	1,116,922
Scaffold. max nt	4,860,115	4,860,865
Scaffold Min nt	9,168	1,971

Table S3. Information on 10 merged contigs of the PC9_AS assembly (identity>99%, overlap length>10-kb).

Scaffold	Contig	Merge length (bp)	Overlap length (bp)	Identity %
scaffold_7	merged_000004F arrow pilon_000014F arrow pilon	3254697	46719	99.07
scaffold_2	merged_000017F arrow pilon_000001F arrow pilon	4530594	29795	99.87
scaffold_4	merged_CRTig00000114 arrow pilon_tig00000062 arrow pilon	3505455	12066	99.15
scaffold_6	merged_tig00000057 arrow pilon_CRTig00002981 arrow pilon	3309613	10406	99.69
scaffold_13	merged_tig00000121 arrow pilon_CRTig00002975 arrow pilon	93884	28837	99.02
Scaffold	Contig	Length (bp)	Contig	Length (bp)
scaffold_7	000004F arrow pilon	2947565	000014F arrow pilon	353851
scaffold_2	000017F arrow pilon	148646	000001F arrow pilon	4411733
scaffold_4	tig00000114 arrow pilon	1116895	tig00000062 arrow pilon	2400614
scaffold_6	tig00000057 arrow pilon	2427394	tig00002981 arrow pilon	892613
scaffold_13	tig00000121 arrow pilon	827676	tig00002975 arrow pilon	93950

364 **Table S4.** Families of transposable elements detected in the PC9_AS assembly.

Name	Classification	Length	Fragments	Copies	Total bp
PC9_TE_1	DNA/Unknown	1090	7	5	2771
PC9_TE_2	DNA/Unknown	2743	35	11	22718
PC9_TE_3	DNA/Unknown	1060	2	0	0
PC9_TE_4	DNA/CMC-EnSpm	4959	20	10	22022
PC9_TE_5	DNA/CMC-EnSpm	846	1	1	846
PC9_TE_6	DNA/CMC-EnSpm	594	1	1	1426
PC9_TE_7	DNA/CMC-EnSpm	1542	1	1	1542
PC9_TE_8	DNA/CMC-EnSpm	1542	6	1	1542
PC9_TE_9	DNA/CMC-EnSpm	624	1	1	624
PC9_TE_10	DNA/CMC-EnSpm	624	3	3	1869
PC9_TE_11	DNA/CMC-EnSpm	568	9	8	3675
PC9_TE_12	DNA/CMC-EnSpm	8773	24	10	53415
PC9_TE_13	DNA/CMC-EnSpm	624	1	1	624
PC9_TE_14	DNA/CMC-EnSpm	825	1	1	825
PC9_TE_15	DNA/hAT-Ac	546	1	1	546
PC9_TE_16	DNA/hAT-Charlie	700	11	11	5823
PC9_TE_17	DNA/hAT-Restless	1947	5	2	3894
PC9_TE_18	DNA/PIF-Harbinger	2939	62	34	25109
PC9_TE_19	DNA/PIF-Harbinger	545	82	65	13367
PC9_TE_20	DNA/RC	5231	31	18	12639
PC9_TE_21	DNA/RC	3283	1	1	3283
PC9_TE_22	DNA/RC	1428	2	1	1428
PC9_TE_23	DNA/RC	1413	1	1	1413
PC9_TE_24	DNA/RC	4815	7	5	6720
PC9_TE_25	DNA/RC	879	1	1	1226
PC9_TE_26	DNA/RC	1482	1	1	1482
PC9_TE_27	DNA/RC	1866	1	1	1866
PC9_TE_28	DNA/RC	4161	3	3	12483
PC9_TE_29	DNA/RC	1494	1	1	1494
PC9_TE_30	DNA/RC	497	1	1	497
PC9_TE_31	DNA/RC	723	1	1	723
PC9_TE_32	DNA/RC	1442	1	1	1442
PC9_TE_33	DNA/RC	3108	4	3	5100
PC9_TE_34	DNA/RC	736	8	7	1308
PC9_TE_35	DNA/RC	1431	2	1	1431
PC9_TE_36	DNA/RC	882	2	2	1393

PC9_TE_37	DNA/TcMar-Ant1	720	2	2	989
PC9_TE_38	DNA/TcMar-Ant1	549	3	3	1075
PC9_TE_39	DNA/TcMar-Fot1	1062	1	1	1062
PC9_TE_40	DNA/TcMar-Fot1	953	1	1	953
PC9_TE_41	DNA/TcMar-Fot1	1246	1	1	1246
PC9_TE_42	DNA/TcMar-Fot1	1170	1	1	1170
PC9_TE_43	DNA/TcMar-Pogo	1070	2	2	2140
PC9_TE_44	DNA/TcMar-Sagan	682	21	13	5420
PC9_TE_45	DNA/TcMar-Sagan	756	13	9	4721
PC9_TE_46	DNA/TcMar-Tc1	984	2	2	1968
PC9_TE_47	DNA/TcMar-Tc1	576	1	1	354
PC9_TE_48	DNA/TcMar-Tc1	1240	8	6	4307
PC9_TE_49	DNA/TcMar-Tc1	969	20	17	12269
PC9_TE_50	LINE/Unknown	456	1	1	456
PC9_TE_51	LINE/Unknown	987	2	1	987
PC9_TE_52	LINE/Unknown	606	2	2	1113
PC9_TE_53	LINE/Unknown	834	1	1	834
PC9_TE_54	LINE/Unknown	867	2	0	0
PC9_TE_55	LINE/I-Jockey	2972	6	3	8915
PC9_TE_56	LINE/I-Jockey	3560	5	2	5884
PC9_TE_57	LINE/I-Jockey	1382	15	3	3717
PC9_TE_58	LINE/L1	1059	3	1	823
PC9_TE_59	LINE/L1	1842	1	1	1842
PC9_TE_60	LINE/L1	2400	5	1	2400
PC9_TE_61	LINE/L1-Tx1	552	1	1	552
PC9_TE_62	LINE/L1-Tx1	750	3	2	1288
PC9_TE_63	LINE/L1-Tx1	1815	1	1	1815
PC9_TE_64	LINE/L1-Tx1	4329	8	1	4329
PC9_TE_65	LINE/L1-Tx1	1560	1	1	1560
PC9_TE_66	LINE/L1-Tx1	2292	1	1	4329
PC9_TE_67	LINE/LOA	1203	2	1	1203
PC9_TE_68	LINE/LOA	915	1	1	1203
PC9_TE_69	LINE/R2-NeSL	1685	4	4	6740
PC9_TE_70	LINE/Tad1	3651	7	5	18225
PC9_TE_71	LINE/Tad1	2871	1	1	2871
PC9_TE_72	LINE/Tad1	3720	3	1	3720
PC9_TE_73	LINE/Tad1	3630	2	1	3630
PC9_TE_74	LINE/Tad1	3630	3	2	3839

PC9_TE_75	LINE/Tad1	3628	3	1	3628
PC9_TE_76	LINE/Tad1	3717	3	2	4249
PC9_TE_77	LINE/Tad1	3636	2	2	6959
PC9_TE_78	LINE/Tad1	765	1	1	765
PC9_TE_79	LINE/Tad1	3546	4	3	4331
PC9_TE_80	LINE/Tad1	3617	6	5	14050
PC9_TE_81	LINE/Tad1	3630	3	2	7260
PC9_TE_82	LINE/Tad1	3882	1	1	3882
PC9_TE_83	LTR/Copia	5463	5	2	5697
PC9_TE_84	LTR/Copia	5477	8	3	10948
PC9_TE_85	LTR/Copia	5225	6	5	6174
PC9_TE_86	LTR/Copia	10786	15	12	36133
PC9_TE_87	LTR/Copia	1557	15	4	3482
PC9_TE_88	LTR/Copia	5462	2	1	5462
PC9_TE_89	LTR/Copia	4326	1	1	4326
PC9_TE_90	LTR/Copia	1563	1	1	1563
PC9_TE_91	LTR/Copia	429	1	1	429
PC9_TE_92	LTR/Copia	1783	96	45	15275
PC9_TE_93	LTR/Copia	6503	20	20	20165
PC9_TE_94	LTR/Copia	5820	12	12	12394
PC9_TE_95	LTR/Copia	5920	21	21	32787
PC9_TE_96	LTR/Copia	5340	11	4	6217
PC9_TE_97	LTR/Copia	6603	5	5	7825
PC9_TE_98	LTR/Copia	5314	5	1	5314
PC9_TE_99	LTR/Copia	4644	15	14	12832
PC9_TE_100	LTR/Copia	774	2	2	1548
PC9_TE_101	LTR/Copia	6602	6	6	7931
PC9_TE_102	LTR/Copia	5984	4	4	20670
PC9_TE_103	LTR/Copia	1400	17	7	8519
PC9_TE_104	LTR/Copia	5225	3	1	5225
PC9_TE_105	LTR/Copia	4404	1	1	119
PC9_TE_106	LTR/Copia	828	1	1	828
PC9_TE_107	LTR/Copia	5466	13	4	6232
PC9_TE_108	LTR/Copia	911	21	4	884
PC9_TE_109	LTR/ERV	1048	14	5	5240
PC9_TE_110	LTR/Gypsy	6701	13	11	12419
PC9_TE_111	LTR/Gypsy	6673	13	6	21776
PC9_TE_112	LTR/Gypsy	9958	1	1	9958

PC9_TE_113	LTR/Gypsy	8294	15	10	14415
PC9_TE_114	LTR/Gypsy	2944	6	2	3145
PC9_TE_115	LTR/Gypsy	1212	1	1	1212
PC9_TE_116	LTR/Gypsy	8765	1	1	8765
PC9_TE_117	LTR/Gypsy	4174	31	16	14437
PC9_TE_118	LTR/Gypsy	8992	4	2	17926
PC9_TE_119	LTR/Gypsy	8253	4	2	8515
PC9_TE_120	LTR/Gypsy	6710	11	9	33115
PC9_TE_121	LTR/Gypsy	6553	1	1	6553
PC9_TE_122	LTR/Gypsy	13648	97	22	78483
PC9_TE_123	LTR/Gypsy	7912	25	15	23944
PC9_TE_124	LTR/Gypsy	1669	9	1	1668
PC9_TE_125	LTR/Gypsy	7634	4	2	7724
PC9_TE_126	LTR/Gypsy	9555	10	2	19109
PC9_TE_127	LTR/Gypsy	15093	2	2	15618
PC9_TE_128	LTR/Gypsy	6721	3	3	14032
PC9_TE_129	LTR/Gypsy	8405	10	5	9439
PC9_TE_130	LTR/Gypsy	10026	9	6	13108
PC9_TE_131	LTR/Gypsy	8429	101	69	36839
PC9_TE_132	LTR/Gypsy	9263	1	1	9263
PC9_TE_133	LTR/Gypsy	8181	14	8	4462
PC9_TE_134	LTR/Gypsy	6690	7	7	29898
PC9_TE_135	LTR/Gypsy	6712	4	4	13433
PC9_TE_136	LTR/Gypsy	6670	3	2	7681
PC9_TE_137	LTR/Gypsy	7947	4	2	12739
PC9_TE_138	LTR/Gypsy	6602	8	7	9440
PC9_TE_139	LTR/Gypsy	6500	2	1	6489
PC9_TE_140	LTR/Gypsy	963	3	1	963
PC9_TE_141	LTR/Gypsy	6761	31	15	23553
PC9_TE_142	LTR/Gypsy	10552	10	7	15927
PC9_TE_143	LTR/Gypsy	9801	32	10	72582
PC9_TE_144	LTR/Gypsy	9124	12	2	9351
PC9_TE_145	LTR/Gypsy	6997	6	6	10672
PC9_TE_146	LTR/Gypsy	6718	6	2	13423
PC9_TE_147	LTR/Gypsy	6674	45	31	53302
PC9_TE_148	LTR/Gypsy	813	3	1	813
PC9_TE_149	LTR/Gypsy	7956	7	6	13221
PC9_TE_150	LTR/Gypsy	5706	8	1	5706

PC9_TE_151	LTR/Gypsy	2733	30	19	6178
PC9_TE_152	LTR/Gypsy	9145	2	1	9145
PC9_TE_153	LTR/Gypsy	6944	6	4	7644
PC9_TE_154	LTR/Gypsy	6555	15	9	30554
PC9_TE_155	LTR/Gypsy	6754	9	7	10018
PC9_TE_156	LTR/Gypsy	6693	8	7	15314
PC9_TE_157	LTR/Gypsy	577	1	1	264
PC9_TE_158	LTR/Gypsy	8428	38	21	25461
PC9_TE_159	LTR/Gypsy	5627	11	3	5994
PC9_TE_160	LTR/Gypsy	1641	2	2	4220
PC9_TE_161	LTR/Gypsy	5067	25	20	10226
PC9_TE_162	LTR/Gypsy	8902	3	2	9158
PC9_TE_163	LTR/Gypsy	6555	3	3	7082
PC9_TE_164	LTR/Gypsy	6650	5	4	7916
PC9_TE_165	LTR/Gypsy	6651	4	4	16068
PC9_TE_166	LTR/Gypsy	12254	56	16	37390
PC9_TE_167	LTR/Gypsy	9940	2	2	11770
PC9_TE_168	LTR/Gypsy	6689	3	3	7778
PC9_TE_169	LTR/Gypsy	10053	1	1	10053
PC9_TE_170	LTR/Gypsy	6761	13	13	14100
PC9_TE_171	LTR/Gypsy	9618	5	2	9808
PC9_TE_172	LTR/Gypsy	6565	1	1	6565
PC9_TE_173	LTR/Gypsy	3228	3	2	6456
PC9_TE_174	LTR/Gypsy	5668	8	6	7171
PC9_TE_175	LTR/Gypsy	9948	8	2	16834
PC9_TE_176	LTR/Gypsy	9976	1	1	9976
PC9_TE_177	LTR/Gypsy	6722	6	4	15919
PC9_TE_178	LTR/Gypsy	9941	1	1	9941
PC9_TE_179	LTR/Gypsy	1668	1	1	1668
PC9_TE_180	LTR/Gypsy	7900	35	25	17699
PC9_TE_181	LTR/Gypsy	6706	7	4	8434
PC9_TE_182	LTR/Gypsy	6861	22	9	41553
PC9_TE_183	LTR/Gypsy	6008	5	3	11046
PC9_TE_184	LTR/Gypsy	7011	4	3	7357
PC9_TE_185	LTR/Gypsy	6982	5	2	7243
PC9_TE_186	LTR/Gypsy	8315	2	1	8315
PC9_TE_187	LTR/Gypsy	6974	8	7	13403
PC9_TE_188	LTR/Gypsy	3801	6	2	1585

PC9_TE_189	LTR/Gypsy	8880	25	17	25978
PC9_TE_190	LTR/Gypsy	6606	8	5	4828
PC9_TE_191	LTR/Gypsy	9170	3	1	9170
PC9_TE_192	LTR/Gypsy	525	24	7	3357
PC9_TE_193	LTR/Gypsy	6553	3	3	8051
PC9_TE_194	LTR/Gypsy	13402	20	8	18318
PC9_TE_195	LTR/Gypsy	5775	4	3	6370
PC9_TE_196	LTR/Gypsy	9953	12	5	11161
PC9_TE_197	LTR/Gypsy	5359	41	29	14106
PC9_TE_198	LTR/Gypsy	9145	1	1	9145
PC9_TE_199	LTR/Gypsy	521	27	19	4260
PC9_TE_200	LTR/Gypsy	10001	6	4	12485
PC9_TE_201	LTR/Gypsy	9423	10	1	9423
PC9_TE_202	LTR/Gypsy	3120	2	1	3225
PC9_TE_203	LTR/Gypsy	9929	5	4	11573
PC9_TE_204	LTR/Gypsy	6340	2	2	6738
PC9_TE_205	LTR/Gypsy	1130	1	1	1130
PC9_TE_206	LTR/Gypsy	9685	12	1	9685
PC9_TE_207	LTR/Gypsy	3138	1	1	261
PC9_TE_208	LTR/Gypsy	8902	3	2	17804
PC9_TE_209	LTR/Gypsy	1558	24	10	5945
PC9_TE_210	LTR/Gypsy	2841	4	1	5626
PC9_TE_211	LTR/Gypsy	453	1	1	453
PC9_TE_212	LTR/Gypsy	6648	19	11	12384
PC9_TE_213	LTR/Gypsy	3380	1	1	395
PC9_TE_214	LTR/Gypsy	6551	1	1	6551
PC9_TE_215	LTR/Gypsy	6554	3	3	13112
PC9_TE_216	LTR/Gypsy	2655	2	2	1275
PC9_TE_217	LTR/Gypsy	6469	7	5	32548
PC9_TE_218	LTR/Gypsy	7679	45	34	20358
PC9_TE_219	LTR/Gypsy	10008	8	8	15623
PC9_TE_220	LTR/Gypsy	10055	9	6	22592
PC9_TE_221	LTR/Gypsy	13711	15	11	24523
PC9_TE_222	LTR/Gypsy	6561	7	6	10199
PC9_TE_223	LTR/Gypsy	6577	3	3	7356
PC9_TE_224	LTR/Gypsy	6268	2	1	6268
PC9_TE_225	LTR/Gypsy	7636	10	2	8071
PC9_TE_226	LTR/Gypsy	6747	29	16	17158

PC9_TE_227	LTR/Gypsy	12641	18	13	21132
PC9_TE_228	LTR/Gypsy	4571	8	5	4379
PC9_TE_229	LTR/Gypsy	7041	6	4	8557
PC9_TE_230	LTR/Gypsy	8021	1	1	8021
PC9_TE_231	LTR/Gypsy	4154	11	1	6713
PC9_TE_232	LTR/Gypsy	7801	57	30	27907
PC9_TE_233	LTR/Gypsy	6770	1	1	585
PC9_TE_234	LTR/Gypsy	6255	2	1	6193
PC9_TE_235	LTR/Gypsy	9745	3	2	10435
PC9_TE_236	LTR/Gypsy	5767	14	6	29858
PC9_TE_237	LTR/Gypsy	9972	1	1	9972
PC9_TE_238	LTR/Gypsy	3042	2	1	8556
PC9_TE_239	LTR/Gypsy	8947	2	1	8947
PC9_TE_240	LTR/Ngaro	1374	1	0	0
PC9_TE_241	LTR/Ngaro	420	1	0	0
PC9_TE_242	LTR/Ngaro	1071	3	3	3213
PC9_TE_243	LTR/Ngaro	1253	1	0	0
PC9_TE_244	LTR/Ngaro	4605	6	3	5122
PC9_TE_245	LTR/Ngaro	5419	3	3	5943
PC9_TE_246	LTR/Ngaro	4603	3	3	4930
PC9_TE_247	LTR/Ngaro	4612	10	5	9794
PC9_TE_248	LTR/Ngaro	4996	23	14	9586
PC9_TE_249	LINE/LOA	915	3	0	0
PC9_TE_250	LINE/LOA	1203	1	0	0
PC9_TE_251	LINE/Unknown	987	2	0	0
PC9_TE_252	LINE/Unknown	834	1	0	0
PC9_TE_253	DNA/CMC-EnSpm	825	1	1	1194

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Table S5. PFAM domains, CAZymes, and KOG/COG classifications for the PC15, PC9_JGI, and PC9_AS genome assemblies.

Annotation	PC9_AS	PC9_JGI	PC15
PFAMs	6770	7914	7972
CAZymes	459	408	562
KOG/COG classification	7192	6321	6410
A: RNA processing and modification	326	373	381
B: Chromatin structure and dynamics	110	170	172
C: Energy production and conversion	321	305	312
D: Cell cycle control, cell division, chromosome partitioning	159	229	232
E: Amino acid transport and metabolism	299	243	243
F: Nucleotide transport and metabolism	114	80	82
G: Carbohydrate transport and metabolism	595	340	342
H: Coenzyme transport and metabolism	118	101	97
I: Lipid transport and metabolism	287	308	302
J: Translation, ribosomal structure and biogenesis	330	328	334
K: Transcription	295	427	439
L: Replication, recombination and repair	207	235	244
M: Cell wall/membrane/envelope biogenesis	58	72	78
N: Cell motility	1	6	6
O: Posttranslational modification, protein turnover, chaperones	581	659	651
P: Inorganic ion transport and metabolism	167	169	170
Q: Secondary metabolites biosynthesis, transport and catabolism	380	320	314
S: Function unknown	1886	407	432
T: Signal transduction mechanisms	447	662	662
U: Intracellular trafficking, secretion, and vesicular transport	371	335	337
V: Defense mechanisms	46	154	163
W: Extracellular structures	2	97	104
Y: Nuclear structure	5	110	100
Z: Cytoskeleton	87	191	213

Table S6. Scaffold sizes (in nucleotides) for our *P. ostreatus* PC9_AS assembly (scaffolds 1-17).

Scaffold	Scaffold size (nt)
PC9_AS_sc1	4859873
PC9_AS_sc2	4530689
PC9_AS_sc3	3655511
PC9_AS_sc4	3510511
PC9_AS_sc5	3500734
PC9_AS_sc6	3307864
PC9_AS_sc7	3271080
PC9_AS_sc8	2797324
PC9_AS_sc9	2134864
PC9_AS_sc10	1695225
PC9_AS_sc11	1369937
PC9_AS_sc12	135750
PC9_AS_sc13	93126
PC9_AS_sc14	62249
PC9_AS_sc15	54081
PC9_AS_sc16	45074
PC9_AS_sc17	9086

Table S7. Scaffold sizes (in nucleotides) for the previously published *P. ostreatus* PC9_JGI genome (scaffolds 1-100; Alfaro et al. 2016).

Scaffold	Scaffold size (nt)	Scaffold	Scaffold size (nt)	Scaffold	Scaffold size (nt)	Scaffold	Scaffold size (nt)
PC9_jgi_sc1	4430591	PC9_jgi_sc26	232132	PC9_jgi_sc51	15574	PC9_jgi_sc76	10585
PC9_jgi_sc2	3355223	PC9_jgi_sc27	195390	PC9_jgi_sc52	15315	PC9_jgi_sc77	10582
PC9_jgi_sc3	3327214	PC9_jgi_sc28	179244	PC9_jgi_sc53	15181	PC9_jgi_sc78	10404
PC9_jgi_sc4	3035439	PC9_jgi_sc29	176908	PC9_jgi_sc54	14718	PC9_jgi_sc79	10219
PC9_jgi_sc5	2563927	PC9_jgi_sc30	162218	PC9_jgi_sc55	14539	PC9_jgi_sc80	10070
PC9_jgi_sc6	2086289	PC9_jgi_sc31	159002	PC9_jgi_sc56	13955	PC9_jgi_sc81	10029
PC9_jgi_sc7	1693221	PC9_jgi_sc32	135498	PC9_jgi_sc57	13695	PC9_jgi_sc82	9937
PC9_jgi_sc8	1456251	PC9_jgi_sc33	114947	PC9_jgi_sc58	13616	PC9_jgi_sc83	9854
PC9_jgi_sc9	1215864	PC9_jgi_sc34	99290	PC9_jgi_sc59	13127	PC9_jgi_sc84	9619
PC9_jgi_sc10	1158825	PC9_jgi_sc35	93408	PC9_jgi_sc60	13062	PC9_jgi_sc85	9584
PC9_jgi_sc11	823721	PC9_jgi_sc36	73952	PC9_jgi_sc61	12936	PC9_jgi_sc86	9566
PC9_jgi_sc12	623273	PC9_jgi_sc37	65148	PC9_jgi_sc62	12473	PC9_jgi_sc87	9545
PC9_jgi_sc13	577815	PC9_jgi_sc38	54882	PC9_jgi_sc63	11699	PC9_jgi_sc88	9468
PC9_jgi_sc14	524972	PC9_jgi_sc39	54229	PC9_jgi_sc64	11564	PC9_jgi_sc89	9372
PC9_jgi_sc15	523842	PC9_jgi_sc40	51136	PC9_jgi_sc65	11483	PC9_jgi_sc90	9295
PC9_jgi_sc16	482463	PC9_jgi_sc41	49577	PC9_jgi_sc66	11391	PC9_jgi_sc91	9279
PC9_jgi_sc17	479568	PC9_jgi_sc42	49327	PC9_jgi_sc67	11281	PC9_jgi_sc92	9173
PC9_jgi_sc18	476552	PC9_jgi_sc43	48231	PC9_jgi_sc68	11143	PC9_jgi_sc93	9065
PC9_jgi_sc19	456527	PC9_jgi_sc44	47637	PC9_jgi_sc69	11128	PC9_jgi_sc94	9029
PC9_jgi_sc20	362764	PC9_jgi_sc45	33979	PC9_jgi_sc70	11031	PC9_jgi_sc95	8970
PC9_jgi_sc21	341089	PC9_jgi_sc46	23569	PC9_jgi_sc71	10991	PC9_jgi_sc96	8956
PC9_jgi_sc22	315898	PC9_jgi_sc47	19536	PC9_jgi_sc72	10945	PC9_jgi_sc97	8840
PC9_jgi_sc23	290907	PC9_jgi_sc48	19420	PC9_jgi_sc73	10890	PC9_jgi_sc98	8812
PC9_jgi_sc24	263270	PC9_jgi_sc49	17084	PC9_jgi_sc74	10838	PC9_jgi_sc99	8526
PC9_jgi_sc25	250080	PC9_jgi_sc50	15720	PC9_jgi_sc75	10613	PC9_jgi_sc100	8476